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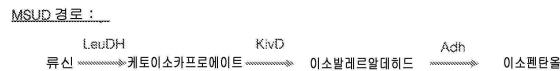
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(54) 발명의 명칭 단풍당밀뇨증 (MSUD)의 치료에 사용하기 위한 효소의 생합성

(57) 요약

본 개시에서는, 일부 실시형태에서, 단풍당밀뇨증 (MSUD) 및 과도한 분지쇄 아미노산을 특징으로 하는 다른 병태를 치료하기 위한 방법 및 조성물을 제공한다.

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명세서

청구범위

청구항 1

류신 데히드로게나제 (LeuDH) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포로서, LeuDH 효소는 서열번호 2, 4, 6, 8, 10, 및 12로부터 선택된 서열과 적어도 90% 동일한 아미노산 서열을 포함하는 것인 숙주 세포.

청구항 2

제1항에 있어서, LeuDH 효소는 서열번호 2와 적어도 90% 동일한 아미노산 서열을 포함하는 것인 숙주 세포.

청구항 3

제2항에 있어서, LeuDH 효소는 서열번호 2를 포함하는 것인 숙주 세포.

청구항 4

제1항 또는 제2항에 있어서, LeuDH 효소는

- a) 서열번호 27의 잔기 13에 상응하는 잔기에 V;
- b) 서열번호 27의 잔기 16에 상응하는 잔기에 W;
- c) 서열번호 27의 잔기 42에 상응하는 잔기에 Q;
- d) 서열번호 27의 잔기 43에 상응하는 잔기에 T, Y, F, E, 또는 W;
- e) 서열번호 27의 잔기 44에 상응하는 잔기에 I, H, K, 또는 Y;
- f) 서열번호 27의 잔기 67에 상응하는 잔기에 T, E, A, S, 또는 K;
- g) 서열번호 27의 잔기 71에 상응하는 잔기에 K;
- h) 서열번호 27의 잔기 73에 상응하는 잔기에 S;
- i) 서열번호 27의 잔기 76에 상응하는 잔기에 R, H, Y, S, K, 또는 W;
- j) 서열번호 27의 잔기 92에 상응하는 잔기에 Y;
- k) 서열번호 27의 잔기 93에 상응하는 잔기에 H;
- l) 서열번호 27의 잔기 95에 상응하는 잔기에 G;
- m) 서열번호 27의 잔기 100에 상응하는 잔기에 G;
- n) 서열번호 27의 잔기 105에 상응하는 잔기에 C;
- o) 서열번호 27의 잔기 111에 상응하는 잔기에 G;
- p) 서열번호 27의 잔기 113에 상응하는 잔기에 M;
- q) 서열번호 27의 잔기 115에 상응하는 잔기에 N 또는 V;
- r) 서열번호 27의 잔기 116에 상응하는 잔기에 R, N, 또는 W;
- s) 서열번호 27의 잔기 120에 상응하는 잔기에 A;
- t) 서열번호 27의 잔기 122에 상응하는 잔기에 D;
- u) 서열번호 27의 잔기 136에 상응하는 잔기에 E;
- v) 서열번호 27의 잔기 140에 상응하는 잔기에 D;

- w) 서열번호 27의 잔기 141에 상응하는 잔기에 M;
 - x) 서열번호 27의 잔기 160에 상응하는 잔기에 S;
 - y) 서열번호 27의 잔기 185에 상응하는 잔기에 F;
 - z) 서열번호 27의 잔기 196에 상응하는 잔기에 N;
 - aa) 서열번호 27의 잔기 228에 상응하는 잔기에 Y;
 - bb) 서열번호 27의 잔기 248에 상응하는 잔기에 M;
 - cc) 서열번호 27의 잔기 256에 상응하는 잔기에 C;
 - dd) 서열번호 27의 잔기 293에 상응하는 잔기에 Q 또는 C;
 - ee) 서열번호 27의 잔기 296에 상응하는 잔기에 K 또는 N;
 - ff) 서열번호 27의 잔기 297에 상응하는 잔기에 R, Q, 또는 K;
 - gg) 서열번호 27의 잔기 300에 상응하는 잔기에 C 또는 D;
 - hh) 서열번호 27의 잔기 302에 상응하는 잔기에 T 또는 S;
 - ii) 서열번호 27의 잔기 305에 상응하는 잔기에 C;
 - jj) 서열번호 27의 잔기 319에 상응하는 잔기에 F; 및/또는
 - kk) 서열번호 27의 잔기 330에 상응하는 잔기에 M
- 을 포함하는 것인 숙주 세포.

청구항 5

제4항에 있어서, LeuDH 효소는 (a)-(kk)의 전부를 포함하는 것인 숙주 세포.

청구항 6

류신 데히드로게나제 (LeuDH) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포로서, 서열번호 27에 대해서, LeuDH 효소는 아미노산 잔기: 42, 43, 44, 67, 71, 76, 78, 113, 115, 116, 136, 293, 296, 297 및/또는 300에 아미노산 치환을 포함하는 것인 숙주 세포.

청구항 7

제6항에 있어서, LeuDH 효소는

- a) 잔기 42에 A, Q, 또는 T;
- b) 잔기 43에 E, F, T, W, 또는 Y;
- c) 잔기 44에 H, I, K, 또는 Y;
- d) 잔기 67에 A, E, K, Q, S, 또는 T;
- e) 잔기 71에 C, D, H, K, M, 또는 T;
- f) 잔기 76에 E, F, H, I, K, M, R, S, T, W, 또는 Y;
- g) 잔기 78에 C, F, H, K, Q, V, 또는 Y;
- h) 잔기 113에 F, M, Q, V, W, 또는 Y;
- i) 잔기 115에 N, Q, S, T, 또는 V;
- j) 잔기 116에 A, L, M, N, R, S, V, 또는 W;
- k) 잔기 136에 E, F, L, R, S, 또는 Y;
- l) 잔기 293에 A, C, Q, S, 또는 T;

- m) 잔기 296에 A, C, E, I, K, L, N, S, 또는 T;
 - n) 잔기 297에 C, D, E, F, H, K, L, M, N, Q, R, T, W, 또는 Y; 및/또는
 - o) 잔기 300에 A, C, D, F, H, K, M, N, Q, R, S, T, W, 또는 Y
- 를 포함하는 것인 숙주 세포.

청구항 8

비-천연 발생 LeuDH 효소로서, 서열번호 27에 대해서, LeuDH 효소는 아미노산 잔기: 42, 43, 44, 67, 71, 76, 78, 113, 115, 116, 136, 293, 296, 297 및/또는 300에 아미노산 치환을 포함하는 것인 비-천연 발생 LeuDH 효소.

청구항 9

제8항에 있어서, LeuDH 효소는

- a) 잔기 42에 A, Q, 또는 T;
 - b) 잔기 43에 E, F, T, W, 또는 Y;
 - c) 잔기 44에 H, I, K, 또는 Y;
 - d) 잔기 67에 A, E, K, Q, S, 또는 T;
 - e) 잔기 71에 C, D, H, K, M, 또는 T;
 - f) 잔기 76에 E, F, H, I, K, M, R, S, T, W, 또는 Y;
 - g) 잔기 78에 C, F, H, K, Q, V, 또는 Y;
 - h) 잔기 113에 F, M, Q, V, W, 또는 Y;
 - i) 잔기 115에 N, Q, S, T, 또는 V;
 - j) 잔기 116에 A, L, M, N, R, S, V, 또는 W;
 - k) 잔기 136에 E, F, L, R, S, 또는 Y;
 - l) 잔기 293에 A, C, Q, S, 또는 T;
 - m) 잔기 296에 A, C, E, I, K, L, N, S, 또는 T;
 - n) 잔기 297에 C, D, E, F, H, K, L, M, N, Q, R, T, W, 또는 Y; 및/또는
 - o) 잔기 300에 A, C, D, F, H, K, M, N, Q, R, S, T, W, 또는 Y
- 를 포함하는 것인 비-천연 발생 LeuDH 효소.

청구항 10

분지쇄 α -케토산 데카르복실라제 (KivD) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포로서, KivD 효소는 서열번호 14, 16, 및 18로부터 선택되는 서열과 적어도 90% 동일한 아미노산 서열을 포함하는 것인 숙주 세포.

청구항 11

제10항에 있어서, KivD 효소는 서열번호 18과 적어도 90% 동일한 아미노산 서열을 포함하는 것인 숙주 세포.

청구항 12

제11항에 있어서, KivD 효소는 서열번호 18을 포함하는 것인 숙주 세포.

청구항 13

제10항 또는 제11항에 있어서, KivD 효소는

- a) 서열번호 29의 잔기 33에 상응하는 잔기에 Y;
 - b) 서열번호 29의 잔기 44에 상응하는 잔기에 Q;
 - c) 서열번호 29의 잔기 117에 상응하는 잔기에 M;
 - d) 서열번호 29의 잔기 129에 상응하는 잔기에 I;
 - e) 서열번호 29의 잔기 185에 상응하는 잔기에 W;
 - f) 서열번호 29의 잔기 190에 상응하는 잔기에 I;
 - g) 서열번호 29의 잔기 225에 상응하는 잔기에 I;
 - h) 서열번호 29의 잔기 227에 상응하는 잔기에 Y;
 - i) 서열번호 29의 잔기 311에 상응하는 잔기에 L;
 - j) 서열번호 29의 잔기 312에 상응하는 잔기에 G;
 - k) 서열번호 29의 잔기 313에 상응하는 잔기에 T;
 - l) 서열번호 29의 잔기 328에 상응하는 잔기에 P;
 - m) 서열번호 29의 잔기 341에 상응하는 잔기에 W;
 - n) 서열번호 29의 잔기 345에 상응하는 잔기에 H;
 - o) 서열번호 29의 잔기 347에 상응하는 잔기에 C;
 - p) 서열번호 29의 잔기 420에 상응하는 잔기에 R;
 - q) 서열번호 29의 잔기 494에 상응하는 잔기에 D;
 - r) 서열번호 29의 잔기 508에 상응하는 잔기에 C; 및/또는
 - s) 서열번호 29의 잔기 550에 상응하는 잔기에 F
- 를 포함하는 것인 숙주 세포.

청구항 14

제13항에 있어서, KivD 효소는 (a)-(s)의 전부를 포함하는 것인 숙주 세포.

청구항 15

알콜 데히드로게나제 (Adh) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포로서, Adh 효소는 서열번호 20, 22, 및 24로부터 선택되는 서열과 적어도 90% 동일한 아미노산 서열을 포함하는 것인 숙주 세포.

청구항 16

제15항에 있어서, Adh 효소는 서열번호 24와 적어도 90% 동일한 아미노산 서열을 포함하는 것인 숙주 세포.

청구항 17

제16항에 있어서, Adh 효소는 서열번호 24를 포함하는 것인 숙주 세포.

청구항 18

제15항 또는 제16항에 있어서, Adh 효소는

- a) 서열번호 31의 잔기 9에 상응하는 잔기에 P;
- b) 서열번호 31의 잔기 16에 상응하는 잔기에 G;
- c) 서열번호 31의 잔기 23에 상응하는 잔기에 Q;
- d) 서열번호 31의 잔기 28에 상응하는 잔기에 R;

- e) 서열번호 31의 잔기 30에 상응하는 잔기에 A;
 - f) 서열번호 31의 잔기 93에 상응하는 잔기에 K;
 - g) 서열번호 31의 잔기 98에 상응하는 잔기에 L;
 - h) 서열번호 31의 잔기 99에 상응하는 잔기에 R;
 - i) 서열번호 31의 잔기 114에 상응하는 잔기에 P;
 - j) 서열번호 31의 잔기 115에 상응하는 잔기에 K;
 - k) 서열번호 31의 잔기 119에 상응하는 잔기에 Y;
 - l) 서열번호 31의 잔기 194에 상응하는 잔기에 Y;
 - m) 서열번호 31의 잔기 242에 상응하는 잔기에 P;
 - n) 서열번호 31의 잔기 249에 상응하는 잔기에 K;
 - o) 서열번호 31의 잔기 255에 상응하는 잔기에 E;
 - p) 서열번호 31의 잔기 260에 상응하는 잔기에 D;
 - q) 서열번호 31의 잔기 269에 상응하는 잔기에 H;
 - r) 서열번호 31의 잔기 281에 상응하는 잔기에 Q;
 - s) 서열번호 31의 잔기 325에 상응하는 잔기에 L;
 - t) 서열번호 31의 잔기 333에 상응하는 잔기에 M;
 - u) 서열번호 31의 잔기 334에 상응하는 잔기에 P; 및/또는
 - v) 서열번호 31의 잔기 348에 상응하는 잔기에 Q
- 를 포함하는 것인 숙주 세포.

청구항 19

제18항에 있어서, Adh 효소는 (a)-(v)의 전부를 포함하는 것인 숙주 세포.

청구항 20

제1항 내지 제7항 및 제10항 내지 제19항 중 어느 하나의 항에 있어서, 숙주 세포는 식물 세포, 조류 세포, 효모 세포, 박테리아 세포, 또는 동물 세포인 숙주 세포.

청구항 21

제20항에 있어서, 숙주 세포는 효모 세포인 숙주 세포.

청구항 22

제21항에 있어서, 효모 세포는 사카로마이세스 (*Saccharomyces*) 세포, 야로위아 (*Yarrowia*) 세포, 또는 피키아 (*Pichia*) 세포인 숙주 세포.

청구항 23

제20항에 있어서, 숙주 세포는 박테리아 세포인 숙주 세포.

청구항 24

제23항에 있어서, 박테리아 세포는 이. 콜라이 (*E. coli*) 세포 또는 바실러스 (*Bacillus*) 세포인 숙주 세포.

청구항 25

제1항 내지 제7항 및 제10항 내지 제24항 중 어느 하나의 항에 있어서, 숙주 세포는 분지쇄 아미노산 수송 시스템

템 2 캐리어 단백질 (BrnQ)을 코딩하는 이중성 폴리뉴클레오티드를 더 포함하는 것인 숙주 세포.

청구항 26

제25항에 있어서, BrnQ 단백질은 서열번호 35의 아미노산 서열과 적어도 90% 동일한 것인 숙주 세포.

청구항 27

제1항 내지 제7항 및 제10항 내지 제26항 중 어느 하나의 항에 있어서, 이중성 폴리뉴클레오티드는 유도성 프로 모터에 작동적으로 연결되는 것인 숙주 세포.

청구항 28

제1항 내지 제7항 및 제10항 내지 제27항 중 어느 하나의 항에 있어서, 이중성 폴리뉴클레오티드는 오페론으로 발현되는 것인 숙주 세포.

청구항 29

제28항에 있어서, 오페론은 하나 초과인 이중성 폴리뉴클레오티드를 발현하고, 리보솜 결합 부위는 각각의 이중 성 폴리뉴클레오티드 사이에 존재하는 것인 숙주 세포.

청구항 30

제1항 내지 제7항 중 어느 하나의 항에 있어서, 숙주 세포는 KivD 효소를 코딩하는 이중성 폴리뉴클레오티드 및 /또는 Adh 효소를 코딩하는 이중성 폴리뉴클레오티드를 더 포함하는 것인 숙주 세포.

청구항 31

제10항 내지 제14항 중 어느 하나의 항에 있어서, 숙주 세포는 LeuDH 효소를 코딩하는 이중성 폴리뉴클레오티드 및/또는 Adh 효소를 코딩하는 이중성 폴리뉴클레오티드를 더 포함하는 것인 숙주 세포.

청구항 32

제15항 내지 제19항 중 어느 하나의 항에 있어서, 숙주 세포는 LeuDH 효소를 코딩하는 이중성 폴리뉴클레오티드 및/또는 KivD 효소를 코딩하는 이중성 폴리뉴클레오티드를 더 포함하는 것인 숙주 세포.

청구항 33

제1항 내지 제7항 및 제10항 내지 제32항 중 어느 하나의 항에 있어서, 숙주 세포는 류신으로부터 이소펜탄올을 생성할 수 있는 것인 숙주 세포.

청구항 34

제33항에 있어서, 숙주 세포는 서열번호 27의 서열을 포함하는 대조군 LeuDH 효소를 코딩하는 이중성 폴리뉴클 레오티드, 서열번호 29의 서열을 포함하는 대조군 KivD 효소를 코딩하는 이중성 폴리뉴클레오티드, 서열번호 31 의 서열을 포함하는 대조군 Adh 효소를 코딩하는 이중성 폴리뉴클레오티드, 및 서열번호 35의 서열을 포함하는 대조군 BrnQ 단백질을 코딩하는 이중성 폴리뉴클레오티드를 포함하는 대조군 숙주 세포에 비해서 적어도 2배 이 상의 류신을 소모하는 것인 숙주 세포.

청구항 35

제1항 내지 제7항 및 제10항 내지 제34항 중 어느 하나의 항의 숙주 세포를 배양하는 단계를 포함하는 방법.

청구항 36

제1항 내지 제7항 및 제10항 내지 제34항 중 어느 하나의 항의 숙주 세포를 배양하는 단계를 포함하는, 류신으 로부터 이소펜탄올의 제조 방법.

청구항 37

서열번호 1, 3, 5, 7, 9, 및 11로부터 선택된 핵산 서열과 적어도 90% 동일한 서열을 포함하는 비-천연 발생 핵

산.

청구항 38

서열번호 13, 15, 및 17로부터 선택된 핵산 서열과 적어도 90% 동일한 서열을 포함하는 비-천연 발생 핵산.

청구항 39

서열번호 19, 21, 및 23으로부터 선택된 핵산 서열과 적어도 90% 동일한 서열을 포함하는 비-천연 발생 핵산.

청구항 40

서열번호 2, 4, 6, 8, 10, 및 12로부터 선택된 서열과 적어도 90% 동일한 서열을 코딩하는 비-천연 발생 핵산.

청구항 41

서열번호 14, 16, 및 18로부터 선택된 서열과 적어도 90% 동일한 서열을 코딩하는 비-천연 발생 핵산.

청구항 42

서열번호 20, 22, 및 24로부터 선택된 서열과 적어도 90% 동일한 서열을 코딩하는 비-천연 발생 핵산.

청구항 43

제37항 내지 제42항 중 어느 하나의 항의 비-천연 발생 핵산을 포함하는 벡터.

청구항 44

제37항 내지 제42항 중 어느 하나의 항의 비-천연 발생 핵산을 포함하는 발현 카세트.

발명의 설명

기술 분야

[0001] 관련 출원에 대한 교차-참조

[0002] 본 출원은 "단풍당밀뇨증 (MSUD)의 치료에 사용하기 위한 효소의 생합성"의 발명의 명칭으로 2019년 6월 21일 출원된 미국 가출원 일련 번호 제62/865,129호 및 "류신, 이소류신, 및/또는 발린의 이화작용이 관여하는 장애를 치료하기 위해 조작된 최적화 박테리아"의 발명의 명칭으로, 2019년 6월 21일 출원된 미국 가출원 일련 번호 제62/864,875호의 35 U.S.C. § 119(e) 하의 이득을 청구한다. 이들 각각의 개시는 그 전문이 참조로 본 명세서에 편입된다.

[0003] EFS-웹을 통한 텍스트 파일로서 제출된 서열 목록에 관한 참조

[0004] 본 출원은 EFS-웹을 통해 ASCII 형식으로 제출된 서열 목록을 함유하고 그 전문을 참조로 본 명세서에 편입시킨다. 상기 ASCII 사본은 2020년 6월 19일 생성되었고, 명칭은 G0919.70033W000-SEQ-OMJ.txt이며, 크기는 1.76 메가바이트 (MB)이다.

[0005] 발명의 분야

[0006] 본 개시는 이소펜탄올로 류신의 전환에 유용한 효소, 핵산, 및 세포에 관한 것이다.

배경 기술

[0007] 단풍당밀뇨증 (MSUD)은 분지쇄 알파-케토산 데히드로게나제 복합체 (BCKDC)의 결핍으로 초래되는 대사 장애로서, 혈액 및 소변 중 분지쇄 아미노산 (류신, 이소류신, 및 발린) 및 그들 독성 부산물 (케토산)의 축적을 야기시킨다. MSUD는 특히 진단 전, 및 급성 질병 시기 동안, 발병 개체의 소변의 특유한 달콤한 냄새로 인해 그 명칭을 얻었다. MSUD 및 과도한 분지쇄 아미노산을 특징으로 하는 다른 병태에 대한 개선된 치료에 대한 요구가 여전히 존재한다.

발명의 내용

- [0008] 본 개시는 적어도 부분적으로 예를 들어, 류신을 이소펜탄올로 전환시켜서, 류신을 소모하기 위한 효소를 함유하는 조작된 세포의 생성을 기반으로 한다. 이러한 세포는 예를 들어 류신의 축적과 연관된 질환 예컨대 MSUD를 치료하는데 유용하다.
- [0009] 본 개시의 양태는 류신 데히드로게나제 (LeuDH) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포에 관한 것으로서, 여기서 LeuDH 효소는 서열번호 2, 4, 6, 8, 10, 및 12로부터 선택된 서열과 적어도 90% 동일한 아미노산 서열을 포함한다. 일부 실시형태에서, LeuDH 효소는 서열번호 2와 적어도 90% 동일한 아미노산 서열을 포함한다. 일부 실시형태에서, LeuDH 효소는 서열번호 2를 포함한다. 일부 실시형태에서, LeuDH 효소는 서열번호 27의 잔기 13에 상응하는 잔기에 V; 서열번호 27의 잔기 16에 상응하는 잔기에 W; 서열번호 27의 잔기 42에 상응하는 잔기에 Q; 서열번호 27의 잔기 43에 상응하는 잔기에 T, Y, F, E, 또는 W; 서열번호 27의 잔기 44에 상응하는 잔기에 I, H, K, 또는 Y; 서열번호 27의 잔기 67에 상응하는 잔기에 T, E, A, S, 또는 K; 서열번호 27의 잔기 71에 상응하는 잔기에 K; 서열번호 27의 잔기 73에 상응하는 잔기에 S; 서열번호 27의 잔기 76에 상응하는 잔기에 R, H, Y, S, K, 또는 W; 서열번호 27의 잔기 92에 상응하는 잔기에 Y; 서열번호 27의 잔기 93에 상응하는 잔기에 H; 서열번호 27의 잔기 95에 상응하는 잔기에 G; 서열번호 27의 잔기 100에 상응하는 잔기에 G; 서열번호 27의 잔기 105에 상응하는 잔기에 C; 서열번호 27의 잔기 111에 상응하는 잔기에 G; 서열번호 27의 잔기 113에 상응하는 잔기에 M; 서열번호 27의 잔기 115에 상응하는 잔기에 N, 또는 V; 서열번호 27의 잔기 116에 상응하는 잔기에 R, N, 또는 W; 서열번호 27의 잔기 120에 상응하는 잔기에 A; 서열번호 27의 잔기 122에 상응하는 잔기에 D; 서열번호 27의 잔기 136에 상응하는 잔기에 E; 서열번호 27의 잔기 140에 상응하는 잔기에 D; 서열번호 27의 잔기 141에 상응하는 잔기에 M; 서열번호 27의 잔기 160에 상응하는 잔기에 S; 서열번호 27의 잔기 185에 상응하는 잔기에 F; 서열번호 27의 잔기 196에 상응하는 잔기에 N; 서열번호 27의 잔기 228에 상응하는 잔기에 Y; 서열번호 27의 잔기 248에 상응하는 잔기에 M; 서열번호 27의 잔기 256에 상응하는 잔기에 C; 서열번호 27의 잔기 293에 상응하는 잔기에 Q 또는 C; 서열번호 27의 잔기 296에 상응하는 잔기에 K 또는 N; 서열번호 27의 잔기 297에 상응하는 잔기에 R, Q, 또는 K; 서열번호 27의 잔기 300에 상응하는 잔기에 C 또는 D; 서열번호 27의 잔기 302에 상응하는 잔기에 T 또는 S; 서열번호 27의 잔기 305에 상응하는 잔기에 C; 서열번호 27의 잔기 319에 상응하는 잔기에 F; 및/또는 서열번호 27의 잔기 330에 상응하는 잔기에 M을 포함한다.
- [0010] 본 개시의 추가 양태는 류신 데히드로게나제 (LeuDH) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포에 관한 것이고, 여기서 LeuDH 효소는 서열번호 27의 잔기 13에 상응하는 잔기에 V; 서열번호 27의 잔기 16에 상응하는 잔기에 W; 서열번호 27의 잔기 42에 상응하는 잔기에 Q; 서열번호 27의 잔기 43에 상응하는 잔기에 T, Y, F, E, 또는 W; 서열번호 27의 잔기 44에 상응하는 잔기에 I, H, K, 또는 Y; 서열번호 27의 잔기 67에 상응하는 잔기에 T, E, A, S, 또는 K; 서열번호 27의 잔기 71에 상응하는 잔기에 K; 서열번호 27의 잔기 73에 상응하는 잔기에 S; 서열번호 27의 잔기 76에 상응하는 잔기에 R, H, Y, S, K, 또는 W; 서열번호 27의 잔기 92에 상응하는 잔기에 Y; 서열번호 27의 잔기 93에 상응하는 잔기에 H; 서열번호 27의 잔기 95에 상응하는 잔기에 G; 서열번호 27의 잔기 100에 상응하는 잔기에 G; 서열번호 27의 잔기 105에 상응하는 잔기에 C; 서열번호 27의 잔기 111에 상응하는 잔기에 G; 서열번호 27의 잔기 113에 상응하는 잔기에 M; 서열번호 27의 잔기 115에 상응하는 잔기에 N, 또는 V; 서열번호 27의 잔기 116에 상응하는 잔기에 R, N, 또는 W; 서열번호 27의 잔기 120에 상응하는 잔기에 A; 서열번호 27의 잔기 122에 상응하는 잔기에 D; 서열번호 27의 잔기 136에 상응하는 잔기에 E; 서열번호 27의 잔기 140에 상응하는 잔기에 D; 서열번호 27의 잔기 141에 상응하는 잔기에 M; 서열번호 27의 잔기 160에 상응하는 잔기에 S; 서열번호 27의 잔기 185에 상응하는 잔기에 F; 서열번호 27의 잔기 196에 상응하는 잔기에 N; 서열번호 27의 잔기 228에 상응하는 잔기에 Y; 서열번호 27의 잔기 248에 상응하는 잔기에 M; 서열번호 27의 잔기 256에 상응하는 잔기에 C; 서열번호 27의 잔기 293에 상응하는 잔기에 Q 또는 C; 서열번호 27의 잔기 296에 상응하는 잔기에 K 또는 N; 서열번호 27의 잔기 297에 상응하는 잔기에 R, Q, 또는 K; 서열번호 27의 잔기 300에 상응하는 잔기에 C 또는 D; 서열번호 27의 잔기 302에 상응하는 잔기에 T 또는 S; 서열번호 27의 잔기 305에 상응하는 잔기에 C; 서열번호 27의 잔기 319에 상응하는 잔기에 F; 및 서열번호 27의 잔기 330에 상응하는 잔기에 M을 포함한다.
- [0011] 본 개시의 추가 양태는 류신 데히드로게나제 (LeuDH) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포에 관한 것으로서, 여기서 서열번호 27에 대해서, LeuDH 효소는 아미노산 잔기: 42, 43, 44, 67, 71, 76, 78, 113, 115, 116, 136, 293, 296, 297 및/또는 300에 아미노산 치환을 포함한다. 일부 실시형태에서, LeuDH 효소는 잔기 42에 A, Q, 또는 T; 잔기 43에 E, F, T, W, 또는 Y; 잔기 44에 H, I, K, 또는 Y; 잔기 67에 A, E, K, Q, S, 또는 T; 잔기 71에 C, D, H, K, M, 또는 T; 잔기 76에 E, F, H, I, K, M, R, S, T, W, 또는 Y; 잔기 78에 C, F, H, K, Q, V, 또는 Y; 잔기 113에 F, M, Q, V, W, 또는 Y; 잔기 115에 N, Q, S, T, 또는 V; 잔

기 116에 A, L, M, N, R, S, V, 또는 W; 잔기 136에 E, F, L, R, S, 또는 Y; 잔기 293에 A, C, Q, S, 또는 T; 잔기 296에 A, C, E, I, K, L, N, S, 또는 T; 잔기 297에 C, D, E, F, H, K, L, M, N, Q, R, T, W, 또는 Y; 및/또는 잔기 300에 A, C, D, F, H, K, M, N, Q, R, S, T, W, 또는 Y를 포함한다.

[0012] 본 개시의 추가 양태는 비-천연 발생 LeuDH 효소에 관한 것으로서, 여기서 서열번호 27에 대해서, LeuDH 효소는 아미노산 잔기: 42, 43, 44, 67, 71, 76, 78, 113, 115, 116, 136, 293, 296, 297 및/또는 300에 아미노산 치환을 포함한다. 일부 실시형태에서, LeuDH 효소는 잔기 42에 A, Q, 또는 T; 잔기 43에 E, F, T, W, 또는 Y; 잔기 44에 H, I, K, 또는 Y; 잔기 67에 A, E, K, Q, S, 또는 T; 잔기 71에 C, D, H, K, M, 또는 T; 잔기 76에 E, F, H, I, K, M, R, S, T, W, 또는 Y; 잔기 78에 C, F, H, K, Q, V, 또는 Y; 잔기 113에 F, M, Q, V, W, 또는 Y; 잔기 115에 N, Q, S, T, 또는 V; 잔기 116에 A, L, M, N, R, S, V, 또는 W; 잔기 136에 E, F, L, R, S, 또는 Y; 잔기 293에 A, C, Q, S, 또는 T; 잔기 296에 A, C, E, I, K, L, N, S, 또는 T; 잔기 297에 C, D, E, F, H, K, L, M, N, Q, R, T, W, 또는 Y; 및/또는 잔기 300에 A, C, D, F, H, K, M, N, Q, R, S, T, W, 또는 Y를 포함한다.

[0013] 본 개시의 추가 양태는 분지쇄 α-케토산 데카르복실라제 (KivD) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포에 관한 것으로서, KivD 효소는 서열번호 14, 16, 및 18로부터 선택되는 서열과 적어도 90% 동일한 아미노산 서열을 포함한다. 일부 실시형태에서, KivD 효소는 서열번호 18과 적어도 90% 동일한 아미노산 서열을 포함한다. 일부 실시형태에서, KivD 효소는 서열번호 18을 포함한다. 일부 실시형태에서, KivD 효소는 서열번호 29의 잔기 33에 상응하는 잔기에 Y; 서열번호 29의 잔기 44에 상응하는 잔기에 Q; 서열번호 29의 잔기 117에 상응하는 잔기에 M; 서열번호 29의 잔기 129에 상응하는 잔기에 I; 서열번호 29의 잔기 185에 상응하는 잔기에 W; 서열번호 29의 잔기 190에 상응하는 잔기에 I; 서열번호 29의 잔기 225에 상응하는 잔기에 I; 서열번호 29의 잔기 227에 상응하는 잔기에 Y; 서열번호 29의 잔기 311에 상응하는 잔기에 L; 서열번호 29의 잔기 312에 상응하는 잔기에 G; 서열번호 29의 잔기 313에 상응하는 잔기에 T; 서열번호 29의 잔기 328에 상응하는 잔기에 P; 서열번호 29의 잔기 341에 상응하는 잔기에 W; 서열번호 29의 잔기 345에 상응하는 잔기에 H; 서열번호 29의 잔기 347에 상응하는 잔기에 C; 서열번호 29의 잔기 420에 상응하는 잔기에 R; 서열번호 29의 잔기 494에 상응하는 잔기에 D; 서열번호 29의 잔기 508에 상응하는 잔기에 C; 및/또는 서열번호 29의 잔기 550에 상응하는 잔기에 F를 포함한다.

[0014] 본 개시의 추가 양태는 분지쇄 α-케토산 데카르복실라제 (KivD) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포에 관한 것으로서, KivD 효소는 서열번호 29의 잔기 33에 상응하는 잔기에 Y; 서열번호 29의 잔기 44에 상응하는 잔기에 Q; 서열번호 29의 잔기 117에 상응하는 잔기에 M; 서열번호 29의 잔기 129에 상응하는 잔기에 I; 서열번호 29의 잔기 185에 상응하는 잔기에 W; 서열번호 29의 잔기 190에 상응하는 잔기에 I; 서열번호 29의 잔기 225에 상응하는 잔기에 I; 서열번호 29의 잔기 227에 상응하는 잔기에 Y; 서열번호 29의 잔기 311에 상응하는 잔기에 L; 서열번호 29의 잔기 312에 상응하는 잔기에 G; 서열번호 29의 잔기 313에 상응하는 잔기에 T; 서열번호 29의 잔기 328에 상응하는 잔기에 P; 서열번호 29의 잔기 341에 상응하는 잔기에 W; 서열번호 29의 잔기 345에 상응하는 잔기에 H; 서열번호 29의 잔기 347에 상응하는 잔기에 C; 서열번호 29의 잔기 420에 상응하는 잔기에 R; 서열번호 29의 잔기 494에 상응하는 잔기에 D; 서열번호 29의 잔기 508에 상응하는 잔기에 C; 및 서열번호 29의 잔기 550에 상응하는 잔기에 F를 포함한다.

[0015] 본 개시의 추가 양태는 알콜 데히드로게나제 (Adh) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포에 관한 것으로서, Adh 효소는 서열번호 20, 22, 및 24로부터 선택되는 서열과 적어도 90% 동일한 아미노산 서열을 포함한다. 일부 실시형태에서, Adh 효소는 서열번호 24와 적어도 90% 동일한 아미노산 서열을 포함한다. 일부 실시형태에서, Adh 효소는 서열번호 24를 포함한다. 일부 실시형태에서, Adh 효소는 서열번호 31의 잔기 9에 상응하는 잔기에 P; 서열번호 31의 잔기 16에 상응하는 잔기에 G; 서열번호 31의 잔기 23에 상응하는 잔기에 Q; 서열번호 31의 잔기 28에 상응하는 잔기에 R; 서열번호 31의 잔기 30에 상응하는 잔기에 A; 서열번호 31의 잔기 93에 상응하는 잔기에 K; 서열번호 31의 잔기 98에 상응하는 잔기에 L; 서열번호 31의 잔기 99에 상응하는 잔기에 R; 서열번호 31의 잔기 114에 상응하는 잔기에 P; 서열번호 31의 잔기 115에 상응하는 잔기에 K; 서열번호 31의 잔기 119에 상응하는 잔기에 Y; 서열번호 31의 잔기 194에 상응하는 잔기에 Y; 서열번호 31의 잔기 242에 상응하는 잔기에 P; 서열번호 31의 잔기 249에 상응하는 잔기에 K; 서열번호 31의 잔기 255에 상응하는 잔기에 E; 서열번호 31의 잔기 260에 상응하는 잔기에 D; 서열번호 31의 잔기 269에 상응하는 잔기에 H; 서열번호 31의 잔기 281에 상응하는 잔기에 Q; 서열번호 31의 잔기 325에 상응하는 잔기에 L; 서열번호 31의 잔기 333에 상응하는 잔기에 M; 서열번호 31의 잔기 334에 상응하는 잔기에 P; 및/또는 서열번호 31의 잔기 348에 상응하는 잔기에 Q를 포함한다.

- [0016] 본 개시의 추가 양태는 알콜 데히드로게나제 (Adh) 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포에 관한 것으로서, Adh 효소는 서열번호 31의 잔기 9에 상응하는 잔기에 P; 서열번호 31의 잔기 16에 상응하는 잔기에 G; 서열번호 31의 잔기 23에 상응하는 잔기에 Q; 서열번호 31의 잔기 28에 상응하는 잔기에 R; 서열번호 31의 잔기 30에 상응하는 잔기에 A; 서열번호 31의 잔기 93에 상응하는 잔기에 K; 서열번호 31의 잔기 98에 상응하는 잔기에 L; 서열번호 31의 잔기 99에 상응하는 잔기에 R; 서열번호 31의 잔기 114에 상응하는 잔기에 P; 서열번호 31의 잔기 115에 상응하는 잔기에 K; 서열번호 31의 잔기 119에 상응하는 잔기에 Y; 서열번호 31의 잔기 194에 상응하는 잔기에 Y; 서열번호 31의 잔기 242에 상응하는 잔기에 P; 서열번호 31의 잔기 249에 상응하는 잔기에 K; 서열번호 31의 잔기 255에 상응하는 잔기에 E; 서열번호 31의 잔기 260에 상응하는 잔기에 D; 서열번호 31의 잔기 269에 상응하는 잔기에 H; 서열번호 31의 잔기 281에 상응하는 잔기에 Q; 서열번호 31의 잔기 325에 상응하는 잔기에 L; 서열번호 31의 잔기 333에 상응하는 잔기에 M; 서열번호 31의 잔기 334에 상응하는 잔기에 P; 및 서열번호 31의 잔기 348에 상응하는 잔기에 Q를 포함한다.
- [0017] 일부 실시형태에서, 숙주 세포는 식물 세포, 조류 세포, 효모 세포, 박테리아 세포, 또는 동물 세포이다. 일부 실시형태에서, 숙주 세포는 효모 세포이다. 일부 실시형태에서, 효모 세포는 사카로마이세스 (*Saccharomyces*) 세포, 야로위아 (*Yarrowia*) 세포 또는 피키아 (*Pichia*) 세포이다. 일부 실시형태에서, 숙주 세포는 박테리아 세포이다. 일부 실시형태에서, 박테리아 세포는 이. 콜라이 (*E. coli*) 세포 또는 바실러스 (*Bacillus*) 세포이다.
- [0018] 일부 실시형태에서, 숙주 세포는 분지쇄 아미노산 수송 시스템 2 캐리어 단백질 (BrnQ)을 코딩하는 이중성 폴리뉴클레오티드를 더 포함한다. 일부 실시형태에서, BrnQ 단백질은 서열번호 35의 아미노산 서열과 적어도 90% 동일하다. 일부 실시형태에서, BrnQ 단백질은 서열번호 35의 아미노산 서열을 포함한다.
- [0019] 일부 실시형태에서, 이중성 폴리뉴클레오티드는 유도성 프로모터에 작동적으로 연결된다. 일부 실시형태에서, 이중성 폴리뉴클레오티드는 오페론으로 발현된다. 일부 실시형태에서, 오페론은 하나 초과와 이중성 폴리뉴클레오티드를 발현하고, 리보솜 결합 부위는 각각의 이중성 폴리뉴클레오티드 사이에 존재할 수 있다.
- [0020] 일부 실시형태에서, 숙주 세포는 KivD 효소를 코딩하는 이중성 폴리뉴클레오티드 및/또는 Adh 효소를 코딩하는 이중성 폴리뉴클레오티드를 더 포함한다.
- [0021] 일부 실시형태에서, 숙주 세포는 LeuDH 효소를 코딩하는 이중성 폴리뉴클레오티드 및/또는 Adh 효소를 코딩하는 이중성 폴리뉴클레오티드를 더 포함한다.
- [0022] 일부 실시형태에서, 숙주 세포는 LeuDH 효소를 코딩하는 이중성 폴리뉴클레오티드 및/또는 KivD 효소를 코딩하는 이중성 폴리뉴클레오티드를 더 포함한다.
- [0023] 일부 실시형태에서, 숙주 세포는 류신으로부터 이소펜탄올을 생성시킬 수 있다. 일부 실시형태에서, 숙주 세포는 서열번호 27의 서열을 포함하는 대조군 LeuDH 효소를 코딩하는 이중성 폴리뉴클레오티드, 서열번호 29의 서열을 포함하는 대조군 KivD 효소를 코딩하는 이중성 폴리뉴클레오티드, 서열번호 31의 서열을 포함하는 대조군 Adh 효소를 코딩하는 이중성 폴리뉴클레오티드, 및 서열번호 35의 서열을 포함하는 대조군 BrnQ 단백질을 코딩하는 이중성 폴리뉴클레오티드를 포함하는 대조군 숙주 세포에 비해서 적어도 2배 이상의 류신을 소모한다.
- [0024] 본 개시의 추가 양태는 본 출원에 개시된 임의의 숙주 세포를 배양하는 단계를 포함하는 방법에 관한 것이다.
- [0025] 본 개시의 추가 양태는 본 출원에서 개시된 임의의 숙주 세포를 배양하는 단계를 포함하는 류신으로부터 이소펜탄올을 제조하기 위한 방법에 관한 것이다.
- [0026] 본 개시의 추가 양태는 서열번호 1, 3, 5, 7, 9, 및 11로부터 선택되는 핵산 서열과 적어도 90% 동일한 서열을 포함하는 비-천연 발생 핵산에 관한 것이다.
- [0027] 본 개시의 추가 양태는 서열번호 13, 15, 및 17로부터 선택되는 핵산 서열과 적어도 90% 동일한 서열을 포함하는 비-천연 발생 핵산에 관한 것이다.
- [0028] 본 개시의 추가 양태는 서열번호 19, 21, 및 23으로부터 선택되는 핵산 서열과 적어도 90% 동일한 서열을 포함하는 비-천연 발생 핵산에 관한 것이다.
- [0029] 본 개시의 추가 양태는 서열번호 2, 4, 6, 8, 10, 및 12로부터 선택되는 서열과 적어도 90% 동일한 서열을 코딩하는 비-천연 발생 핵산에 관한 것이다.
- [0030] 본 개시의 추가 양태는 서열번호 14, 16, 및 18로부터 선택되는 서열과 적어도 90% 동일한 서열을 코딩하는 비-

천연 발생 핵산에 관한 것이다.

[0031] 본 개시의 추가 양태는 서열번호 20, 22, 및 24로부터 선택되는 서열과 적어도 90% 동일한 서열을 코딩하는 비-천연 발생 핵산에 관한 것이다.

[0032] 본 개시의 추가 양태는 본 출원에서 개시된 임의의 비-천연 발생 핵산을 포함하는 벡터에 관한 것이다.

[0033] 본 개시의 추가 양태는 본 출원에 개시된 임의의 비-천연 발생 핵산을 포함하는 발현 카세트에 관한 것이다.

[0034] 본 발명의 각각의 제한은 본 발명의 다양한 실시형태를 포괄할 수 있다. 그러므로, 임의의 하나의 구성요소 또는 구성요소의 조합을 포함하는 본 발명의 각각의 제한이 본 발명의 각 양태에 포함될 수 있다는 것을 예상한다. 본 발명은 하기 설명에 기재되거나 또는 도면에 예시된 성분의 구성 및 배열의 상세설명으로 본 출원을 제한하지 않는다. 본 발명의 다른 실시형태가 가능할 수 있고 다양한 방식으로 실시 또는 수행될 수 있다.

도면의 간단한 설명

[0035] 첨부된 도면은 일정 비율로 작성된 것은 아니다. 도면에서, 다양한 수치로 예시된 각각의 동일하거나 또는 거의 동일한 성분은 유사한 번호로 표시된다. 명확함의 목적을 위해서, 모든 성분이 모든 도면에서 표시되지 않을 수 있다. 도면에서,

도 1a-1c는 서열 유사성 네트워크를 도시한다. 각각의 스폿은 서열 데이터베이스에서 이용가능한 단일 아미노산 서열을 나타낸다. 밀접하게 관련된 아미노산 서열이 더 많을수록, 스폿은 서로에 대해 더 가깝다. 각각의 서열 유사성 네트워크는 효소의 출처 또는 주석과 관련된 정보와 함께 해당 클러스터 열쇠를 갖는다. **도 1a**는 류신 데히드로게나제 (LeuDH)에 대한 서열 유사성 네트워크를 도시한다. 클러스터 열쇠는 효소의 주석을 의미한다. **도 1b**는 케토이스발레레이트 데카르복실라제 (KivD)에 대한 서열 유사성 네트워크를 도시한다. 주석 각 스폿은 효소가 공급된 계통발생 분기군을 나타낸다. **도 1c**는 알콜 데히드로게나제 (Adh)에 대한 서열 유사성 네트워크를 도시한다. 각 스폿의 주석은 효소가 공급된 계통발생 분기군을 나타낸다.

도 2는 LeuDH 효소의 스크리닝으로부터의 데이터를 보여주는 그래프를 도시한다. 220 LeuDH 효소가 생물학적 복제물 (n=4)에서 스크리닝되어 효소 활성 및 순위가 검증되었다. 활성은 비. 세레우스 (*B. cereus*) LeuDH 활성에 대비하여 기록된다.

도 3는 LeuDH 효소의 활성 및 특이성의 비교로부터의 데이터를 보여주는 그래프를 도시한다. 상위 ~ 200 LeuDH 효소는 Leu, Val, 및 Ile에 대한 활성에 대해서 스크리닝되었다. Leu에 대한 LeuDH 효소의 활성은 비. 세레우스 LeuDH 활성에 대비하여 기록된다. 특이성은 Val/Leu 대비 Leu에 대한 활성의 비율로서 측정된다. 좌측 패널에서, Leu에 대한 효소 활성은 Leu/Val 특이성에 대비하여 기록된다. 우측 패널에서, 효소 활성은 Leu/Ile 특이성에 대비하여 기록된다. 추론적으로 조작된 활성 부위 변이체는 채워지지 않은 원형으로서 표시된다. 공급된 LeuDH 효소는 채워진 원형으로 표시된다. 음성 대조군 및 양성 대조군 비. 세레우스 LeuDH가 또한 도시된다.

도 4는 LeuDH 효소에 대한 특이성의 비교로부터의 데이터를 도시한다. 상위 ~ 200 LeuDH 효소는 Leu, Val, 및 Ile에 대한 활성에 대해서 스크리닝되었다. 특이성은 Val/Leu 대비 Leu에 대한 활성의 비율로서 측정된다. 추론적으로 조작된 활성 부위 변이체는 채워지지 않은 원형으로 표시된다. 공급된 LeuDH 효소는 채워진 원형으로 표시된다. 음성 대조군 및 양성 대조군 비. 세레우스 LeuDH가 도시된다.

도 5는 KivD 효소의 스크리닝으로부터의 데이터를 보여주는 그래프를 도시한다. 55 KivD 효소는 생물학적 복제물 (n=4)로 활성에 대해 스크리닝되었다. 활성은 이중으로 발현된 에스. 아우레우스 (*S. aureus*) KivD (이의 활성은 용해물의 측정가능한 배경 활성과 구별불가하여 배경치와 동일시함)를 함유하는 용해물의 활성에 대비하여 기록된다.

도 6는 Adh 효소의 스크리닝으로부터의 데이터를 도시한다. 55 Adh 효소는 생물학적 복제물 (n=4)로 스크리닝하였다. 활성은 이중으로 발현된 에스. 세레비시아에 (*S. cerevisiae*) ADH2 (이의 활성은 용해물의 측정가능한 배경 활성과 구별불가하여 배경치와 동일시함)를 함유하는 용해물의 활성에 대비하여 기록된다.

도 7는 LeuDH 효소의 선택성의 데이터를 도시한다. 총 21 후보 LeuDH 효소가 시험되었다. 각각의 막대 세트는 좌측에서 우측으로, 소모된 Leu, 소모된 Ile, 및 소모된 Val을 도시한다.

도 8는 상위 Leu 소모 균주 (5941, 5942 및 5943) 및 원형 균주 (1980) 간 시간 경과에 따른 Leu 소모율의 비교를 도시한다. 8 mM 류신을 최소 배지에 첨가하였고 샘플은 혐기성 인큐베이션 이후 0시간, 2시간, 및 4시간

시점에 채취하였다.

도 9는 이소펜탄올로 류신의 전환을 위한 MSUD 경로를 도시한다.

도 10은 Ambr15 생물반응기 (n=2)에서 어세이된 균주 5941에 대한 이소펜탄올 경로 중간체의 세포외 프로파일을 도시한다. 오차 막대는 이중 생물반응기 전반의 표준 편차를 반영한다. "총합"에 상응하는 데이터는 도시된 중간체의 총합 농도를 나타낸다. Leu = 류신, 산 = 2-옥소이소카프로에이트, 알데히드 = 이소발레르알데히드, 알콜 = 이소펜탄올.

발명을 실시하기 위한 구체적인 내용

[0036] 본 개시는 일부 양태에서, 류신 소모를 위해 조작된 분지쇄 아미노산 (BCAA) 경로의 효소 조합 및 세포를 제공한다. 이들 BCAA 경로 효소는 류신 데히드로게나제 (LeuDH), 케토이소발레레이트 데카르복실라제 (KivD), 및 알콜 데히드로게나제 (Adh)를 포함한다. 개시된 효소 및 이러한 효소를 포함하는 숙주 세포는 예를 들어, BCAA (예를 들어, 류신)의 축적과 연관된 장애 예컨대 단풍당밀노증 (MSUD)을 앓는 대상체에서, 그리고 다른 의학적 및 산업적 상황에서, 류신 소모를 촉진하는데 사용될 수 있다.

[0037] **류신 데히드로게나제 (LeuDH)**

[0038] 본 개시에서 사용되는 "류신 데히드로게나제 (LeuDH)"는 분지쇄 L-아미노산 (예를 들어, L-류신, L-발린, L-이소류신)의 그들 2-옥소 유사체로의 가역적 탈아미노화를 촉매하는 효소를 의미한다. LeuDH 효소는 기질로서 L-류신을 사용할 수 있다. 일부 실시형태에서, LeuDH는 L-발린 및/또는 L-이소류신과 비교하여 L-류신에 대한 특이성을 나타낸다. 일부 실시형태에서, LeuDH는 L-류신으로부터 케토이소카프로에이트 (2-옥소이소카프로에이트로도 알려짐)를 생산한다.

[0039] 일부 실시형태에서, 숙주 세포는 LeuDH 효소 및/또는 이러한 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함한다. 일부 실시형태에서, 숙주 세포는 서열번호 2, 4, 6, 8, 10, 12, 또는 257-475 중 어느 하나와 적어도 80% (예를 들어, 적어도 80%, 적어도 85%, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100%) 동일한 아미노산 서열을 포함하는 LeuDH 효소, 표 3 또는 표 4의 LeuDH 효소, 또는 달리 본 개시에 기술된 LeuDH 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함한다. 일부 실시형태에서, 숙주 세포는 서열번호 1, 3, 5, 7, 9, 11, 또는 37-255 중 어느 하나와 적어도 90% (예를 들어, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100%) 동일한 이중성 폴리뉴클레오티드, 표 3 또는 표 4의 LeuDH 효소, 또는 달리 본 개시에 기술된 LeuDH 효소를 코딩하는 폴리뉴클레오티드를 포함한다.

[0040] 일부 실시형태에서, 숙주 세포는 바실러스 세레우스 (*Bacillus cereus*) 유래의 LeuDH를 포함한다. 다른 실시형태에서, 숙주 세포는 바실러스 세레우스 유래의 LeuDH를 포함하지 않는다.

[0041] 바실러스 세레우스 유래의 LeuDH는 UniProtKB - P0A392의 아미노산 서열 (서열번호 27)을 포함할 수 있다:

```
MTLEIFEYLEKYDYEQVFCQDKESGLKAIHDTTLGPPALGGTRMWTYDSEEAIEDALRLAKGMTY
KNAAGLNLGGAKTVIIGDPRKDKSEAMFRALGRYIQGLNGRYITAEDVGTVDMDIIHEETDFVTGISPSFGS
SGNPSPVTAYGVYRGMAAAKEAFGTDNLEGVIAVQGVGNVAYHLCKHLHAEGAKLIVTDINKEAVQRAVEEFG
ASAVEPNEIYGVECDIYAPCALGATVNDTIPQLKAKVIAGSANNQLKEDRHGDIHEMGIVYAPDYVINAGGVI
NVADELYGYNRERALKRVESIYDTIAKVIEISKRDGIATYVAADRLAEERIASLKNRSSTYLRNGHDIISRR
(서열번호 27)
```

[0042]

[0043] 일부 실시형태에서, 서열번호 27의 아미노산 서열은 하기 핵산 서열에 의해 코딩된다:

```
ATGACCCTTGAGATTTTGAATACCTCGAAAAATATGATTATGAGCAGGTCGTTTTCTGTCAAGACAAG
GAATCAGGACTGAAAGCGATCATTGCTATCCATGATACTACACTGGGGCCAGCCTTAGGTGGCAGCCGTATGTGG
ACGTACGACTCGGAAGAAGCGGCAATTGAGGATGCCTTGAGGTTAGCTAAGGGCATGACGTATAAAAAACGCGCA
GCCGGTTTGAATCTGGGCGGTGCGAAAACCGTGATTATCGGGGATCCCCGCAAGACAAATCTGAAGCAATGTTT
CGGGCGCTGGGCGGATACATACAGGGACTAAATGGTCGCTATATCACCGCTGAAGATGTAGGAACACCGTGGAT
GATATGGACATAATTACGAAGAAACGGAATTCGTACCGGCATTAGCCCTAGTTTTGGTAGCTCCGGGAACCCG
TCTCCGGTTACCGCCTATGGCGGTACCGTGGCATGAAGGCAGCAGCGAAAGAGGCCCTTTGGTACAGACAACTG
GAGGGGAAAGTGATCGCGGTTCAAGGGGTAGGTAATGTGGCGTATCATCTGTGCAAACTTACATGCCGAGGGC
GCCAAGCTGATTGTCTACGGATATCAACAAAGAAGCGGTACAGCGTGCAGTGAAGAATTGGCGCTTCCGCCGTT
GAGCGGAATGAAATCTACGGCGTGAATGCGATATTTACGCGCCGTGTGCTCTTGGTGCAGTCAACGATGAA
ACGATCCCTCAGCTGAAAGCAAAGGTAATTGCGGGTTCGGCTAATAACCGATTAAAGAAGACAGACATGGAGAC
ATAATTCACGAGATGGGTATTGTTTATGCACAGATTATGTAATCAATGCGGGCGGCGTTATTAACGTCGCAGAT
GAATGTATGGTACAAACCGCAACGCGCCCTCAAACGTGTGGAGTCAATTTATGACACCATGCCAAAGTGATC
GAAATCAGCAAGCGCGATGAATCGCCACTTATGTGGCTGCCGATCGTCTGGCGGAAGAACGCATTGCAAGTCTC
AAAAATAGCCGTTCCACCTACCTTCGCAATGGCCATGATATTATAAGTCGGCGTTGA (서열번호 28)←
```

[0044]

[0045] 일부 실시형태에서, LeuDH 효소를 코딩하는 이중성 폴리뉴클레오티드를 발현하는 숙주 세포는 대조군에 비해서 0.5배, 1배, 1.5배, 2배, 2.5배, 3배, 3.5배, 4배, 4.5배, 5배, 5.5배, 또는 6배 이상 (예를 들어, 2배 내지 6배 이상)으로 케토이소카프로에이트로 류신의 전환을 증가시킬 수 있다. 일부 실시형태에서, 대조군은 서열번호 27을 코딩하는 이중성 폴리뉴클레오티드를 발현하는 숙주 세포이다. 일부 실시형태에서, 대조군은 이. 콜라이 (*E. coli*) 니슬 (Nissle) 균주 SYN1980 Δ leuE, Δ ilvC, lacZ:tetR-Ptet-livKHMGE, tetR-Ptet-leuDH(Bc)-kivD-adh2-brnQ-rrnB ter (pSC101), 예컨대 미국 특허 출원 공개 번호 제US20170232043호에 기술된 것이다.

[0046]

일부 실시형태에서, LeuDH 효소를 코딩하는 이중성 폴리뉴클레오티드를 발현하는 숙주 세포는 발린에 비해서 류신에 대해 적어도 0.5배, 1배, 1.5배, 2배, 2.5배, 3배, 3.5배, 4배, 4.5배, 5배, 5.5배, 또는 6배 이상 (예를 들어, 2배 내지 6배 이상)의 활성을 나타낼 수 있다. 일부 실시형태에서, LeuDH 효소를 코딩하는 이중성 폴리뉴클레오티드를 발현하는 숙주 세포는 이소류신에 비해서 류신에 대해 적어도 0.5배, 1배, 1.5배, 2배, 2.5배, 3배, 3.5배, 4배, 4.5배, 5배, 5.5배, 또는 6배 이상 (예를 들어, 2배 내지 6배 이상)의 활성을 나타낼 수 있다.

[0047]

일부 실시형태에서, LeuDH는 서열번호 27, 서열번호 2, 4, 6, 8, 10, 12, 또는 257-475 중 어느 하나, 서열번호 1, 3, 5, 7, 9, 11, 또는 37-255 중 어느 하나와 적어도 5%, 적어도 10%, 적어도 15%, 적어도 20%, 적어도 25%, 적어도 30%, 적어도 35%, 적어도 40%, 적어도 45%, 적어도 50%, 적어도 55%, 적어도 60%, 적어도 65%, 적어도 70%, 적어도 71%, 적어도 72%, 적어도 73%, 적어도 74%, 적어도 75%, 적어도 76%, 적어도 77%, 적어도 78%, 적어도 79%, 적어도 80%, 적어도 81%, 적어도 82%, 적어도 83%, 적어도 84%, 적어도 85%, 적어도 86%, 적어도 87%, 적어도 88%, 적어도 89%, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100% 동일한 서열, 표 3 또는 표 4의 LeuDH 효소, 또는 달리 본 개시에 기술된 LeuDH 효소의 아미노산 또는 폴리뉴클레오티드 서열을 포함한다.

[0048]

일부 실시형태에서, 이러한 LeuDH 효소는 서열번호 27의 잔기 13에 상응하는 잔기에 V; 서열번호 27의 잔기 16에 상응하는 잔기에 W; 서열번호 27의 잔기 42에 상응하는 잔기에 Q; 서열번호 27의 잔기 43에 상응하는 잔기에 T, Y, F, E, 또는 W; 서열번호 27의 잔기 44에 상응하는 잔기에 I, H, K, 또는 Y; 서열번호 27의 잔기 67에 상응하는 잔기에 T, E, A, S, 또는 K; 서열번호 27의 잔기 71에 상응하는 잔기에 K; 서열번호 27의 잔기 73에 상응하는 잔기에 S; 서열번호 27의 잔기 76에 상응하는 잔기에 R, H, Y, S, K, 또는 W; 서열번호 27의 잔기 92에 상응하는 잔기에 Y; 서열번호 27의 잔기 93에 상응하는 잔기에 H; 서열번호 27의 잔기 95에 상응하는 잔기에 G; 서열번호 27의 잔기 100에 상응하는 잔기에 G; 서열번호 27의 잔기 105에 상응하는 잔기에 C; 서열번호 27의 잔기 111에 상응하는 잔기에 G; 서열번호 27의 잔기 113에 상응하는 잔기에 M; 서열번호 27의 잔기 115에 상응하는 잔기에 N, 또는 V; 서열번호 27의 잔기 116에 상응하는 잔기에 R, N, 또는 W; 서열번호 27의 잔기 120에 상응하는 잔기에 A; 서열번호 27의 잔기 122에 상응하는 잔기에 D; 서열번호 27의 잔기 136에 상응하는 잔기에 E; 서열번호 27의 잔기 140에 상응하는 잔기에 D; 서열번호 27의 잔기 141에 상응하는 잔기에 M; 서열번호 27의 잔기 160에 상응하는 잔기에 S; 서열번호 27의 잔기 185에 상응하는 잔기에 F; 서열번호 27의 잔기 196에 상응하는 잔기에 N; 서열번호 27의 잔기 228에 상응하는 잔기에 Y; 서열번호 27의 잔기 248에 상응하는 잔기에 M; 서열번호 27의 잔기 256에 상응하는 잔기에 C; 서열번호 27의 잔기 293에 상응하는 잔기에 Q 또는 C; 서열번호 27의 잔기 296에 상응하는 잔기에 K 또는 N; 서열번호 27의 잔기 297에 상응하는 잔기에 R, Q, 또는 K; 서열번호

27의 잔기 300에 상응하는 잔기에 C 또는 D; 서열번호 27의 잔기 302에 상응하는 잔기에 T 또는 S; 서열번호 27의 잔기 305에 상응하는 잔기에 C; 서열번호 27의 잔기 319에 상응하는 잔기에 F; 및/또는 서열번호 27의 잔기 330에 상응하는 잔기에 M을 포함한다.

[0049] 일부 실시형태에서, LeuDH 효소는 서열번호 27의 잔기 13에 상응하는 잔기에 V; 서열번호 27의 잔기 16에 상응하는 잔기에 W; 서열번호 27의 잔기 42에 상응하는 잔기에 Q; 서열번호 27의 잔기 43에 상응하는 잔기에 T, Y, F, E, 또는 W; 서열번호 27의 잔기 44에 상응하는 잔기에 I, H, K, 또는 Y; 서열번호 27의 잔기 67에 상응하는 잔기에 T, E, A, S, 또는 K; 서열번호 27의 잔기 71에 상응하는 잔기에 K; 서열번호 27의 잔기 73에 상응하는 잔기에 S; 서열번호 27의 잔기 76에 상응하는 잔기에 R, H, Y, S, K, 또는 W; 서열번호 27의 잔기 92에 상응하는 잔기에 Y; 서열번호 27의 잔기 93에 상응하는 잔기에 H; 서열번호 27의 잔기 95에 상응하는 잔기에 G; 서열번호 27의 잔기 100에 상응하는 잔기에 G; 서열번호 27의 잔기 105에 상응하는 잔기에 C; 서열번호 27의 잔기 111에 상응하는 잔기에 G; 서열번호 27의 잔기 113에 상응하는 잔기에 M; 서열번호 27의 잔기 115에 상응하는 잔기에 N, 또는 V; 서열번호 27의 잔기 116에 상응하는 잔기에 R, N, 또는 W; 서열번호 27의 잔기 120에 상응하는 잔기에 A; 서열번호 27의 잔기 122에 상응하는 잔기에 D; 서열번호 27의 잔기 136에 상응하는 잔기에 E; 서열번호 27의 잔기 140에 상응하는 잔기에 D; 서열번호 27의 잔기 141에 상응하는 잔기에 M; 서열번호 27의 잔기 160에 상응하는 잔기에 S; 서열번호 27의 잔기 185에 상응하는 잔기에 F; 서열번호 27의 잔기 196에 상응하는 잔기에 N; 서열번호 27의 잔기 228에 상응하는 잔기에 Y; 서열번호 27의 잔기 248에 상응하는 잔기에 M; 서열번호 27의 잔기 256에 상응하는 잔기에 C; 서열번호 27의 잔기 293에 상응하는 잔기에 Q 또는 C; 서열번호 27의 잔기 296에 상응하는 잔기에 K 또는 N; 서열번호 27의 잔기 297에 상응하는 잔기에 R, Q, 또는 K; 서열번호 27의 잔기 300에 상응하는 잔기에 C 또는 D; 서열번호 27의 잔기 302에 상응하는 잔기에 T 또는 S; 서열번호 27의 잔기 305에 상응하는 잔기에 C; 서열번호 27의 잔기 319에 상응하는 잔기에 F; 및 서열번호 27의 잔기 330에 상응하는 잔기에 M을 포함한다.

[0050] 일부 실시형태에서, LeuDH 효소는 서열번호 27, 서열번호 2, 4, 6, 8, 10, 12, 또는 257-475 중 어느 하나, 표 3 또는 표 4의 LeuDH 효소, 또는 달리 본 개시에 기술된 LeuDH 효소에 비해서, 적어도 1, 적어도 2, 적어도 3, 적어도 4, 적어도 5, 적어도 6, 적어도 7, 적어도 8, 적어도 9, 적어도 10, 적어도 11, 적어도 12, 적어도 13, 적어도 15, 적어도 16, 적어도 17, 적어도 18, 적어도 19, 적어도 20, 적어도 21, 적어도 22, 적어도 23, 적어도 24, 적어도 25, 적어도 26, 적어도 27, 적어도 28, 적어도 29, 적어도 30, 적어도 31, 적어도 32, 적어도 33, 적어도 34, 적어도 35, 적어도 36, 적어도 37, 적어도 38, 적어도 39, 적어도 40, 적어도 41, 적어도 42, 적어도 43, 적어도 44, 적어도 45, 적어도 46, 적어도 47, 적어도 48, 적어도 49, 적어도 50, 적어도 60, 적어도 70, 적어도 80, 적어도 90, 또는 적어도 100의 아미노산 치환, 결실, 삽입, 또는 첨가를 포함한다.

[0051] 일부 실시형태에서, LeuDH 효소는 서열번호 27에 비해서 하나 이상의 잔기에 아미노산 치환을 포함한다. 일부 실시형태에서, LeuDH 효소는 서열번호 27의 위치 42에 상응하는 잔기에, 서열번호 27의 위치 43에 상응하는 잔기에, 서열번호 27의 위치 44에 상응하는 잔기에, 서열번호 27의 위치 67에 상응하는 잔기에, 서열번호 27의 위치 71에 상응하는 잔기에, 서열번호 27의 위치 76에 상응하는 잔기에, 서열번호 27의 위치 78에 상응하는 잔기에, 서열번호 27의 위치 113에 상응하는 잔기에, 서열번호 27의 위치 115에 상응하는 잔기에, 서열번호 27의 위치 116에 상응하는 잔기에, 서열번호 27의 위치 136에 상응하는 잔기에, 서열번호 27의 위치 293에 상응하는 잔기에, 서열번호 27의 위치 296에 상응하는 잔기에, 서열번호 27의 위치 297에 상응하는 잔기에, 및/또는 서열번호 27의 위치 300에 상응하는 잔기에 아미노산 치환을 포함한다. 일부 실시형태에서, LeuDH 효소는 서열번호 27의 위치 42에 상응하는 잔기에 A, Q, 또는 T; 서열번호 27의 위치 43에 상응하는 잔기에 E, F, T, W, 또는 Y; 서열번호 27의 위치 44에 상응하는 잔기에 H, I, K, 또는 Y; 서열번호 27의 위치 67에 상응하는 잔기에 A, E, K, Q, S, 또는 T; 서열번호 27의 위치 71에 상응하는 잔기에 C, D, H, K, M, 또는 T; 서열번호 27의 위치 76에 상응하는 잔기에 E, F, H, I, K, M, R, S, T, W, 또는 Y; 서열번호 27의 위치 78에 상응하는 잔기에 C, F, H, K, Q, V, 또는 Y; 서열번호 27의 위치 113에 상응하는 잔기에 F, M, Q, V, W, 또는 Y; 서열번호 27의 위치 115에 상응하는 잔기에 N, Q, S, T, 또는 V; 서열번호 27의 위치 116에 상응하는 잔기에 A, L, M, N, R, S, V, 또는 W; 서열번호 27의 위치 136에 상응하는 잔기에 E, F, L, R, S, 또는 Y; 서열번호 27의 위치 293에 상응하는 잔기에 A, C, Q, S, 또는 T; 서열번호 27의 위치 296에 상응하는 잔기에 A, C, E, I, K, L, N, S, 또는 T; 서열번호 27의 위치 297에 상응하는 잔기에 C, D, E, F, H, K, L, M, N, Q, R, T, W, 또는 Y; 및/또는 서열번호 27의 위치 300에 상응하는 잔기에 A, C, D, F, H, K, M, N, Q, R, S, T, W, 또는 Y를 포함한다.

[0052] 일부 실시형태에서, 서열번호 27에 대해서, LeuDH 효소는 아미노산 잔기: 42, 43, 44, 67, 71, 76, 78, 113, 115, 116, 136, 293, 296, 297 및/또는 300에 아미노산 치환을 포함한다. 일부 실시형태에서, LeuDH 효소는 잔

기 42에 A, Q, 또는 T; 잔기 43에 E, F, T, W, 또는 Y; 잔기 44에 H, I, K, 또는 Y; 잔기 67에 A, E, K, Q, S, 또는 T; 잔기 71에 C, D, H, K, M, 또는 T; 잔기 76에 E, F, H, I, K, M, R, S, T, W, 또는 Y; 잔기 78에 C, F, H, K, Q, V, 또는 Y; 잔기 113에 F, M, Q, V, W, 또는 Y; 잔기 115에 N, Q, S, T, 또는 V; 잔기 116에 A, L, M, N, R, S, V, 또는 W; 잔기 136에 E, F, L, R, S, 또는 Y; 잔기 293에 A, C, Q, S, 또는 T; 잔기 296에 A, C, E, I, K, L, N, S, 또는 T; 잔기 297에 C, D, E, F, H, K, L, M, N, Q, R, T, W, 또는 Y; 및/또는 잔기 300에 A, C, D, F, H, K, M, N, Q, R, S, T, W, 또는 Y를 포함한다.

[0053] **케토이소발레레이트 데카르복실라제 (KivD)**

[0054] 본 개시에서 사용되는, "케토이소발레레이트 데카르복실라제 (KivD)"는 아미노산 아미노전달반응으로부터 유래된 알파-케토산의 알데히드로의 탈카르복실화를 촉매하는 효소를 의미한다. KivD는 기질로서 케토이소카프로에이트를 사용할 수 있다. 일부 실시형태에서, KivD는 케토이소카프로에이트로부터 이소발레르알데히드를 생성한다.

[0055] 일부 실시형태에서, 숙주 세포는 KivD 효소 및/또는 이러한 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함한다. 일부 실시형태에서, 숙주 세포는 서열번호 14, 16, 18, 또는 533-588 중 어느 하나와 적어도 80% (예를 들어, 적어도 80%, 적어도 85%, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100%) 동일한 아미노산 서열을 포함하는 KivD 효소, 표 3 또는 표 5의 KivD 효소, 또는 달리 본 개시에 기술된 KivD 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함한다. 일부 실시형태에서, 숙주 세포는 서열번호 13, 15, 17 또는 477-532 중 어느 하나와 적어도 90% (예를 들어, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100%) 동일한 이중성 폴리뉴클레오티드, 표 3 또는 표 5의 kivD 효소를 코딩하는 폴리뉴클레오티드, 또는 달리 본 개시에 기술된 KivD 효소를 코딩하는 폴리뉴클레오티드를 포함한다.

[0056] 일부 실시형태에서, 숙주 세포를 락토코커스 락티스 (*Lactococcus lactis*) 유래의 KivD를 포함한다. 다른 실시형태에서, 숙주 세포는 락토코커스 락티스 유래의 KivD를 포함하지 않는다.

[0057] 락토코커스 락티스 유래의 KivD는 UniProtKB - Q684J7의 아미노산 서열 (서열번호 29)을 포함할 수 있다:

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MYTVGDYLLDRLHELGIIEIFGVPGDYNLQFLDQIIISHKDMKWVGNANELNASYMDGYARTKKAAAFLL
TTFGVGELSAVNGLAGSYAENLPVVEIVGSPTSQVQNEGKQFVHHTLADGDFKHFMKHEPVTAARTLLTAENATV
EIDRVLSALLKERKPVYINLPVDVAAAIAEKPSLPLKKENSTNTSDQEIILNKIQESLKNAKKPIVITGHEIISF
GLEKTVTQFISKTKLPITTLNFGKSSVDEALPSFLGIYNGTLSEPNLKEFVESADFILMLGVKLTDSSTGAFTHH
LNENKMISLNIIDEGKIFNERIQNFDFESLISSLLDLSEIEYKGYIDKKQEDFVPSNALLSQDRLWQAVENLTQS
NETIVAEQGTSTFFGASSIFLKSQSHFQPLWGSIGYTFPAALGSQIADKESRHLLEFGDGLQLTVQELGLAIR
EKINPICFIIINNDGYTVEREIHGPNQSYNDIPMWNYSKLPESFGATEDRVVSKIVRTENEFVSVMKEAQADPNRM
YWIELILAKEGAPKVLKMGKLFQEQNKS (서열번호 29)
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[0058]

[0059] 일부 실시형태에서, 서열번호 29의 아미노산 서열은 하기 핵산 서열에 의해 코딩된다:

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ATGTACACAGTCGGTGATTATCTTTTAGACCGACTGCACGAACTCGGAATCGAGGAAATTTTGGCGTG
CCCGGGGATTATAACTTGCAGTTCCTGGACCAAATAATTTCCCATAGGATATGAAATGGGTAGGCAATGCTAAC
GAACTGAATGCGTCTTACATGCGCGATGTTATGCACGGACCAAAAAAGCGGCAGCCTTTCTGACGACTTTTCGGC
GTTGGTGAGTTAAGCGCGGTGAACGGCCTGGCGGGGTACATCGCCGAAAATCTACAGTTGTCGAAATCGTGGGC
TCGCCGACCAGCAAAGTTTCAAGACGAGGGTAAGTTTGTGCATCACACCTTGTGACGGAGATTTTAAACATTTTC
ATGAAAATGCACGAACCTGTAAACGGCAGCGCACACTGTTGACTGCGGAGAACGCCACCGTCGAAATTGATCGC
GTCCTGAGTGCTCTTCTGAAGGAACGTAAACCGGTGTATATCAATCTCCCGTTGACGTGGCGGCAGCTAAAGCC
GAAAAACCGAGTTTGGCCTTAAAGAAAGAGAATAGCACGTCTAACACGTCTGACCAAGAAATTTGAACAAAATT
CAGGAATCCCTCAAAAATGCGAAAAAACCTATCGTCATACCGGTGATGAAATAATTTTCAATTTGGACTGGAGAAA
ACCGTTACACAGTTTCTCAAGACGAAACTGCCAATTACCACCTAAATTTTGGCAAATCGTCCGTAGACGAA
GCCCTGCCGAGCTTCTTGGGGATCTATAACGGCACTTTAAGCGAACCGAATTTAAAGGAATTTGTGGAGAGCGCC
GATTTTCATTCTCATGCTGGGTGTTAAGCTGACAGATTCCAGTACGGGCGCGTTCACTCATCACCTGAACGAGAAC
AAAAATGATCTCGTTGAACATTGATGAAGGAAAAATATTTAATGAACGTATTCAAAATTCGATTTTGAATCGCTG
ATTTCTTCCCTACTGGACCTCAGCGAGATCGAATACAAAGGTAATATATTGATAAAAAACAGGAAGACTTTGTG
CCGAGTAACGCACCTGTTGTCTCAGGATCGCTGTGGCAAGCTGTGAAAATCTGACCCAGAGTAACGAAACGATT
GTCGCGGAACAGGGGACCTCTTTCTTGTGTCTCGTCAATCTTTTAAAGTCAAAATCACATTTTATTGGCCAA
CCACTTTGGGGTAGTATCGGCTACACTTTCCCTGCGGCACCTGGGTAGTCAGATTGCCGATAAAGAGTCGCGTCAC
CTTTTGTATTATTGGGGATGGCTCGCTACAAATTGACCGTTTCAGGAGTTAGGTCTTGTCTATACGCGAAAAAATCAAT
CCGATCTGTTTTCATTATCAATAATGACGGCTATACCGTGGAGCGCGAAATCCATGGTCCGAATCAGAGCTATAAC
GATATACCGATGTGGAATTACAGCAAACTCCCGAGAGCTTTGGCGCAACAGAAGATAGGGTTGTCTCCAAGATC
GTGCGTACGGAACGAATTTGTAAAGTGAATGAAAGAAGCGCAAGCGGACCTAATCGAATGTACTGGATTGAA
CTTATTCTGGCAAAAGAAGGGGCCCTAAAGTCCTCAAGAAAATGGGGAAGTTGTTCCCGGAACAAAACAAAAGC
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[0060] TGA (서열번호 30)⁴

[0061] 일부 실시형태에서, KivD 효소를 코딩하는 이중성 폴리뉴클레오티드를 발현하는 숙주 세포는 대조군에 비해서 0.5배, 1배, 1.5배, 2배, 2.5배, 3배, 3.5배, 4배, 4.5배, 5배, 5.5배, 또는 6배 이상 (예를 들어, 2배 내지 6배 이상)으로 케토이소카프로에이트의 이소발레르알데히드로의 전환을 증가시킬 수 있다. 일부 실시형태에서, 대조군은 서열번호 29를 코딩하는 이중성 폴리뉴클레오티드를 발현하는 숙주 세포이다. 일부 실시형태에서, 대조군은 이. 콜라이 니슬 (Nissle) 균주 SYN1980 Δ leuE, Δ ilvC, lacZ:tetR-Ptet-livKHMgf, tetR-Ptet-leuDh(Bc)-kivD-adh2-brnQ-rrnB ter (pSC101), 예컨대 미국 특허 출원 공개 번호 제US20170232043호에 기술된 것이다.

[0062] 일부 실시형태에서, KivD 효소는 서열번호 29, 서열번호 14, 16, 18, 또는 533-588 중 어느 하나, 서열번호 13, 15, 17 또는 477-532 중 어느 하나와 적어도 5%, 적어도 10%, 적어도 15%, 적어도 20%, 적어도 25%, 적어도 30%, 적어도 35%, 적어도 40%, 적어도 45%, 적어도 50%, 적어도 55%, 적어도 60%, 적어도 65%, 적어도 70%, 적어도 71%, 적어도 72%, 적어도 73%, 적어도 74%, 적어도 75%, 적어도 76%, 적어도 77%, 적어도 78%, 적어도 79%, 적어도 80%, 적어도 81%, 적어도 82%, 적어도 83%, 적어도 84%, 적어도 85%, 적어도 86%, 적어도 87%, 적어도 88%, 적어도 89%, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100% 동일한 서열, 표 3 또는 표 5의 KivD 효소, 또는 달리 본 개시에 기술된 KivD 효소를 코딩하는 아미노산 또는 폴리뉴클레오티드 서열을 포함한다.

[0063] 일부 실시형태에서, KivD 효소는 서열번호 29, 서열번호 14, 16, 18, 또는 533-588 중 어느 하나, 표 3 또는 표 5의 KivD 효소, 또는 달리 본 개시에 기술된 KivD 효소에 비해서, 적어도 1, 적어도 2, 적어도 3, 적어도 4, 적어도 5, 적어도 6, 적어도 7, 적어도 8, 적어도 9, 적어도 10, 적어도 11, 적어도 12, 적어도 13, 적어도 14, 적어도 15, 적어도 16, 적어도 17, 적어도 18, 적어도 19, 적어도 20, 적어도 21, 적어도 22, 적어도 23, 적어도 24, 적어도 25, 적어도 26, 적어도 27, 적어도 28, 적어도 29, 적어도 30, 적어도 31, 적어도 32, 적어도 33, 적어도 34, 적어도 35, 적어도 36, 적어도 37, 적어도 38, 적어도 39, 적어도 40, 적어도 41, 적어도 42, 적어도 43, 적어도 44, 적어도 45, 적어도 46, 적어도 47, 적어도 48, 적어도 49, 적어도 50, 적어도 60, 적어도 70, 적어도 80, 적어도 90, 또는 적어도 100의 아미노산 치환, 결실, 삽입, 또는 첨가를 포함한다.

[0064] 일부 실시형태에서, KivD 효소는 서열번호 29의 잔기 33에 상응하는 잔기에 Y; 서열번호 29의 잔기 44에 상응하는 잔기에 Q; 서열번호 29의 잔기 117에 상응하는 잔기에 M; 서열번호 29의 잔기 129에 상응하는 잔기에 I; 서열번호 29의 잔기 185에 상응하는 잔기에 W; 서열번호 29의 잔기 190에 상응하는 잔기에 I; 서열번호 29의 잔기 225에 상응하는 잔기에 I; 서열번호 29의 잔기 227에 상응하는 잔기에 Y; 서열번호 29의 잔기 311에 상응하는

잔기에 L; 서열번호 29의 잔기 312에 상응하는 잔기에 G; 서열번호 29의 잔기 313에 상응하는 잔기에 T; 서열번호 29의 잔기 328에 상응하는 잔기에 P; 서열번호 29의 잔기 341에 상응하는 잔기에 W; 서열번호 29의 잔기 345에 상응하는 잔기에 H; 서열번호 29의 잔기 347에 상응하는 잔기에 C; 서열번호 29의 잔기 420에 상응하는 잔기에 R; 서열번호 29의 잔기 494에 상응하는 잔기에 D; 서열번호 29의 잔기 508에 상응하는 잔기에 C; 및/또는 서열번호 29의 잔기 550에 상응하는 잔기에 F를 포함한다.

[0065] 일부 실시형태에서, KivD 효소는 서열번호 29의 잔기 33에 상응하는 잔기에 Y; 서열번호 29의 잔기 44에 상응하는 잔기에 Q; 서열번호 29의 잔기 117에 상응하는 잔기에 M; 서열번호 29의 잔기 129에 상응하는 잔기에 I; 서열번호 29의 잔기 185에 상응하는 잔기에 W; 서열번호 29의 잔기 190에 상응하는 잔기에 I; 서열번호 29의 잔기 225에 상응하는 잔기에 I; 서열번호 29의 잔기 227에 상응하는 잔기에 Y; 서열번호 29의 잔기 311에 상응하는 잔기에 L; 서열번호 29의 잔기 312에 상응하는 잔기에 G; 서열번호 29의 잔기 313에 상응하는 잔기에 T; 서열번호 29의 잔기 328에 상응하는 잔기에 P; 서열번호 29의 잔기 341에 상응하는 잔기에 W; 서열번호 29의 잔기 345에 상응하는 잔기에 H; 서열번호 29의 잔기 347에 상응하는 잔기에 C; 서열번호 29의 잔기 420에 상응하는 잔기에 R; 서열번호 29의 잔기 494에 상응하는 잔기에 D; 서열번호 29의 잔기 508에 상응하는 잔기에 C; 및 서열번호 29의 잔기 550에 상응하는 잔기에 F를 포함한다.

[0066] 알콜 데히드로게나제 (Adh)

[0067] 본 개시에서 사용되는 "알콜 데히드로게나제 (Adh)"는 에탄올의 아세트알데히드로의 전환을 촉매하는 효소를 의미한다. Adh는 기질로서 이소발레르알데히드를 사용할 수 있다. 일부 실시형태에서, Adh는 이소발레르알데히드로부터 이소펜탄올을 생산한다.

[0068] 일부 실시형태에서, 숙주 세포는 Adh 효소 및/또는 이러한 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함한다. 일부 실시형태에서, 숙주 세포는 서열번호 20, 22, 24, 또는 645-700 중 어느 하나와 적어도 80% (예를 들어, 적어도 80%, 적어도 85%, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100%) 동일한 아미노산 서열을 포함하는 Adh 효소, 표 3 또는 표 6의 Adh 효소, 또는 달리 본 개시에 기술된 Adh 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함한다. 일부 실시형태에서, 숙주 세포는 서열번호 19, 21, 23 또는 589-644 중 어느 하나와 적어도 90% (예를 들어, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100%) 동일한 이중성 폴리뉴클레오티드, 표 3 또는 표 6의 Adh 효소, 또는 달리 본 개시에 기술된 Adh 효소를 코딩하는 폴리뉴클레오티드를 포함한다.

[0069] 일부 실시형태에서, 숙주 세포는 사카로마이세스 세레비지아에 (*Saccharomyces cerevisiae*) 유래의 Adh를 포함한다. 다른 실시형태에서, 숙주 세포는 사카로마이세스 세레비지아에 유래 Adh를 포함하지 않는다.

[0070] 사카로마이세스 세레비지아에 유래의 Adh는 UniProtKB - P00331의 아미노산 서열 (서열번호 31)을 포함할 수 있다:

```
MSIPETQKAIIFYESNGKLEHKDIPVPKPKPNELLINVKYSQVCHTDLHAWHGDWPLPTKLPVGGHEG
AGVVVGMGENVKGWKIGDYAGIKWLNGSCMACEYCELGNESNCPHADLSGYTHDGSFQYATADAVQAAHIPQGT
DLAEVAPILCAGITVYKALKSANLRAGHWAAISGAAGGLGSLAVQYAKAMGYRVLGIDGGPGKEELFTSLGGEVF
IDFTKEKDIVSAVVKATNGGAHGIINVSVSEAAIEASTRYCRANGTVVLVGLPAGAKCSSDVFNVHVKISIVGS
YVGNRADTREALDFFARGLVKSPIKVVGLSSLPEIYEKMEKGQIAGRYVVDTSK (서열번호 31)44
```

[0071]

[0072] 일부 실시형태에서, 서열번호 31의 아미노산 서열은 하기 핵산 서열에 의해 코딩된다:

```
ATGTCGATCCCAGAACTCAGAAGGCTATTATATTTATGAGTCAAACGGCAAACCTCGAACATAAAGACATTCCC
GTGCTTAAACCGAAACCGAATGAACCTTCTGATTAACGTAAAGTACAGCGGAGTCTGCCACACGGATTGCGATGCC
TGGCAGGGGATTGGCCGTACCGACCAAACTGCCTCTGGTGGGTGGTCATGAGGGCGCGGGCGTTGTTGTGGGT
ATGGGAGAAAATGTCAAAGGCTGGAAAATCGGCGACTATGCAGGGATCAAGTGGCTGAACGGGTCTTGTATGGCG
TGCGAGTACTGTGAATTAGGTAATGAATCCAACCTGCCACACGCAGATCTGAGTGGTTATACCCATGACGGCAGC
TTCCAAGAATACGCCACAGCGGATGCCGTGCAGGCAGCTCACATTCGCAAGGAAGTATCTTGCAGGAAGTAGCC
CCAATTCGTGCGCGGGCATCACGGTATATAAAGCTCTCAAAGTGCAAACCTTGCAGCGCGGTCTTGGGCTGCG
ATTCGCGGTGCCGCGGGCGGGCTGGGATCATTAGCTGTTTCAGTACGCGAAGGCAATGGGTTATCGAGTCTGGGC
ATCGACGGCGGGCCCGGTAAAGAAGAGCTATTTACCAGCCTCGGCGGTGAGGTCTTCATCGATTTTACCAAAGAA
AAAGATATCGTTCGCGAGTCGTGAAAGCAACCAATGGCGGCGCTCACGGAATTATAAATGTGTCTGTATCAGAA
GCGGCGATTGAAGCCAGCAGCGCTTATTGTGCGCGCAACGGCACAGTGGTCTTGGTAGGCCTGCCCGCGGTGCG
AAATGTAGCTCGGAGCTGTTCAATCATGTGGTGAAGAGTATTTCCATTGTTGGATCTTACGTAGGGAACCGTGCG
GATACGCGGGAGGCACTGGATTTTTTTGCAAGGGGCTTGGTTAAAGCCCGATCAAAGTCGTGGGTCTGTCGTCT
CTACCTGAAATATATGAGAAAATGGAAGGACAGATCGCGGAGCGCTACGTCGTCGACACCTCAAAGTGA
(서열번호 32)
```

[0073]

[0074] 일부 실시형태에서, Adh 효소를 코딩하는 이중성 폴리뉴클레오티드를 발현하는 숙주 세포는 대조군에 비해서 0.5배, 1배, 1.5배, 2배, 2.5배, 3배, 3.5배, 4배, 4.5배, 5배, 5.5배, 또는 6배 이상 (예를 들어, 2배 내지 6배 이상)으로 이소발레르알데히드의 이소펜탄올로의 전환을 증가시킬 수 있다. 일부 실시형태에서, 대조군은 서열번호 31을 코딩하는 이중성 폴리뉴클레오티드를 발현하는 숙주 세포이다. 일부 실시형태에서, 대조군은 서열번호 31을 코딩하는 이중성 폴리뉴클레오티드를 발현하는 숙주 세포이다. 일부 실시형태에서, 대조군은 이. 콜라이 니슬 균주 SYN1980 Δ leuE, Δ ilvC, lacZ:tetR-Ptet-livKHMGE, tetR-Ptet-leuD(Hc)-kivD-adh2-brnQ-rnB ter (pSC101), 예컨대 미국 특허 출원 공개 번호 제US20170232043호에 기술된 것이다.

[0075]

일부 실시형태에서, Adh는 서열번호 31, 서열번호 20, 22, 24, 또는 645-700 중 어느 하나, 서열번호 19, 21, 23 또는 589-644 중 어느 하나와 적어도 5%, 적어도 10%, 적어도 15%, 적어도 20%, 적어도 25%, 적어도 30%, 적어도 35%, 적어도 40%, 적어도 45%, 적어도 50%, 적어도 55%, 적어도 60%, 적어도 65%, 적어도 70%, 적어도 71%, 적어도 72%, 적어도 73%, 적어도 74%, 적어도 75%, 적어도 76%, 적어도 77%, 적어도 78%, 적어도 79%, 적어도 80%, 적어도 81%, 적어도 82%, 적어도 83%, 적어도 84%, 적어도 85%, 적어도 86%, 적어도 87%, 적어도 88%, 적어도 89%, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100% 동일한 서열, 표 3 또는 표 6의 Adh 효소, 또는 달리 본 개시에 개시된 Adh 효소를 코딩하는 아미노산 또는 폴리뉴클레오티드 서열을 포함한다.

[0076]

일부 실시형태에서, Adh는 서열번호 31, 서열번호 20, 22, 24, 또는 645-700 중 어느 하나, 표 3 또는 표 6의 Adh 효소, 또는 달리 본 개시에 개시된 Adh 효소에 비해서, 적어도 1, 적어도 2, 적어도 3, 적어도 4, 적어도 5, 적어도 6, 적어도 7, 적어도 8, 적어도 9, 적어도 10, 적어도 11, 적어도 12, 적어도 13, 적어도 15, 적어도 16, 적어도 17, 적어도 18, 적어도 19, 적어도 20, 적어도 21, 적어도 22, 적어도 23, 적어도 24, 적어도 25, 적어도 26, 적어도 27, 적어도 28, 적어도 29, 적어도 30, 적어도 31, 적어도 32, 적어도 33, 적어도 34, 적어도 35, 적어도 36, 적어도 37, 적어도 38, 적어도 39, 적어도 40, 적어도 41, 적어도 42, 적어도 43, 적어도 44, 적어도 45, 적어도 46, 적어도 47, 적어도 48, 적어도 49, 적어도 50, 적어도 60, 적어도 70, 적어도 80, 적어도 90, 또는 적어도 100의 아미노산 치환, 결실, 삽입, 또는 첨가를 포함한다.

[0077]

일부 실시형태에서, Adh는 서열번호 31의 잔기 9에 상응하는 잔기에 P; 서열번호 31의 잔기 16에 상응하는 잔기에 G; 서열번호 31의 잔기 23에 상응하는 잔기에 Q; 서열번호 31의 잔기 28에 상응하는 잔기에 R; 서열번호 31의 잔기 30에 상응하는 잔기에 A; 서열번호 31의 잔기 93에 상응하는 잔기에 K; 서열번호 31의 잔기 98에 상응하는 잔기에 L; 서열번호 31의 잔기 99에 상응하는 잔기에 R; 서열번호 31의 잔기 114에 상응하는 잔기에 P; 서열번호 31의 잔기 115에 상응하는 잔기에 K; 서열번호 31의 잔기 119에 상응하는 잔기에 Y; 서열번호 31의 잔기 194에 상응하는 잔기에 Y; 서열번호 31의 잔기 242에 상응하는 잔기에 P; 서열번호 31의 잔기 249에 상응하는 잔기에 K; 서열번호 31의 잔기 255에 상응하는 잔기에 E; 서열번호 31의 잔기 260에 상응하는 잔기에 D; 서열번호 31의 잔기 269에 상응하는 잔기에 H; 서열번호 31의 잔기 281에 상응하는 잔기에 Q; 서열번호 31의 잔기 325에 상응하는 잔기에 L; 서열번호 31의 잔기 333에 상응하는 잔기에 M; 서열번호 31의 잔기 334에 상응하는 잔기에 P; 및/또는 서열번호 31의 잔기 348에 상응하는 잔기에 Q를 포함한다.

[0078]

일부 실시형태에서, Adh는 서열번호 31의 잔기 9에 상응하는 잔기에 P; 서열번호 31의 잔기 16에 상응하는 잔기

에 G; 서열번호 31의 잔기 23에 상응하는 잔기에 Q; 서열번호 31의 잔기 28에 상응하는 잔기에 R; 서열번호 31의 잔기 30에 상응하는 잔기에 A; 서열번호 31의 잔기 93에 상응하는 잔기에 K; 서열번호 31의 잔기 98에 상응하는 잔기에 L; 서열번호 31의 잔기 99에 상응하는 잔기에 R; 서열번호 31의 잔기 114에 상응하는 잔기에 P; 서열번호 31의 잔기 115에 상응하는 잔기에 K; 서열번호 31의 잔기 119에 상응하는 잔기에 Y; 서열번호 31의 잔기 194에 상응하는 잔기에 Y; 서열번호 31의 잔기 242에 상응하는 잔기에 P; 서열번호 31의 잔기 249에 상응하는 잔기에 K; 서열번호 31의 잔기 255에 상응하는 잔기에 E; 서열번호 31의 잔기 260에 상응하는 잔기에 D; 서열번호 31의 잔기 269에 상응하는 잔기에 H; 서열번호 31의 잔기 281에 상응하는 잔기에 Q; 서열번호 31의 잔기 325에 상응하는 잔기에 L; 서열번호 31의 잔기 333에 상응하는 잔기에 M; 서열번호 31의 잔기 334에 상응하는 잔기에 P; 및 서열번호 31의 잔기 348에 상응하는 잔기에 Q를 포함한다.

[0079] **분지쇄 아미노산 수송 시스템 2 캐리어 단백질 (BrnQ)**

[0080] 본 개시에서 사용되는, "분지쇄 아미노산 수송 시스템 2 캐리어 단백질 (BrnQ)"은 분지쇄 아미노산을 위한 LIV-II 수송 시스템의 성분을 의미한다. BrnQ는 분지쇄 아미노산, 예를 들어 류신을 세포 예컨대 숙주 세포로 수송하는데 사용될 수 있다.

[0081] 일부 실시형태에서, 숙주 세포는 BrnQ 단백질 및/또는 이러한 단백질을 코딩하는 이중성 폴리뉴클레오티드를 포함한다. 일부 실시형태에서, 숙주 세포는 본 출원에서 기술된 바와 같은 BrnQ 단백질, 예를 들어, 서열번호 35와 적어도 80% (예를 들어, 적어도 80%, 적어도 85%, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100%) 동일한 아미노산 서열을 포함하는 BrnQ 단백질을 코딩하는 이중성 폴리뉴클레오티드를 포함한다. 일부 실시형태에서, BrnQ 단백질은 UniProtKB - B7MD59에 기재된 아미노산 서열을 포함한다.

[0082] UniProtKB - B7MD59는 하기 아미노산 서열을 갖는다:

```
MTHQLRSRDIIALGFMFTALFVAGAGNIIFPPMVGLQAGEHVWTAAGFLITAVGLPVLTVVALAKVGGVDSLST
PIGVAGVLLATVCYLAVGLPLFATPRATATVSFEVGIAPLTGDSALPLFIYSLVYFAIVILVSLYPGKLLDTVGNF
LAPLKIILVILSVAAIWPAGSISTATEAYQNAAFSNGFVNGYLTMDTLGAMVFGIVIVNAARSRGVTEARLLT
RYTVWAGLMAGVGLTLLYLALFRLGSDSASLVDQSANGAAILHAYVQHTFGGGGSFLLAALIFIACLVTAVGLTC
ACAEFFAQYVPLSYRTLVLVILGGFSMVVSNLGLSGLIQLISVPVLTATYPPCIALVVLSTFRSWHNSRVIAPPM
FISLLFGILDGIKASAFSDILPSWAQRLPLAEQGLAWLMPTVVMVLAIIWDRAAGRQVTSSAH (서열번호
35)
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[0083]

[0084] 일부 실시형태에서, 서열번호 35는 하기 핵산 서열에 의해 코딩된다:

```
ATGACCCATCAATTAAGATCGCGCATATCATCGCTCTGGGCTTTATGACATTGCGTTGTTTCGTCGCGCGCAGGT
AACATTATTTTCCCTCCAATGGTCGGCTTGCAGGCAGGCGAACACGCTCTGGACTGCGGCATTGCGCTTCTCTCATT
ACTGCCGTTGGCCTACCGGTATTAACGGTAGTGGCGCTGGCAAAAGTTGGCGCGGTGTTGACAGTCTCAGCACG
CCAATTGGTAAAGTCGCTGGCGTACTGCTGGCAACAGTTTGTACCTGGCGGTGGGGCCGCTTTTGTCTACGCCG
CGTACAGCTACCGTTTCTTTGAAGTGGGCATTGCGCCGCTGACGGGTGATTCCGCGCTGCCGCTGTTTATTTAC
AGCCTGGTCTATTTTCGCTATCGTTATTTCTGGTTTCGCTCTATCCGGCAAGCTGCTGGATACCGTGGGCAACTTC
CTTGCGCCGCTGAAAATTATCGCGCTGGTCATCCTGTCTGTGTCGCAATTATCTGGCCGGCGGGTCTATCAGT
ACGGCGACTGAGGCTTATCAAAACGCTGCGTTTTCTAACGGCTTCGTCAACGGCTATCTGACCATGGATACGCTG
GGCGCAATGGTGTGGTATCGTTATTGTTAACGCGCGCGTTCCTGTTGGCGTTACCGAAGCGCGTCTGCTGACC
CGTTATACCGCTCTGGGCTGGCCTGATGGCGGGTGTGGTGTGACTCTGCTGTACCTGGCGCTGTTCCGCTCTGGGT
TCAGACAGCGCGTCTGCTGGTCGATCAGTCTGCAACGGTGGCGGATCCTGCATGCTTACGTTTACGATACCTTT
GGCGCGCGCGGTAGCTTCTGCTGGCGCGGTTAATCTTCATCGCCTGCCTGGTCACGGCGGTTGGCCTGACCTGT
GCTTGTGCGAATTCTTCGCCAGTACGTACCGCTCTCTTATCGTACGCTGGTGTATCTCTCGCGCGCTTCTCG
ATGGTGGTGTCTAACCTCGGCTTGAGCCAGCTGATTCAGATCTCTGTACCGGTGCTGACCGCCATTATCCGCCG
TGTATCGCACTGGTGTATTAAGTTTTACACGCTCATGGTGGCATAATTCGTCGCCGCTGATTGCTCCGCCGATG
TTTATCAGCCTGCTTTTTGGTATTCTCGACGGGATCAAGGCATCTGCATTACGCGATATCTTACCGTCTGGGCG
CAGCGTTTACCGCTGGCCGAACAAGGTCTGGCGTGGTTAATGCCAACAGTGGTGATGGTGGTCTGGCCATTATC
TGGGATCGTGGCGCAGGTCGTACAGTGACCTCCAGCGCTCACTAA (서열번호 36)
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[0085]

[0086] **변이체**

[0087] 본 개시에 기술된 효소 및 단백질의 변이체 (예를 들어, LeuDh, KivD, 또는 Adh 및 핵산 및 아미노산 서열에 대한 변이체 포함)는 또한 본 개시에 포괄된다. 변이체는 그 사이의 모든 값을 포함하여, 기준 서열과 적어도 5%,

적어도 10%, 적어도 15%, 적어도 20%, 적어도 25%, 적어도 30%, 적어도 35%, 적어도 40%, 적어도 45%, 적어도 50%, 적어도 55%, 적어도 60%, 적어도 65%, 적어도 70%, 적어도 71%, 적어도 72%, 적어도 73%, 적어도 74%, 적어도 75%, 적어도 76%, 적어도 77%, 적어도 78%, 적어도 79%, 적어도 80%, 적어도 81%, 적어도 82%, 적어도 83%, 적어도 84%, 적어도 85%, 적어도 86%, 적어도 87%, 적어도 88%, 적어도 89%, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100% 서열 동일성을 공유할 수 있다.

- [0088] 달리 표시하지 않으면, 당분야에 공지된 바와 같은 용어 "서열 동일성"은 서열 비교 (정렬)를 통해 결정된, 2개 폴리펩티드 또는 폴리뉴클레오티드의 서열 간 상관성을 의미한다. 일부 실시형태에서, 서열 동일성은 서열 (예를 들어, LeuDH, KivD, 또는 Adh 서열)의 전체 길이 전반에서 결정된다. 일부 실시형태에서, 서열 동일성은 서열 (예를 들어, LeuDH, KivD, 또는 Adh 서열)의 영역 (예를 들어, 아미노산 또는 핵산의 스트레치, 예를 들어 활성 부위를 포괄하는 서열) 상에서 결정된다.
- [0089] 동일성은 또한 둘 이상의 잔기 (예를 들어, 핵산 또는 아미노산 잔기)의 스트링 간 일치수를 통해 결정된 2개 서열 간 서열 관련도를 의미할 수 있다. 동일성은 특정 수학 모델 또는 컴퓨터 프로그램 (예를 들어, 알고리즘)을 통해 해결된 (있다면) 갭 정렬에 의한 둘 이상의 서열 간 동일한 일치 백분율을 측정한다.
- [0090] 관련 폴리펩티드 또는 핵산 서열의 동일성은 당업자에게 공지된 임의 방법으로 쉽게 계산할 수 있다. 2개 서열 (예를 들어, 핵산 또는 아미노산 서열)의 "동일성 백분율"은 예를 들어 문헌 [Karlin and Altschul *Proc. Natl. Acad. Sci. USA* 90:5873-77, 1993]에서 처럼 변형된, [Karlin and Altschul *Proc. Natl. Acad. Sci. USA* 87:2264-68, 1990]의 알고리즘을 사용해 결정할 수 있다. 이러한 알고리즘은 [Altschul et al., *J. Mol. Biol.* 215:403-10, 1990]의 NBLAST® 및 XBLAST® 프로그램 (버전 2.0)에 통합된다. BLAST® 단백질 검색은 본 출원에 기술된 단백질에 상동성인 아미노산 서열을 수득하기 위해서, 예를 들어, XBLAST 프로그램, 점수=50, 단어길이=3를 사용하여 수행될 수 있다. 2개 서열 간에 갭이 존재하는 경우에, Gapped BLAST®는 예를 들어, [Altschul et al., *Nucleic Acids Res.* 25(17):3389-3402, 1997]에 기술된 바와 같이 이용될 수 있다. BLAST® 및 Gapped BLAST® 프로그램을 이용하는 경우에, 개별 프로그램 (예를 들어, XBLAST® 및 NBLAST®)의 디폴트 매개변수가 사용될 수 있거나, 또는 매개변수는 당업자가 이해하게 되는 바와 같이 적절하게 조정될 수 있다.
- [0091] 사용할 수 있는 다른 국소 정렬 기술은 예를 들어, 스미스-워터만 (Smith-Waterman) 알고리즘 (Smith, T.F. & Waterman, M.S. (1981) "Identification of common molecular subsequences." *J. Mol. Biol.* 147:195-197)을 기반으로 한다. 사용할 수 있는 일반 전역 정렬 기술은 동적 프로그래밍을 기반으로 하는, 예를 들어 니들만-분치 (Needleman-Wunsch) 알고리즘 (Needleman, S.B. & Wunsch, C.D. (1970) "A general method applicable to the search for similarities in the amino acid sequences of two proteins." *J. Mol. Biol.* 48:443-453)이다.
- [0092] 보다 최근에, 니들만-분치 알고리즘을 포함하여, 다른 최적 전역 정렬 방법에 비해 더 빠른 핵산 및 아미노산 서열의 전역 정렬을 알려진 대로 생산하는 신속 최적 전역 서열 정렬 알고리즘 (Fast Optimal Global Sequence Alignment Algorithm) (FOGSAA)이 개발되었다. 일부 실시형태에서, 2개 폴리펩티드의 동일성은 2개 아미노산 서열을 정렬하고, 동일한 아미노산의 수를 계산하고 나서, 아미노산 서열 중 하나의 길이로 나뉘어 결정된다. 일부 실시형태에서, 2개 핵산의 동일성은 2개 뉴클레오티드 서열을 정렬하고, 동일한 뉴클레오티드의 수를 계산하고 나서, 핵산 중 하나의 길이로 나뉘어 결정된다.
- [0093] 다중 서열 정렬을 위해서, Clustal Omega (Sievers et al., *Mol Syst Biol.* 2011 Oct 11;7:539)를 포함한 컴퓨터 프로그램이 사용될 수 있다.
- [0094] 바람직한 실시형태에서, 핵산 또는 아미노산 서열을 포함한 서열은 서열 동일성이 문헌 [Karlin and Altschul *Proc. Natl. Acad. Sci. USA* 90:5873-77, 1993]에서 처럼 변형된, 문헌 [Karlin and Altschul *Proc. Natl. Acad. Sci. USA* 87:2264-68, 1990]의 알고리즘 (예를 들어, 개별 프로그램의 디폴트 매개변수를 사용하는, BLAST®, NBLAST®, XBLAST® 또는 Gapped BLAST® 프로그램)을 사용해 결정될 때 기준 서열 예컨대 청구항에서 인용되고/되거나 본 출원에서 개시된 서열과 명시된 동일성 백분율을 갖는 것으로 확인된다.
- [0095] 일부 실시형태에서, 핵산 또는 아미노산 서열을 포함한, 서열은 서열 동일성이 디폴트 매개변수를 사용하여 스미스-워터만 알고리즘 (Smith, T.F. & Waterman, M.S. (1981) "Identification of common molecular subsequences." *J. Mol. Biol.* 147:195-197) 또는 니들만-분치 알고리즘 (Needleman, S.B. & Wunsch, C.D. (1970) "A general method applicable to the search for similarities in the amino acids of two

proteins." J. Mol. Biol. 48:443-453)을 사용해 결정될 때 기준 서열, 예컨대 본 출원에 개시되고/되거나 청구항에서 인용되는 서열과 명시된 동일성 백분율을 갖는 것으로 확인된다.

[0096] 일부 실시형태에서, 핵산 또는 아미노산 서열을 포함하는, 서열은 서열 동일성이 디폴트 매개변수를 사용한 FOGSAA (Fast Optimal Global Sequence Alignment Algorithm)를 사용해 결정될 때 기준 서열, 예컨대 본 출원에 개시되고/되거나 청구항에 인용된 서열과 명시된 동일성 백분율을 갖는 것으로 확인된다.

[0097] 일부 실시형태에서, 핵산 또는 아미노산 서열을 포함하는, 서열은 서열 동일성이 디폴트 매개변수를 사용한 Clustal Omega (Sievers et al., *Mol Syst Biol.* 2011 Oct 11;7:539)를 사용해 결정될 때 기준 서열, 예컨대 본 출원에 개시되고/되거나 청구항에 인용된 서열과 명시된 동일성 백분율을 갖는 것으로 확인된다.

[0098] 본 개시에서 사용되는, 서열 "X"의 잔기 (예컨대 핵산 잔기 또는 아미노산 잔기)는 서열 X 및 Y가 당분야에 공지된 아미노산 서열 정렬 도구, 예컨대, 예를 들어, Clustal Omega 또는 BLAST®를 사용해 정렬될 때 서열 "X"의 잔기가 서열 "Y" 중 "Z"의 대응 위치에 있는 경우 상이한 서열 "Y" 중 위치 또는 잔기 (예컨대 핵산 잔기 또는 아미노산 잔기) "Z"에 상응하는 것을 의미한다.

[0099] 본 개시에서 사용되는, 변이체 서열은 상동성 서열일 수 있다. 본 개시에서 사용되는, 상동성 서열은 소정 동일성 백분율 (예를 들어, 그 사이의 모든 값을 포함하여, 적어도 5%, 적어도 10%, 적어도 15%, 적어도 20%, 적어도 25%, 적어도 30%, 적어도 35%, 적어도 40%, 적어도 45%, 적어도 50%, 적어도 55%, 적어도 60%, 적어도 65%, 적어도 70%, 적어도 71%, 적어도 72%, 적어도 73%, 적어도 74%, 적어도 75%, 적어도 76%, 적어도 77%, 적어도 78%, 적어도 79%, 적어도 80%, 적어도 81%, 적어도 82%, 적어도 83%, 적어도 84%, 적어도 85%, 적어도 86%, 적어도 87%, 적어도 88%, 적어도 89%, 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 적어도 99%, 또는 100%의 동일성 백분율)을 공유하는 서열 (예를 들어, 핵산 또는 아미노산 서열)이다. 상동성 서열은 파라로그 또는 오솔로그 서열을 포함하지만, 이에 제한되지 않는다. 파라로그 서열은 종의 계통 내 유전자의 중복으로 발생하는 반면, 오솔로그 서열은 종분화 사건 이후에 분기된다.

[0100] 일부 실시형태에서, 폴리펩티드 변이체 (예를 들어, LeuDH, KivD, 또는 Adh 효소 변이체)는 기준 폴리펩티드 (예를 들어, 기준 LeuDH, KivD, 또는 Adh 효소)와 2차 구조 (예를 들어, 알파 헬릭스, 베타 시트)를 공유하는 도메인을 포함한다. 일부 실시형태에서, 폴리펩티드 변이체 (예를 들어, LeuDH, KivD, 또는 Adh 효소 변이체)는 기준 폴리펩티드 (예를 들어, 기준 LeuDH, KivD, 또는 Adh 효소)와 3차 구조를 공유한다. 비제한적인 예로서, 변이체 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소 변이체)는 기준 폴리펩티드와 비교하여 낮은 1차 서열 동일성 (예를 들어, 80% 미만, 75% 미만, 70% 미만, 65% 미만, 60% 미만, 55% 미만, 50% 미만, 45% 미만, 40% 미만, 35% 미만, 30% 미만, 25% 미만, 20% 미만, 15% 미만, 10% 미만, 또는 5% 미만 서열 동일성)을 갖지만, 하나 이상의 2차 구조 (예를 들어, 루프, 알파 헬릭스, 또는 베타 시트를 포함하나, 이에 제한되지 않음)를 공유하거나, 또는 기준 폴리펩티드와 동일한 3차 구조를 가질 수 있다. 예를 들어, 루프는 베타 시트와 알파 헬릭스 사이, 2개 알파 헬릭스 사이, 또는 2개 베타 시트 사이에 위치될 수 있다. 상동성 모델링을 사용하여 둘 이상의 3차 구조를 비교할 수 있다.

[0101] 환형 치환 (Yu and Lutz, *Trends Biotechnol.* 2011 Jan;29(1):18-25)을 포함한, 임의의 적합한 방법을 사용하여 이러한 변이체를 생산할 수 있다. 환형 치환에서, 폴리펩티드의 선형 1차 서열은 (예를 들어, 서열의 N-말단부 및 C-말단부를 연결하여) 원형화될 수 있고 폴리펩티드는 상이한 위치에서 절단 ("파단")될 수 있다. 따라서, 새로운 폴리펩티드의 선형 1차 서열은 선형 서열 정렬 방법 (예를 들어, Clustal Omega 또는 BLAST)으로 결정하여 낮은 서열 동일성 (예를 들어, 그 사이의 모든 값을 포함하여, 80% 미만, 75% 미만, 70% 미만, 65% 미만, 60% 미만, 55% 미만, 50% 미만, 45% 미만, 40% 미만, 35% 미만, 30% 미만, 25% 미만, 20% 미만, 15% 미만, 10% 미만, 또는 5% 미만)을 가질 수 있다. 그러나, 2개 폴리펩티드의 위상학적 분석은 그들의 3차 구조가 유사하다는 것을 밝혀줄 수 있다. 특정 이론에 국한하지 않고, 기준 폴리펩티드의 환형 치환을 통해서, 그리고 기준 폴리펩티드와 유사한 3차 구조를 갖게 생성된 변이체 폴리펩티드는 유사한 기능적 특징 (예를 들어, 효소 활성, 효소 반응속도론, 기질 특이성 또는 생성물 특이성)을 공유할 수 있다. 일부 예에서, 환형 치환은 2차 구조, 3차 구조, 또는 4차 구조를 변경시킬 수 있고 상이한 기능적 특징 (예를 들어, 증가되거나 또는 감소된 효소 활성, 상이한 기질 특이성, 또는 상이한 생성물 특이성)을 갖는 효소를 생산할 수 있다. 예를 들어, 문헌 [Yu and Lutz, *Trends Biotechnol.* 2011 Jan;29(1):18-25]을 참조한다.

[0102] 환형 치환을 겪은 단백질에서, 단백질의 선형 아미노산 서열은 환형 치환을 겪지 않은 기준 단백질과 상이할 수 있다는 것을 이해해야 한다. 그러나, 당업자는 환형 치환을 겪은 단백질 중 어떠한 잔기가 예를 들어, 서열을

정렬하여 보존된 모티프를 검출하고/하거나, 단백질의 구조 또는 예측 구조를 예를 들어, 상동성 모델링을 통해 비교하여, 환경 치환을 겪지 않은 기준 단백질 중 잔기들에 상응하는 가를 쉽게 결정할 수 있을 것이다. 본 출원에 기술된 변이체는 본 출원에 기술된 서열의 환경으로 치환된 변이체를 포함한다.

[0103] 일부 실시형태에서, 관심 서열과 본 출원에 기술된 기준 서열 간 동일성 백분율을 결정하는 알고리즘이 서열 간 환경 치환의 존재를 설명한다. 환경 치환의 존재는 예를 들어, RASPODOM (Weiner et al., *Bioinformatics*. 2005 Apr 1;21(7):932-7)을 포함한, 당분야에 공지된 임의 방법을 사용해 검출될 수 있다. 일부 실시형태에서, 환경 치환의 존재는 관심 서열 및 본 출원에 기술된 서열 간 동일성 백분율의 계산 이전에 보정된다 (예를 들어, 적어도 하나의 서열 중 도메인을 재정렬함). 본 출원의 청구항은 기준 서열의 동일성 백분율이 서열의 잠재적 환경 치환을 고려한 이후에 계산된 서열을 포괄한다는 것을 이해해야 한다.

[0104] 본 출원에 개시된 재조합 LeuDh, KivD, 또는 Adh 효소의 기능적 변이체가 또한 본 개시에 포괄된다. 예를 들어, 기능적 변이체는 하나 이상의 동일 기질에 결합할 수 있거나 또는 하나 이상의 동일한 생성물을 생산할 수 있다. 기능적 변이체는 당분야에 공지된 임의 방법을 사용해 확인할 수 있다. 예를 들어, 상기 기술된 문헌 [Karlin and Altschul *Proc. Natl. Acad. Sci. USA* 87:2264-68, 1990]의 알고리즘은 기지 기능을 갖는 상동성 단백질을 확인하는데 사용될 수 있다.

[0105] 추정된 기능적 변이체가 또한 기능적으로 주석달린 도메인을 갖는 폴리펩티드를 검색하여 확인될 수 있다. Pfam을 포함한 데이터베이스 (Sonnhammer et al., *Proteins*. 1997 Jul;28(3):405-20)는 특정 도메인을 갖는 폴리펩티드를 확인하는데 사용될 수 있다.

[0106] 상동성 모델링은 또한 기능에 영향을 미치지 않고 돌연변이될 수 있는 아미노산 잔기를 확인하는데 사용될 수 있다. 이러한 방법의 비제한적인 예는 위치-특이적 채점 매트릭스 (PSSM) 및 에너지 최소화 프로토콜의 사용을 포함할 수 있다.

[0107] 위치-특이적 채점 매트릭스 (PSSM)는 공통 서열 (예를 들어, 모티프)을 확인하기 위해 위치 가중 매트릭스를 사용한다. PSSM은 핵산 또는 아미노산 서열에 대해 수행될 수 있다. 서열을 정렬하고 방법은 분석된 서열의 수 및 특정 위치에서 특정 잔기 (예를 들어, 아미노산 또는 뉴클레오티드)의 관찰된 빈도를 고려한다. 예를 들어, 문헌 [Stormo et al., *Nucleic Acids Res.* 1982 May 11;10(9):2997-3011]을 참조한다. 소정 위치에서 특정 잔기를 관찰할 가능성을 계산할 수 있다. 특정 이론에 국한하지 않고, 높은 가변성을 갖는 서열 중 위치는 기능적 상동체를 생산하도록 돌연변이될 수 있다 (예를 들어, PSSM 점수 ≥ 0).

[0108] PSSM은 야생형 및 단일-점 돌연변이체 간 편차를 결정하는, 로제타 에너지 함수의 계산과 쌍형성될 수 있다. 로제타 에너지 함수는 ($\Delta \Delta G_{calc}$)로서 이러한 편차를 계산한다. 로제타 함수를 사용하여, 돌연변이된 잔기와 주변 원자 간 결합 상호작용을 사용해 돌연변이가 단백질 안정성을 증가 또는 감소시키는지 여부를 결정한다. 예를 들어, PSSM 점수 (예를 들어, PSSM 점수 ≥ 0)를 통해서 유리하다고 지정된 돌연변이는 단백질 안정성에 대한 돌연변이의 잠재적 영향을 결정하기 위해서 로제타 에너지 함수를 사용해 분석될 수 있다. 특정 이론에 국한하지 않고, 잠재적으로 안정한 돌연변이가 단백질 조작 (예를 들어, 기능적 상동체의 생산)에 바람직하다. 일부 실시형태에서, 잠재적으로 안정한 돌연변이는 -0.1 미만 (예를 들어, -0.2 미만, -0.3 미만, -0.35 미만, -0.4 미만, -0.45 미만, -0.5 미만, -0.55 미만, -0.6 미만, -0.65 미만, -0.7 미만, -0.75 미만, -0.8 미만, -0.85 미만, -0.9 미만, -0.95 미만, 또는 -1.0 미만)의 로제타 에너지 유닛 (R.e.u.)의 $\Delta \Delta G_{calc}$ 값을 갖는다. 예를 들어, 문헌 [Goldenzweig et al., *Mol Cell*. 2016 Jul 21;63(2):337-346. Doi: 10.1016/j.molcel.2016.06.012]을 참조한다.

[0109] 일부 실시형태에서, LeuDh, KivD, 또는 Adh 효소 코딩 서열은 기준 (예를 들어, LeuDh, KivD, 또는 Adh 효소) 코딩 서열에 상응하는 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100 또는 100 초과 위치에 돌연변이를 포함한다. 일부 실시형태에서, LeuDh, KivD, 또는 Adh 효소 코딩 서열은 기준 (예를 들어, LeuDh, KivD, 또는 Adh 효소) 코딩 서열에 비해서 코딩 서열의 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83,

84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100 이상의 코돈 중에 돌연변이를 포함한다. 당업자가 이해하게 되는 바와 같이, 코돈 내 돌연변이는 유전자 코드의 축퇴성에 기인하여 코돈에 의해 코딩되는 아미노산을 변화시킬 수 있거나 또는 변화시키지 않을 수도 있다. 일부 실시형태에서, 코딩 서열 중 하나 이상의 돌연변이는 기준 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소)의 아미노산 서열에 비해서 코딩 서열 (예를 들어, LeuDH, KivD, 또는 Adh 효소)의 아미노산 서열을 변경시키지 않는다.

[0110] 일부 실시형태에서, 재조합 LeuDH, KivD, 또는 Adh 효소 서열 중 하나 이상의 돌연변이는 기준 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소)의 아미노산 서열에 비해서 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소)의 아미노산 서열을 변경시킨다. 일부 실시형태에서, 하나 이상의 돌연변이는 기준 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소)의 아미노산 서열에 비해서 재조합 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소)의 아미노산 서열을 변경시키고, 기준 폴리펩티드에 비해서 폴리펩티드의 활성을 변경 (증강 또는 감소)시킨다.

[0111] 본 개시에 기술된 임의의 재조합 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소)의 활성 (예를 들어, 비활성)은 통상의 방법을 사용해 측정될 수 있다. 비제한적인 예로서, 재조합 폴리펩티드의 활성은 이의 기질 특이성, 생산된 생성물(들), 생산된 생성물(들)의 농도, 또는 이의 임의의 조합을 측정하여 결정할 수 있다. 본 개시에서 사용되는 재조합 폴리펩티드의 "비활성"은 단위 시간 당 재조합 폴리펩티드의 소정 양 (예를 들어, 농도)에 대한 생성된 특정 생성물의 양 (예를 들어, 농도)을 의미한다.

[0112] 당업자는 또한 재조합 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소) 코딩 서열 중 돌연변이가 전술한 폴리펩티드의 기능적으로 동등한 변이체, 예를 들어, 폴리펩티드의 활성을 보유하는 변이체를 제공하도록 보존성 아미노산 치환을 야기시킬 수 있다는 것을 또한 인식할 것이다. 본 개시에서 사용되는 "보존성 아미노산 치환"은 아미노산 치환이 만들어진 단백질의 상대적 전하 또는 크기 특징 또는 기능적 활성을 변경시키지 않는 아미노산 치환을 의미한다.

[0113] 일부 예에서, 아미노산은 이의 R 기 (예를 들어, 표 1 참조)를 특징으로 한다. 예를 들어, 아미노산은 비극성 지방족 R 기, 양으로 하전된 R 기, 음으로 하전된 R 기, 비극성 방향족 R 기, 또는 극성 비하전 R 기를 포함할 수 있다. 비극성 지방족 R 기를 포함하는 아미노산의 비제한적인 예는 알라닌, 글리신, 발린, 류신, 메티오닌, 및 이소류신을 포함한다. 양으로 하전된 R 기를 포함하는 아미노산의 비제한적인 예는 리신, 아르기닌, 및 히스티딘을 포함한다. 음으로 하전된 R 기를 포함하는 아미노산의 비제한적인 예는 아스파테이트 및 글루타메이트를 포함한다. 비극성, 방향족 R 기를 포함하는 아미노산의 비제한적인 예는 페닐알라닌, 티로신, 및 트립토판을 포함한다. 극성 비하전 R 기를 포함하는 아미노산의 비제한적인 예는 세린, 트레오닌, 시스테인, 프롤린, 아스파라긴, 및 글루타민을 포함한다.

[0114] 변이체는 당업자에게 공지된 폴리펩티드 서열을 변경시키기 위한 방법, 예컨대 이러한 방법을 편집한 참조 문헌, 예를 들어, [Molecular Cloning: A Laboratory Manual, J. Sambrook, et al., eds., Fourth Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2012], 또는 [Current Protocols in Molecular Biology, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York, 2010]에서 확인되는 것과 같은 방법에 따라서 제조될 수 있다.

[0115] 폴리펩티드의 기능적으로 균등한 변이체의 비제한적인 예는 본 출원에 개시된 단백질의 아미노산 서열 중 보존성 아미노산 치환을 포함할 수 있다. 본 개시에서 사용되는 "보존성 치환"은 "보존성 아미노산 치환"과 상호교환적으로 사용되고 표 1에 제공된 아미노산 치환 중 어느 하나를 의미한다.

[0116] 일부 실시형태에서, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 또는 20 초과와 같은 변이체 폴리펩티드를 제조할 때 변화될 수 있다. 일부 실시형태에서, 아미노산은 보존성 아미노산 치환으로 치환된다.

표 1. 보존성 아미노산 치환.

본래 잔기	R 기 유형	보존성 아미노산 치환
Ala	비극성 지방족 R 기	Cys, Gly, Ser
Arg	양으로 하전된 R 기	His, Lys
Asn	극성 비하전 R 기	Asp, Gln, Glu
Asp	음으로 하전된 R 기	Asn, Gln, Glu
Cys	극성 비하전 R 기	Ala, Ser
Gln	극성 비하전 R 기	Asn, Asp, Glu
Glu	음으로 하전된 R 기	Asn, Asp, Gln
Gly	비극성 지방족 R 기	Ala, Ser
His	양으로 하전된 R 기	Arg, Tyr, Trp
Ile	비극성 지방족 R 기	Leu, Met, Val
Leu	비극성 지방족 R 기	Ile, Met, Val
Lys	양으로 하전된 R 기	Arg, His
Met	비극성 지방족 R 기	Ile, Leu, Phe, Val
Pro	극성 비하전 R 기	
Phe	비극성 방향족 R 기	Met, Trp, Tyr
Ser	극성 비하전 R 기	Ala, Gly, Thr
Thr	극성 비하전 R 기	Ala, Asn, Ser
Trp	비극성 방향족 R 기	His, Phe, Tyr, Met
Tyr	비극성 방향족 R 기	His, Phe, Trp
Val	비극성 지방족 R 기	Ile, Leu, Met, Thr

[0117]

[0118]

바람직한 성질 및/또는 활성을 갖는 재조합 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소) 변이체를 생산하기 위한 폴리펩티드의 아미노산 서열 중 아미노산 치환은 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소)의 코딩 서열의 변경을 통해 만들어질 수 있다. 유사하게, 폴리펩티드의 기능적으로 균등한 변이체를 생성시키기 위한 폴리펩티드의 아미노산 서열 중 보존성 아미노산 치환은 전형적으로 재조합 폴리펩티드 (예를 들어, LeuDH, KivD, 또는 Adh 효소)의 코딩 서열의 변경을 통해 만들어진다.

[0119]

돌연변이 (예를 들어, 치환)는 당업자에게 공지된 다양한 방법을 통해 뉴클레오티드 서열 내에 만들어질 수 있다. 예를 들어, 돌연변이는 PCR-유도 돌연변이, Kunkel의 방법에 따른 부위-지정 돌연변이유발법 (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), 폴리펩티드를 코딩하는 유전자의 화학 합성, 유전자 편집 기술, 또는 삽입, 예컨대 태그 (예를 들어, HIS 태그 또는 GFP 태그)의 삽입을 통해서 만들어질 수 있다.

[0120]

분지쇄 아미노산 (BCAA) 경로 효소를 코딩하는 핵산

[0121]

본 개시의 양태는 재조합 효소, 이의 기능적 변형 및 변이체를 비롯하여, 이와 관련된 용도에 관한 것이다. 예를 들어, 본 출원에 기술된 효소 및 세포는 예를 들어, 류신을 이소펜탄올로 전환시켜서, 류신 소모를 촉진시키는데 사용될 수 있다. 방법은 본 출원에 개시된 하나 이상의 효소를 포함하는 숙주 세포, 세포 용해물, 단리된 효소, 또는 이의 임의의 조합을 사용하는 단계를 포함할 수 있다. 숙주 세포에서 본 출원에 개시된 효소를 코딩하는 폴리뉴클레오티드의 재조합 발현 단계를 포함하는 방법이 본 개시에 포괄된다. 적어도 하나의 BCAA 경로 효소 (예를 들어, LeuDH, KivD, 또는 Adh 효소)를 포함하는 숙주 세포를 이를 필요로 하는 대상체에게 투여하는 단계를 포함하는 방법이 본 개시에 포괄된다. 반응 혼합물 중 하나 이상의 분지쇄 아미노산 (BCAA)을 본 출원에 개시된 BCAA 경로 효소와 반응시키는 단계를 포함하는 시험관내 방법이 또한 본 개시에 포괄된다. 일부 실시형태에서, BCAA 경로 효소는 LeuDH, KivD, 또는 Adh 효소, 또는 이의 조합이다.

[0122]

임의의 하나 이상의 재조합 폴리펩티드 (예를 들어, LeuDH, KivD, Adh, 및/또는 BrnQ)를 코딩하는 핵산은 본 개시에 포괄되고 숙주 세포 내에 포함될 수 있다. 일부 실시형태에서, 핵산은 오피론의 형태로 존재한다. 일부 실시형태에서, 적어도 하나의 리보솜 결합 부위는 핵산에 존재하는 하나 이상의 코딩 서열 사이에 존재한다.

[0123]

일부 실시형태에서, 본 개시에 포괄되는 LeuDH, KivD, Adh, 및/또는 BrnQ 핵산 서열은 중간 또는 고 엄격 조건 하에서 본 개시에서 제공하는 LeuDH, KivD, Adh, 및/또는 BrnQ 핵산 서열과 혼성화하고 생물학적으로 활성인 핵산 서열이다. 예를 들어, 65°C에서 0.2 내지 1 x SSC에 이어서 65°C에서 0.2 x SSC 중 세척의 고엄격 조건 하에

서 LeuDH, KivD, Adh, 및/또는 BrnQ를 코딩하는 핵산과 혼성화되는 핵산을 사용할 수 있다. 실온에서 6 x SSC에 이어서 실온에서 2 x SSC 중 세척의 저엄격 조건 하에서 LeuDH, KivD, Adh, 및/또는 BrnQ를 코딩하는 핵산과 혼성화하는 핵산이 사용될 수 있다. 다른 혼성화 조건은 40℃ 또는 50℃에서 3 x SSC에 이어서, 20℃, 30℃, 40℃, 50℃, 60℃, 또는 65℃에서 1 또는 2 x SSC 중 세척을 포함한다.

[0124] 혼성화는 혼성화의 엄격도를 더 증가시키는, 예를 들어, 10%, 20%, 30% 40% 또는 50%의 포름알데히드의 존재 하에서 수행될 수 있다. 핵산 혼성화의 이론 및 실시는 예를 들어 문헌 [S. Agrawal (ed.) *Methods in Molecular Biology*, volume 20]에 기술되어 있고; 문헌 [Tijssen (1993) *Laboratory Techniques in biochemistry and molecular biology-hybridization with nucleic acid probes*, 예를 들어, part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays," Elsevier, New York]은 핵산 혼성화에 대한 기본 지침을 제공한다. 예시적인 단백질은 LeuDH, KivD, 또는 Adh 단백질 또는 이의 도메인, 예를 들어, 촉매 도메인과 적어도 약 50%, 70%, 80%, 90%, 바람직하게 적어도 약 95%, 보다 더 바람직하게 적어도 약 98% 및 가장 바람직하게 적어도 99% 상동성 또는 동일성을 가질 수 있다. 다른 예시적인 단백질은 LeuDH, KivD, 또는 Adh 핵산, 예를 들어, 본 출원에 기술된 것과 적어도 약 90%, 바람직하게 적어도 약 95%, 보다 더 바람직하게 적어도 약 98% 및 가장 바람직하게 적어도 99% 상동성 또는 동일성인 핵산에 의해 코딩될 수 있다.

[0125] 본 출원에서 기술되는 임의의 하나 이상의 재조합 폴리펩티드 (예를 들어, LeuDH, KivD, Adh 및/또는 BrnQ)를 코딩하는 핵산은 당분야에 공지된 임의의 방법을 통해서 임의의 적절한 벡터에 도입될 수 있다. 예를 들어, 벡터는 바이러스 벡터 (예를 들어, 렌티바이러스, 레트로바이러스, 아데노바이러스, 또는 아데노-연관 바이러스 벡터), 일시적 발현에 적합한 임의의 벡터, 항상성 발현에 적합한 임의의 벡터, 또는 유도성 발현에 적합한 임의의 벡터 (예를 들어, 갈락토스-유도성 또는 독시시클린-유도성 벡터)를 포함하지만, 이에 제한되지 않는, 발현 벡터일 수 있다.

[0126] 일부 실시형태에서, 벡터는 세포에서 자율적으로 복제된다. 일부 실시형태에서, 벡터는 세포 내 염색체에 통합된다. 벡터는 세포에서 복제될 수 있는 재조합 벡터를 생산하기 위해서 본 출원에 기술된 유전자를 함유하는 핵산을 삽입 및 결찰시키도록 제한 엔도뉴클레아제를 통해 절단되는 하나 이상의 엔도뉴클레아제 제한 부위를 함유할 수 있다. 벡터는 전형적으로 DNA로 구성되지만, RNA 벡터도 이용가능하다. 클로닝 벡터는 플라스미드, 포스미드, 파지미드, 바이러스 게놈, 및 인공 염색체를 포함하지만, 이에 제한되지 않는다. 본 출원에서 사용되는 용어 "발현 벡터" 또는 "발현 구성체"는 숙주 세포 (예를 들어, 미생물), 예컨대 효모 세포에서 특정 핵산의 전사를 허용하는 일련의 명시된 핵산 구성요소를 갖는, 재조합적으로 또는 합성적으로 생성된, 핵산 구성체를 의미한다. 일부 실시형태에서, 본 출원에 기술된 유전자의 핵산 서열은 조절 서열에 작동적으로 연결되어서, 일부 실시형태에서, RNA 전사물로서 발현되도록 클로닝 벡터에 삽입된다. 일부 실시형태에서, 벡터는 재조합 벡터가 형질전환되거나 또는 형질감염된 세포를 확인하기 위해서, 본 출원에 기술된 바와 같은 선택 마커같은, 하나 이상의 마커를 함유한다. 일부 실시형태에서, 본 출원에 기술된 유전자의 핵산 서열은 코돈-최적화된다. 코돈 최적화는 코돈-최적화되지 않은 기준 서열에 비해서, 그 사이의 모든 값을 포함하여, 적어도 10%, 적어도 15%, 적어도 20%, 적어도 25%, 적어도 30%, 적어도 35%, 적어도 40%, 적어도 45%, 적어도 50%, 적어도 55%, 적어도 60%, 적어도 65%, 적어도 70%, 적어도 75%, 적어도 80%, 적어도 85%, 적어도 90%, 적어도 95%, 또는 100% 까지 유전자 생성물의 생산을 증가시킬 수 있다.

[0127] 일부 실시형태에서, 본 출원에 기술된 핵산 서열은 플라스미드로 발현된다. 예를 들어, 본 출원에 기술된 핵산 서열은 클로닝 플라스미드로 발현될 수 있다. 본 출원에 기술된 핵산 서열은 일시적 발현을 위한 플라스미드로 발현될 수 있다. 본 출원에 기술된 핵산 서열은 또한 게놈 DNA로 핵산 서열의 도입을 위한 플라스미드로 발현될 수 있다.

[0128] 코딩 서열 및 조절 서열은 코딩 서열 및 조절 서열이 공유적으로 연결되어 코딩 서열의 발현 또는 전사가 조절 서열의 영향 또는 제어 하에 있을 때 "작동적으로 결합" 또는 "작동적으로 연결"되었다고 한다. 코딩 서열이 기능성 단백질로 번역시키려는 경우에, 코딩 서열 및 조절 서열은 5' 조절 서열에서 프로모터의 유도가 코딩 서열이 전사되도록 허용하고 코딩 서열과 조절 서열 간 연결의 속성이 (1) 프레임-시프트 돌연변이의 유도를 일으키지 않거나, (2) 코딩 서열의 전사를 유도하는 프로모터 영역의 능력을 방해하지 않거나, 또는 (3) 단백질로 번역시키려는 해당 RNA 전사물의 능력을 방해하지 않으면 작동적으로 연결되었다고 한다.

[0129] 일부 실시형태에서, 본 출원에 기술된 임의의 하나 이상의 단백질을 코딩하는 핵산은 조절 서열 (예를 들어, 인핸서 서열)의 제어 하에 있다. 일부 실시형태에서, 핵산은 프로모터의 제어 하에 발현된다. 프로모터는 천연 프로모터, 예를 들어 유전자의 발현의 정상 조절을 제공하는, 이의 내생성 환경에서의 유전자의 프로모터일 수 있

다. 대안적으로, 프로모터는 유전자의 천연 프로모터와 상이한 프로모터일 수 있고, 예를 들어, 프로모터는 이의 내생성 상황에서 유전자의 프로모터와 상이하다.

[0130] 일부 실시형태에서, 프로모터는 진핵생물 프로모터이다. 진핵생물 프로모터의 비제한적인 예는 당업자에게 공지된 바와 같은, TDH3, PGK1, PKC1, PDC1, TEF1, TEF2, RPL18B, SSA1, TDH2, PYK1, TP11, GAL1, GAL10, GAL7, GAL3, GAL2, MET3, MET25, HXT3, HXT7, ACT1, ADH1, ADH2, CUP1-1, ENO2, 및 SOD1을 포함한다 (예를 들어, Addgene 웹사이트: blog.addgene.org/plasmids-101-the-promoter-region 참조). 일부 실시형태에서, 프로모터는 원핵생물 프로모터 (예를 들어, 박테리오파지 또는 박테리아 프로모터)이다. 박테리오파지 프로모터의 비제한적인 예는 Pls1con, T3, T7, SP6, 및 PL을 포함한다. 박테리아 프로모터의 비제한적인 예는 Pbad, PmgrB, Ptrc2, PCI857, Plac/ara, Plac/fnr, Ptac, Ptet, Pcmt, 및 Pm을 포함한다.

[0131] 일부 실시형태에서, 프로모터는 유도성 프로모터이다. 본 출원에서 사용되는 "유도성 프로모터"는 분자의 존재 또는 부재에 의해 제어되는 프로모터이다. 이것은 예를 들어 효소의 발현을 제어가능하게 유도시키기 위해 사용될 수 있다. 일부 실시형태에서, 유도성 프로모터가 LeuDH, KivD 및/또는 Adh에 연결되는 경우에, LeuDH, KivD 및/또는 Adh의 발현은 일정 시점에 유도될 수 있거나 또는 유도되지 않을 수 있다. 예를 들어, 일부 실시형태에서, 발현은 류신 소모가 제한되도록 일정 시간 (예를 들어, 세포 성장 동안)에 유도되지 않을 수 있다. 유도성 프로모터의 비제한적인 예는 화학적으로 조절되는 프로모터 및 물리적으로 조절되는 프로모터를 포함한다. 화학적으로 조절되는 프로모터의 경우에, 전사 활성은 하나 이상의 화합물, 예컨대 알콜, 테트라사이클린, 갈락토스, 스테로이드, 금속, 또는 다른 화합물에 의해 조절될 수 있다. 물리적으로 조절되는 프로모터 경우에, 전사 활성은 현상 예컨대 빛 또는 온도에 의해 조절될 수 있다. 테트라사이클린-조절된 프로모터의 비제한적인 예는 언히드로테트라사이클린 (aTc)-반응성 프로모터 및 다른 테트라사이클린-반응성 프로모터 시스템 (예를 들어, 테트라사이클린 리프레서 단백질 (tetR), 테트라사이클린 오퍼레이터 서열 (tetO) 및 테트라사이클린 트랜스활성인자 융합 단백질 (tTA))을 포함한다. 스테로이드-조절된 프로모터의 비제한적인 예는 래트 글루코코르티코이드 수용체, 인간 에스트로겐 수용체, 나방 액티온 수용체를 기반으로 하는 프로모터, 및 스테로이드/레티노이드/갑상선 수용체 슈퍼패밀리로부터의 프로모터를 포함한다. 금속-조절된 프로모터의 비제한적인 예는 메탈로티오네인 (금속 이온에 결합하여 격리시키는 단백질) 유전자로부터 유래된 프로모터를 포함한다. 발병기전-조절된 프로모터의 비제한적인 예는 살리실산, 에틸렌 또는 벤조티아디아졸 (BTH)에 의해 유도되는 프로모터를 포함한다. 온도/열-유도성 프로모터의 비제한적인 예는 열충격 프로모터를 포함한다. 빛-조절된 프로모터의 비제한적인 예는 식물 세포 유래의 빛 반응성 프로모터를 포함한다. 일정 실시형태에서, 유도성 프로모터는 갈락토스-유도성 프로모터이다. 일부 실시형태에서, 유도성 프로모터는 하나 이상의 생리적 조건 (예를 들어, pH, 온도, 방사선, 삼투압, 염수 구배, 세포 표면 결합, 또는 하나 이상의 외인성 또는 내인성 유도제의 농도)에 의해 유도된다. 외인성 유도인자 또는 유도제의 비제한적인 예는 아미노산 및 아미노산 유사체, 당류 및 다당류, 핵산, 단백질 전사 활성인자 및 리프레서, 사이토카인, 독소, 석유-기반 화합물, 금속 함유 화합물, 염, 이온, 효소 기질 유사체, 호르몬 또는 이의 임의 조합을 포함한다.

[0132] 일부 실시형태에서, 프로모터는 항상성 프로모터이다. 본 출원에서 사용되는 "항상성 프로모터"는 유전자의 연속 전사를 허용하는 비조절 프로모터를 의미한다. 항상성 프로모터의 비제한적인 예는 TDH3, PGK1, PKC1, PDC1, TEF1, TEF2, RPL18B, SSA1, TDH2, PYK1, TP11, HXT3, HXT7, ACT1, ADH1, ADH2, ENO2, 및 SOD1을 포함한다.

[0133] 당업자에게 공지된 다른 유도성 프로모터 또는 항상성 프로모터가 또한 본 출원에서 고려된다.

[0134] 유전자 발현에 필요한 조절 서열의 정밀한 속성은 종 또는 세포 유형 간에 다양할 수 있지만, 일반적으로 필요에 따라, 각각 전사 및 번역의 개시에 관여되는 5' 비-전사 및 5' 비-번역 서열, 예컨대 TATA 박스, 캡핑 서열, CAAT 서열 등을 포함한다. 특히, 이러한 5' 비-전사 조절 서열은 작동적으로 연결된 유전자의 전사 제어를 위한 프로모터 서열을 포함하는 프로모터 영역을 포함하게 될 것이다. 조절 서열은 또한 인핸서 서열 또는 상류 활성화자 서열을 포함할 수 있다. 본 출원에 개시된 벡터는 5' 리더 또는 신호 서열을 포함할 수 있다. 조절 서열은 또한 종결자 서열을 포함할 수 있다. 일부 실시형태에서, 종결자 서열은 전사 동안 DNA 내 유전자의 끝을 표시한다. 이중성 유기체에서 본 출원에 기술된 하나 이상의 유전자의 발현을 유도하는데 적합한 하나 이상의 적절한 벡터의 선택 및 디자인은 당업자의 능력 및 재량 내에 있다.

[0135] 발현에 필수적인 구성요소를 함유하는 발현 벡터는 상업적으로 입수가 가능하고 당업자에게 공지되어 있다 (예를 들어, 문헌 [Sambrook et al., Molecular Cloning: A Laboratory Manual, Fourth Edition, Cold Spring Harbor Laboratory Press, 2012] 참조).

[0136] **숙주 세포**

- [0137] 개시된 방법 및 조성물 및 숙주 세포는 이. 콜라이 세포 (예를 들어, 이. 콜라이 니슬 1917)를 예로 들지만, 일부 실시형태에서, 다른 숙주 세포에 적용가능하다.
- [0138] 적합한 숙주 세포는 효모 세포, 박테리아 세포, 조류 세포, 식물 세포, 진균 세포, 곤충 세포, 및 포유동물 세포를 포함한, 동물 세포를 포함하지만, 이에 제한되지 않는다. 예시적인 일 실시형태에서, 적합한 숙주 세포는 이. 콜라이 (예를 들어, New England BioLabs (Ipswich, Mass)에서 입수가능한 Shuffle™ 컴피턴트 이. 콜라이 또는 독일 생물자원 센터 (German Collection of Microorganisms and cell Cultures)에서 입수가능한 이. 콜라이 니슬 1917 (DSMZ Braunschweig, 이. 콜라이 DSM 6601))를 포함한다.
- [0139] 적합한 효모 숙주 세포는 칸디다 (*Candida*), 한세놀라 (*Hansenula*), 사카로마이세스 (*Saccharomyces*), 스킴조사카로마이세스 (*Schizosaccharomyces*), 피키아 (*Pichia*), 클루이베로마이세스 (*Kluyveromyces*), 및 야로위아 (*Yarrowia*)를 포함하지만, 이에 제한되지 않는다. 일부 실시형태에서, 효모 세포는 한세놀라 폴리모르파 (*Hansenula polymorpha*), 사카로마이세스 세레비시아에 (*Saccharomyces cerevisiae*), 사카로마이세스 칼스베르겐시스 (*Saccaromyces carlsbergensis*), 사카로마이세스 디아스타티쿠스 (*Saccharomyces diastaticus*), 사카로마이세스 노르벤시스 (*Saccharomyces norbensis*), 사카로마이세스 클루이베리 (*Saccharomyces kluyveri*), 스킴조사카로마이세스 폼베 (*Schizosaccharomyces pombe*), 피키아 파스토리스 (*Pichia pastoris*), 피키아 핀란드카 (*Pichia finlandica*), 피키아 트레할로필라 (*Pichia trehalophila*), 피키아 코다마에 (*Pichia kodamae*), 피키아 멤브라나에피엔스 (*Pichia membranaefaciens*), 피키아 오펜티아에 (*Pichia opuntiae*), 피키아 써모톨레란스 (*Pichia thermotolerans*), 피키아 살릭타리아 (*Pichia salictaria*), 피키아 쿠에르쿠움 (*Pichia quercuum*), 피키아 피지페리 (*Pichia pijperi*), 피키아 스티피티스 (*Pichia stipitis*), 피키아 메타놀리카 (*Pichia methanolica*), 피키아 안구스타 (*Pichia angusta*), 클루이베로마이세스 락티스 (*Kluyveromyces lactis*), 칸디다 알비칸스 (*Candida albicans*), 또는 야로위아 리폴리티카 (*Yarrowia lipolytica*) 이다.
- [0140] 일부 실시형태에서, 효모 균주는 산업용 배수체 효모 균주이다. 진균 세포의 다른 비제한적인 예는 아스퍼질러스 (*Aspergillus*) spp., 페니실리움 (*Penicillium*) spp., 푸사리움 (*Fusarium*) spp., 리조푸스 (*Rhizopus*) spp., 아크레모니움 (*Acremonium*) spp., 뉴로스포라 (*Neurospora*) spp., 솔다리아 (*Sordaria*) spp., 마그나포르테 (*Magnaporthe*) spp., 알로마이세스 (*Allomyces*) spp., 우스틸라고 (*Ustilago*) spp., 보트리티스 (*Botrytis*) spp., 및 트리코더마 (*Trichoderma*) spp.로부터 수득된 세포를 포함한다.
- [0141] 일정 실시형태에서, 숙주 세포는 조류 세포 예컨대 클라미도모나스 (*Chlamydomonas*) (예를 들어, 씨. 레인하르티 (*C. Reinhardtii*)) 및 포르미디움 (*Phormidium*) (*P. sp.* ATCC29409)이다.
- [0142] 다른 실시형태에서, 숙주 세포는 원핵생물 세포이다. 적합한 원핵생물 세포는 그람 양성, 그람 음성, 및 그람-가변성 박테리아 세포를 포함한다. 숙주 세포는 아그로박테리움 (*Agrobacterium*), 알리시클로바실러스 (*Alicyclobacillus*), 아나바에나 (*Anabaena*), 아나시스티스 (*Anacystis*), 아시네토박터 (*Acinetobacter*), 아시도써머스 (*Acidothermus*), 아르트로박터 (*Arthrobacter*), 아조박터 (*Azobacter*), 바실러스 (*Bacillus*), 비피도박테리움 (*Bifidobacterium*), 브레비박테리움 (*Brevibacterium*), 부티리비브리오 (*Butyrivibrio*), 부크네라 (*Buchnera*), 캄페스트리스 (*Campestris*), 캄필로박터 (*Campylobacter*), 클로스트리듐 (*Clostridium*), 코리네박테리움 (*Corynebacterium*), 크로마티움 (*Chromatium*), 코프로코커스 (*Coprococcus*), 에스케리치아 (*Escherichia*), 엔테로코커스 (*Enterococcus*), 엔테로박터 (*Enterobacter*), 어위니아 (*Erwinia*), 푸소박테리움 (*Fusobacterium*), 파에칼리박테리움 (*Faecalibacterium*), 프란시셀라 (*Francisella*), 플라보박테리움 (*Flavobacterium*), 지오바실러스 (*Geobacillus*), 헤모필러스 (*Haemophilus*), 헬리코박터 (*Helicobacter*), 클렙시엘라 (*Klebsiella*), 락토바실러스 (*Lactobacillus*), 락토코커스 (*Lactococcus*), 일리오박터 (*Ilyobacter*), 미크로코커스 (*Micrococcus*), 마이크로박테리움 (*Microbacterium*), 메소리조비움 (*Mesorhizobium*), 메틸로박테리움 (*Methylobacterium*), 메틸로박테리움 (*Methylobacterium*), 미코박테리움 (*Mycobacterium*), 네이세리아 (*Neisseria*), 판토에아 (*Pantoea*), 슈도모나스 (*Pseudomonas*), 프로클로로코커스 (*Prochlorococcus*), 로도박터 (*Rhodobacter*), 로도슈도모나스 (*Rhodopseudomonas*), 로도슈도모나스 (*Rhodospseudomonas*), 로세부리아 (*Roseburia*), 로도스피릴럼 (*Rhodospirillum*), 로도코커스 (*Rhodococcus*), 세네데스무스 (*Scenedesmus*), 스트렙토마이세스 (*Streptomyces*), 스트렙토코커스 (*Streptococcus*), 시네코커스 (*Syneccoccus*), 사카로모노스포라 (*Saccharomonospora*), 사카로폴리스포라 (*Saccharopolyspora*), 스태필로코커스 (*Staphylococcus*), 세라티아 (*Serratia*), 살모넬라 (*Salmonella*), 시겔라 (*Shigella*), 써모아나에로박테리움 (*Thermoanaerobacterium*), 트로페리마 (*Tropheryma*), 툴라렌시스 (*Tularensis*), 테머쿨라 (*Temecula*), 써모시네코코커스 (*Thermosynechococcus*), 써모코커스 (*Thermococcus*), 우레아플라스마 (*Ureaplasma*), 잔토모나스 (*Xanthomonas*), 자일렐라 (*Xylella*), 여시니아 (*Yersinia*), 및 자이모모나스 (*Zymomonas*)의 종일 수 있지만,

이에 제한되지 않는다.

- [0143] 일부 실시형태에서, 박테리아 숙주 균주는 산업용 균주이다. 수많은 박테리아 산업 균주가 공지되어 있고 본 출원에 기술된 방법 및 조성물에 적합하다.
- [0144] 일부 실시형태에서, 박테리아 숙주 세포는 아그로박테리움 (*Agrobacterium*) 종 (예를 들어, 에이. 라디오박터 (*A. radiobacter*), 에이. 리조게네스 (*A. rhizogenes*), 에이. 루비 (*A. rubi*)), 아르트로박터 (*Arthrobacter*) 종 (예를 들어, 에이. 아우레센스 (*A. aureus*), 에이. 시트레우스 (*A. citreus*), 에이. 글로보포르미스 (*A. globiformis*), 에이. 히드로카르보글루타미커스 (*A. hydrocarboglutamicus*), 에이. 미소렌스 (*A. mysorens*), 에이. 니코티아나에 (*A. nicotianae*), 에이. 파라피네우스 (*A. paraffineus*), 에이. 프로토포니아에 (*A. protophoniae*), 에이. 로세오파라피네스 (*A. roseoparaffinus*), 에이. 술폴레우스 (*A. sulfureus*), 에이. 우레아파시엔스 (*A. ureafaciens*)), 바실러스 (*Bacillus*) 종 (예를 들어, 비. 투링지엔시스 (*B. thuringiensis*), 비. 안트라시스 (*B. anthracis*), 비. 메가테리움 (*B. megaterium*), 비. 서브틸리스 (*B. subtilis*), 비. 렌투스 (*B. lentus*), 비. 서큘러스 (*B. circularis*), 비. 푸밀러스 (*B. pumilus*), 비. 라우투스 (*B. lautus*), 비. 코아굴란스 (*B. coagulans*), 비. 브레비스 (*B. brevis*), 비. 퍼머스 (*B. firmus*), 비. 알카오피우스 (*B. alkaophilus*), 비. 리체니포르미스 (*B. licheniformis*), 비. 클라우시이 (*B. clausii*), 비. 스테아로써모필러스 (*B. stearothermophilus*), 비. 할로두란스 (*B. halodurans*) 및 비. 아밀로리케파시엔스 (*B. amyloliquefaciens*))의 것이다. 특정 실시형태에서, 숙주 세포는 비. 서브틸리스 (*B. subtilis*), 비. 푸밀러스 (*B. pumilus*), 비. 리체니포르미스 (*B. licheniformis*), 비. 메가테리움 (*B. megaterium*), 비. 클라우시이 (*B. clausii*), 비. 스테아로써모필러스 (*B. stearothermophilus*) 및 비. 아밀로리케파시엔스 (*B. amyloliquefaciens*)를 포함하지만, 이에 제한되지 않는 산업용 바실러스 균주일 것이다. 일부 실시형태에서, 숙주 세포는 산업용 클로스트리듐 종 (예를 들어, 씨. 아세토부틸리컴 (*C. acetobutylicum*), 씨. 테타니 (*C. tetani*) E88, 씨. 리투세부렌스 (*C. lituseburens*), 씨. 사카로부틸리컴 (*C. saccharobutylicum*), 씨. 퍼프린젠스 (*C. perfringens*), 씨. 베이제린키이 (*C. beijerinckii*))일 것이다. 일부 실시형태에서, 숙주 세포는 산업용 코리네박테리움 종 (예를 들어, 씨. 글루타미컴 (*C. glutamicum*), 씨. 아세트아시도필럼 (*C. acetoacidophilum*))일 것이다. 일부 실시형태에서, 숙주 세포는 산업용 에스케리치아 종 (예를 들어, 이. 콜라이 (*E. coli*))일 것이다. 일부 실시형태에서, 숙주 세포는 산업용 어위니아 종 (예를 들어, 이. 우레도보라 (*E. uredovora*), 이. 카로토보라 (*E. carotovora*), 이. 아나나스 (*E. ananas*), 이. 허비콜라 (*E. herbicola*), 이. 푼타타 (*E. punctata*), 이. 테레우스 (*E. terreus*))일 것이다. 일부 실시형태에서, 숙주 세포는 산업용 판토에아 종 (예를 들어, 피. 시트레아 (*P. citrea*), 피. 아글로머란스 (*P. agglomerans*))일 것이다. 일부 실시형태에서, 숙주 세포는 산업용 슈도모나스 종 (예를 들어, 피. 푸티다 (*P. putida*), 피. 에어루지노사 (*P. aeruginosa*), 피. 메발로니이 (*P. mevalonii*))일 것이다. 일부 실시형태에서, 숙주 세포는 산업용 스트렙토코커스 종 (예를 들어, 에스. 에퀴시밀레스 (*S. equisimiles*), 에스. 피오게네스 (*S. pyogenes*), 에스. 우베리스 (*S. uberis*))일 것이다. 일부 실시형태에서, 숙주 세포는 산업용 스트렙토마이세스 종 (예를 들어, 에스. 암보파시엔스 (*S. ambofaciens*), 에스. 아크로모게네스 (*S. achromogenes*), 에스. 아버미틸리스 (*S. avermitilis*), 에스. 코엘리콜러 (*S. coelicolor*), 에스. 아우레오파시엔스 (*S. aureofaciens*), 에스. 아우레우스 (*S. aureus*), 에스. 푼지시디커스 (*S. fungicidicus*), 에스. 그리세우스 (*S. griseus*), 에스. 리비단스 (*S. lividans*))일 것이다. 일부 실시형태에서, 숙주 세포는 산업용 자이모모나스 종 (예를 들어, 지. 모빌리스 (*Z. mobilis*), 지. 리폴리티카 (*Z. lipolytica*)) 등일 수 있다.
- [0145] 본 개시는 또한 포유동물 세포, 예를 들어, 인간 (293, HeLa, WI38, PER.C6 및 바우스 흑색종 세포 포함), 마우스 (3T3, NS0, NS1, Sp2/0 포함), 햄스터 (CHO, BHK), 원숭이 (COS, FRhL, Vero), 및 하이브리도마 세포주를 포함한, 다양한 동물 세포 유형과 사용하기에 적합하다.
- [0146] 다양한 실시형태에서, 원핵생물 및 진핵생물 균주 둘 모두를 포함하여 본 개시의 실시에서 사용될 수 있는 균주이고, 수많은 생물자원 센터 예컨대 미국 생물자원 센터 (American Type Culture Collection) (ATCC), 독일 생물자원 센터 (Deutsche Sammlung von Mikroorganismen and Zellkulturen GmbH) (DSMZ), 네덜란드 곰팡이 자원 센터 (Centraalbureau Voor Schimmelcultures) (CBS), 및 농업 특허 자원 센터, 북부 연구소 (Agricultural Research Service Patent Culture Collection, Northern Regional Research Center) (NRRL)에서 공공으로 쉽게 접근가능하다. 본 개시는 또한 다양한 식물 세포 유형으로 사용에 적합하다.
- [0147] 본 출원에서 사용되는 용어 "세포"는 단일 세포 또는 세포의 개체군, 예컨대 동일한 세포주 또는 균주에 속하는 세포의 개체군을 의미할 수 있다. 단수 용어 "세포"의 사용은 세포의 개체군이 아닌 단일 세포를 명시적으로 의

미하는 것으로 해석되어서는 안된다. 숙주 세포는 야생형 대응물에 비해 유전자 변형을 포함할 수 있다.

- [0148] 본 출원에 기술된 임의의 하나 이상의 재조합 폴리펩티드 (예를 들어, LeuDH, KivD, Adh 효소 및/또는 BrnQ)를 코딩하는 벡터는 당분야에 공지된 임의 방법을 사용하여 적합한 숙주 세포에 도입시킬 수 있다. 숙주 세포는 당업자가 이해하는 바와 같이 적합한 임의의 조건 하에 배양될 수 있다. 예를 들어, 당분야에 공지된 임의 배지, 온도, 및 인큐베이션 조건이 사용될 수 있다. 유도성 벡터를 보유하는 숙주 세포 경우에, 세포는 발현을 촉진시키기 위해 적절한 유도제와 함께 배양될 수 있다.
- [0149] 본 출원에 개시된 임의의 세포는 핵산의 접촉 및/또는 통합 이전, 그 동안, 및/또는 그 이후에 임의 조성 및 임의 유형 (풍부 또는 최소)의 배지에서 배양될 수 있다. 배양 조건 또는 배양 과정은 당업자가 이해하는 바와 같이 통상의 실험을 통해 최적화될 수 있다. 일부 실시형태에서, 선택된 배지는 다양한 성분이 보충된다. 일부 실시형태에서, 보충 성분의 양 및 농도는 최적화된다. 일부 실시형태에서, 배지 및 성장 조건의 다른 양태 (예를 들어, pH, 온도 등)는 통상의 실험을 통해 최적화된다. 일부 실시형태에서, 하나 이상의 보충 성분이 배지에 보충되는 빈도, 및 세포가 배양되는 시간량이 최적화된다.
- [0150] 본 출원에서 기술되는 세포의 배양은 당분야에서 공지되고 사용되는 배양 용기에서 수행될 수 있다. 일부 실시형태에서, 통기형 반응 용기 (예를 들어, 교반식 탱크 반응기)가 세포를 배양하는데 사용된다. 일부 실시형태에서, 생물반응기 또는 발효기가 세포를 배양하는데 사용된다. 따라서, 일부 실시형태에서, 세포는 발효배양에서 사용된다. 본 출원에서 사용되는 용어 "생물반응기" 및 "발효기"는 상호교환적으로 사용되고 생유기체 또는 생유기체의 일부를 포함하는, 생물학적, 생화학적, 및/또는 화학적 반응이 일어나는, 인클로저, 또는 부분 인클로저를 의미한다. "대규모 생물반응기" 또는 "산업적 규모 생물반응기"는 상업적 또는 준-상업적 규모로 생성물을 생성시키는데 사용되는 생물반응기이다. 대규모 생물반응기는 전형적으로 리터 범위, 수백 리터, 수천 리터 이상의 부피를 갖는다.
- [0151] 일부 실시형태에서, 생물반응기는 세포 (예를 들어, 박테리아 세포) 또는 세포 배양물 (예를 들어, 박테리아 세포 배양물), 예컨대 본 출원에 기술된 세포 또는 세포 배양물을 포함한다. 일부 실시형태에서, 생물반응기는 단리된 미생물의 포자 및/또는 휴면 세포 유형 (예를 들어, 건조 상태에서 휴면인 세포)을 포함한다.
- [0152] 생물반응기의 비제한적인 예는 교반식 탱크 발효기, 회전식 혼합 장치, 케모스타트에 의해 교반되는 생물반응기, 진탕 장치로 교반되는 생물반응기, 에어리프트 발효기, 충전층 반응기, 고정층 반응기, 유동층 생물반응기, 파동 유발 교반을 적용한 생물반응기, 롤러병, 및 중공 섬유 생물반응기, 롤러 장비 (예를 들어, 벤치탑, 카트-장착, 및/또는 자동화 버라이어티), 수직-적층 플레이트, 스피너 플라스크, 교반식 또는 진동식 플래스크, 진탕 다중-웰 플레이트, MD 병, T-플래스크, 루 (Roux) 병, 다중-표면 조직 배양 전파기, 변형식 발효기, 및 코팅된 비드 (예를 들어, 세포 부착을 방지하기 위해 혈청 단백질, 니트로셀룰로스, 또는 카르복시메틸셀룰로스로 코팅된 비드)를 포함한다.
- [0153] 일부 실시형태에서, 생물반응기는 세포 (예를 들어, 박테리아 세포)가 이동하는 액체 및/또는 가스 버블과 접촉하는 세포 배양 시스템을 포함한다. 일부 실시형태에서, 세포 또는 세포 배양물은 현탁 성장된다. 다른 실시형태에서, 세포 또는 세포 배양물은 고정층 담체에 부착된다. 담체 시스템의 비제한적인 예는 마이크로담체 (다공성 또는 비-다공성일 수 있는 예를 들어, 중합체구, 마이크로비드, 및 마이크로디스크), 특별한 화학기 (예를 들어, 4차 아민 기)가 충전된 가교된 비드 (예를 들어, 텍스트란), 비다공성 중합체 섬유에 포획된 세포를 포함하는 2D 마이크로담체, 3D 담체 (예를 들어, 캐리어 섬유, 중공 섬유, 다중카트리지 반응기, 및 다공성 섬유를 포함할 수 있는 반투과성막), 이온 교환 능력이 감소된 마이크로담체, 캡슐화 세포, 모세관, 및 응집체를 포함한다. 일부 실시형태에서, 담체는 텍스트란, 젤라틴, 유리, 또는 셀룰로스같은 재료로 제작된다.
- [0154] 일부 실시형태에서, 산업적 규모의 과정은 연속, 반-연속, 또는 비-연속 방식으로 작업된다. 작업 방식의 비제한적인 예는 회분식, 유가식, 확장형 회분식, 반복형 회분식, 추출/충전, 회전-벽, 스피닝 플라스크, 및/또는 관류 작업 방식을 포함한다. 일부 실시형태에서, 생물반응기는 기질 원료, 예를 들어, 탄수화물 공급원의 연속 또는 반-연속 보충 및/또는 생물반응기로부터, 생성물의 연속 또는 반-연속 분리를 허용한다.
- [0155] 일부 실시형태에서, 생물반응기 또는 발효기는 반응 매개변수를 측정하고/하거나 조정하기 위한 센서 및/또는 제어 시스템을 포함한다. 반응 매개변수의 비제한적인 예는 생물학적 매개변수 (예를 들어, 성장 속도, 세포 크기, 세포수, 세포 밀도, 세포 유형, 또는 세포 상태 등), 화학적 매개변수 (예를 들어, pH, 산화환원 전위, 반응 기질 및/또는 생성물의 농도, 용존 가스의 농도, 예컨대 산소 농도 및 CO₂ 농도, 영양소 농도, 대사산물 농도, 올리고펩티드의 농도, 아미노산의 농도, 비타민의 농도, 호르몬의 농도, 첨가제의 농도, 혈청 농도, 이온

강도, 이온의 농도, 상대 습도, 물농도, 삼투압 농도, 다른 화학물, 예를 들어 완충제, 보강제 또는 반응 부산물의 농도), 물리적/기계적 매개변수 (예를 들어, 밀도, 전도율, 교반도, 압력, 및 유속, 전단 응력, 전단율, 점도, 색상, 탁도, 흡광도, 혼합율, 전환율을 비롯하여, 열역학적 매개변수, 예컨대 온도, 및 강도/품질 등)를 포함한다. 본 출원에 기술된 매개변수를 측정하기 위한 센서는 관련 기계 및 전자 분야의 당업자에게 충분히 공지되어 있다. 본 출원에 기술된 센서로부터 투입될 기반으로 생물반응기 중 매개변수를 조정하기 위한 제어 시스템은 생물반응기 조작의 당업자에게 충분히 공지되어 있다.

[0156] 일부 실시형태에서, 방법은 회분식 발효배양 (예를 들어, 진탕 플라스크 발효배양)을 포함한다. 회분식 발효배양 (예를 들어, 진탕 플라스크 발효배양)에 대한 일반 고려사항은 산소 및 포도당의 수준을 포함한다. 예를 들어, 회분식 발효배양 (예를 들어, 진탕 플라스크 발효배양)은 산소 및 포도당이 제한될 수 있어서, 일부 실시형태에서, 잘-디자인된 유가식 발효배양을 수행하는 균주의 능력은 과소평가된다. 또한, 최종 생성물은 가용성, 독성, 세포 축적 및 분비의 관점에서 기질과 일부 편차를 나타낼 수 있고 일부 실시형태에서 상이한 발효배양 동역학을 가질 수 있다.

[0157] 일부 실시형태에서, 본 개시의 세포는 생체내에서 류신을 소모하도록 조정된다. 일부 실시형태에서, 세포는 이소펜타놀로의 전환을 통해서 류신 소모를 위한 하나 이상의 효소 (예를 들어, LeuDH, KivD, 및/또는 Adh)를 생산하도록 조정된다. 이러한 실시형태에서, 효소는 시험관내 또는 생체의 과정으로 생물전환을 통해서 류신의 소모를 위한 반응을 촉매할 수 있다.

[0158] 본 개시의 임의의 단백질 또는 효소는 숙주 세포에서 발현될 수 있다. 본 출원에서 사용되는, 숙주 세포는 (예를 들어, 본 출원에 기술된 바와 같은 단백질 또는 효소를 코딩하는) 적어도 하나의 이중성 폴리뉴클레오티드를 발현하는데 사용될 수 있는 세포이다. 폴리뉴클레오티드, 예컨대 유전자를 포함하는 폴리뉴클레오티드에 대한 용어 "이중성"은 용어 "외생성" 및 용어 "재조합"과 상호교환적으로 사용되고 생물학적 시스템에 인공적으로 공급된 폴리뉴클레오티드; 생물학적 시스템 내에서 변형된 폴리뉴클레오티드, 또는 그의 발현 또는 조절이 생물학적 시스템 내에서 조작된 폴리뉴클레오티드를 의미한다. 숙주 세포에 도입되거나 또는 그에서 발현되는 이중성 폴리뉴클레오티드는 숙주 세포와 상이한 유기체 또는 종에서 기원하는 폴리뉴클레오티드일 수 있거나, 또는 합성 폴리뉴클레오티드일 수 있거나, 또는 숙주 세포와 동일한 유기체 또는 종에서 역시 내생적으로 발현되는 폴리뉴클레오티드일 수 있다. 예를 들어, 숙주 세포에서 내생적으로 발현되는 폴리뉴클레오티드는 숙주 세포 내에서 비-천연적으로 놓이게 되는 경우; 안정하게 또는 일시적으로 숙주 세포에서 재조합적으로 발현되는 경우; 숙주 세포 내에서 변형되는 경우; 숙주 세포 내에서 선택적으로 편집되는 경우; 숙주 세포 내에서 천연적으로 발생되는 카피수와 상이한 카피수로 발현되는 경우; 또는 예컨대 폴리뉴클레오티드의 발현을 제어하는 조절 영역을 조작하여, 숙주 세포 내에서 비-천연적인 방식으로 발현하는 경우에 이중성으로 간주될 수 있다. 일부 실시형태에서, 이중성 폴리뉴클레오티드는 숙주 세포에서 내생적으로 발현되지만 그의 발현이 폴리뉴클레오티드의 발현을 천연적으로 조절하지 않는 프로모터에 의해 구동되는 폴리뉴클레오티드이다. 다른 실시형태에서, 이중성 폴리뉴클레오티드는 숙주 세포에서 내생적으로 발현되지만 그의 발현이 폴리뉴클레오티드의 발현을 천연적으로 조절하는 프로모터에 의해 구동되는 폴리뉴클레오티드이지만, 프로모터 또는 다른 조절 영역이 변형되어 있다. 일부 실시형태에서, 프로모터는 재조합적으로 활성화되거나 또는 억제된다. 예를 들어, 유전자-편집 기반 기술은 내생성 프로모터를 포함하여, 프로모터로부터, 내생성 폴리뉴클레오티드를 포함하는, 폴리뉴클레오티드의 발현을 조절하는데 사용될 수 있다. 예를 들어, 문헌 [Chavez *et al.*, Nat Methods. 2016 Jul; 13(7): 563-567]을 참조한다. 이중성 폴리뉴클레오티드는 기준 폴리뉴클레오티드 서열과 비교하여 돌연변이체 서열 또는 야생형 서열을 포함할 수 있다.

[0159] 임의의 적합한 숙주 세포는 진핵생물 세포 또는 원핵생물 세포를 포함하는, 본 출원에 개시된 임의의 재조합 폴리펩티드 (예를 들어, LeuDH, KivD, 및/또는 Adh)를 생산하는데 사용될 수 있다.

[0160] 조성물

[0161] 본 개시는 본 출원에 기술된 숙주 세포 (예를 들어, LeuDH, KivD, 및 Adh로 이루어진 군으로부터 선택되는 적어도 하나의 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포) 또는 본 출원에 기술된 하나 이상의 효소 (예를 들어, LeuDH, KivD, 및/또는 Adh), 및 경우에 따라, 약학적으로 허용되는 부형제를 포함하는, 약학 조성물을 포함한다, 조성물을 제공한다.

[0162] 일정 실시형태에서, 본 출원에 기술된 숙주 세포는 조성물, 예컨대 약학 조성물 중에 유효량으로 제공된다. 일정 실시형태에서, 본 출원에 기술된 하나 이상의 효소는 조성물, 예컨대 약학 조성물 중에 유효량으로 제공한다. 일정 실시형태에서, 유효량은 치료적 유효량이다. 일정 실시형태에서, 유효량은 예방학적

유효량이다. 일부 실시형태에서, 유효량은 MSUD의 하나 이상의 증상을 치료하거나 또는 경감시키는데 충분한 양이다.

[0163] 일정 실시형태에서, 대상체는 동물이다. 일정 실시형태에서, 대상체는 인간이다. 다른 실시형태에서, 대상체는 인간 이외의 동물이다. 일정 실시형태에서, 대상체는 포유동물이다. 일정 실시형태에서, 대상체는 인간 이외의 포유동물이다. 일부 실시형태에서, 대상체는 비-포유동물이다. 일정 실시형태에서, 대상체는 가축, 예컨대 개, 고양이, 소, 돼지, 말, 양, 닭 또는 염소이다. 일정 실시형태에서, 대상체는 반려 동물, 예컨대 개 또는 고양이이다. 일정 실시형태에서, 대상체는 가축, 예컨대 소, 돼지, 말, 양, 닭, 또는 염소이다. 일정 실시형태에서, 대상체는 동물원 동물이다. 다른 실시형태에서, 대상체는 연구 동물, 예컨대 설치류 (예를 들어, 마우스, 래트), 개, 돼지, 또는 인간 이외의 영장류이다.

[0164] 본 출원에 기술된 조성물, 예컨대 약학 조성물은 당분야에 공지된 임의 방법으로 제조될 수 있다. 일반적으로, 이러한 제조 방법은 본 출원에 기술된 화합물 (예를 들어, "활성 성분")을 담체 또는 부형제, 및/또는 하나 이상의 다른 보조 성분과 혼합되게 하는 단계, 및 이어서 필요하고/하거나 바람직하다면, 바람직한 단일 단위 용량 또는 다수 단위 용량으로 생성물을 성형 및/또는 포장하는 단계를 포함한다.

[0165] **방법**

[0166] 일부 양태에서, 본 개시는 숙주 세포를 사용하는 방법을 제공한다. 일부 실시형태에서, 본 개시는 본 출원에 기술된 숙주 세포 (예를 들어, LeuDH, KivD, 및 Adh로 이루어진 군으로부터 선택되는 적어도 하나의 효소를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포)를 배양하는 단계를 포함하는 방법을 제공한다. 세포를 배양하기 위한 방법은 본 출원의 다른 곳에 기술되어 있다. 일부 실시형태에서, 본 개시는 본 출원에 기술된 숙주 세포 (예를 들어, LeuDH, KivD, 및 Adh를 코딩하는 이중성 폴리뉴클레오티드를 포함하는 숙주 세포)를 배양하는 단계를 포함하는 류신으로부터 이소펜탄올을 제조하는 방법을 제공한다. 일부 실시형태에서, 제조 및 배양은 생체 내에서, 예를 들어, 숙주 세포가 투여된 인간 대상체에서, 일어난다. 일부 실시형태에서, 제조는 생체외에서, 예를 들어, 시험관내 세포 배양 환경에서 일어난다. 본 출원에 기술된 조성물, 세포, 효소, 및 방법은 또한 분지쇄 아미노산 (예를 들어, 류신, 이소류신, 및 발린)의 축적이 존재할 수 있는 임의 적용분야를 포함하여 산업적 상황에서 적용가능하다.

[0167] 본 발명은 하기 실시예를 통해 더욱 예시하지만, 임의 방식으로 제한하는 것으로 해석되어서는 안된다. 본 출원 전반에서 인용되는 모든 참조 (문헌 참조, 발행 특허, 공개 특허 출원, 및 계류중 특허 출원 포함)의 전체 내용은 본 명세서에서 명확하게 참조로 편입된다. 본 출원에 편입된 참조는 그의 정의가 본 개시에 정의된 바와 동일한 용어의 정의와 모순되거나 또는 양립하지 않으면, 본 출원의 용어에 부여된 의미가 우선될 것이다. 그러나, 본 출원에서 인용되는 임의 참조, 논문, 공개물, 특허, 특허 공개물, 및 특허 출원의 언급은 그들이 유효한 선행 기술을 구성하거나 또는 전세계 임의 국가에서 공통 일반 지식의 일부를 형성한다는 제안의 임의 형태 또는 승인으로서 간주되어서는 안된다.

[0168] **실시예**

[0169] 본 출원에 기술된 본 발명을 보다 완전히 이해하기 위해서, 하기 실시예가 기재된다. 본 출원에 기술된 실시예는 본 출원에서 제공하는 시스템 및 방법을 예시하기 위해 제공되며 임의 방식으로 그들 범주를 제한하려는 것으로 해석되어서는 안된다.

[0170] **실시예 1: 효소 라이브러리 디자인 및 합성**

[0171] 재료 및 방법

[0172] **메타게놈 효소 발굴**

[0173] 기계-학습-기반 생물정보학 도구를 사용하여 공공 서열 데이터베이스 (함께 UniProt으로 알려진, SwissProt 및 TrEMBL)에서 각각 3가지 바람직한 활성 (류신 데히드로게나제, 1.4.1.9; 케토이소발레이트 데카르복실라제, 4.1.1.1; 및 알콜 데히드로게나제 1.1.1.1)에 대한 효소 후보를 동정하였다. LeuDH 및 Adh 경우, 서열 다양성은 이전에 개발된 알고리즘을 사용해 최대화시켰다. KivD 경우, 계층화된 샘플채취 접근법을 사용하였다. 효소 후보의 총 개수는 1175 LeuDH 서열, 1296 KivD 서열 및 1177 Adh 서열이었다.

[0174] **추론적 효소 디자인**

[0175] LeuDH 및 Adh 경우, 효소-전이 상태 복합체의 분자 모델은 로제타 소프트웨어를 사용하여 구축되었고, 20개 아

미노산 각각에 대한 활성 부위 잔기의 체계적 돌연변이를 디자인하였다.

[0176] **라이브러리 합성**

[0177] LeuDH, KivD, 및 Adh 효소 전부에 대한 DNA 서열은 이. 콜라이에서의 발현을 위해 코돈 최적화되었다. 코딩 서열은 T7 프로모터의 제어 하에 있는 유도성 이. 콜라이 발현 벡터로 합성되었다.

[0178] **결과**

[0179] 류신-소모 분지쇄 아미노산 (BCAA) 경로를 개선시키기 위해서, 원형 균주 (1980, SYN1980로도 공지됨)의 부모 효소에 비해서 우수한 활성을 갖는 LeuDH, KivD, 및 Adh 효소를 동정하기 위한 실험을 수행하였고, 부모 균주는 바실러스 세레우스 LeuDH, 락토코커스 락티스 KivD, 및 사카로마이세스 세레비지아에 ADH2를 포함하였다. 원형 균주는 또한 분지쇄 아미노산, 예컨대 류신을 세포로 수송할 수 있는 분지쇄 아미노산에 대한 수송체인, 이. 콜라이 유래의 BrnQ를 포함하였다. 부모 LeuDH 효소는 류신 이외에도 발린 및 이소류신을 탈아미노화시키는, 기질 난잡성을 나타내었다. BCAA 경로에 의한 류신의 특이적 소모를 개선시키기 위해서, 경로 디자인에 대한 추가 목표는 발린 (Val) 및 이소류신 (Ile)에 비해서 증가된 특이성을 갖는 LeuDH 효소를 동정하는 것이었다.

[0180] 2가지 상보적 접근법을 사용하여 각각의 효소 패밀리 (LeuDH, KivD, 및 Adh)에 대한 라이브러리를 디자인하는데 사용되었다: 메타게놈 공급 및 추론적 디자인 (표 2). 각 효소의 경우에, >1000 효소의 메타게놈 라이브러리를 디자인하여 서열 데이터베이스에서 입수가능한 전체 메타게놈 서열 스페이스를 샘플채취하였다 (도 1a-1c). LeuDH 및 Adh 라이브러리 경우에, 입수가능한 구조 데이터는 비. 세레우스 LeuDH 및 에스. 세레비지아에 Adh 효소의 추론적 디자인에 사용되었다. 모든 라이브러리에 대한 효소 서열은 이. 콜라이에서 발현을 위해 최적화되었고 유도성 이. 콜라이 발현 벡터로 합성되었으며 고속 대량 스크리닝을 위해 이. 콜라이를 형질전환시켰다.

표 2. 효소 라이브러리 조성.

라이브러리	박테리아	진균	동물	식물	추론	총 디자인
LeuDH	1129	11	23	12	270	1445
KivD	783	508	1	4	0	1296
Adh	654	273	128	122	140	1317

[0181]

[0182] **실시예 2: 경로 효소 라이브러리의 특징규명**

[0183] **재료 및 방법**

[0184] **세포 성장 및 효소 제조**

[0185] 스크리닝된 효소 라이브러리의 각각의 경우에, 라이브러리 플라스미드를 보유하는 균주는 이. 콜라이 T7 발현 숙주 세포를 형질전환시켰다. 해동된 글리세롤 스톱 중 5 μ l/웰은 절반-높이 심부웰 플레이트 중 500 μ l/웰의 LB + 100 μ g/mL 카르베니실린 (LB-Carb100)에 넣고, AeraSeals로 밀봉하였다. 샘플은 37°C에 인큐베이션시켰고 80% 습도 중에서 1000 RPM으로 밤새 진탕하였다. 최종 사전배양물 중 50 μ l/웰을 절반-높이 심부웰 플레이트 중 450 μ l/웰의 LB-Carb100 + 1 mM IPTG에 넣고, AeraSeals로 밀봉하였다. 샘플을 30°C에서 인큐베이션하였고 80% 습도 중에서 1000 RPM으로 밤새 진탕시켰다. 최종 생산 배양물 중 250 μ l/웰을 500 μ l의 포스페이트 완충 염수 (PBS)를 함유하는 심부웰 플레이트에 넣고 10분 동안 4000*G로 원심분리하였다. 상등액을 제거하였고 최종 세포 펠렛은 200 μ l의 BugBuster 단백질 추출 시약 + 1 μ l/mL 정제된 벤조나제 + 1 μ l/6 mL 정제된 리소자임 중에 재현탁하였다. 샘플은 10분동안 실온에서 인큐베이션시켜서 시험관내 효소 어세이에서 사용되는 세포 용해물을 생성시켰다.

[0186] **LeuDH 활성 어세이**

[0187] LeuDH 라이브러리 균주에 대한 10 μ l의 용해물은 90 μ l/웰 어세이 완충액 (20 mM 아미노산 [L-류신, L-발린, 또는 L-이소류신], 200 mM 글리신, 200 mM KCl, 0.4 mM NAD, pH 10.5)을 함유하는 절반-면적 편평-바닥 플레이트로 옮겼다. 광학 측정을 플레이트 판독기 상에서 수행하였고, 10분 동안 340 nm에서 흡광 판독치를 얻었다. 최종 동역학 데이터는 LeuDH 활성을 대리하여, NAD⁺ 환원의 최대 속도를 해결하는데 사용되었다.

[0188] **KivD 활성 어세이**

[0189] KivD 라이브러리 균주에 대한 10 μ l의 용해물은 90 μ l/웰 어세이 완충액 (100 mM PIPES-KOH, 100 mM 칼륨 글루타메이트, 1 mM 디티오프레이트, 0.4 mM NAD, 1.5 mM 티아민 파이로포스페이트, 10 mM 마그네슘 글루타메이트, 20 mM 케토이소카프로에이트 (KIC), pH 7.5)를 함유하는 절반-면적 편평-바닥 플레이트로 옮겼다. 커플링 효소는 KIC에 대한 KivD 활성을 간접적으로 측정하는데 사용되었다. 광학 흡광도 측정은 10분 동안 수행되었다. 최

중 동역학 데이터는 KivD 활성을 결정하는데 사용되었다.

[0190] **Adh 활성 어세이**

[0191] Adh 라이브러리 군주에 대한 10 μ l의 용해물은 90 μ l/웰 어세이 완충액 (50 mM MOPS 완충제, 0.4 mM NADH, 및 30 mM 이소발레르알데히드, pH 7.0)을 함유하는 절반-면적 편평-바닥 플레이트로 옮겼다. 광학 흡광도 측정은 10분 동안 340 nm에서 플레이트 판독기 상에서 수행하였다. 최종 동역학 데이터는 ADH 활성에 대한 대리로서, NADH 산화의 최대 속도를 해결하는데 사용되었다.

[0192] **LeuDH 선택성 어세이**

[0193] LeuDH 선택성 (L-Ile 및 L-Val의 존재 하에서 L-Leu의 특이적 탈아미노화)을 측정하기 위해서, 용해물은 용해 완충액 중에 4배로 희석하였고, 10 μ l/웰의 새롭게 희석된 용해물은 0.5 mM의 각각의 아미노산 (L-류신, L-이소류신, L-발린), 200 mM 글리신, 200 mM 염화칼륨, 및 4 mM NAD을 특징으로 하는, 상기로부터의 변형된 어세이 완충액의 90 μ l/웰에 넣었다. 반응은 상이한 시점에 켄칭하였고 류신, 이소류신, 및 발린의 LC-MS 정량화를 수행하였다.

[0194] **결과**

[0195] 3 x ~1300-구성원 효소 라이브러리를 스크리닝하기 위해서, 고속 대량 (HTP) 방법을 개발하여 이. 콜라이 세포 용해물 중 LeuDH, KivD, 및 Adh 효소 활성에 대해 스크리닝되었다. 간략하게, 군주는 96웰 심부웰 플레이트에서 배양하여 단백질 생산을 유도하였고, 양성 및 음성 대조군 군주가 각 플레이트에 포함되었다. 세포를 용해하였고, 효소 활성은 본 명세서에 기술된 효소-특이적 분광광도 어세이를 사용해 세포 용해물에서 측정하였다. 효소 어세이는 완전 자동 로봇식 워크셀에서 수행되었다. 각각의 효소 패밀리 경우에, 전체 라이브러리 (~1300 구성원 각각)는 생물학적 중복물에서 측정되었고, 각 효소 패밀리에서 최고 활성을 갖는 50-200 효소가 그 패밀리에 대한 1차 "히트"로서 선택되었다. 1차 히트는 효소 순위를 검증하기 위해서 추가 복제물 (4 생물학적 복제물)로 2차 스크린에서 재스크리닝하였다.

[0196] **류신 데히드로게나제 (LeuDH)**

[0197] 총 1378 LeuDH 효소는 Leu를 탈아미노화시키는 능력에 대해 먼저 스크리닝되었다. 스크리닝의 초기 라운드는 비. 서브틸리스 유래의 부모 LeuDH 효소와 유사하거나 또는 그보다 양호한 활성을 갖는 220 효소를 동정하였다 (표 4). 이들 1차 히트는 2차 스크린에서 더욱 분석되었다 (도 2). 2차 스크린에서, Leu에 대한 LeuDH 활성이 최대 1.8배 증가된 LeuDH 효소가 검증되었다.

[0198] 활성은 배경 효소 활성 빼기 1로 효소 활성을 나누어서 계산하였다. 대조군은 0으로 설정하였고, > 0의 값을 갖는 군주는 잠재적 히트로서 간주되었다. 값은 대조군에 비해 미소한 개선을 나타낸다. 비제한적인 예로서, 50% 개선된 군주는 0.5의 값으로 표 4에 표시되어 있다.

[0199] 임의의 1차 LeuDH 히트가 Ile 및 Val에 비해 증가된 특이성을 나타내는지 여부를 결정하기 위해서, 모든 220 1차 히트는 또한 Val 및 Ile에 대한 활성에 대해 스크리닝되었다. 특이성은 Leu에 대한 활성 대 Ile 또는 Val에 대한 활성의 비율로서 측정하였다. 도 3에 도시된 바와 같은, 1차 스크린에서 히트였던 효소들은 Val에 비해 Leu에 대해 최대 ~2.7배 선호도, 및 Ile에 비해 Leu에 대해 최대 5배 선호도를 나타냈다. 양성 대조군 비. 세레우스 LeuDH는 이러한 어세이에서 측정했을 때 Leu, Val, 및 Ile에 대한 동등한 선호도를 보였다.

[0200] Leu 활성에 대한 Leu 특이성의 균형이 이러한 라이브러리에서 관찰되었고, 여기서 가장 특이적인 LeuDH 효소가 가장 활성인 LeuDH 효소는 아니었다. Leu/Ile에 대한 특이성을 Leu/Val에 대한 특이성과 비교함으로써, Leu 및 Val에 비해서 Leu에 대한 특이성이 증가된 히트를 동정하였다 (도 4). 대조군 비. 세레우스 LeuDH는 Leu, Val, 및 Ile에 대해 대략 동등한 선호도를 나타내었다.

[0201] **케토이소발레레이트 데카르복실라제 (KivD)**

[0202] 총 1248 KivD 효소는 케토이소카프로에이트에 대한 데카르복실라제 활성에 대해서 스크리닝되었다. 스크리닝의 초기 라운드는 이 어세이에서 배경 용해물 데카르복실라제 활성에 비해서 더 큰 활성을 나타내지 않고, 0이 아닌 측정가능한 배경 활성과 동등한, 에스. 아우레우스 유래 부모 KivD 효소에 비해 더 높은 활성을 갖는 55 효소 (표 5)를 동정하였다. 이들 1차 KivD 히트는 2차 스크린에서 더욱 분석되었다 (도 5) (표 5). 2차 스크린에서, 이 어세이에서 배경 용해물 활성에 비해서 KivD 활성이 적어도 6배 내지 8배 증가된 >40 KivD 효소가 동정되었다. KivD 활성은 배경 효소 활성 빼기 1로 효소 활성을 나누어서 계산하였다.

[0203] **알콜 데히드로게나제 (Adh)**

[0204] 총 1215 Adh 효소가 이소발레르알데히드를 이소펜탄올로 환원시키는 능력에 대해서 스크리닝되었다. 스크리닝의 초기 라운드는 이러한 어세이에서 배경 용해물 알콜 데히드로게나제 활성에 비해서 더 큰 활성을 나타내지 않고 0이 아닌 측정가능한 배경 활성과 동등한, 에스. 세레비지아에 유래 부모 ADH2 효소에 비해 더 높은 활성을 갖는 55 효소 (표 6)를 동정하였다. 에스. 세레비지아에의 ADH2 효소의 활성이 용해물의 배경 활성과 구별불가하기 때문에, 배경 활성에 비해 더 높은 활성을 갖는 에쿠우스 카발리스 (*Equus caballus*) Adh가 스크리닝에 대한 양성 대조군으로서 사용되었다. 이들 1차 히트는 2차 스크린에서 더욱 분석되었다 (도 6) (표 6). 2차 스크린에서, 배경 용해물 활성에 비해서 Adh 활성이 적어도 20배 증가된 5 Adh 효소가 동정되었다. 에스. 세레비지아에 대한 ADH2 효소가 2차 스크리닝에 대한 대조군으로서 사용되었다. Adh 활성은 배경 효소 활성 빼기 1로 효소 활성을 나누어서 계산하였다.

[0205] **실시예 3: 상위 LeuDH 후보 효소의 선택성**

[0206] **재료 및 방법**

[0207] **LeuDH 선택성 어세이**

[0208] LeuDH 선택성 (L-Ile 및 L-Val의 존재 하에서 L-Leu의 특이적 탈아미노화)을 측정하기 위해서, 용해물을 용해 완충액에 4배로 희석하였고, 새롭게 희석된 용해물 중 10 μ l/웰을 0.5 mM의 각각의 아미노산 (L-류신, L-이소류신, L-발린), 200 mM 글리신, 200 mM 염화칼륨, 및 4 mM NAD를 특징으로 하는, 상기 변형된 어세이 완충액의 90 μ l/웰에 넣었다. 반응물을 상이한 시점에 켄칭하였고 류신, 이소류신, 및 발린의 LC-MS 정량화를 수행하였다.

[0209] **결과**

[0210] LeuDH는 Leu, Val 및 Ile의 탈아미노화를 촉매하고, 결과로서 모든 기질은 기질 풀이 혼합되는 생체내 상황에서 경쟁인자로서 작용할 가능성을 갖는다. 혼합된-기질 풀과 관련하여 상위 LeuDH 히트의 성능을 더욱 잘 예측하기 위해서, Leu에 대한 LeuDH 효소의 선택성 (즉, Leu, Val, 및 Ile이 반응 혼합물 중에 모두 존재할 때 Leu에 대한 LeuDH의 선호도)을 측정하였다. 반응 혼합물이 1:1:1 몰비율로 Leu, Val 및 Ile를 함유한다는 것을 제외하고, HTP 스크린과 유사한 세포 용해물 어세이에서 총 21 LeuDH 효소가 스크리닝되었다. Leu, Val, 및 Ile 소멸 속도는 반응 혼합물 중에서 모니터링되었다. 도 7은 각 LeuDH 효소에 대한 반응 혼합물 내 Leu, Ile, 및 Val의 소모를 도시한다. 적어도 10 LeuDH 효소가 부모 비. 서브틸리스 LeuDH와 비교했을 때 Val 및 Ile에 비해 Leu에 대해 개선된 선호도를 보였다. 거의 모든 LeuDH 효소 경우에, 발린에 대해 최소 선호도를 보였다.

[0211] **실시예 4: 경로 효소 히트 선택 및 오페론 조립**

[0212] BCAA 경로의 전체 Leu 소모를 개선시키기 위해서, 부모 효소에 비해 우수한 성능이 입증된 각 단계에 대한 다수 효소가 선택되었다. LeuDH 경우, 2개 기준: Leu에 대한 효소 활성 및 Val 및 Ile 대비 Leu에 대한 특이성을 기반으로 6 히트가 선택되었다. LeuDH 선택성 분석은 오페론 조립과 동시에 실시되었으므로, 선택성 데이터 세트는 LeuDH 선택을 위한 인자로서 포함시키지 않았다. KivD 및 ADH 경우, 3 히트는 시험관내 효소 활성을 기반으로 각 효소 패밀리에 대해 선택되었다. 전체로, 12 효소가 최종 오페론 디자인으로 진행되었다 (표 3). 오페론은 하기 순서로 효소에 대한 4개 코딩 서열로 구성되었다: LeuDH-KivD-Adh-BrnQ. Leu 소모를 위해 바람직한 오페론이 선택되었고 하기 기술된 바와 같이 더욱 시험되었다.

표 3. 오페론 디자인으로 발전을 위해 선택된 효소

효소	식별자	출처	서열번호 (핵산)	서열번호 (아미노산)
LeuDH	t160946	세토박테리움 세티	1	2
LeuDH	t160389	하이메노박터 다에케온센시스	3	4
LeuDH	t160283	하이메노박터 sp. CRA2	5	6
LeuDH	t160434	아페니모나스 sp SCN 70-307	7	8
LeuDH	t160048	칸디다투스 카파박테리아 sp. 59-99	9	10
LeuDH	t160141	펠토코카세아에 박테리움 CEB3	11	12
KivD	t163988	칸디다 아우리스	13	14
KivD	t164076	바실러스 sp. FJ AT-1801	15	16
KivD	t163842	어워니아 이니엑타	17	18
Adh	t159319	토르티스포라 카세이놀리티카 NRRL Y-17797	19	20
Adh	t159028	리조비알레스 박테리움 NRL2	21	22
Adh	t158538	알카니보박스 디에셀콜레이	23	24

[0213]

[0214]

실시예 5: 오페론 시험

[0215]

재료 및 방법

[0216]

세포 제조

[0217]

분지쇄 아미노산 (BCAA) 경로 오페론 플라스미드로 독일 생물자원 센터 (German Collection of Microorganisms and Cell Cultures)에서 구매한, 이. 콜라이 니슬 균주 1917 (DSMZ Braunschweig, 이. 콜라이 DSM 6601)을 형질전환시켰다. 형질전환된 세포를 얼음 상에서 해동시켰고 세포 밀도는 600 nm에서의 흡광도 (OD₆₀₀)로 측정되었다. 1.0의 OD₆₀₀ 은 이 방법에서 10⁹ 세포/mL과 동등한 것으로 추정되었다. 부피는 1 mL의 2 x 10⁹ 세포/mL 세포 재현탁액을 표적화하도록 계산되었고, 세포는 96-심부웰 플레이트로 옮겨졌고 1회 냉 PBS로 세척되었다. 원심분리 (4000 rpm, 4℃, 10분) 이후에, PBS를 버리고, 이어서 세포 펠렛을 1 mL의 1x M9 + 50 mM MOPS + 0.5% 포도당 (MMG) 완충액에 재현탁시켰다. 800 μL의 각 샘플을 새로운 96-심부웰 플레이트로 옮겼고 16 mM 류신을 함유하는 800 μL의 MMG를 첨가하였고, 파이펫팅으로 충분히 혼합하였다. 0시로 지정된 샘플 (200 μL)을 이 시점에 수집하였다. 다음으로 플레이트는 통기성 막으로 덮었고 혐기성 챔버로 이동시켜 37℃에서 인큐베이션시켰다. 샘플은 또한 혐기성 챔버에서 인큐베이션 동안 2시간 및 4시간에 수집하였다. 샘플은 수집 직후에 10분 동안 4000 rpm으로 4℃에서 원심분리되었다. 100 μL의 상등액을 새로운 96-웰 플레이트로 옮겼고 향후 분석을 위해 -80℃에 저장하였다.

[0218]

류신 활성 어세이

[0219]

류신은 Ultimate 3000 UHPLC-TSQ Quantum 또는 Vanquish UHPLC-TSQ Altis 시스템을 사용하여 탠덤 질량 분광분석과 커플링된 액체 크로마토그래피 (LC-MS/MS)를 통해서 박테리아 상등액 중에서 정량되었다. 샘플은 내부 표준으로서 1 μg/mL 류신-d3를 함유하는 9부 2:1 아세토니트릴:물로 추출하였고, 와류시키고, 원심분리하였다. 상등액은 9부 0.1% 포름산으로 희석시켰고 0.8 내지 1000 μg/mL의 상기와 같이 처리된 표준물과 동시에 분석되었다. 샘플은 Phenomenex Synergi 4 μm Hydro-RP 80A, 75 x 2 mm 상에서 0.1% 포름산 (A), 0.1% 포름산/아세토니트릴 (B)을 사용하여 0.3 mL/분 및 50℃에서 분리되었다. 2 μL 주입 및 초기 5% B를 0분 내지 0.5분 동안 유지시키고 나서, 피분석물은 0.5분 내지 1.5분 동안 5 내지 90% B로 농도구배 용리하고, 이어서 높은 유기 세척 및 수성 평형 단계를 후속하였다. 피분석물은 전자분무 양성 이온 방식 (류신: 132>86, 이소류신: 류신-d3: 135>89)으로 화합물 특이적 충돌 유도 단편의 SRM (Selected Reacting Monitoring)을 사용해 검출하였다. SRM 크로마토그램을 통합시켰고, 미지/내부 표준물 피크 면적 비율은 표준 곡선에 대한 농도를 계산하는데 사용되었

다.

[0220] **결과**

[0221] HTP 스크리닝을 통해서 동정된 상위 Leu 소모 오페론으로 이. 콜라이 니슬을 형질전환시켰고 (균주 5941, 5942 및 5943로서 표시됨), 원형 균주 1980과 비교하였다. 균주 5941은 세토박테리움 세티 (*Cetobacterium ceti*)의 LeuDH 효소, 어위니아 이니엑타 (*Erwinia iniecta*)의 KivD 효소, 및 알카니보락스 디에셀롤레이 (*Alcanivorax dieselolei*)의 Adh 효소를 함유한다. 균주 5942는 세토박테리움 세티의 LeuDH 효소, 어위니아 이니엑타의 KivD 효소, 및 리조비알레스 (*Rhizobiales*) 박테리아 NRL2의 Adh 효소를 갖는다. 균주 5943은 세토박테리움 세티의 LeuDH 효소, 어위니아 이니엑타의 KivD 효소, 및 리조비알레스 박테리아 NRL2의 Adh 효소를 갖는다. 오페론은 이. 콜라이의 BrnQ를 더 함유한다. 원형 균주는 바실러스 세레우스 LeuDH, 락토코커스 락티스 KivD, 사카로마이세스 세레비지아에 ADH2를 비롯하여, 이. 콜라이 BrnQ를 함유한다.

[0222] 상위 Leu 소모 오페론 및 원형 균주로부터의 샘플은 Leu 소모에 대해 분석되었다 (도 8). 상위 Leu 소모 오페론-함유 균주 (5941, 5942 및 5943)는 원형 균주 (1980)에 비해 유의하게 더 빠른 속도로 Leu를 소모하는 것으로 확인되었다.

[0223] **실시예 6: LeuDH 효소의 조작 및 활성 LeuDH 효소의 생물정보학적 분석.**

[0224] 표 4에 표시된 바와 같이, 바실러스 세레우스 유래의 UniProt P0A392 (서열번호 27)의 돌연변이체를 생성시켰고 돌연변이체들이 UniProt P0A392 (서열번호 27)에 비해서 개선된 활성 또는 효소 발현을 보이는지 여부를 결정하기 위해 시험되었다. 실시예 2에 기술된 LeuDH 활성 어레이가 사용되었다. 하기 고유한 위치에서 점 돌연변이가 활성 또는 효소 발현을 개선시키는 것으로 관찰되었다: 42, 43, 44, 67, 71, 76, 78, 113, 115, 116, 136, 293, 296, 297, 및 300.

[0225] UniProt P0A392 (서열번호 27)의 하기 점 돌연변이는 활성 또는 단백질 발현을 개선시키는 것으로 관찰되었다: A115N, A115Q, A115S, A115T, A115V, A297C, A297D, A297E, A297F, A297H, A297K, A297L, A297M, A297N, A297Q, A297R, A297T, A297W, A297Y, E116A, E116L, E116M, E116N, E116R, E116S, E116V, E116W, G43E, G43F, G43T, G43W, G43Y, G44H, G44I, G44K, G44Y, I113F, I113M, I113Q, I113V, I113W, I113Y, L300A, L300C, L300D, L300F, L300H, L300K, L300M, L300N, L300Q, L300R, L300S, L300T, L300W, L300Y, L42A, L42Q, L42T, L76E, L76F, L76H, L76I, L76K, L76M, L76R, L76S, L76T, L76W, L76Y, L78C, L78F, L78H, L78K, L78Q, L78V, L78Y, M67A, M67E, M67K, M67Q, M67S, M67T, N71C, N71D, N71H, N71K, N71M, N71T, T136E, T136F, T136L, T136R, T136S, T136Y, V293A, V293C, V293Q, V293S, V293T, V296A, V296C, V296E, V296I, V296K, V296L, V296N, V296S, 및 V296T.

[0226] 생물정보학 분석은 히트인 메타게놈 라이브러리로부터의 서열 및 서열번호 27의 돌연변이체에 대해 수행되었다. 히트에서 확인된 고유 잔기의 목록은 하기 표 7에 제공된다. 서열번호 27의 해당 위치가 표시된다. 히트는 서열번호 27에 비해서 증가된 활성 (0 초과)을 갖는 LeuDH이다. 다중 서열 정렬에서 각 위치 경우에, 개별 잔기 정체는 히트 및 비-히트로 구간화하였고, 세트 편차를 계산하였다. 이들은 체계적 점 돌연변이 라이브러리 또는 메타게놈 서열을 통해서, 히트 세트에 고유한 잔기들이다.

[0227] **실시예 7: 활성 KivD 효소의 생물정보학적 분석.**

[0228] 생물정보학 분석은 서열번호 29에 비해서 증가된 활성을 보인 히트 KivD 효소에 대해 수행되었다. 히트에서 확인된 고유한 잔기의 목록은 표 8에 제공된다. 다중 서열 정렬에서 각 위치 경우에, 개별 잔기 정체는 히트 및 비-히트로 구간화하였고, 세트 편차를 계산하였다. 이들은 히트 세트에 고유한 잔기들이다. 서열번호 29의 해당 위치는 표 8에 표시된다.

[0229] UniProt Q684J7은 락토코커스 락티스 유래로서, 버터밀크 및 치즈의 생산에서 광범위하게 사용되는 미생물이다. 천연 효소에 대해 명명된 반응은 아니지만, KivD는 4-메틸-2-옥소펜타노에이트의 탈카르복실화를 촉매하여 이소펜탄올을 형성한다. KivD 효소 라이브러리로부터의 히트는 α-케토이소발레레이트인 그들 천연 기질을 넘어서 기질 특이성을 확장시켰다는 것을 발견하였다.

[0230] **실시예 8: 활성 ADH 효소의 생물정보학적 분석.**

[0231] 생물정보학 분석은 서열번호 31에 비해서 증가된 활성을 보인 히트 ADH 효소에 대해 수행되었다. 히트에서 확인된 고유한 잔기의 목록은 표 9에 제공된다. 다중 서열 정렬에서 각 위치 경우에, 개별 잔기 정체는 히트 및 비-히트로 구간화시켰고, 세트 편차를 계산하였다. 이들은 히트 세트에 고유한 잔기들이다. 서열번호 31의 해당 위

치는 표 9에 표시된다.

[0232] **실시예 9: 이소펜탄올 경로의 물 평형 폐쇄**

[0233] 균주 5941에서 이소펜탄올 경로의 성능 및 물 평형 폐쇄는 AMBR®15 생물반응기에서 평가하였다. 균주 5941은 서열번호 2의 LeuDH 효소, 서열번호 18의 KivD 효소, 및 서열번호 24의 Adh 효소를 포함한다. 반응기는 0.5% 포도당, 10 mM Leu, 10 mM Val, 및 5 mM Ile이 존재하는 M9 배지를 17 mL까지 충전시켰다. 조건은 0% 용존 산소 및 7.0의 pH로 제어되었다. 활성화된 생물량은 1의 OD₆₀₀까지 접종되었고, 상등액의 샘플은 시간 경과에 따라 채취하여 대사산물 농도를 모니터링하였다.

[0234] 경로 중간체의 세포의 농도 프로파일은 도 10에 도시되어 있다. 180분의 과정 동안, 4.1 ± 0.3 mM의 류신이 소모되었고 4.4 ± 0.5 mM의 이소펜탄올이 배지에 축적되었다. 케토-산 (2-옥소이소카프로에이트) 및 알데히드 (이소발레르알데히드)는 상등액에서 관찰되지 않았다. 따라서, 경로를 통한 흐름은 균형을 이루고 처리된다. 이것은 또한 경로 중간체의 총 물의 보존으로도 확인된다 (도 10에서 "총합"에 해당하는 데이터).

[0235] **방법 - 발효배양**

[0236] 어세이는 Sartorius의 미세생물반응기 시스템, AMBR15f에서 수행되었다. 용기는 2.0 mM MgSO₄, 0.1 mM CaCl₂, 5% 포도당, 10 mM L-류신, 5 mM L-이소류신, 및 10mM 발린이 보충된, 1x M9 배지 염을 17 mL까지 충전시켰다. 용기는 접종 전 18시간에 충전되어서, pH 및 DO 광전극 둘 모두를 수화시킬 수 있었다. 반응기의 온도는 37°C로 유지시켰고, pH는 2 N NaOH를 사용하여 7로 유지시켰으며, 용존 산소는 0.14vvm N₂ 유속을 사용해 0으로 유지시켰다. 실험 전반에서 양호한 혼합이 가능하도록 교반은 500 RPM으로 설정하였다. 생물반응기는 Synlogic가 공급한 활성화 생물량으로부터, 1의 OD₆₀₀까지 접종되었다. 생물반응기는 접종 후 0분, 30분, 90분, 150분, 및 180분에 샘플채취되었다. 샘플은 미세원심분리기에서 30초 동안 15000xg로 바로 원심분리되었고 상등액은 분석을 위해 제거하였다. 상등액은 분석 준비까지 -20°C에 저장하였다.

[0237] **방법 - 분석**

[0238] 2개 방법에 대한 분석법이 개발되었다. 제1 방법은 류신 (Leu), 케토이소카프로에이트 산 (Leu 산), 및 이소발레르알데히드 (Leu 알데히드)의 정량을 위한 액상 크로마토그래피 질량 분광법 (LCMS)을 포함하였다. 이러한 방법은 또한 검증되었고 발린 및 이소류신 (및 그들의 개발 산 및 알데히드 생성물)의 정량을 위해 사용되었다. 제2 방법은 이소펜탄올 (Leu 알콜)의 정량을 위한 가스 크로마토그래피 질량 분광법 (GCMS)을 포함하였다. 함께, 이들 분석 방법은 균주 5941에 대한 모든 경로 중간체의 정량을 허용하였다. GCMS 방법이 또한 검증되었고 발린 및 이소류신 알콜 생성물의 정량에 사용되었다.

[0239] LCMS 분석은 하기 용리 용매를 사용하여 Thermo Q-Exactive 사중극자-오비트랩 질량 검출기 및 Thermo Accucore PFP 컬럼 (2.1x100 mm, 2.6 μm 패키징)이 구비된 Thermo Ultimate 3000 UPLC 시스템에서 수행되었다: A= 수중 0.1% 포름산 및 0.1% TFA; B= 아세트니트릴 중 0.1% 포름산. 농도구배는 60초 동안 A 중 1% B의 0.5 mL/분에 이어서, 270초 동안 A 중 1% 내지 40% B의 선형 경사를 후속하였다. 다음으로 컬럼은 60초 동안 A 중 95% B로 씻어냈고, 180초 동안 A 중 1% B로 재평형화시켰다. MS 획득은 0.8분 내지 5.3분 사이였다.

[0240] 컬럼 유출액은 +3800V에서 양성 방식 이온화, 400°C의 기화기 온도, 및 375°C의 이온 전달관 온도로 표준 Thermo ESI 소스를 통해 질량 분광계로 유입되었다. Thermo는 STP에서 L/분으로 가능하게 근사치로 계산되는 임의 단위의 가스 유속을 기록한다. 설정점은 차단 가스, 60; 보조 가스, 30; 스위프 가스, 1이었다. 데이터 획득 속도를 증가시키기 위해서, 오비트랩 해상도를 17,500로 설정하였다. 사중극자 해상도는 1 m/z였다.

[0241] 이 방법은 또한 알데히드 및 케토 산을 유도체화하여, 이들 피분석물의 안정성을 개선시킨다. 수많은 유도체화제가 분석되었고, 메탄올 중 2-(디메틸아미노)에틸히드라진이 양성 방식에서 최선의 감도를 일으키는 것으로 확인되었다. 메탄올 중 0.5M 아세트산 및 0.5M 아세트산나트륨의 완충액이 LEU 산 및 LEU 알데히드의 정량에 사용된 한편, 또한 비-유도체화된 LEU를 측정하였다.

[0242] GC-MS 분석은 J&W DB-WAX GC 컬럼 (15m) 및 추출 용매로서 클로로포름을 사용하여, Gerstel 자동샘플러가 구비된 Agilent GCMS/MSD에서 수행되었다. 전방 주입기는 250°C 및 1 mL/분의 유속으로 설정되었다. 오븐 온도는 1분 동안 40°C에서 유지시키고 나서, 130°C (15°C/분)까지 단계적으로 승온시킨 후에, 200°C (65°C/분)까지 단계적 승온시켰다. Ms 획득 스캔 창은 40-150 m/z였고, MS 소스 및 MS quad는 각각 250C 및 200C였다.

[0243] 고속 대량 및 자동화를 용이하게 하기 위해서, Gerstel 자동샘플러를 사용하여 생성물 증발을 방지하도록 오버

레이로서 작용하는 수성 ambr15 배양 매트릭스가 상부에 존재하는 96웰 플레이트 형식 중 추출된 바닥 클로로포름 층을 주입하였다. 임의의 다른 잠재적 알콜 생성물 증발을 설명하기 위해서, 2-헵탄올이 내부물로서 클로로포름에 첨가되었다.

표 3 의 효소 서열

LeuDH (식별자: t160946; 등록: A0A1T4PGG9)

ATGAACATCTTCAAGAAAATGGAGGAATTTAATTATGAACAACCTGGTCTACTTCTACGACAGCGA
AACGGAACTCAAAGGTATTACCTGTATACACAACAACCTTTAGGGCCGGCATTGGGCGGTACCC
GCCTTTGGAACATAAATCTGAGGAAAGATGCCGTTGAAAGACGTAATCCGCTCGGCTCGGGCATGA
CTTACAAAGCGGCTTGGCGCGGTCTGAATCTGGGCGGGGTAACCCGCTGCTGATCGGTGATGCTA
AAAAGATTAAATCAGAGTCCTACTTCGCTGGACTGGGCGCTACGTTACGTCGCTGAACGGCAGA
TATATCACCCGGGAAGACGTAAATCTCTACGAAAGGATATGGCATACGTTGCTATGGAAACGTGA
CTATGTGGTAGGGCTGGGAGGTAAATCCGGCAACCCCTAGTCCAGTTACTGCTTACGGTGCAATTTAT
GGGTATCAAGCGGCGCTGATGAAAAAATTTGAGGATAGCTCTATTGAAGGCCGAACCTTCGCAG
TGCAGGGTGTCTGGGCAGACGGGTACTATCTTATCGATTACCTCCTAGGCAACAACAAGTTCAAAG
AAAAGGCTAAAAAATTTACTTCACCGAAATTAACGAGAGCTATATCGAGCGTATGAACAAAGAA
CATCCGGAAGTTGAATTTATTTCCCGGACAAAATCTACTCGTGGAAGTAGACGCTTTCGTGCC
TGCGCCCTGGGCAAAATCGTTAATGACAAAACATCGATGAATTTAAGTGTCCGATCATCGCAGGT
ACTGCAACAAACGCTACTGGAAAGGGAAGCGCACGGCAACATGCTTAAAGAACGTGGCATTTCTTA
CGCCCCGACTATGTGATCAATGCTGGTGGGCTGATCAACGTTTACCACGAGCTGAACGGTTACAA
TAAAGAGAACGCTATTCTGGAAGTGGAATTAATTTATGATCGCCTACTGGAATATTCAACATCGC
TGATTCTCTGAACATCAGCACCAATATCGCTGCCAACGAGTTCGCGGAAAAACGTATCAAGCAAA
TTAAGTCCTTGAACAACTTCATTAACGC (서열번호 1)

MNIFKKMEEFNYEQLVYFYDSETELKGITCIHNTTLGPALGGTRLWNYNSEEDAVEDVIRLARGMTYK
AACAGLNLGGGKTVLIGDAKKIKSESYFRGLGRYVQSLNGRYITAEDVNTSTKDMAYVAMETDYVVG
LGKSGNPSVPTAYGAFMGIKAAALMKKFEDSSIEGRFAVQAGQGTGYLIDYLLGNKFKKAKKIY
FTEINESYIERMKNKEHPEVEFISPDKIYSLEVDFVPCALGKIVNDKTIDEFKCPILAGTANNVLEREAHG
NMLKERGILYAPDYVDNAGGLINVYHELNGYNKENAILEVELIYDRILLEIFNIADSLNISTNIAANFAEK
RIKQIKSLKNFEIKR (서열번호 2)

LeuDH (식별자: t160389; 등록: A0A1M6BE59)

ATGGTAGAGATCAAGGCTTTGACGGACACTCCGTGTTTGGGCAAAATTCAGAACACCAGCATGA
ACAGGTCGTTTTCTGCCACGATCACGAAACCGGCCCTCCGTGCGATCATCGGTATTCATAACACAGT
TCTTGGCCCCGCCCTAGGTGGAACCTCGCATGTGGCACTATGCTTCTGACGCAGAGGCGCTGAATGA
TGTTCTCGCTCTGTGCGCGGTATGACCTACAAAGCTGCTATAAGTGGCCTGAACCTGGGTGGCGG
TAAAGCAGTGATCATTGGGGACGCCAAAACCCCTGAAAACCGAAGCGCTGCTGCGGAAGTTCGGCA
GATTCGTAACAAAACCTGAATGGTAAATACATCACTGCTGAAGATGTCAACATGACTACAAAAGAC
ATGGAGTACATCAGGATGGAACCAAGCACGTTGCTGGCTTACCTGAATCAATGGGTGGAAGCGG
TGATCCGTCCCGGTGACTGCAATTTGGTACGTATATGGGCATGAAAGCGCGGCCAAAAAGCGT
TCGGCTCTGACTCTGTGGTGGCAACGATCGCTGTTCAAGGTGTAGGTCATGTGCGCACTTACC
TGTTGGAGTATTTGCAGAAAGGAAGGTGCTAAGCTGGTACTGACTGACTACTATGAAGATCGTGCC
TGGAGGCAGCAACGCGTTTTGGCGCAAAAATGGTTGGCCTGGACGAAATTTACGATCAAGACGTT
GATATCTACAGTCCATGTGCTCTTGGAGCTACCATTAACGATGACACTATCGGTGCGCTGAAATGC
CAGGTTATCGCTGGTTGCGCAAAACACGCTGCAAAACGAAATGTGCTGGCCCGGCCCTCGT
GGAGCGGGGATTGTGTACGCTCCGATTTCTGATCAACGCCGGCGGCTGATCAACGTTTACTC
GGAAGTAGTGGTAGCTCCCGTCAAGGTGCTTGAACCGAGCCGAAAAATTTTCGACATCACCA
CTCAGGTTCTAAACAAAGCGGAACAAGAGGGTTCTCACCCGAGCGCGCAGCTACTAAGCAGGCT
GAAGAGCGTATTGCAAGCCTGGGCAAAAGTTAAGAGCACCTAC (서열번호 3)

[0244]

MVEIKALTDTSVFGQIAEHQHEQVVFCHDHETGLRAIIGIHNTVLGPALGGTRMWHYASDAEALNDVLR
LSRGMITYKAAISGLNLGGGKAVIIGDAKTLKTEALLRKFRFVKNLNGKYITAEDVNMTTKDMEYIR
METKHVAGLPESMGSGDSPVTAFGTVMGMKAAAKKAFGSDSLAGKRIAVQGVGHVGTLYLLEYLQ
KEGAKLVLTDYYEDRALEAAATRFGAKMVGLEIYDQDVVDIYSPCALGATINDDTIGRLKCQVIAGCAN
NQLQENNVHGPALVERGIVYAPDFLINAGGLINVYSEVVGSSRQGALNQTEKIFDITTVLNLKAEQEGS
HPQAAATKQAEERIAIAGLVKSTY (서열번호 4)

LeuDH (식별자: t160283; 등록: A0A1S9B636)

ATGGTAGAGATCCAGGCTTTGCCGGAACCTCCATTTTGGGCAATCGCAGACCACCGCATGAA
CAGGTGGTCTTCTGCCACGATCACGAAACCGGCCTCCGTGCCGATAATCGGTATTCATAACACGGTT
CTTGGCCCCGCCTTAGGTGGAACCTCGCATGTGGCACTATGCTACCGAGGCAGAAGCGCTGAATGA
CGTTCTGCGTCTGCTCGCGGTATGACCTACAAGGCTGCTATCTCGGGCTGAACCTGGGTGGCGG
TAAAGCAGTAATCATTGGGGATGCCAAAACAATCAAAACCGAAGCGCTGCTGCGGAAATTCGGCA
GATTCGTGCAGAACCTGAATGGTAAATACATCACTGCTGAAGACGTTAAACATGACTACAAAGGAT
ATGGAATACATTAGATGGAAACCAACACGTCGCTGGCTTACCTGAAAGTATGGGTGGAAGCGG
TGACCCGTCACCGGTAACCTGCATATGGTACGTACATGGGCATGAAAGCGCGCGCCAAAAGGCGT
TTGGCTCTGATTCCCTGGCTGGCAACGATATCGCTGTTCAAGGTGTGGGTGATGTTGGCACTTATCT
GCTTGAGCATTTTGACCAAAAGAGGTGCTCAGATTGTGCTGACTGACTACTATAAGGAACGTGCGG
AGGAAGCAGCGCGCGCTTTTGGCGCACAGGTTGTTGGCTGGACGATATCTACGATCAAGAGGTG
GACATTTACTCTCCATGCTCTCGGTGCTACCATCAACGATGACACTATCGATCGCCTGCGTTGGC
CTGTTGTAGCCGGTTGCGCAAAACACAGCTGAAAGAAAGAAAACGTCCACGGTCCGCGCGCTGGT
GAGCGCGGATAGTATACGCCCCAGACTTCTGATCAATGCAAGGTGGCTGATTAAAGTGTATAGC
GAAGTTACAGGGTCTACCCGTCAGGGGGGCTTAACTCAGACCGAAAAAATCTATGACTACACACT
CCAAGTTCTGGAAAAAGCGCGGCTGAAGGTCTGCACCCGACGAGGCTGCGATCCGTCAGGCGG
AACAACGCATCGCTGCAATTGGTAAGGTGAAAGCACCTAC (서열번호 5)

MVEIQALPETSIFGQIADHQHEQVVFCHDHETGLRAIIGIHNTVLGPALGGTRMWHYATEAEALNDVLR
LSRGMITYKAAISGLNLGGGKAVIIGDAKTLKTEALLRKFRFVQNLNGKYITAEDVNMTTKDMEYIRM
ETKHVAGLPESMGSGDSPVTAFGTVMGMKAAAKKAFGSDSLAGKRIAVQGVGHVGTLYLLEHLTK
EGAQIVLTDYYKERAEEAGARFQAQVVGLEIYDQDVVDIYSPCALGATINDDTIDRLRCAVVGACANN
QLKEENVHGPALVERGIVYAPDFLINAGGLINVYSEVTGSTRQGALTQTEKIYDYTLQVLEKAAAEGLH
PQQAIRQAERQIAAIGLVKSTY (서열번호 6)

LeuDH (식별자: t160434; 등록: A0A1D2RXB2)

ATGATCTTCGAGACAATTTCTACGTCGAATCACGAAGAAGTGTGTATTGCCATAACAAGGACGCC
GGCTTGAAAGCAATCATCGCGATTCAACACTGTACTCGGTCCGGCTCTGGGTGGCACTCGCATG
TGGCCCTACGCTAGCGAAGAGGAAGCACTGAAAGATGCTCTCGTTATCCCGTGGGATGACCTAC
AAAGCTCGCGTTTCAGGTCTAAACCTGGGCGGCGGTAAGCTGTGATCTGGGGTATCCGAATAA
AGACAAGTCTGAAGCGCTGTTAGAGCCTTCGGACGGTTTGTAAACAGCCTGGGCGGACGCTACA
TTACCGCGGAGGACGTTGGCATTGATGTTAACGACATGGAATATGTGCTGCGTGAAACTGATTACG
TCACCGGTGTACATCAGGTTACGCTGGGAGTGGTGATCCTTCTCATTACCCGATATGGCACTC
TGCAAGGCTGTATGCGCGCTCTGCAAGTGAAATTCGGTAACGAAGACGTAGGCAATTACAGCTAC
GCTGTTCAAGGTGTGGGTGACGTTGGCATGGAATTTGTTAAACTGCTGCGTGAGCGCGGTGCAAG
GTTTTCTGCTACATGACATCAACAAAGATGCGGTCCAGCGTGCTGTGGACGAATTTGGTTGTAGGCA
GTAGCCCTGGATGAAATCTATGACGTTGATTGCGACGCTGACTCCCGACCGCTCTGGGCGGCACC
GTGAACGATAAACTTTACCGGCTCTGAAATGTAAGGTAACTGCGGTGCGGCAACAAACAGTT
AGCTAATGATGAGATAGCGGTGGAACCTGGAATAAAAGGCATCCTCTATGCTCCGGAACACGCGG
TCAACGCGGGTGGGCTGATGAACGTTAGCCTGGAATCGATGGATACAACCGCGAACGTCGGATG
CGTATGATCGTACCATTTATTACAATTTGGGTGCAATTTTCAAAATCTCTAAGCGCGACCGGATC
CTACATTTCCGAGCGCGCATCGTATGGTGAAAGACGCATAACGGCCATCGGTAAACTGCGTTTA
CGCATTTGGGCGCTGCGGCACCGCGCTTCCAGGGCCGACGTGGCAAC (서열번호 7)

MIFETISTSNEEVVYCHNKDAGLKAIHNTVLGPALGGTRMWPYASEEEALKDVLRLSRGMITYKA
AVSGLNLGGGKAVIIGDPNKKSEALFRAFGRFVNSLGGRYITAEDVGIDVNDMEYVLRDITYVTGV
HQVHGGSGDSPFTAYGTLQGLMAALQVKFGNEDVGNYSYAVQGVGHVGMFVKLLRERGAQV
TDINKDAVQRAVDFEGCEAVLEIYDVCDDVYSPTALGGTVNDKTLRLKCKVICGAANNQLANDEI

GVELEKKGLYAPDYAVNAGGLMNVSLIEDGYNRERAMRMRTIYYNLGRIFEISKRDGIPTFRAADR
MAERITAIGKLRRLPHLGAAAPRFQORRG (서열번호 8)

LeuDH (식별자: t160048)
ATGCAGATCTTCGACACTTTGCAATCAATGGGCCATGAGCAGGTGGTCTATGTAGCGATAAGACC
ACGGGTCTGCGCGCCATTATCGCTATACACGATACATCCTTAGGGCCGGCGTTGGTGGTACCCGT
ATGTGGCAGTATGCAACTGACGACGATGCTATTACTGACGCACTCCGTCTGTCTCGGGGATGACC
TACAAAGCTGCGGTTTCTGCGCTAAATCTGGGCGGTGGTAAAGCCGTTATCATCGGAAACCCCTCAC
AGTGATAAAAGCGAAGCGCTGTTTCGCGCTTACGGCAGAAATGGTGGAAATCCAGCGTGGGCGTTA
CATCACCGCCGAAGACGTTGGTACTAGCGTACGTGATATGGAGTGGATTCCGATGGAAACCAAAT
ATGTAACGGGCGTGGGTGGCAACGGAGGCTCTGGTGACCCCTCTCCAGTTACCGCTCTGGGTGTTT
ACTCGGGCATGAAGGCATGCGCTAAATCAGTCTATGGTACTGATGCGCTGAGCGGTAAAAGGATC
GTGGTTACGGGCGCGGTAACTGATCCCATCTGGTTCACAGTCTGGTAAAAGAGGCGGTGTG
GTTTTCTGCTACTGACATCTACGAAGAAAAGGCCAAAGCATTAGCGGCTGAAACGGGCGCTACCGT
GATTGCGACCGACGAGGTTTTTACTACACAATGCGATATCTTCTCCGAACGCTCTGGGGGCGGT
CCTGAACGATGAAACTATTCGCGAGCTCACATGCGCTATCGTAGCTGGTGGTGCAACAATCAGCT
TAAATCGAACAACGTCACGCCACGGCTCTGCAAGAGAAAGGCATTCTGTATGCGCCGATTACG
TAATCAACGCCGGGCGCTCATGAATGTGGCGAGCGAAGTTGACGGCTACAACCGTGAAAAGGTT
ATGCGCCAGGCTGAAGGTATTTACGATATTACTATGAACATCTAAATACCGCGCGTGAGCGTAAC
ATCTCGACCATCGAAGCATCCAAACGCGATTGCTGAAGAGCGGATCAACAAAGTTGCGCATGTTC
CGGGAACCTTCATCGGTTCCCGCTCTATTGCGGGAGTA (서열번호 9)

MQIFDTLQSMGHEQVVLCSDKTTLGLRAIIHDTSLGPALGGTRMWQYATDDDAITDALRLSRGMTYK
AAVSGVNLGGGKAVIIGNPHSDKSEALFRAYGRMVESQGRYITAEDVGTSVRDMEWIRMETKYVTG
VGGNGSGDPSVFTALGVYSGMKACAKSVYGTDLALSGKRIVVQAGNVASHLVHSLVKEGAVVFT
DIYEKAKALAAETGATVIRTDEVFTTQCDIFSPNALGAVLNDETIPQLTCAIVAGGANNQLKIEQRHAT
ALQEKGLYAPDYVINAGGLMNVASEVDGYNREKVMRQAEGIYDITMNLNTARERNILTIEASNAIAE
ERINKVRHVHGNFIGSPSIRGV (서열번호 10)

LeuDH (식별자: t160141; 등록: A0A0J1FEE3)

ATGACAACGTCGAGTATATGGAAAAGTACGACTACGAACAACCTGGTCTTTGTGAGGATAACAC
TTCTGGCCTCAAAGCAGTAATTTGCATCCATGACACCACTCTGGGGCCAGCTTTGGGTGGCACCCG
TATGTGGAATTACGCCAGTGAAGAAGATGCTATCCTGGATGCGTTACGCTGGCGCGAGGTATGA
CTTATAAAAAACGCTGCCGCGAGTCTGAACCTGGGCGGCGGTAAAGCTGTTATTATGGGCGACAGC
CGTACCCAGAAATCAGAGGAACTTTTCGCGCGTTTCGGTCTGTTACGTGCAGGCGCTGAACGGCCGT
TATATACCGCTGAGGACGTTGGTACTAACGTACAAGATATGGACTGGATACACATGGAAACAAA
GTTTGTGACCGGGATCTCCTCTTCGTACGGTGCTAGCGGAGATCCGTCCCTCTGACCGCACTGGG
CGTTTACCGCGGTATGAAAGCCGCGCAAAAGAACGCTTCGGCAGCGACTCTTTAGAGGGTAAAA
CTGTTGCTATTACGGGTCTTTGGCCACGTCGGCTATTACCTGGCAAAACACCTCACTGATGAAGCG
CTAACTGATCGTGACGGATATCAATTCTGAAGCCGTTAAGAGGGTAGCGCGTGAGTTCTGTTGCTA
CCGAGTCCGTACCGAAGAAATTTTCGGCGTTAAATGCGACATCTTTGCGCCCTGTGCTCTGGGTG
CAGTTATCAACGATGAACCATTCGCGAGCTGAAGTGCCAGGTAGTTGCGCGTGCTGCGAACAAT
GTGTTGAAAGAGGATCGCCATGGTGACGAACATAACGAAAAGGAATCCTGTACGCTCCGACTA
TGTAATTAACGGGGCGCGGTATCAACGTGGCCGACGAACCTGGAAGGTTACAACGCTGAACGTG
CTCTGAAAAAAGTTGAGATGGTATATGATAATGTGGCACGCGTATCGCTATTGCCAAGCGTGACC
ATATCCGCACTTATAAAGCAGCGGACCGAATGGCTGAGGAACGATTGCGAAAAATGGCAAGTT
TCCAACACTTTCCTGCGC (서열번호 11)

MTTFEYMEKYDYEQVLVCQDNTSLGLKAVICIHDTTLGPALGGTRMWNYASEEDAILDALRLARGMTY
KNAAAGLNLGGGKAVIMGDSRTQKSEELFRAFGRYVQALNGRYITAEDVGTNVQDMWDHMETKVFV
TGSSSYGASGDPSPALTALGVYRGMKAAAKEAFGSDSLGKTVAIQGLGHVGYLAKHLTDEGAKLIV
TDINSEAVKRVAREFVATAVRTEEIFGVKCDIFAPCALGAVINDETIPQLKQVAVAGAAANNVLKEDRHG
DELYEKGILYAPDYVINAGGVINVADELEGYNAERALKKVEMVYDYNVARVIAIAKRHDHIPTYKAADR
MAEERIAIKGVSNFTLR (서열번호 12)

KivD (식별자: t163988; 등록: A0A0L0P8D8)

ATGTCGGAGATCACATTGGGTAGATACCTTTTCGAACGCTTAAACCACTGCAAGTGAGACTATT
TTTGGGCTGCCCGGCGACTTCAATCTGTCCTGCTGGATAAGATCTATGAAGTTGATGGCATCGGT
TGGCGAGGTAAACGCTAACGAACCAACGCGCTTACGCGGCTGACGGTTATAGCCGTGTCAAAGG
CCTCGCATGTCTGGTTACCACTTTTGGTGTAGGCGAGCTAAGTGCCTGAATGGTGTGGGTGGCGC
TTACGCGAAGAACAGCTTGGGCTGCTGCATGTAGTGGGCTGCCATCAATCTAGCCAGGCGAAACA
GCTGCTGCTGCAACATACCTGGGTAAACGAGATTTACGGTTTTCCACCGCATGTCCAACAACAT
TTCTCAGACCAGCGCTTTATCAGCGACATTAACTCTGCTCCTGGTGAAATCGATAGGTGCATCCGT
GAGGCTGGGTACATCAGCGTCCGGTTTACGTCGGCTGCCGGCGAACCTAGTTGACCTGACTGTG
CCGGCGTCTCTGTTAGACACTCCGATCGATCTGCTCTTGAACCAACGACCCGGATGCCAGGAA
GAAGTTATTGAACCGCTCTGATCTGGTAGACAAGTCTAAAAACCTATAATCTTAGTTGACGCA
TGCCTAGCCGCTACTCATGCCGCGATGAAGTACGCGGTTGGTGGACTCCACCGCTTCCCGGTT
TTCGTTACTCCAATGGGTAATCTGCTGTAATGAGAGTCAACCGCGTTTGGCGGTGTTTACGTG
GGCAGCCTCAGCGACCAACGTAAGAAAGCCGTTGAAACGCTGACCTGGTGTCTTCCATAGG
CGCCTGTTGAGCGACTTCAACACTGGATCGTTCTTATTCTACAAAACTAAGAACATTGTTGA
ATTTCACTCTGATTATACCAAAATCCGTCAAGCAACGTTCCCGGTTGTTAGATGAAGAAAGCACT
GAATGTCCTGTTGGAAAAAATCCCGAGCCATGTCGCTAACTACAAACCTCTGCGGTTCCGAGCG
TCGCGTTATTCGAGCCAGGGGATAAGGCTGCGATCTCTCAGGAGTGGCTGGTGGCGTCTGTC
TAGCTGGTTCCCGAGGGCGACATCGTCATTACAGAAACCGGTACCAAGTGGTTTGAATTGTACA
GTCTATTTCACAGATAACTGCATCGGCATCAGTCAGGTGCTGGGGTTTCGATCGGCTTCCCGT
AGGTGCAACGCTGGGCGCGGTGATGGCTGCAACAAGAAATCGATCCGAAAAACGTTGATTTAT
TTGTCGGTGACGGTTCTCTGCAACTACTGTACAGGAAATTTTACCATGGTTAAGTGGGAAACCA
CGCCTACCTGTTTGTGCTGAACAACGATGGGTACACTATCGAACCGCTTATCCATGGCGAGACTG
CTACGTAATAACGATATTACGCGTGGGATAATCTGGGCTGTTGCGCGCTGTTCAAAGCTCTGACT
ACGAAACCAACCGAGTTGCGACTGTAGGCGAAATTGAAGCGCTATTCAACAATTCAGCTTTCAAT
GAGAATACAAAGATCCGTATGGTGGAGGTATGCTGCCGCGGATGGATGCACCACAGAACCTGGT
TAAACAGGCTGAATTTCTCCAAAGCAACACGCGAAAAAC(서열번호 13)

MSEITLGRYLFERLNLQVQTFGLPGDFNLSLLDKIYVDGMRWAGNANELNAAYAADGYSRVKGL
ACLVTTFGVGLSALNGVGGAYAEHVGLLHVGVPSISSQAKQLLHHTLGNGDFTVFRMNSNISQT
TAFISDINSAPGEIDRCIREAWVHQRPVYVGLPANLVDLTPASLLDPIDLKKNPDPAQEEVETVL
DLVDKSKNPILVDACASRHSRDEVRRLVDSTSPFVFTPMGKSAVNESHPRFGGVYVGLSEPNVKE
AVENADLVLSIGALLSDFNTGSFSYKTKNIVEFHSYDKIRQATFPVQMKEALNVLEKIPSHVAN
YKPLVPQRRVPSPGDKAALSQEWLWSRLSSWFREGDIVITETGTSFQVQSYFPDNCIGISQVLWGS
GFTVGATLGAUVAQIDPKKRVILFVGDGSLQLTVQEISTMVKWETTPYLFVLNNDGYTIERLIHGET
ATYNDIQPWDLNLLPLFKARDYETNRVATVGEIEALFNNSAFNENTKIRMVEMVLMRMDAPQNLVK
QAEFSSKTNSEN(서열번호 14)

KivD (식별자: t164076; 등록: A0A0M5JJZ2)

ATGACAAGCATGGACAATTCTAGTCAGCAAAATCCCATGGGTGAGAAAACCGTCGGGGAGTACTT
GTTTCGATTGCCTAAGCAGGAAGGCATAACGGAATCTTTGGTGTGCGGGCGATTATAACTTCAC
CTTACTGGACGCGCTGCAAGAATACAACGGTATTCTGTTCTATAACGGCGCAACGAGCTGAATGC
TGGTACGCGAGCTGACGGTTACGCGCGTATTAAGGAATCTCCGCGCTAATCACTACTTTTGGTGT
TGTTGAAGTGTACGCACTAACGCTATTGCGGCGCGAACAGCGAACACGTACCTATCATCCATAT
TGTTGGGTCCCAACCGAAAAAGCTCAGAAGGAGCGCAAACTGATGCACCATACCTGATGGATG
GCAACTTCGACGTATTCCGTAAAGTTTACGAACCGCTTACCGCTTATACTACCATCGTCACGGCAG
ATAACGCGCGGATGGAGATCCCGGCTGCTATCCGTATTGCCAAAGAACGAAAGGCCAGTGTAC
CTGTTGTTGCGGATGACGTAGTGGCTAAACCGATTACTGGTCGTGAAGTCCCGGCATCTCCTCTG
CCGGCTAGCAATCAGGACAACTGCTTGTGCGGTTGAGCACGTTAGGCGTCTTCTGGAACCTGCA
CGCCAGCCGGTAATATTGGTTGATGTGAAAGCCATGCGCTTTGGATTACAGACCGCGCTCAGGGA
ACTGGCAACACTATGAATGTTCCAGTGGCTACAATGATGTATGGCAAGGCACTTTCGACGAAA
CCCATCCAACTACATCGGCGTATATGCGGGTACGTTGCGTTGCTGCTGAAGTTCAATCTATCGTAG
AAAACCTCGGACTGTGTTATCGCGTGGTTTGGTGTGGAGCGATACTAACACCGCAAACTTACTG
CGAAATTAAACCGCACAAATACCATGAGGTTTACGCGACAAAAGTGAAATCGCTGAGTCCGAG
TACCCCGATGTCCGTGCGCGAGACATCTGCAAGAAATGCAAGAGCTGGAATTATCGTAGCCAGTCT
AAACCGGAAAAATCTCATTTCCGTACGAAGAGATAACCGGGTCCAGTGATGAACCGCTCCGCGC
AGAAAACACTTCCCTCGTTTTCAGCGCATGCTGAAGGAAACGATATTGTTATCGCTGAGACCGG

[0247]

CACGTTCTACTACGGTATGAGTCAAGTTAACTGCCCGGAACTACGTACATCATGCAGGGCGG
CTGGCAGAGCAATTGGTTATGCCACCCCGGCGGCATACGGCGCTCTATCGCTGCTCCGACCGTCTG
CGCTTACTGTCTACTGGTGATGGCTCCATGCAGCTGACCGCACAGGAAATCTCTCTATGCTTTAT
TACGGTTGCAAGCCGATTATCTTTGTACTGAAACAATGACGGGTACACCATGAGCGGTATCTGAAT
GTAGAAATCTCCCTGACGAACAACTATAACGATATTCGAACTGGTCTTATACTAACTGGCT
GAGCGGTTCGGTGGTGAACGTCTTCACTAAACAGTGGTACCAATGAAGAATTGGATGAAGCGAT
CACACAGGCTGAGCAAGAGTACGCCGAAAACTGTGCCTGATCGAGATGATTGCTGCTGATCCAA
TGACGCACCCGGAATACATGCACCGTATCCGTAACCATAAGCAGGAACAGAAAAAG (서열번호 15)

MTSMDNSSQQIPMGQKTVGEYLFDCLEKQEGITEIFGVPGDYNFTLLDALQEYNGIRFYNGRNELNAGY
AADGYARIKGISALITTFGVGELSATNAIAGANSEHVPIIHVGSPEKAQKERKLMHHTLMDGNFDFVR
KVYEPLTAYTTIVTADNARMEIPAAIRIAKERRKPVVLVVADDVVAKPITGREVPASPLASNQDKLLA
AVEHVRRLLEPARQPVILVDVKAMRFGQLTAVRELANTMNVVATMMYKGTDFETHPNYIGVYAG
TFGSSEVQSIVENSDCVIAVGLVWSDTNTANFTAKLNPHTIEVQPTKVIAESQYPDVRAADILQEMQ
KLDYRSQSKPEKISFPYEEITGSSDEPLRAENYFPRFQRLKENDIVIAETGTFYYGMSQVKLPANTTYI
MQGGWQSIGYATPAAYGASIAAPDRRVLLFTGDSMQLTAQEISSMLYYGCKPIIFVLNNDGYTIERYL
NVEISPDEQNYNDIPNWSYTKLAEAFGGELFTKTVRTNEELDEAITQAEQYAEKLCLEIMIAADPMDA
PEYMHRIRNHRKQEQK (서열번호 16)

KivD (식별자: t163842; 등록: A0A0L7TB96)

ATGTCGACGACAACCGTTGGTGAAGTACTGCTGTATCGCTTAAACGAAATCGGCATTGAGCACCTC
TTCCGAGTGCCAGGTGATTACAATCTGCAATTTCTGGATCATGTAATCGACACCCCTCAGCTGACT
TGGGTGCGCTGCCTAACGAACTTAACGCTGCCTACGCAGCTGATGGTTATGCGCGTTGTCGTCGG
GCTGCGGCACTGCTGACCACTTCGGGGTTCGCGAACTGAGCGCTATTAATGGCATCGCAGGTTCC
TACGCGGAGTATCTGCCGGTAATACATATCGTTGGTGACCGAGTCTATCAGCCAGCAGCAGGGC
GACCTGATTACCACTCTCTTGGCGAAGGTGATTTTTCCAGCTTCCTGAGGATGTCCCAACCGGTGT
CTGTTGCGCAGGCTGCTCTGACTCTGATAACGCATGCAAGGAAATCGACCGCTACTGGCGGAA
GTCTCTATTACAGCGTCGTCGGGTACCTGCTGTCTACCGACGTGGTGTGCGCGCGCGGCT
CTGCCAAGAGCACTCTTTCTTTGCGGACCGCCCGGATCATCGCGCAGTTCTGGTGTCTTCAGCG
ACGCTGCTGAGCAGATGCTGGCTCAGGCCAAAAGCGTCTCTACTGCGGCACTTTCTGGTGTATC
GTTTCGGTGTACTCGAGCACTGCGCGGTGGCTTACGAGGTTCCGCTACCGCACGCCACTCTGT
TAATGGGTAAAGCGGTCTGAGTGAAACAGCAACCGAGGTTCTGGGTACCTACGCTGGTGCGGCA
TCTATCGATTGCGCGGTGGCGCAATCGAAGAAGCTGGGGTAATTATCGGAGTGGGAGTTAGATT
TCCGACACTATCACAGCAGCGCTTCTCGCAGCAGATCGACGCCCGCGTTTATAGACATTCAACCC
TTCTCTCTCGTATTGGCGATCGCCAGTTTGATCACTGCCGATGACGGCTGCCGTGCGCAGCCCTGC
ATCAACTGTGTCTTCGTTATCAGCAGCAGTGGTCTATCACCGCTCTAGCCCGCTGCATGCGCGC
GGCTGCTGGTAGCGAGCTGTCCAGAACGCAATTCGGCAGGCGATGCAGAACTTATCCGCGCTGG
GGACCTGTTGTGGCGGACCAAGGTACTGCGGCGTTTCGGCGCAGCGCGCTGCGCTTACCGCAGA
ATTGCCAGCTGCTTGTGACGCGCTGTGGGGCTCAATCGGTTACAGTCTGCGCGCCACCTTTGGTG
CTCAGACGGCAGATACAGAGCGTCTGTGTAATCTTAATCATTGGCGATGGTTACGCGCAATTAAC
TTAGGAACTTTCCAGTATGATGCGTGACGGCTTGAACCTATCATCTTTCTCCTGAACAACAACG
GTTACACCGTTGAACGGGCGATTACGGCGCGGAGCAACGTTATAACGATATCGCTGCTTGAATT
GGACCAACTGCCCCAGGCGCTGAGTGTTCATTGCCAGCGCAGAGCTGGCGAGTCTGTTGAACG
GTGACGCTGACCGACGTAATGAAAGTCATCGCTGCTTCTCCGCGCTGAGCTTGGTAGAAGTTGTT
CTGCCTGCAATGGATGTCCCAACCGCTGTCGAAGCAGTGAGTCCGCTCTGAACAGCGCAACTCC
TCT (서열번호 17)

MSTTTVGDYLLYRLNEIGIEHLFGVPGDYNLQFLDHVIDHPQLTWVGCTNELNAAYAADGYARCRPA
AALLTTFGVGSALINGIAGSYAEYLPVIHVGAPSLAQQQGDLIHSLGEGDFSFLRMSQPVSVAAQ
ALTPDNACKIEDRVLAEVLIQRRPGYLLSTDVAAAPALPQSTLSLPTAPDHRVLAAFSDAEQMLA
QAKSVSLADFLADRFVTRALAAWLQVPLPHATLLMGKGVLEQQQPFVGTAGAAASIDSTRGAE
EAGVIIGVGVYRFSDDTITAGFSQOIDARRFDIQPFSSRIGDRQFDHLPMAAVALHOLCLRYQQQWSIT
APSPPALPPAAGSELSONAFWQAMQNFIRPGDLLVADQGTAAFGAAALRLPONCQLLVQPLWGSIGYS
LPATFGAQTADTERRVILIGDGSACLTIQELSSMMRDGLKPIIFLLNNNGYTVRAIHGAEQRYNDIAA
WNNWTQLPQALSVHCPAQSWRVVETVQLTDVMKVIAASPRLSLVEVLPAMDVPPLQAVSAALNQR
NSS (서열번호 18)

[0248]

Adh (식별자: t159319; 등록: A0A1E4TMA4)

ATGCAGACGGCGTCTCTGTATAAGCCAGGTCACGAAAACTTAGTGCCTCGGAGATCCCGATACCT
AAAGCTGGCGCTGGCGAAGTCGTTCTGGAAATTAAAGCCGCTGGCATGTGCCATTCCGATCTGCAC
GTCTCGACGGTGGGAATCCCTGCCGGGTCAATTGTAATGGGCCATGAAATCGTTGGTACTATT
CACGAGATCGGCCAGGACGTGACCGGTTTCAAACAGGGCGATCTGTACGCAGTCCACGGCCCGAA
TCCGTGTGGTATTTCACCCCTGTGCAGAGAAAGGATTGATAACGACTGCACACAGTGGCGAAAA
CGGTCAATGGTTCCGACTGGGTCTTGACGGCGGCTACCAGAAATATATCCGTATCCCGAACGTAAG
GTCTATCGTTAAAGTTCAGAAAGTGTTCAGCTGAGGCAAGCTGCGAGCTGACTGATGCAGTACT
GACCCCGTACCGTGCCTAAAACAGGCTGGCGCCAGCAACTCTACTCGGCTACTGATTCTGGGTCT
GGGTGGCTTAGGTGTAATGCCCTTAACTGGCTAAGACCTTCGGCAGTTACGTTTACGCATCTGA
CCTGAAACCTTCTGCGCGTGAAGCTGCTAAGGCCGCTGGGCGGATGAAGTCTGGAGTCCCTGC
CCGAAGACCCGCTGGGTGTTGATATCGTGTAGACGCTGTTGGCGTGCAGAGCACCTTCAACCTCG
CTCAAAAACAGCTGGCCCGCGTGGCATCATTTGTACCTGTAGGCGTGGCATCCCGACAGCTTTCGT
TTAACCTAACGGATCTGGCGCTCCGCGAAATTCGTGTTACAGGCACTTTTGGGGCAGCAGCAATG
AGCTGGCTGAATGTCTGCGCTGTGCCAGCTGGGCTGATCAACCCGAAATATACTGTGGTGCCTC
TTGAAGAAGCGCGGAAATATATGAAGCAATGGCTCATGGGAAAGTAGAAGGTGCTATCGTTTTTC
CACCCG (서열번호 19)

MQTAFLYKPGHENLVSEIPKAGRGEVVEIKAAGMCHSDHLVLDGGIPLPGQFVGMHEIVGTIHEIG
QDVTGFKQGDLYAVHGPNPCIGICTLREGFDNDCTTVAKTGQWFLGLDGGYQKIRIPNVRSIVKVP
EGVSAEAAASCTDAVLTPYRALKQAGASNSTRLVILGLGLNLALKLAKTFGSYVYASDLKPSAREA
AKAAGADEVLESLEPDLGVLDVVGVSSTFNLAKQHVGFPRGIIVPGLASPQLSFNLTDLALREIR
VQGTFWGTSNELAECLRLCQLGLINPKYTVVPLEEAPKYMEAMAHGKVEGRIVFHP (서열번호 20)

Adh (식별자: t159028; 등록: A0A192IDS9)

ATGCGCAGCATGCAGTTTGATGAGTACGGTGCACCCCTGAAAGCGTTTCATATGAAGACCCGACC
CCGAAGGGAAGGAAGTAGTCGTAGGATCGAAGCCTGTGGTGTGTGCCACTCTGATATTATCTTT
CACGAGGGCTACTTCGACATGGCGGTGGCAATAAAGCTGATGTTACTCGTCTCGCGAACTCCCT
TTTACATTGGGTGATGAAATCGTTGGCGAAGTGTAGCAACTGGACAGGTGTACCCGGCGCTAA
ACCGGCGCAACACGTAATTGTGTACCGTGGATCGGGTGGCGGACTGCCGAAATGCAACAGTG
GTGAGGATCAGTCTGTGCGCTCCACGTAACCTGGGTGTTACGTTGACGGTGGCTATTGACGCG
ACGTAAAGATACCGGACGAAAAATTCCTGTTGCGCTACGATGGTATTCTACTGAGTTAGCGGAA
CCTATGCTTGACGCGCATCACCGCTTATGGTGCATGATGAAAGCAAGGAAGCGGTGAAAGA
TCTGGCTACATCGGTCTGATTGGCGCTGGTGGCGTGGCATGGCTGGTCTGATGCTGGCGAAAGCA
GCGATCGGGGTGAAAACTGTAGTCTTTGATATCGACGACGCAAACTGGAAGCTGCGACCCGTGC
CGGGGCGGATTACGTGTTCAACTCGGTGCAAAAGAAACACGCAAGGAAGTTATGAACTAACGTA
ATGGTGGCTGTCTGTGCTGTTGATTTCGTTGGCAGCGATAAAAGCGCTCTGTTTGAATCAACG
CCTTGGGTGCAAGCGCGTGTGTCATAATGGACTGTTGGTGGCGCTATGACTGTTCCGGTAC
CCCTGTTCCCGCTGAAAGGATCACCGTACGTGGCTCATACGTAGGTTCCCTGCAAGAGATGAGTG
ATATGATGGAGTTAGTTGCGCTGGGAAAGTTCCTCCGATGCCGTAAGAACTCGGCCACTGGAC
GCTGCTGGGAAACCCCTGAGGATCTACGCCATGTTAAATCGTGGGCGGTGTTGTTCTGACCCCA
(서열번호 21)

MRSMQFDEYGAFLKAFSYEDPTPQGKEVVRIEACGVCHSDIHLHEGYFDMGGGNKADVTRARELPF
TLGHEIVGEVVATGPGVTGAKPGDKRIVYPWIGCGDPCPKNSGEDQSCARPNLGVHVDGGYSTHVKI
PDEKFLFAYDGPTELAGTYACSGITAYGALMKAKEAAERSGYVIGLAGGVMAGLMLAKAAGAKT
VVFDIDDAKLEAATRAGADYVFNAGAKETRKEVMKLTNGGLSGAVDFVSGDKSALFGINALGQNGVL
VHGLFGGAMTVVPVPLFPLKGTIVRGSYVGSLEQMSDMMELVRAGKVPMPVKTRPLDAAWETLEDLR
HGKIVGRVVLTP (서열번호 22)

Adh (식별자: t158538; 등록: A0A0P1JIW4)

ATGACAGCGGAGCAGCAAAATGGGGTATCCGACTCACGCCGTTTCGAATTTACAGAAATTTGGTGG
CCCTATCGCCCCACAGACCTATCAGCTCCCCGCACCGGCTAGCGATGAAGTTTTGTTAAAGGTGAA

[0249]

CTACTCGGTGTCTGTACAGTATGTTTCACTTACGACGGCTACTTCGAGCTGGGTGGCGATAA
ACGCTTGAATCTTCCGCTATGCCGCTGCCGCTGACGCTGGGTACGAAAGTAATTTGACCCGTTGTGGC
TGTCGGCGACCAAGTTACTGGTGTAAAACCGGGGACCGGACTGATCTATCCGTGGATAGGTT
GCGGAAAATGCGGCGCGTGTCAAAAAGGAGAAGAAACCTGTGCGTTACTCTCGACATCTGGGC
GTGAACAAGCGGGCGGTTACGCTGATCAGTGTGTAACCCCTTCTGCTACCTTCTGGACATT
TCGGGTCTGAACCCGGGTGATGCCCTACCTCGCTGCTCCGGCTGACCACTTTCAGCGCGATC
AACAAAGTGTGCGGCTTGCGCATGACGAGTACGAGTGGATTGTTGTTATCGGTTGTGGTGGCTCGGCCAG
ATGGCGCTGCTATCTGCAAGCTATGGAAATTGGCAATGTTATCGGTTATTGACCTGTCTGAAGAG
AAACGGAACTGGCTATGAAAGCGGTGACGCTACTCTTCGATCCAAACACTCCGAAGCTGAA
CCCGGTGGTCCCGCAACCTGCCGGGTACGGTACAGGCCGCGTTAGACTTTGTGGCAATGAGC
AACTGCTCAGCTGGCAGTCTCTGCTTGGAAAAGGTGGCAAAATATGTTCTGTGCGGCTGCACG
GCGGCGAGCTGGCTTACCCATTGCCGATCATCAGAAACAAAGCTGTAAGTATCATCGGTTCTTACG
TTGGTACCCGTGAAAGAACTGGAAGACTTAGTTGCTTCCGCCAAGGAAAAAATCTGCGCGCAATTC
ATATTGAACACCGCCCGCTGGAATCGGGCGCTCAGGCCGTAGAGGACCTGGAAAAAGGACAGGT
GCTGGCGGTGTTATCTCGGATGACAGGTAAC (서열번호 23)

MTAEQNGVSDSRREFQEFGGPIAQTYQLPAPASDEVLLKVNYCGVCHSDVHLHDGYFELGGDKR
LNFAMPLPLTLGHEVIGTVVAVGDQVTGVKPGDQRLIYPWIGCGKCGACQKGEENLCVTPAHLGVNK
PGGYADHIVPHSRYLDDISGLNPGDAATLACSLTTFSAINKVLPLADDQWTVVIGCGGLGQMALRIL
QAMGIGNVIGIDLSEEKRLAHESGARHSFDPNPKLNRVVAETCPGTVQAALDFVNEQTAQLALS
LGKGGKVVPVGLHGGELRYPLPIITNKAVSIIGSYVGLKELEDLVAFAKEKNLPPHIEHRPLESAAQA
VEDLEKQVAGRVLDAGN (서열번호 24)

GFP (음성 대조군)

ATGACCGCACTTACGGAAGGGGCAAACTGTTTGAGAAAGAGATACCGTATATAACCGAACTGGA
AGGCGAGCTAGAAAGGATGAAATTTATAATTAAAGCGAGGGGACCGGGGACCGGACCGACCGGG
ACCATTAAGCGAAATACATATGCACTACGGGCGACCTGCCGGTACCGTGGGCAACCCCTGGTGA
CACCTTGAGCTACGGGGTCCAGTGTTCGCCAAGTACCCGAGCCACATAAAGGATTTCTTTAAGAG
CGCCATGGCGGAAGGGTATACCAAGAGCGTACCATAAGCTTCGAAGGCGACGGCGTGTACAAGA
CGCGTCTATGCTACCTACGCAACGCGGGTCTATATACAATCGTGTAAACGCTGACTGGGGAGAAT
TTAAGAAAGACGGGCACATTCTGCGTAAAGAACGTCGATTCCAATGCCGCCAAGCAATTCTGTATA
TTCTGCTGACACCGTCAACAATGGCATACGCGTCGAGTTCAACAGGCGTACGATATTGAAGGG
GTGACCGAAAAAAGTGGTACCAATGACGCCAAATGAATCGTCCGCTTGGCGGCGAGTGGCGGAGT
GCATATACCGGTTATCATCATCATTAACCTACACACCAAACTGAGCAAAAGACCGGCGACGCGCC
GTGATCATATGTGCTGGTTGAGGTAGTGAAAGCGGTGATGCTGGACAGTATCATGTA (서열번호
25)

MTALTEGAKLFEKEIPYITELEGDVEGMKFIKGEGTGDTTGTIKAKYICTTGDLPVPWATLVSTLSYG
VQCFAYKPSHKDFKSAAMPEGYTQERTISFEGDGVYKTRAMVITYERGSIVNRVLTGENFKKDGHLR
KNVAFQCPSSLYILPDTVNNIRVEFNQAYDIEGVTEKLVTKCSQMNRLAGSAVHIPRHHYHTYHK
LSKDRDERRDHMCLVEVVKAVDLDTYQ (서열번호 26)

[0250]

효소 스크리닝 데이터

표 4. LeuDH 효소 및 대조군 대비 활성

등록	단백질 돌연변이	군주	대조군 대비 개선 배수	뉴클레오티드 서열번호	단백질 서열번호
P0A392	wt	대조군	0	37	257
A0A1T4PGG9	wt	t160946	2.846	38	258
A4CBM3	wt	t161014	2.188	39	259
A0A0C1US13	wt	t160854	2.178	40	260
A0A1M6BE59	wt	t160389	2.166	41	261
K2M7H0	wt	t160943	2.027	42	262
A0A1Q6ZIF7	wt	t160092	2.005	43	263
A0A075JPW8	wt	t160267	2.002	44	264
A0A0B5AS65	wt	t160288	1.910	45	265
A0A0V8JFL2	wt	t160337	1.826	46	266
A0A1S2LUY1	wt	t160524	1.804	47	267
A0A0A8UN70	wt	t161111	1.792	48	268
P0A392	G43T	t159984	1.775	49	269
A0A1E7PTP0	wt	t161162	1.751	50	270
A0A1S9B636	wt	t160283	1.741	51	271
P0A392	E116V	t160562	1.553	52	272
A0A1D2RXB2	wt	t160434	1.550	53	273
K4KRS4	wt	t160706	1.548	54	274
P0A392	L76F	t160502	1.538	55	275
P0A392	T136R	t160559	1.521	56	276
P0A392	A297C	t160202	1.509	57	277
A0A1I1INGX1	wt	t160947	1.501	58	278
A0A142ITE6	wt	t161198	1.401	59	279
I1DTY5	wt	t160169	1.364	60	280
P0A392	A297Y	t160199	1.364	61	281
A0A0A0EMP0	wt	t160499	1.359	62	282
W4PY11	wt	t160682	1.359	63	283
R8B531	wt	t161210	1.359	64	284
A0A1Q2KY34	wt	t160573	1.340	65	285
L1QQC1	wt	t161091	1.333	66	286
D6XVM2	wt	t160162	1.301	67	287
P0A392	L78V	t160587	1.281	68	288
A0A1G8KLY7	wt	t160351	1.267	69	289
A0A0J6CNT2	wt	t160438	1.254	70	290
P0A392	L300K	t160181	1.196	71	291
U3HCY1	wt	t161117	1.191	72	292
A0A1K1TVW4	wt	t160461	1.188	73	293
A0A1Y6CWJ6	wt	t160154	1.186	74	294
A0A154W9T2	wt	t160973	1.171	75	295

[0251]

IID544	wt	t161185	1.149	76	296
A0A165NUD8	wt	t161204	1.149	77	297
A0A0A8JN83	wt	t160338	1.144	78	298
P0A392	N71T	t160401	1.144	79	299
F7RX04	wt	t160786	1.110	80	300
A0A1U9K9A9	wt	t160671	1.108	81	301
A0A0K6GVS2	wt	t160957	1.105	82	302
A0A136MKS4	wt	t160417	1.095	83	303
A0A0A5GIG6	wt	t160609	1.076	84	304
A0A143BJV1	wt	t160627	1.051	85	305
K6YKY7	wt	t161088	1.046	86	306
A0A0T5PG63	wt	t160158	1.032	87	307
A0A1M6L5E8	wt	t160479	1.032	88	308
P0A392	L42Q	t160013	1.029	89	309
A0A0A2TA47	wt	t160286	1.017	90	310
P0A392	A297H	t160636	1.012	91	311
A0A0Q5UT14	wt	t160279	1.002	92	312
I4D8U4	wt	t160598	1.000	93	313
P0A392	I113V	t160129	0.993	94	314
A0A1G3WLY4	wt	t159999	0.976	95	315
P0A392	A297N	t160134	0.968	96	316
P0A392	A297M	t160503	0.954	97	317
A0A1X4MV49	wt	t160926	0.949	98	318
P0A392	A297L	t160497	0.912	99	319
A0A0J1FEE3	wt	t160141	0.897	100	320
P0A392	E116A	t160512	0.892	101	321
P0A392	M67T	t160125	0.883	102	322
A0A0F7HKR2	wt	t160291	0.873	103	323
K0AAV5	wt	t160552	0.870	104	324
A0A1Q4XJW1	wt	t160891	0.868	105	325
P0A392	L300N	t160557	0.866	106	326
A0A0K9GVI6	wt	t160443	0.863	107	327
W7D8C3	wt	t160771	0.858	108	328
F7NG13	wt	t160215	0.851	109	329
A0A1H8Q403	wt	t160870	0.836	110	330
P0A392	L42T	t160357	0.829	111	331
E1WZZ8	wt	t160664	0.797	112	332
A0A0K9GC14	wt	t160444	0.790	113	333
P0A392	V296N	t160184	0.787	114	334
A0A1F3SFY8	wt	t160002	0.785	115	335
P0A392	L78K	t160487	0.782	116	336
P0A392	T136S	t160176	0.768	117	337
A0A1Y5EK08	wt	t160841	0.768	118	338
P0A392	T136F	t160489	0.763	119	339
N0AUJ4	wt	t160823	0.751	120	340
P0A392	M67Q	t159980	0.748	121	341
C4L3E4	wt	t160256	0.748	122	342
A0A1I6TTT1	wt	t160115	0.733	123	343
P0A392	A297R	t160509	0.733	124	344
A0A1H7JVK8	wt	t160952	0.733	125	345
A0A1U7M8J0	wt	t160255	0.724	126	346

[0252]

P0A392	L300Q	t160226	0.721	127	347
A1S7B6	wt	t160188	0.719	128	348
P0A392	V293S	t160602	0.711	129	349
C1A7X5	wt	t160733	0.709	130	350
A0A0W0TJD2	wt	t161212	0.697	131	351
P0A392	I113F	t160504	0.689	132	352
P0A392	M67E	t160064	0.685	133	353
A0A1U7JH14	wt	t160966	0.685	134	354
P0A392	L300A	t160612	0.680	135	355
P0A392	E116S	t160543	0.675	136	356
P0A392	G43F	t160059	0.672	137	357
P0A392	A297F	t160588	0.670	138	358
M8DS05	wt	t160310	0.663	139	359
P0A392	L300C	t160633	0.658	140	360
P0A392	L300F	t160128	0.655	141	361
M7N8L2	wt	t160152	0.655	142	362
P0A392	L78F	t160584	0.653	143	363
G8R2S3	wt	t160212	0.650	144	364
A0A0P8B102	wt	t161073	0.650	145	365
S2YPJ0	wt	t160830	0.643	146	366
A0A1M5CX03	wt	t159964	0.636	147	367
P0A392	L76E	t160245	0.626	148	368
A0A1M5IEB6	wt	t160988	0.626	149	369
A0A0F6SHW7	wt	t160860	0.619	150	370
A0A0U3AUS4	wt	t160964	0.619	151	371
A0A081G3H3	wt	t160968	0.604	152	372
A0A1Q4UNH5	wt	t161006	0.599	153	373
P0A392	A297D	t160548	0.597	154	374
P0A392	V293Q	t160249	0.594	155	375
P0A392	T136E	t160648	0.594	156	376
P0A392	L300D	t160248	0.587	157	377
P0A392	L300T	t160270	0.587	158	378
P0A392	L76H	t160546	0.587	159	379
P0A392	L76W	t160139	0.579	160	380
P0A392	L76M	t160274	0.575	161	381
P0A392	L300M	t160541	0.548	162	382
T0CG61	wt	t160808	0.538	163	383
A0A166W971	wt	t160538	0.535	164	384
P0A392	V296C	t160206	0.533	165	385
P0A392	A297E	t160567	0.533	166	386
K2JU58	wt	t160877	0.523	167	387
P0A392	G44I	t160011	0.516	168	388
A0A0M4FMC6	wt	t160371	0.516	169	389
P0A392	M67S	t160060	0.509	170	390
A0A0K1JA83	wt	t160995	0.509	171	391
P0A392	A115T	t159988	0.504	172	392
A0A1N6U8W9	wt	t160814	0.504	173	393
A0A075LQK1	wt	t160493	0.499	174	394
P0A392	G44Y	t160080	0.494	175	395
P0A392	L300H	t160197	0.494	176	396
A0A0K3QRE8	wt	t160626	0.489	177	397

[0253]

A0A1M6M3I5	wt	t160912	0.487	178	398
A0A0F7JZ22	wt	t161016	0.477	179	399
P0A392	L78H	t160634	0.469	180	400
A0A1Y6BX33	wt	t160700	0.460	181	401
P0A392	V296L	t160146	0.447	182	402
A0A1L8CTI5	wt	t161020	0.445	183	403
P0A392	L300Y	t160145	0.443	184	404
P0A392	E116N	t160539	0.428	185	405
A0A171DN74	wt	t160716	0.423	186	406
P0A392	A297K	t160491	0.416	187	407
P0A392	L78Y	t160594	0.416	188	408
E6TXR8	wt	t160618	0.416	189	409
P0A392	N71H	t160120	0.411	190	410
A0A1G3X1T7	wt	t160910	0.411	191	411
P0A392	E116W	t160246	0.408	192	412
U4KND6	wt	t160852	0.408	193	413
P0A392	E116R	t160131	0.399	194	414
P0A392	N71C	t160385	0.399	195	415
A0A1G0BBA9	wt	t160899	0.396	196	416
A0A1Y2L717	wt	t160990	0.396	197	417
P0A392	A297T	t160227	0.389	198	418
A0A0M4UKZ2	wt	t160340	0.379	199	419
P0A392	A297W	t160596	0.357	200	420
P0A392	L78C	t160406	0.350	201	421
E2SC01	wt	t161059	0.350	202	422
A0A1K1PP57	wt	t160629	0.347	203	423
P0A392	G44K	t159990	0.345	204	424
P0A392	A115S	t160495	0.342	205	425
P0A392	L300S	t160275	0.337	206	426
P0A392	L300W	t160639	0.337	207	427
A0A1G0A9I7	wt	t160875	0.337	208	428
A0A0W7WYJ8	wt	t161047	0.337	209	429
P0A392	V296E	t160520	0.325	210	430
P0A392	T136Y	t160638	0.325	211	431
P0A392	A115V	t160123	0.320	212	432
A0A1V0ADI4	wt	t160970	0.318	213	433
W7ZGF1	wt	t160812	0.315	214	434
P0A392	A115Q	t159982	0.311	215	435
A0A1H6CJX7	wt	t161141	0.308	216	436
P0A392	M67K	t160356	0.296	217	437
P0A392	L78Q	t160581	0.296	218	438
P0A392	T136L	t160589	0.293	219	439
P0A392	E116L	t160604	0.293	220	440
P0A392	I113M	t160628	0.291	221	441
P0A392	L76Y	t160516	0.289	222	442
P0A392	V293A	t160655	0.274	223	443
P0A392	V296K	t160243	0.267	224	444
P0A392	L76R	t160153	0.264	225	445
P54531	wt	t160721	0.262	226	446
P0A392	V296I	t160271	0.259	227	447
P0A392	L300R	t160560	0.254	228	448

[0254]

K9ARW8	wt	t160789	0.252	229	449
P0A392	L76S	t160133	0.249	230	450
P0A392	I113W	t160094	0.244	231	451
P0A392	A115N	t160194	0.240	232	452
P0A392	V296S	t160644	0.240	233	453
P0A392	E116M	t160643	0.235	234	454
P0A392	L42A	t160402	0.232	235	455
P0A392	V293C	t160500	0.225	236	456
P0A392	N71M	t160324	0.220	237	457
P0A392	V296A	t160143	0.213	238	458
P0A392	G43W	t160099	0.210	239	459
P0A392	A297Q	t160140	0.196	240	460
P0A392	V293T	t160221	0.191	241	461
P0A392	I113Y	t160098	0.188	242	462
P0A392	L76I	t160601	0.188	243	463
P0A392	G44H	t160029	0.176	244	464
P0A392	L76K	t160585	0.171	245	465
P0A392	G43Y	t159996	0.169	246	466
P0A392	N71D	t160415	0.142	247	467
P0A392	I113Q	t160632	0.139	248	468
P0A392	M67A	t160055	0.127	249	469
P0A392	V296T	t160630	0.122	250	470
P0A392	L76T	t160603	0.115	251	471
A0A1Q4VRJ4	wt	t161033	0.112	252	472
B2A513	wt	t160167	0.108	253	473
P0A392	G43E	t160096	0.083	254	474
P0A392	N71K	t160101	0.044	255	475

[0255]

표 5. KiVD 효소 및 대조군 대비 활성

등록	표지	대조군 비교 개선 배수	뉴클레오타이드 서열번호	단백질 서열번호
Q684J7	대조군	0	477	533
A0A085UD38	t163850	1.958	478	534
A0A090DYV6	t163542	3.986	479	535
A0A0A6W4H3	t163732	4.354	480	536
A0A0B1U4F6	t163805	2.972	481	537
A0A0D0SDJ9	t163730	3.292	482	538
A0A0D2CSK3	t163274	3.965	483	539
A0A0D2GWW0	t163016	4.354	484	540
A0A0H4KFT8	t163716	3.958	485	541
A0A0J8UR79	t163869	2.250	486	542
A0A0K2Y209	t163916	3.944	487	543
A0A0L0P8D8	t163988	5.097	488	544
A0A0L7TB96	t163842	4.833	489	545
A0A0M5JJZ2	t164076	4.944	490	546
A0A0M5MY84	t163914	4.139	491	547
A0A0Q4N500	t164007	4.493	492	548
A0A0T9T7Y7	t163705	3.694	493	549
A0A0T9UPI9	t163338	3.493	494	550
A0A0U1CW59	t163964	3.201	495	551
A0A0U2NS09	t163656	2.222	496	552
A0A198FEB4	t163871	4.382	497	553
A0A1B1NY37	t163888	3.646	498	554
A0A1B7ILY5	t163742	3.792	499	555
A0A1B9AUW4	t162995	3.889	500	556
A0A1D4X3F2	t163818	4.708	501	557
A0A1F2KK66	t163546	3.403	502	558
A0A1G7WAJ7	t163085	5.076	503	559
A0A1M7EHD4	t163474	1.813	504	560
A0A1Q4T3V5	t163704	4.535	505	561
A0A1T1GFV6	t163784	3.500	506	562
A0A1U4TJK1	t163702	4.722	507	563
A0A1V2L8B3	t164100	3.229	508	564
A0A1V2YXQ3	t163766	2.319	509	565
A0A1V4SV36	t163852	4.396	510	566
A0A1V6TQU7	t162902	3.118	511	567
A0A1W6B724	t163806	3.639	512	568
A0A1X0AE10	t163798	3.104	513	569
A0A1X1XPA7	t163472	3.826	514	570
A0A1X2FKJ1	t163432	3.035	515	571
A0A1Y6E4E9	t163406	3.486	516	572
A0A205J7X5	t163837	3.910	517	573

[0256]

A0A2B1L7A1	t163722	4.215	518	574
B9DJU8	t163844	4.597	519	575
D4B725	t163868	4.111	520	576
D4C3A5	t163661	2.139	521	577
D4F0I3	t163478	0.896	522	578
D7UWC4	t163880	3.785	523	579
F58QV4	t163740	2.535	524	580
G9YCD8	t163678	0.090	525	581
I1CGS4	t163934	3.785	526	582
J2LV57	t163902	2.667	527	583
Q6C9L5	t163155	4.222	528	584
R5SST3	t163337	3.014	529	585
R8AV71	t163285	4.535	530	586
S3IST7	t163983	2.979	531	587
W0L941	t163973	3.396	532	588

[0257]

표 6. Adh 효소 및 대조군 대비 활성

등록	표지	대조군 대비 개선 배수	뉴클레오타이드 서열 서열번호	단백질 서열 서열번호
P00331	대조군	0	589	645
A0A011RFM0	t159061	-0.581	590	646
A0A068NM64	t159163	4.815	591	647
A0A081B9F7	t159282	5.992	592	648
A0A0F7S860	t159174	-0.411	593	649
A0A0F8XA97	t159080	-0.250	594	650
A0A0L8BIH2	t158526	0.629	595	651
A0A0M2SIC1	t158995	0.323	596	652
A0A0M8TKC3	t158267	2.427	597	653
A0A0N1F703	t159004	9.032	598	654
A0A0P1J1W4	t158538	10.516	599	655
A0A0Q6FH05	t159022	-0.113	600	656
A0A0Q9AMT3	t158946	1.476	601	657
A0A163KUH6	t159154	0.710	602	658
A0A192IDS9	t159028	10.581	603	659
A0A1A0K0C6	t159162	0.645	604	660
A0A1E4TMA4	t159319	11.113	605	661
A0A1E7X363	t159283	4.234	606	662
A0A1Q7HM90	t159036	-0.492	607	663
A0A1V1TTZ9	t158998	-0.613	608	664
A0A1V2EYM1	t159040	3.750	609	665
A0A1V6E459	t159120	1.008	610	666
A0A1Y0G594	t159236	1.645	611	667
A2V8B3	t159176	4.758	612	668
A9MKQ8	t158774	-0.548	613	669
C0SPA5	t158820	1.113	614	670
D8MZF3	t159280	6.234	615	671
F0IX07	t159318	0.371	616	672
H1ZV38	t158442	1.694	617	673
J1KN15	t158976	4.008	618	674
J5T2P7	t159183	-0.161	619	675
K4IPR3	t158247	5.444	620	676
M1LUC5	t158246	0.073	621	677
M2N9N4	t159152	0.669	622	678
M2QHN1	t159090	0.282	623	679
M2YNQ9	t159054	3.629	624	680
M5FVU5	t158291	0.565	625	681
O74822	t158955	-0.500	626	682
P08843	t158458	0.460	627	683
P0DMQ6	t158893	-0.444	628	684
P13603	t158263	0.645	629	685

[0258]

P14219	t158869	-0.048	630	686
P14673	t158726	0.952	631	687
P14675	t158728	6.056	632	688
P20368	t158816	0.798	633	689
P25141	t158333	3.677	634	690
P28032	t158454	2.887	635	691
P39451	t158390	5.500	636	692
P39849	t158243	0.516	637	693
P40394	t158613	3.460	638	694
P42328	t158520	2.065	639	695
Q2FJ31	t158326	1.024	640	696
Q38707	t158580	-0.105	641	697
Q99W07	t158330	1.597	642	698
S0EJ18	t159328	11.185	643	699
W5YKG3	t159122	0.782	644	700

[0259]

표 7. 서열번호 27 대비 LeuDH 활성 증가된 효소 중 보존된 아미노산.

서열번호 27 중 해당 위치	아미노산
13	V
16	W
42	Q
43	T, Y, F, E, W
44	I, H, K, Y
67	T, E, A, S, K
71	K
73	S
76	R, H, Y, S, K, W
92	Y
93	H
95	G
100	G
105	C
111	G
113	M
115	N, V
116	R, N, W
120	A
122	D
136	E
140	D
141	M
160	S
185	F
196	N
228	Y
248	M
256	C
293	Q, C
296	K, N
297	R, Q, K
300	C, D
302	T, S
305	C
319	F
330	M

[0260]

표 8. 서열번호 29 대비 KivD 활성 증가된 효소 중 보존된 아미노산.

서열번호 29의 위치 중 해당 위치	아미노산
33	Y
44	Q
117	M
129	I
185	W
190	I
225	I
227	Y
311	L
312	G
313	T
328	P
341	W
345	H
347	C
420	R
494	D
508	C
550	F

[0261]

표 9. 서열번호 31 대비 ADH 활성이 증가된 효소 중 보존된 아미노산.

서열번호 31 중 해당 위치	아미노산
9	P
16	G
23	Q
28	R
30	A
93	K
98	L
99	R
114	P
115	K
119	Y
194	Y
242	P
249	K
255	E
260	D
269	H
281	Q
325	L
333	M
334	P
348	Q

[0262]

[0263]

등가물

[0264]

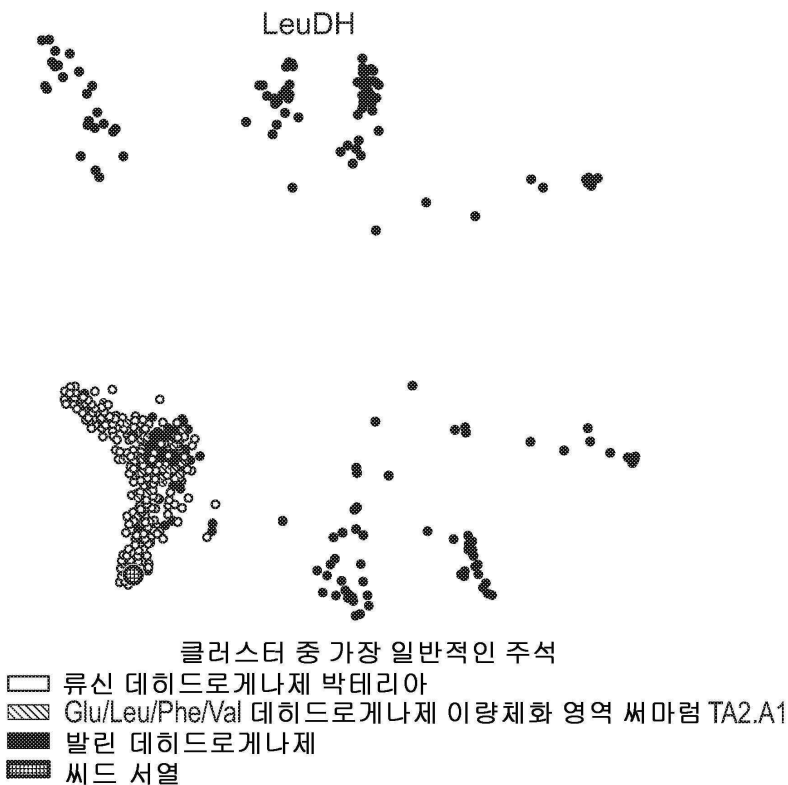
당업자는 단지 통상의 실험을 사용하여, 본 개시에 기술된 본 발명의 특별한 실시형태에 대한 많은 등가물을 인식하거나 또는 확인할 수 있을 것이다. 이러한 등가물은 하기 청구항에 포괄시키고자 한다.

[0265]

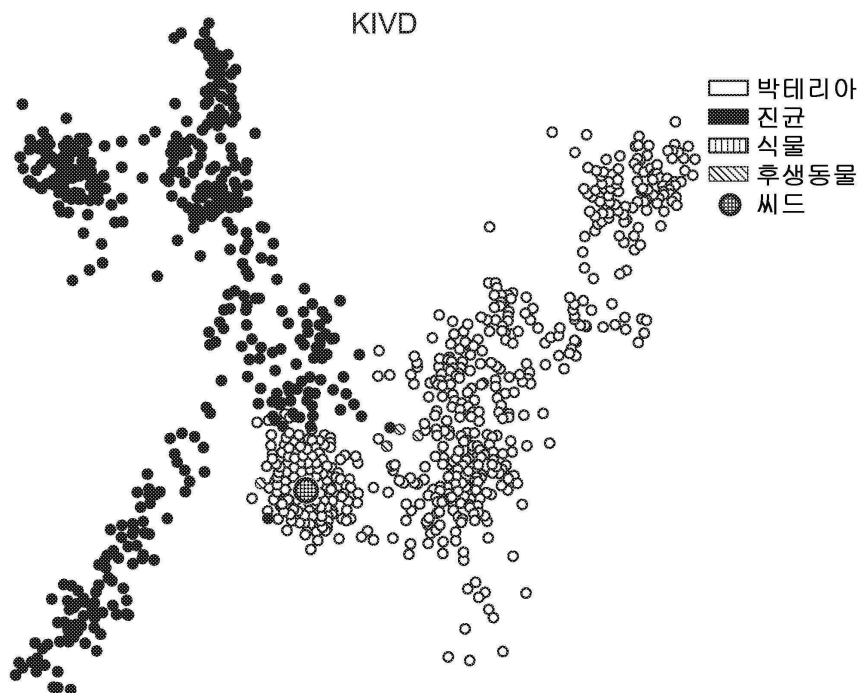
본 출원에 개시된, 특허 문헌을 포함한 모든 참조는 특히 본 개시에서 참조하는 개시에 대해서, 그들 전체로 참조로 편입시킨다.

도면

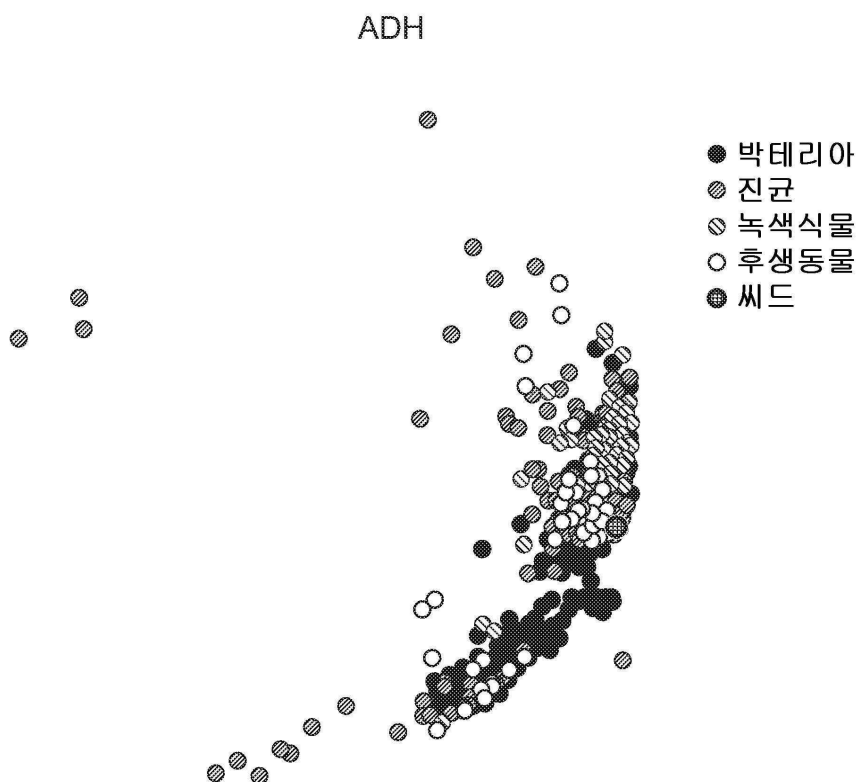
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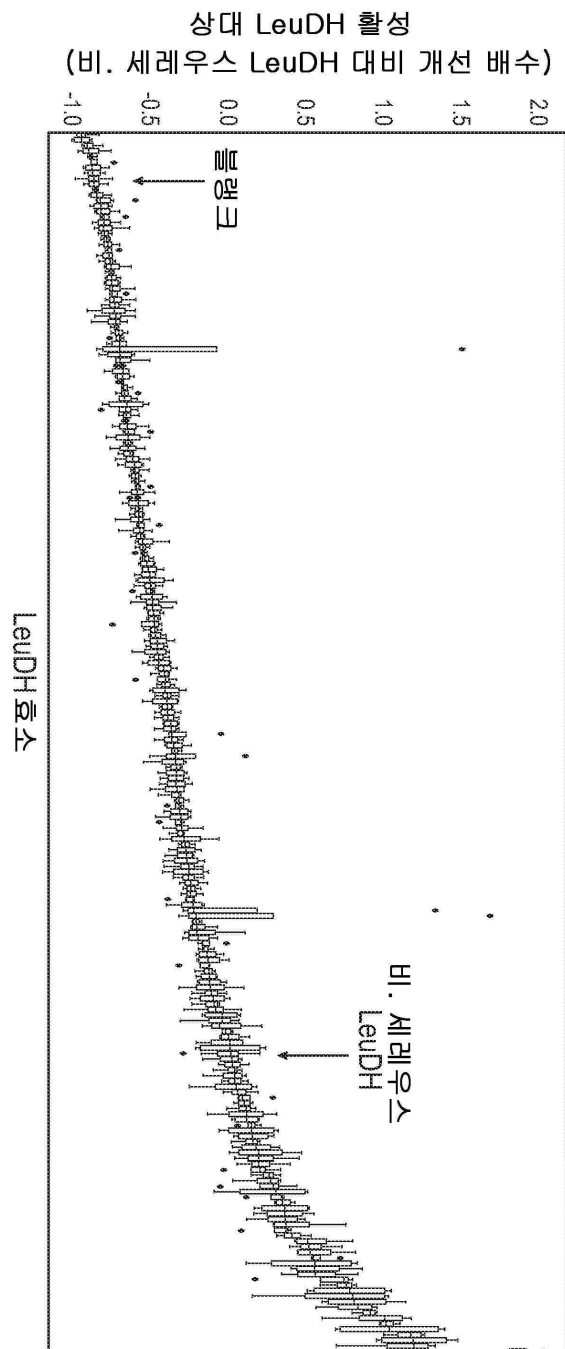
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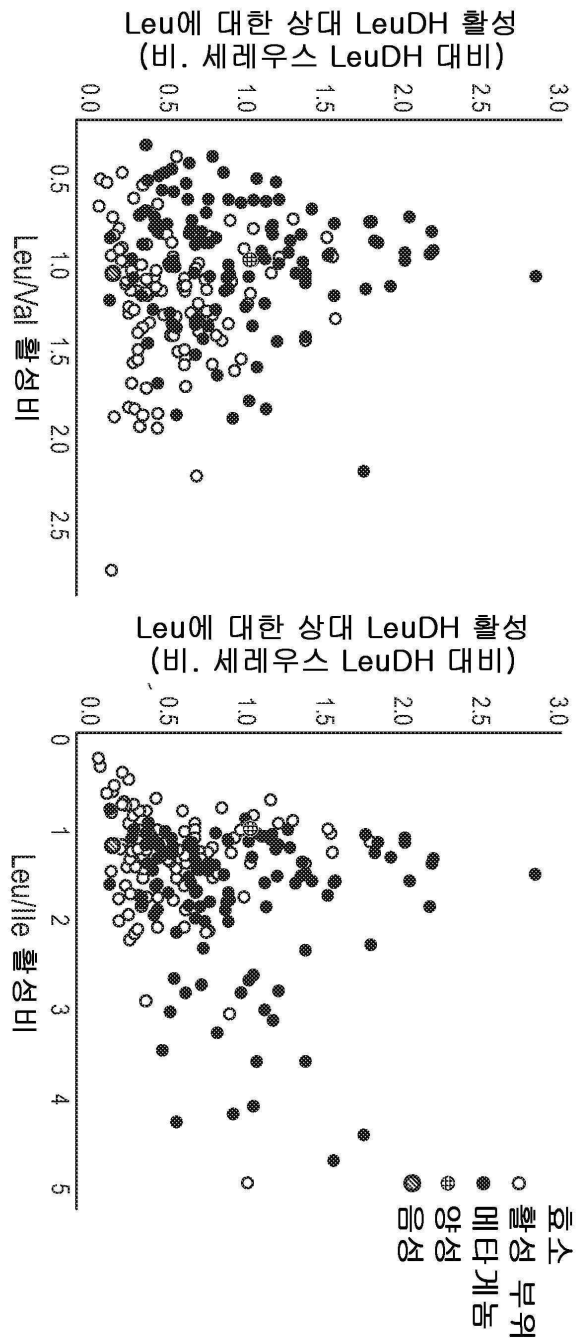
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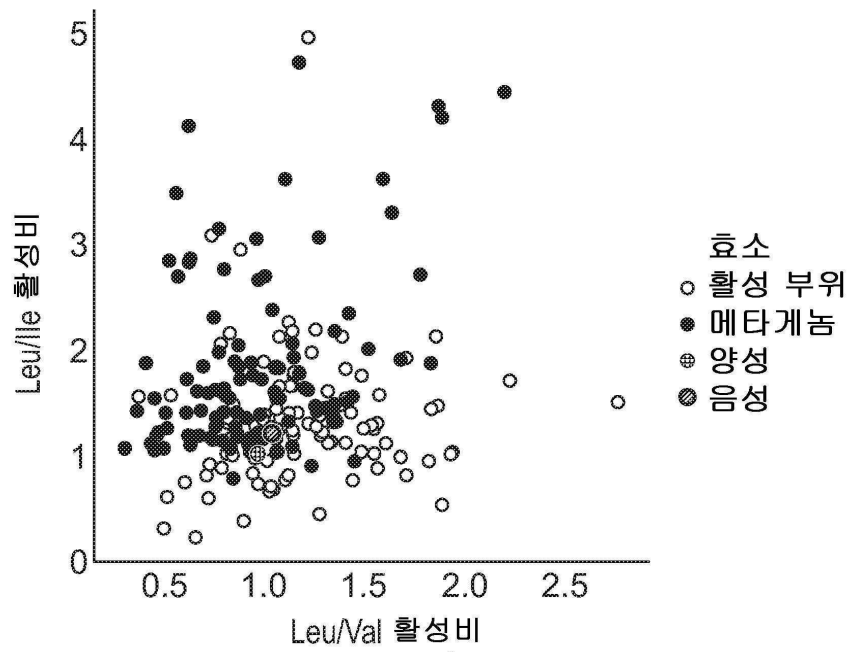
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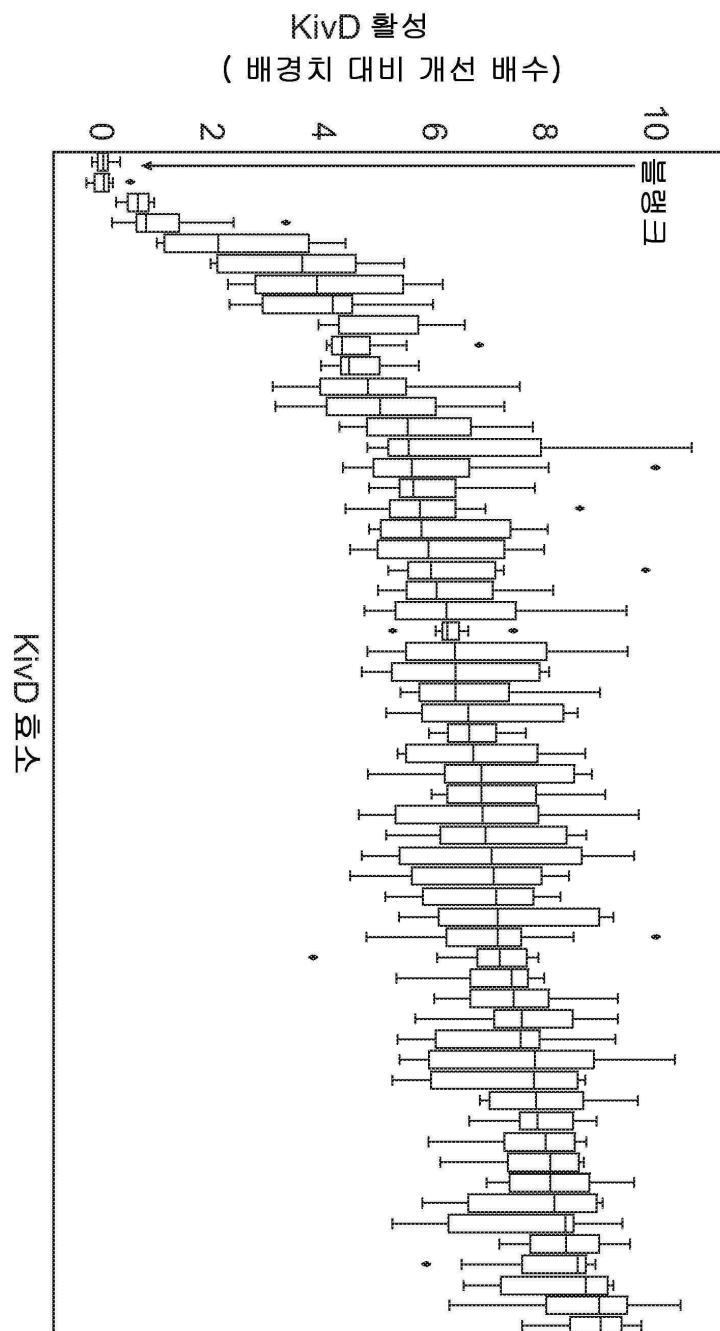
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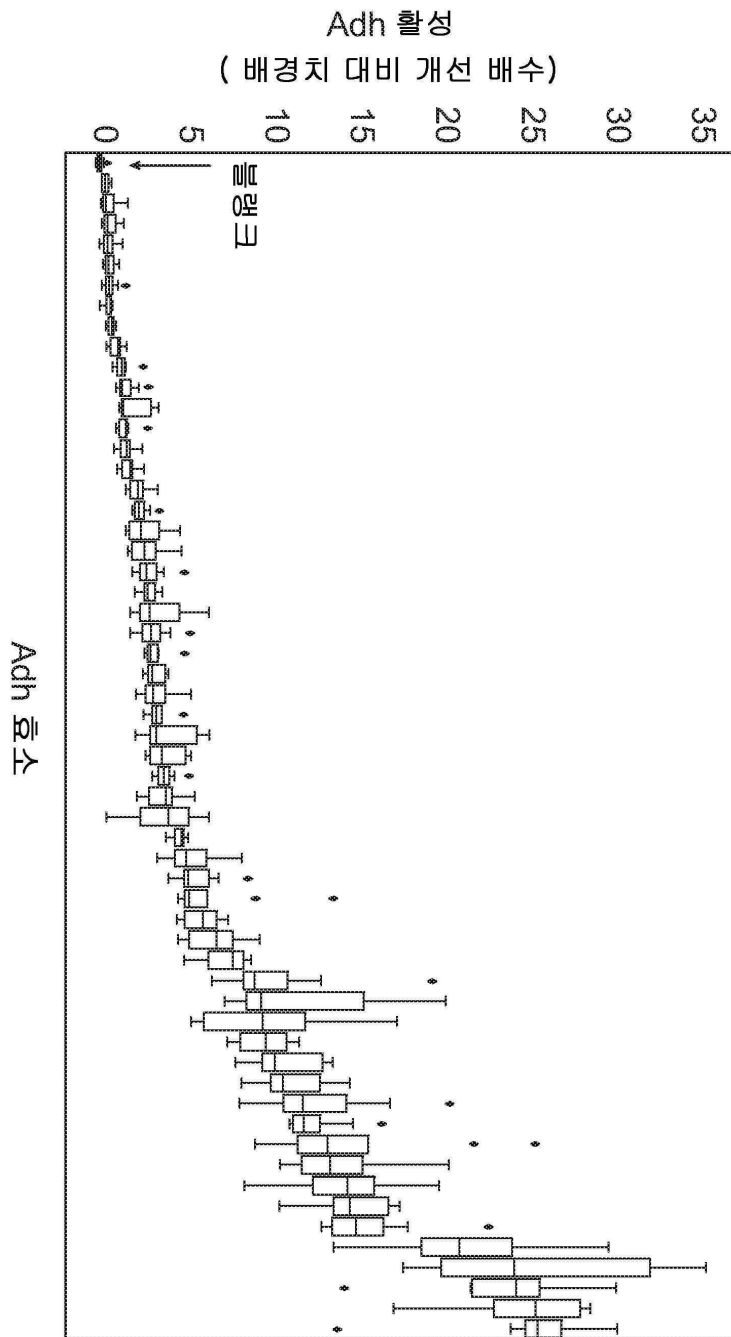
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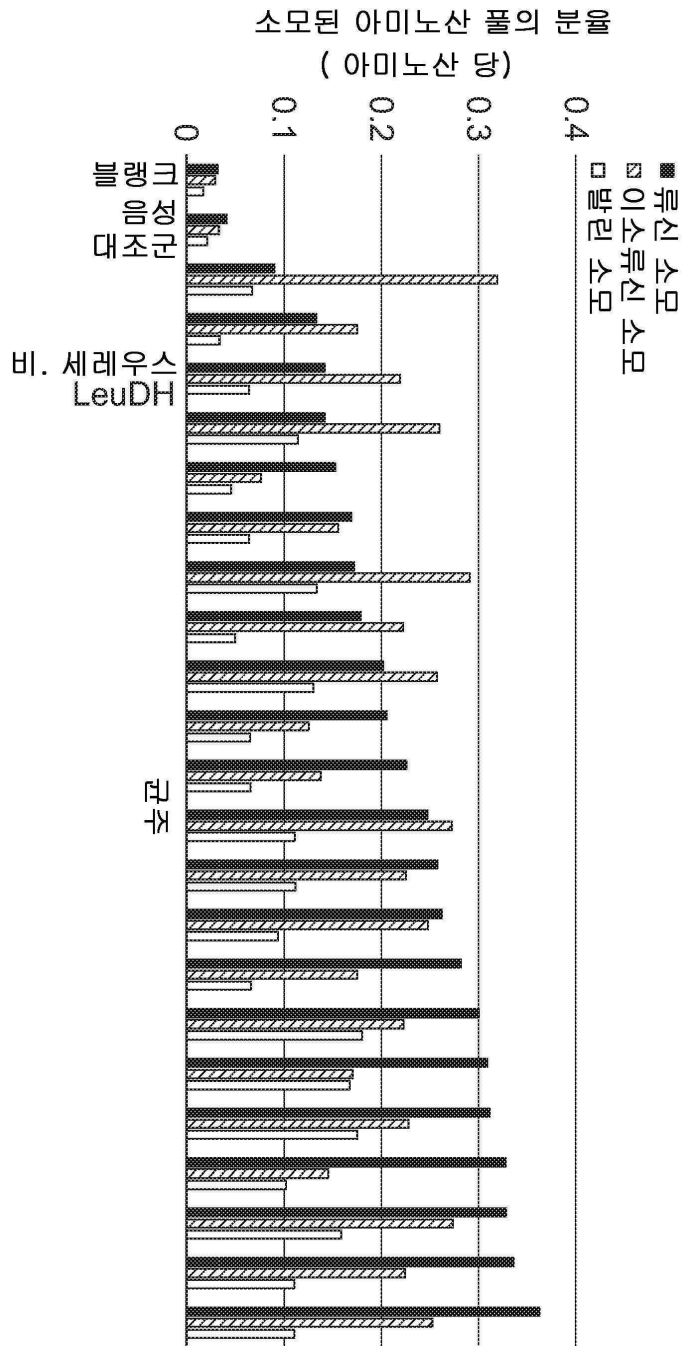
도면5



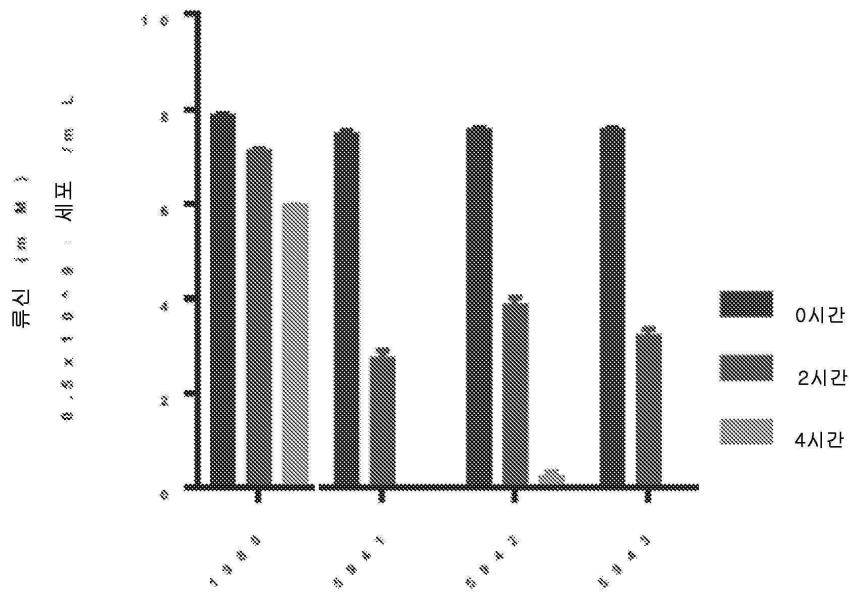
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도면7

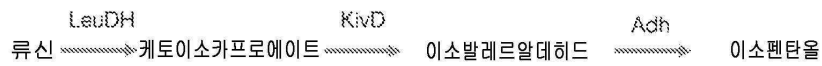


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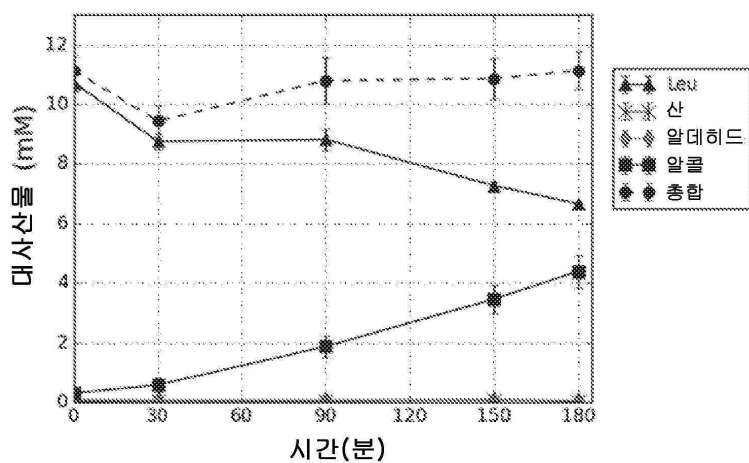


도면9

MSUD 경로 :



도면10



서열 목록

SEQUENCE LISTING

<110> Ginkgo Bioworks, Inc.

Synlogic Operating Company, Inc.

<120> BIOSYNTHESIS OF ENZYMES FOR USE IN TREATMENT OF MAPLE SYRUP URINE
DISEASE (MSUD)

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<151> 2019-06-21

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<151> 2019-06-21

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35 40 45

Asn Ser Glu Glu Asp Ala Val Glu Asp Val Ile Arg Leu Ala Arg Gly

50 55 60

Met Thr Tyr Lys Ala Ala Cys Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80

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

85 90 95

Arg Gly Leu Gly Arg Tyr Val Gln Ser Leu Asn Gly Arg Tyr Ile Thr

100 105 110

Ala Glu Asp Val Asn Thr Ser Thr Lys Asp Met Ala Tyr Val Ala Met

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

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 180 185 190
 Val Gly Thr Tyr Leu Leu Glu Tyr Leu Gln Lys Glu Gly Ala Lys Leu
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 Phe Gly Ala Lys Met Val Gly Leu Asp Glu Ile Tyr Asp Gln Asp Val

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Glu Lys Ile Phe Asp Ile Thr Thr Gln Val Leu Asn Lys Ala Glu Gln
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gctggcaaac gtatcgctgt tcaagggtgt ggtcatgttg gcacttatct gcttgagcat	600
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gcaggcgcgc gttttggcgc acaggttgtt ggcttgacg atatctacga tcaagaggtc	720
gacatttact ctccatgtgc tctcgggtgt accatcaacg atgacactat cgatcgctg	780
cgttgcgctg ttgtagccgg ttgcgcaaac aaccagctga aagaagaaaa cgtccacggt	840
ccggcgctgg ttgagcgcgg gatagtatac gccccagact tctgatcaa tgcaggtggc	900
ctgattaacg tgiatagcga agttacaggg tctaccgctc agggggcttt aactcagacc	960
gaaaaaatct atgactacac actccaagtt ctggaaaaag ccgcggctga aggtctgcac	1020
ccgcagcagg ctgcgatccg tcaggcggaa caacgcatcg ctgcaattgg taagtgaaa	1080
agcacctac	1089

<210> 6

<211> 363

<212> PRT

<213> Unknown

<220><223> Hymenobacter sp. CRA2

<400> 6

Met Val Glu Ile Gln Ala Leu Pro Glu Thr Ser Ile Phe Gly Gln Ile

1 5 10 15

Ala Asp His Gln His Glu Gln Val Val Phe Cys His Asp His Glu Thr

20 25 30

Gly Leu Arg Ala Ile Ile Gly Ile His Asn Thr Val Leu Gly Pro Ala

35 40 45

Leu Gly Gly Thr Arg Met Trp His Tyr Ala Thr Glu Ala Glu Ala Leu

50 55 60

Asn Asp Val Leu Arg Leu Ser Arg Gly Met Thr Tyr Lys Ala Ala Ile

65 70 75 80

Ser Gly Leu Asn Leu Gly Gly Gly Lys Ala Val Ile Ile Gly Asp Ala

85 90 95

Lys Thr Ile Lys Thr Glu Ala Leu Leu Arg Lys Phe Gly Arg Phe Val

100 105 110

Gln Asn Leu Asn Gly Lys Tyr Ile Thr Ala Glu Asp Val Asn Met Thr

115 120 125

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

130 135 140

Leu Pro Glu Ser Met Gly Gly Ser Gly Asp Pro Ser Pro Val Thr Ala

145 150 155 160

Tyr Gly Thr Tyr Met Gly Met Lys Ala Ala Ala Lys Lys Ala Phe Gly

165 170 175

Ser Asp Ser Leu Ala Gly Lys Arg Ile Ala Val Gln Gly Val Gly His

180 185 190

Val Gly Thr Tyr Leu Leu Glu His Leu Thr Lys Glu Gly Ala Gln Ile

195 200 205

Val Leu Thr Asp Tyr Tyr Lys Glu Arg Ala Glu Glu Ala Gly Ala Arg
 210 215 220
 Phe Gly Ala Gln Val Val Gly Leu Asp Asp Ile Tyr Asp Gln Glu Val
 225 230 235 240
 Asp Ile Tyr Ser Pro Cys Ala Leu Gly Ala Thr Ile Asn Asp Asp Thr
 245 250 255

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

Glu Lys Ile Tyr Asp Tyr Thr Leu Gln Val Leu Glu Lys Ala Ala Ala
 325 330 335
 Glu Gly Leu His Pro Gln Gln Ala Ala Ile Arg Gln Ala Glu Gln Arg
 340 345 350
 Ile Ala Ala Ile Gly Lys Val Lys Ser Thr Tyr
 355 360

<210> 7

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 7

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ggcactcgca tgtggcccta cgctagcgaa gaggaagcac tgaaagatgt ccttcgttta 180

tcccgtggga tgacctaaa agctgcggtt tcaggtctaa acctgggcgg cggtaaagct 240

gtgatctggg gtgatccgaa taaagacaag tctgaagcgc tgtttagagc cticggacgg 300

tttgtaaaca gcctgggcgg acgtacatt accgcggagg acgttggcat tgatgttaac 360

gacatggaat atgtgctgcg tgaaactgat tacgtcaccg gtgtacatca ggttcacggt 420
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 gccctggatg aaatctatga cgttgattgc gacgtgtact ccccgaccgc tctgggcggc 720
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<210> 8

<211> 366

<212> PRT

<213> Unknown

<220><223> Arenimonas sp SCN 70-307

<400> 8

Met Ile Phe Glu Thr Ile Ser Thr Ser Asn His Glu Glu Val Val Tyr

1 5 10 15

Cys His Asn Lys Asp Ala Gly Leu Lys Ala Ile Ile Ala Ile His Asn

20 25 30

Thr Val Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Pro Tyr Ala

35 40 45

Ser Glu Glu Glu Ala Leu Lys Asp Val Leu Arg Leu Ser Arg Gly Met

50 55 60

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

65 70 75 80

Val Ile Trp Gly Asp Pro Asn Lys Asp Lys Ser Glu Ala Leu Phe Arg

85 90 95

Ala Phe Gly Arg Phe Val Asn Ser Leu Gly Gly Arg Tyr Ile Thr Ala
100 105 110

Glu Asp Val Gly Ile Asp Val Asn Asp Met Glu Tyr Val Leu Arg Glu
115 120 125

Thr Asp Tyr Val Thr Gly Val His Gln Val His Gly Gly Ser Gly Asp
130 135 140

Pro Ser Pro Phe Thr Ala Tyr Gly Thr Leu Gln Gly Leu Met Ala Ala
145 150 155 160

Leu Gln Val Lys Phe Gly Asn Glu Asp Val Gly Asn Tyr Ser Tyr Ala
165 170 175

Val Gln Gly Val Gly His Val Gly Met Glu Phe Val Lys Leu Leu Arg
180 185 190

Glu Arg Gly Ala Lys Val Phe Val Thr Asp Ile Asn Lys Asp Ala Val
195 200 205

Gln Arg Ala Val Asp Glu Phe Gly Cys Glu Ala Val Ala Leu Asp Glu
210 215 220

Ile Tyr Asp Val Asp Cys Asp Val Tyr Ser Pro Thr Ala Leu Gly Gly
225 230 235 240

Thr Val Asn Asp Lys Thr Leu Pro Arg Leu Lys Cys Lys Val Ile Cys
245 250 255

Gly Ala Ala Asn Asn Gln Leu Ala Asn Asp Glu Ile Gly Val Glu Leu
260 265 270

Glu Lys Lys Gly Ile Leu Tyr Ala Pro Asp Tyr Ala Val Asn Ala Gly
275 280 285

Gly Leu Met Asn Val Ser Leu Glu Ile Asp Gly Tyr Asn Arg Glu Arg
290 295 300

Ala Met Arg Met Met Arg Thr Ile Tyr Tyr Asn Leu Gly Arg Ile Phe
305 310 315 320

Glu Ile Ser Lys Arg Asp Gly Ile Pro Thr Phe Arg Ala Ala Asp Arg
325 330 335

Met Ala Glu Glu Arg Ile Thr Ala Ile Gly Lys Leu Arg Leu Pro His

340	345	350	
Leu Gly Ala Ala Ala Pro Arg Phe Gln Gly Arg Arg Gly Asn			
355	360	365	
<210> 9			
<211> 1086			
<212> DNA			
<213> Artificial Sequence			
<220><223> Synthetic polynucleotide			
<400> 9			
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aagaccacgg gtctgcgcgc cattatcgct atacacgata catccttagg gccggcgctt			120
ggtggtaccc gtatgtggca gtatgcaact gacgacgatg ctattactga cgcactccgt			180
ctgtctcggg gcatgacctt caaagctgcg gtttctggcg taaatctggg cgggtgtaaa			240
gccgttatca tcggaacccc tcacagtgat aaaagcgaag cgctgtttcg cgcttacggc			300
agaatggtgg aatcccacgg tgggcgttac atcaccgccg aagacgttgg tactagcgta			360
cgatgatagg agtggattcg catggaacc aaatatgtaa cgggcgtggg tggcaacgga			420
ggctctgggtg acccctctcc agttaccgct ctgggtgttt actcgggcat gaaggcatgc			480
gctaaatcag tctatggtag tgatgcgctg agcggtaaaa ggatcgtggg tcagggcgcg			540
ggtaacgttg catcccatct gggtcacagt ctggtaaaag aaggcgctgt ggttttcgtc			600
actgacatct acgaagaaaa ggccaaagca ttagcggctg aaacgggcgc taccgtgatt			660
cgcaccgacg aggtttttac tacacaatgc gatattctct ctccgaacgc tctgggggcc			720
gtcctgaacg atgaaactat tccgcagctc acatgcgcta tcgtagctgg tggtgcaaac			780
aatcagctta aaatcgaaca acgtcacgcc acggctctgc aagagaaagg cattctgtat			840
gcgccggatt acgtaatcaa gcgccggggc ctcatgaatg tggcgagcga agttgacggc			900
tacaaccgtg aaaaggttat gcgccaggct gaaggatatt acgatattac tatgaacatc			960
ctaaataccg cgcgtgagcg taacatcctg accatcgaag catccaacgc gattgctgaa			1020
gagcggatca acaaagtctg ccatgttcac gggaacttca tcggttcccc gtctattcgc			1080
ggagta			1086
<210> 10			
<211> 362			
<212> PRT			
<213> Candidatus kapabacteria			

<400> 10

Met Gln Ile Phe Asp Thr Leu Gln Ser Met Gly His Glu Gln Val Val

1 5 10 15

Leu Cys Ser Asp Lys Thr Thr Gly Leu Arg Ala Ile Ile Ala Ile His

20 25 30

Asp Thr Ser Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Gln Tyr

35 40 45

Ala Thr Asp Asp Asp Ala Ile Thr Asp Ala Leu Arg Leu Ser Arg Gly

50 55 60

Met Thr Tyr Lys Ala Ala Val Ser Gly Val Asn Leu Gly Gly Gly Lys

65 70 75 80

Ala Val Ile Ile Gly Asn Pro His Ser Asp Lys Ser Glu Ala Leu Phe

85 90 95

Arg Ala Tyr Gly Arg Met Val Glu Ser Gln Arg Gly Arg Tyr Ile Thr

100 105 110

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

115 120 125

Glu Thr Lys Tyr Val Thr Gly Val Gly Gly Asn Gly Gly Ser Gly Asp

130 135 140

Pro Ser Pro Val Thr Ala Leu Gly Val Tyr Ser Gly Met Lys Ala Cys

145 150 155 160

Ala Lys Ser Val Tyr Gly Thr Asp Ala Leu Ser Gly Lys Arg Ile Val

165 170 175

Val Gln Gly Ala Gly Asn Val Ala Ser His Leu Val His Ser Leu Val

180 185 190

Lys Glu Gly Ala Val Val Phe Val Thr Asp Ile Tyr Glu Glu Lys Ala

195 200 205

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

210 215 220

Val Phe Thr Thr Gln Cys Asp Ile Phe Ser Pro Asn Ala Leu Gly Ala

225 230 235 240

Val Leu Asn Asp Glu Thr Ile Pro Gln Leu Thr Cys Ala Ile Val Ala

245 250 255

Gly Gly Ala Asn Asn Gln Leu Lys Ile Glu Gln Arg His Ala Thr Ala

260 265 270

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

275 280 285

Gly Gly Leu Met Asn Val Ala Ser Glu Val Asp Gly Tyr Asn Arg Glu

290 295 300

Lys Val Met Arg Gln Ala Glu Gly Ile Tyr Asp Ile Thr Met Asn Ile

305 310 315 320

Leu Asn Thr Ala Arg Glu Arg Asn Ile Leu Thr Ile Glu Ala Ser Asn

325 330 335

Ala Ile Ala Glu Glu Arg Ile Asn Lys Val Arg His Val His Gly Asn

340 345 350

Phe Ile Gly Ser Pro Ser Ile Arg Gly Val

355 360

<210> 11

<211> 1065

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 11

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ggtggcaccg gtatgtggaa ttacgccagt gaagaagatg ctatcctgga tgcgttacgc 180

ctggcgcgag gtatgactta taaaacgct gccgcaggtc tgaacctggg cggcggtaaa 240

gctgttatta tgggcgacag ccgtaccagc aaatcagagg aactgtttcg cgcgttcggt 300

cgttacgtgc aggcgctgaa cggccgttat atcaccgctg aggacgttgg tactaacgta 360

caagatatgg actggataca catggaaaca aagtttgtga cgggatctc ctcttcgtac 420

ggtgctagcg gagatccgtc cctctgacc gactgggagc ttaccgcgg tatgaaagcc 480

gccgcaaaag aagcgttcgg cagcgactct ttagagggtg aaactgttgc tattcagggt 540

cttggccacg tcggctatta cctggcaaaa cacctcactg atgaaggcgc taaactgatc 600

gtgacggata tcaattctga agccgttaag agggtagcgc gtgagttcgt tgctaccgca 660

gtccgtaccg aagaaatfff cggcggtaaa tgcgacatct ttgcgccctg tgctctgggt 720

gcagttatca acgatgaaac cattccgcag ctgaagtgcc aggtagttgc cgggtgctgcg 780

aacaatgtgt tgaagagga tcgcatgtgt gacgaactat acgaaaaagg aatcctgtac 840

gctccggact atgtaattaa cgccggcggc gttatcaacg tggccgacga actggaaggt 900

tacaacgtg aacgtgctct gaaaaaagtt gagatggtat atgataatgt ggcacgcgtc 960

atcgctattg ccaagcgtga ccatatcccg acttataaag cagcggaccg aatggctgag 1020

gaacgtattg cgaaaattgg caaagtttcc aacactttcc tgcgc 1065

<210> 12

<211> 355

<212> PRT

<213> Peptococcaceae bacterium

<400> 12

Met Thr Thr Phe Glu Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val

1 5 10 15

Leu Cys Gln Asp Asn Thr Ser Gly Leu Lys Ala Val Ile Cys Ile His

20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr

35 40 45

Ala Ser Glu Glu Asp Ala Ile Leu Asp Ala Leu Arg Leu Ala Arg Gly

50 55 60

Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80

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

85 90 95

Arg Ala Phe Gly Arg Tyr Val Gln Ala Leu Asn Gly Arg Tyr Ile Thr

100 105 110

Ala Glu Asp Val Gly Thr Asn Val Gln Asp Met Asp Trp Ile His Met

115 120 125

Glu Thr Lys Phe Val Thr Gly Ile Ser Ser Ser Tyr Gly Ala Ser Gly

130 135 140

Asp Pro Ser Pro Leu Thr Ala Leu Gly Val Tyr Arg Gly Met Lys Ala
 145 150 155 160
 Ala Ala Lys Glu Ala Phe Gly Ser Asp Ser Leu Glu Gly Lys Thr Val
 165 170 175
 Ala Ile Gln Gly Leu Gly His Val Gly Tyr Tyr Leu Ala Lys His Leu
 180 185 190
 Thr Asp Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Ser Glu Ala
 195 200 205
 Val Lys Arg Val Ala Arg Glu Phe Val Ala Thr Ala Val Arg Thr Glu
 210 215 220
 Glu Ile Phe Gly Val Lys Cys Asp Ile Phe Ala Pro Cys Ala Leu Gly
 225 230 235 240
 Ala Val Ile Asn Asp Glu Thr Ile Pro Gln Leu Lys Cys Gln Val Val
 245 250 255
 Ala Gly Ala Ala Asn Asn Val Leu Lys Glu Asp Arg His Gly Asp Glu
 260 265 270
 Leu Tyr Glu Lys Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala
 275 280 285
 Gly Gly Val Ile Asn Val Ala Asp Glu Leu Glu Gly Tyr Asn Ala Glu
 290 295 300
 Arg Ala Leu Lys Lys Val Glu Met Val Tyr Asp Asn Val Ala Arg Val
 305 310 315 320
 Ile Ala Ile Ala Lys Arg Asp His Ile Pro Thr Tyr Lys Ala Ala Asp
 325 330 335
 Arg Met Ala Glu Glu Arg Ile Ala Lys Ile Gly Lys Val Ser Asn Thr
 340 345 350
 Phe Leu Arg
 355
 <210> 13
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 13

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gatggcatgc gttgggcagg taacgctaac gaactcaacg ccgcttacgc ggctgacggt	180
tatagccgtg tcaaaggcct cgcatgtctg gttaccactt ttggtgtagg cgagctaagt	240
gcgctgaatg gtgtgggtgg cgcttacgca gaacacgttg ggctgctgca tgtagtgggc	300
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cgtcgggttt acgtcggcct gccggcgaac ctagttagacc tgactgtgcc ggctgtcttg	540
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attgaaacgg tccttgatct ggtagacaag tctaaaaacc ctataatctt agttgacgca	660
tgcgctagcc gtcactcatg ccgcatgaa gtacgccggg ttggtggactc caccagcttc	720
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accactccct acctgtttgt gctgaacaac gatgggtaca ctatcgaac ccttatccat	1440
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ttcaaagctc gtgactacga aaccaaccga gttgcgactg taggcgaaat tgaagcgcta	1560
ttcaacaatt cagctttcaa tgagaataca aagatccgta tgggtggaggt catgctgccg	1620
cggatggatg caccacagaa cctggttaaa caggctgaat tttctccaa gaccaacagc	1680

gaaaac

1686

<210> 14

<211> 562

<212> PRT

<213> Candida auris

<400> 14

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1 5 10 15

Leu Gln Val Gln Thr Ile Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser

20 25 30

Leu Leu Asp Lys Ile Tyr Glu Val Asp Gly Met Arg Trp Ala Gly Asn

35 40 45

Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ser Arg Val

50 55 60

Lys Gly Leu Ala Cys Leu Val Thr Thr Phe Gly Val Gly Glu Leu Ser

65 70 75 80

Ala Leu Asn Gly Val Gly Gly Ala Tyr Ala Glu His Val Gly Leu Leu

85 90 95

His Val Val Gly Val Pro Ser Ile Ser Ser Gln Ala Lys Gln Leu Leu

100 105 110

Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met

115 120 125

Ser Asn Asn Ile Ser Gln Thr Thr Ala Phe Ile Ser Asp Ile Asn Ser

130 135 140

Ala Pro Gly Glu Ile Asp Arg Cys Ile Arg Glu Ala Trp Val His Gln

145 150 155 160

Arg Pro Val Tyr Val Gly Leu Pro Ala Asn Leu Val Asp Leu Thr Val

165 170 175

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

180 185 190

Asp Pro Asp Ala Gln Glu Glu Val Ile Glu Thr Val Leu Asp Leu Val

195 200 205
 Asp Lys Ser Lys Asn Pro Ile Ile Leu Val Asp Ala Cys Ala Ser Arg
 210 215 220
 His Ser Cys Arg Asp Glu Val Arg Arg Leu Val Asp Ser Thr Ser Phe
 225 230 235 240
 Pro Val Phe Val Thr Pro Met Gly Lys Ser Ala Val Asn Glu Ser His

 245 250 255
 Pro Arg Phe Gly Gly Val Tyr Val Gly Ser Leu Ser Glu Pro Asn Val
 260 265 270
 Lys Glu Ala Val Glu Asn Ala Asp Leu Val Leu Ser Ile Gly Ala Leu
 275 280 285
 Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
 290 295 300
 Asn Ile Val Glu Phe His Ser Asp Tyr Thr Lys Ile Arg Gln Ala Thr

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

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

 435 440 445

Thr Val Gln Glu Ile Ser Thr Met Val Lys Trp Glu Thr Thr Pro Tyr
 450 455 460
 Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Arg Leu Ile His
 465 470 475 480
 Gly Glu Thr Ala Thr Tyr Asn Asp Ile Gln Pro Trp Asp Asn Leu Gly
 485 490 495
 Leu Leu Pro Leu Phe Lys Ala Arg Asp Tyr Glu Thr Asn Arg Val Ala
 500 505 510
 Thr Val Gly Glu Ile Glu Ala Leu Phe Asn Asn Ser Ala Phe Asn Glu
 515 520 525
 Asn Thr Lys Ile Arg Met Val Glu Val Met Leu Pro Arg Met Asp Ala
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 Pro Gln Asn Leu Val Lys Gln Ala Glu Phe Ser Ser Lys Thr Asn Ser
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 Glu Asn

<210> 15

<211> 1698

<

212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 15

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 aacagcgaac acgtacctat catccatatt gttgggtccc caccggaaaa agctcagaag 360
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 tacgaaccgc ttaccgctta tactaccatc gtcacggcag ataacgcgcg gatggagatc 480
 ccggctgcta tccgtattgc caaagaacga agaaagccag tgtacctggt tgttgcgat 540
 gacgtagtgg ctaaaccgat tactggtcgt gaagtcgccg catctcctct gccggctagc 600

aatcaggaca aactgcttgc tgcggttgag cacgttaggc gtcttctgga acctgcacgc 660
cagccggtaa tattggttga tgtgaaagcc atgcgctttg gattacagac cgccgtcagg 720
gaactggcaa aactatgaa tgttcagtg gctacaatga tgtatggcaa aggcactttc 780

gacgaaaccc atccaaacta catcgccgta tatgcgggta cgttcggttc gtctgaagtt 840
caatctatcg tagaaaactc ggactgtgtt atgcgcttg gtttgggtg gagcgatact 900
aacaccgcaa actttactgc gaaattaaac ccgcacaata ccattgaggt tcagccgaca 960
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gagataaccg ggtccagtga tgaaccgtc cgcgagaaa actacttccc tcgttttcag 1140
cgcatgctga aggaaaacga tattgttatc gctgagaccg gcacgttcta ctacggtatg 1200

agtcaagtta aactgccgcg gaacactacg tacatcatgc agggcggctg gcagagcatt 1260
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tacggttgca agccgattat ctttgtactg aacaatgacg ggtacacat tgagcggat 1440
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gaattggatg aagcgatcac acaggctgag caagagtacg ccgaaaaact gtgcctgac 1620

gagatgattg ctgctgatcc aatggacgca ccggaatata tgcaccgtat ccgtaacat 1680
aagcaggaac agaaaaag 1698

<210> 16

<211> 566

<212> PRT

<213> Unknown

<220><223> Bacillus sp. FJ AT-1801

<400> 16

Met Thr Ser Met Asp Asn Ser Ser Gln Gln Ile Pro Met Gly Gln Lys

1 5 10 15

Thr Val Gly Glu Tyr Leu Phe Asp Cys Leu Lys Gln Glu Gly Ile Thr

20 25 30

Glu Ile Phe Gly Val Pro Gly Asp Tyr Asn Phe Thr Leu Leu Asp Ala

35 40 45

Leu Gln Glu Tyr Asn Gly Ile Arg Phe Tyr Asn Gly Arg Asn Glu Leu
 50 55 60
 Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Ala Arg Ile Lys Gly Ile Ser
 65 70 75 80
 Ala Leu Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Thr Asn Ala
 85 90 95

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

 Pro Ala Ala Ile Arg Ile Ala Lys Glu Arg Arg Lys Pro Val Tyr Leu
 165 170 175
 Val Val Ala Asp Asp Val Val Ala Lys Pro Ile Thr Gly Arg Glu Val
 180 185 190
 Pro Ala Ser Pro Leu Pro Ala Ser Asn Gln Asp Lys Leu Leu Ala Ala
 195 200 205
 Val Glu His Val Arg Arg Leu Leu Glu Pro Ala Arg Gln Pro Val Ile
 210 215 220

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

 Cys Val Ile Ala Val Gly Leu Val Trp Ser Asp Thr Asn Thr Ala Asn

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

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

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

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

Ala Asp Pro Met Asp Ala Pro Glu Tyr Met His Arg Ile Arg Asn His

545 550 555 560

Lys Gln Glu Gln Lys Lys

565

<210> 17

<211> 1653

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 17

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cacctcttcg gagtgccagg tgattacaat ctgcaatttc tggatcatgt aatcgaccac 120
cctcagctga ctgggtcgg ctgcactaac gaacttaacg ctgcctacgc agctgatggt 180

tatgcgcgtt gtcgtccggc tgcggcactg ctgaccacct tcgggggttgg cgaactgagc 240
gctattaatg gcatcgaggc ttccctacgcg gagtatctgc cggtaataca tatcgttggc 300
gcaccgagtc tatcagccca gcagcagggc gacctgattc accactctct tggcgaaggt 360
gatttttcca gcttctctgag gatgtcccaa ccggtgtctg ttgcgcaggc tgctctgact 420
cctgataacg catgcaagga aatcgaccgc gtactggcgg aagtcctcat tcagcgtcgt 480
cccggctacc tgctgtctgc taccgacgtg gctgtctgcg cggcggctct gccacaaagc 540
actctttctt tgccgaccgc cccggatcat cgcgcagttc tggtctgttt cagcgacgct 600

gctgagcaga tgctggctca ggccaaaagc gtctctctac tggcggactt tctggctgat 660
cgtttcgggtg ttactcgagc actggccgcg tggtcttcagc aggttccgct accgcacgcc 720
actctgttaa tgggtaaagg cgttctgagt gaacagcaac cagggttcgt gggtacctac 780
gctgggtcgg catctatcga ttgcacgcgt ggcgcaatcg aagaagctgg ggtaattatc 840
ggagtgggag ttagattttc cgacactatc acagcaggct tctcgagca gatcgacgcc 900
cgccgtttta tagacattca acccttcttc tctcgtattg gcgatcgcca gtttgatcac 960
ctgccgatgc aggtgcccgt cgcagccctg catcaactgt gtcttcgtta tcagcagcag 1020

tggtctatca ccgtcctag cccgcctgca ctgccgccgg ctgctggtag cgagctgtcc 1080
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cttgtgcagc cgctgtgggg ctcaatcggc tacagtctgc cggccacctt tgggtgctcag 1260
acggcagata cagagcgtcg tgtaatccta atcattggcg atggttcagc gcaattaact 1320

attcaggaac tticcagtat gatgcgtgac ggcttgaaac ctatcatctt tctcctgaac 1380
aacaacgggt acaccgttga acgggcgatt cacggcgcgg agcaacgtta taacgatatc 1440

gctgcttgga attggacceca actgccccag gcgctgagtg ttcattgccc agcgcagagc 1500
tggcgagtcg ttgaaacggt gcagctgacc gacgtaatga aagtcatcgc tgcttctccg 1560
cgtctgagct tggtagaagt tgttctgcct gcaatggatg tcccaccgct gctgcaagca 1620
gtgagtgcgg ctctgaacca gcgcaactcc tct 1653

<210> 18
<211> 551
<212> PRT
<213> Erwinia iniecta
<400> 18

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1 5 10 15

Ile Gly Ile Glu His Leu Phe Gly Val Pro Gly Asp Tyr Asn Leu Gln
20 25 30

Phe Leu Asp His Val Ile Asp His Pro Gln Leu Thr Trp Val Gly Cys
35 40 45

Thr Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Cys
50 55 60

Arg Pro Ala Ala Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu Ser
65 70 75 80

Ala Ile Asn Gly Ile Ala Gly Ser Tyr Ala Glu Tyr Leu Pro Val Ile
85 90 95

His Ile Val Gly Ala Pro Ser Leu Ser Ala Gln Gln Gln Gly Asp Leu
100 105 110

Ile His His Ser Leu Gly Glu Gly Asp Phe Ser Ser Phe Leu Arg Met
115 120 125

Ser Gln Pro Val Ser Val Ala Gln Ala Ala Leu Thr Pro Asp Asn Ala
130 135 140

Cys Lys Glu Ile Asp Arg Val Leu Ala Glu Val Leu Ile Gln Arg Arg
145 150 155 160

Pro Gly Tyr Leu Leu Leu Ser Thr Asp Val Ala Ala Ala Pro Ala Ala
165 170 175

Leu Pro Gln Ser Thr Leu Ser Leu Pro Thr Ala Pro Asp His Arg Ala
180 185 190

Val Leu Ala Ala Phe Ser Asp Ala Ala Glu Gln Met Leu Ala Gln Ala
195 200 205

Lys Ser Val Ser Leu Leu Ala Asp Phe Leu Ala Asp Arg Phe Gly Val
210 215 220

Thr Arg Ala Leu Ala Ala Trp Leu Gln Gln Val Pro Leu Pro His Ala
225 230 235 240

Thr Leu Leu Met Gly Lys Gly Val Leu Ser Glu Gln Gln Pro Gly Phe
245 250 255

Val Gly Thr Tyr Ala Gly Ala Ala Ser Ile Asp Ser Thr Arg Gly Ala
260 265 270

Ile Glu Glu Ala Gly Val Ile Ile Gly Val Gly Val Arg Phe Ser Asp
275 280 285

Thr Ile Thr Ala Gly Phe Ser Gln Gln Ile Asp Ala Arg Arg Phe Ile
290 295 300

Asp Ile Gln Pro Phe Phe Ser Arg Ile Gly Asp Arg Gln Phe Asp His
305 310 315 320

Leu Pro Met Gln Ala Ala Val Ala Ala Leu His Gln Leu Cys Leu Arg
325 330 335

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

Pro Ala Ala Gly Ser Glu Leu Ser Gln Asn Ala Phe Trp Gln Ala Met
355 360 365

Gln Asn Phe Ile Arg Pro Gly Asp Leu Leu Val Ala Asp Gln Gly Thr
370 375 380

Ala Ala Phe Gly Ala Ala Ala Leu Arg Leu Pro Gln Asn Cys Gln Leu
385 390 395 400

Leu Val Gln Pro Leu Trp Gly Ser Ile Gly Tyr Ser Leu Pro Ala Thr

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

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

 Leu Pro Ala Met Asp Val Pro Pro Leu Leu Gln Ala Val Ser Ala Ala
 530 535 540
 Leu Asn Gln Arg Asn Ser Ser
 545 550

 <210> 19
 <211> 993
 <212> DNA
 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 19

 atgcagacgg cgttcttgta taagccaggt cagaaaact tagtgcgctc ggagatcccg 60
 atacctaaag ctgggcgtgg cgaagtcgtt ctggaaatta aagccgctgg catgtgccat 120
 tccgatctgc acgttctcga cgggtggaatc ccctgccgg gtcaatttgt aatgggccat 180

 gaaatcgttg gtactattca cgagatcggc caggacgtga ccggtttcaa acagggcgat 240
 ctgtacgcag tccacggccc gaatccgtgt ggtatttgca ccctgtgcag agaaggattt 300
 gataacgact gcactacagt ggcgaaaacc ggtcaatggt tcggactggg tcttgacggc 360
 ggctaccaga agtatatccg tatccgaac gtaaggtcta tcgttaaagt tccagaaggt 420

gtttcagctg aggagctgc gagctgtact gatgcagtac tgaccccgta cegtgcacta 480
 aaacaggctg ggcagcaaa ctctactcgg gtactgattc tgggtctggg tggcttaggt 540
 ctgaatgccc ttaaacctggc taagaccttc ggcagttacg ttacgcatac tgacctgaaa 600

ccttctgcgc gtgaagctgc taaggccgct ggggcggatg aagtgcctga gtccctgccc 660
 gaagaccgcg tgggtgttga tatcgtgtta gacgtcgttg gcgtgcagag caccttcaac 720
 ctgcgtcaaa aacacgttgg cccgcgtggc atcattgtac ctgtaggcct ggcaccccca 780
 cagctttcgt ttaacctaac ggatctggcg ctccgcgaaa ttcgtgttca gggcactttt 840
 tggggcacga gcaatgagct ggctgaatgt ctgcgcctgt gccagctggg cctgatcaac 900
 ccgaaatata ctgtgtgtcc tcttgaagaa gcgccgaaat atatggaagc aatggctcat 960
 gggaaagtag aaggctgtat cgttttccac ccg 993

<210> 20

<211> 331

<212> PRT

<213> Tortispora caseinolytica

<400> 20

Met Gln Thr Ala Phe Leu Tyr Lys Pro Gly His Glu Asn Leu Val Arg

1 5 10 15

Ser Glu Ile Pro Ile Pro Lys Ala Gly Arg Gly Glu Val Val Leu Glu

20 25 30

Ile Lys Ala Ala Gly Met Cys His Ser Asp Leu His Val Leu Asp Gly

35 40 45

Gly Ile Pro Leu Pro Gly Gln Phe Val Met Gly His Glu Ile Val Gly

50 55 60

Thr Ile His Glu Ile Gly Gln Asp Val Thr Gly Phe Lys Gln Gly Asp

65 70 75 80

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

85 90 95

Arg Glu Gly Phe Asp Asn Asp Cys Thr Thr Val Ala Lys Thr Gly Gln

100 105 110

Trp Phe Gly Leu Gly Leu Asp Gly Gly Tyr Gln Lys Tyr Ile Arg Ile

115 120 125

Pro Asn Val Arg Ser Ile Val Lys Val Pro Glu Gly Val Ser Ala Glu
130 135 140
Ala Ala Ala Ser Cys Thr Asp Ala Val Leu Thr Pro Tyr Arg Ala Leu
145 150 155 160
Lys Gln Ala Gly Ala Ser Asn Ser Thr Arg Val Leu Ile Leu Gly Leu
165 170 175
Gly Gly Leu Gly Leu Asn Ala Leu Lys Leu Ala Lys Thr Phe Gly Ser
180 185 190
Tyr Val Tyr Ala Ser Asp Leu Lys Pro Ser Ala Arg Glu Ala Ala Lys
195 200 205
Ala Ala Gly Ala Asp Glu Val Leu Glu Ser Leu Pro Glu Asp Pro Leu
210 215 220
Gly Val Asp Ile Val Leu Asp Val Val Gly Val Gln Ser Thr Phe Asn
225 230 235 240
Leu Ala Gln Lys His Val Gly Pro Arg Gly Ile Ile Val Pro Val Gly
245 250 255
Leu Ala Ser Pro Gln Leu Ser Phe Asn Leu Thr Asp Leu Ala Leu Arg
260 265 270
Glu Ile Arg Val Gln Gly Thr Phe Trp Gly Thr Ser Asn Glu Leu Ala
275 280 285
Glu Cys Leu Arg Leu Cys Gln Leu Gly Leu Ile Asn Pro Lys Tyr Thr
290 295 300
Val Val Pro Leu Glu Glu Ala Pro Lys Tyr Met Glu Ala Met Ala His
305 310 315 320
Gly Lys Val Glu Gly Arg Ile Val Phe His Pro
325 330

<210> 21

<211> 1050

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 21

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 gatattcatc ttcacgaggg ctacttcgac atgggcggtg gcaataaagc tgatgttact 180
 cgtgctcgcg aactcccttt tacattgggt catgaaatcg ttggcgaagt ggtagcaact 240

ggaccagggtg tcaccggcgc taaaccgggc gacaaacgta ttgtgtaccc gtggatcggg 300
 tgcggcgact gcccgaaatg caacagtggg gaggatcagt cctgtgcgcg tccacgtaac 360
 ctgggtgttc acgttgacgg tggctattcg acgcacgtaa agataccgga cgaaaaattc 420
 ctgttcgct acgatggtat tcctactgag ttagcgggaa cctatgcttg cagcggcatc 480
 accgcttatg gtgcactgat gaaagcaaag gaagcggctg aaagatctgg ctacatcggt 540
 ctgattggcg ctggtggcgt tggcatggct ggtctgatgc tggccaaagc agcgatcggg 600
 gctaaaaactg tagtctttga tatcgacgac gcaaaactgg aagctgcgac ccgtgccggg 660

gcggattacg tgttcaactc cggtgcaaaa gaaacacgca aggaagttat gaaactaacg 720
 aatgggtggc tgtctggtgc tgttgatttc gttggcagcg ataaaagcgc tctgtttgga 780
 atcaacgcct tgggtcagaa cggcgtgctg gtcataattg gactgttcgg tggcgtatg 840
 actgttcgg taccctgtt cccgtgaaa gggatcaccg tacgtggctc atacgtaggt 900
 tcctgcaag agatgagtga tatgatggag ttagttcgcg ctgggaaagt tcctccgatg 960
 ccggtaaaaa ctcgccact ggacgtgcc tgggaaacce ttgaggatct acgcatggt 1020
 aaaatcgtgg gccgtgttgt tctgaccca 1050

<210> 22

<211> 350

<212> PRT

<213> Rhizobiales bacterium

<400> 22

Met Arg Ser Met Gln Phe Asp Glu Tyr Gly Ala Pro Leu Lys Ala Phe

1 5 10 15

Ser Tyr Glu Asp Pro Thr Pro Gln Gly Lys Glu Val Val Val Arg Ile

20 25 30

Glu Ala Cys Gly Val Cys His Ser Asp Ile His Leu His Glu Gly Tyr

35 40 45

Phe Asp Met Gly Gly Gly Asn Lys Ala Asp Val Thr Arg Ala Arg Glu

50

55

60

Leu Pro Phe Thr Leu Gly His Glu Ile Val Gly Glu Val Val Ala Thr
 65 70 75 80
 Gly Pro Gly Val Thr Gly Ala Lys Pro Gly Asp Lys Arg Ile Val Tyr
 85 90 95
 Pro Trp Ile Gly Cys Gly Asp Cys Pro Lys Cys Asn Ser Gly Glu Asp
 100 105 110
 Gln Ser Cys Ala Arg Pro Arg Asn Leu Gly Val His Val Asp Gly Gly
 115 120 125
 Tyr Ser Thr His Val Lys Ile Pro Asp Glu Lys Phe Leu Phe Ala Tyr
 130 135 140
 Asp Gly Ile Pro Thr Glu Leu Ala Gly Thr Tyr Ala Cys Ser Gly Ile
 145 150 155 160
 Thr Ala Tyr Gly Ala Leu Met Lys Ala Lys Glu Ala Ala Glu Arg Ser
 165 170 175
 Gly Tyr Ile Gly Leu Ile Gly Ala Gly Gly Val Gly Met Ala Gly Leu
 180 185 190
 Met Leu Ala Lys Ala Ala Ile Gly Ala Lys Thr Val Val Phe Asp Ile
 195 200 205
 Asp Asp Ala Lys Leu Glu Ala Ala Thr Arg Ala Gly Ala Asp Tyr Val
 210 215 220
 Phe Asn Ser Gly Ala Lys Glu Thr Arg Lys Glu Val Met Lys Leu Thr
 225 230 235 240
 Asn Gly Gly Leu Ser Gly Ala Val Asp Phe Val Gly Ser Asp Lys Ser
 245 250 255
 Ala Leu Phe Gly Ile Asn Ala Leu Gly Gln Asn Gly Val Leu Val Ile
 260 265 270
 Ile Gly Leu Phe Gly Gly Ala Met Thr Val Pro Val Pro Leu Phe Pro
 275 280 285
 Leu Lys Gly Ile Thr Val Arg Gly Ser Tyr Val Gly Ser Leu Gln Glu
 290 295 300
 Met Ser Asp Met Met Glu Leu Val Arg Ala Gly Lys Val Pro Pro Met

305					310					315					320	
Pro	Val	Lys	Thr	Arg	Pro	Leu	Asp	Ala	Ala	Trp	Glu	Thr	Leu	Glu	Asp	
				325					330					335		
Leu	Arg	His	Gly	Lys	Ile	Val	Gly	Arg	Val	Val	Leu	Thr	Pro			
				340					345					350		
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<211>	1080															
<212>	DNA															
<213>	Artificial Sequence															
<220><223>	Synthetic polynucleotide															
<400>	23															
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ttaaaggtga	actactgcgg	tgtctgtcac	agtgatgttc	atcttcacga	cggtacttc											180
gagctgggtg	gcgataaacg	tctgaacttc	gctatgccgc	tgccgtgac	gctgggtcac											240
gaagtaattg	gcaccgttgt	ggctgtcggc	gaccaggtta	ctgggttaaa	accgggggac											300
cagcgactga	tctatccgtg	gataggttgc	ggaaaatcgc	gcgcgtgtca	aaaaggagaa											360
gaaaacctgt	gcgttactcc	tgcacatctg	ggcgtgaaca	agccgggcgg	ttacgtgat											420
cacatcgttg	taccccatcc	tcgtacctt	ctggacattt	cgggtctgaa	cccgggtgat											480
gccgtaccc	tcgcgtgctc	cggcctgacc	acttcagcg	cgatcaacaa	agtgttgccg											540
cttgcagatg	accagtggat	tgttgttata	ggttgtggtg	gcctcggcc	gatggcgtg											600
cgtatcctgc	aagctatggg	aattggcaat	gttatcggtg	ttgacctgtc	tgaagagaaa											660
cggaaactgg	ctcatgaaag	cgggtgcacgt	cactccttcg	atccaaacac	tccgaagctg											720
aaccgcgtgg	tcgccgaaac	ctgcccgggt	acggtacagg	ccgcgttaga	ctttgtgggc											780
aatgagcaaa	ctgctcagct	ggcactgtct	ctgcttgtaa	aaggtggcaa	atatgttcct											840
gtcgggctgc	acggcggcga	gctgcgttac	ccattgccga	tcatacagaa	caaagctgta											900
agtatcatcg	gttcttacgt	tggtaccctg	aaagaactgg	aagacttagt	tgctttcgcc											960
aaggaaaaaa	atctgccgcc	aattcatatt	gaacaccgcc	cgctggaatc	ggcggctcag											1020
gccgtagagg	acctggaaaa	aggacaggtt	gctgggcgtg	ttatcctgga	tgcaggtaac											1080
<210>	24															
<211>	360															
<212>	PRT															

<213> Alcanivorax dieselolei

<400> 24

Met Thr Ala Glu Gln Gln Asn Gly Val Ser Asp Ser Arg Arg Phe Glu

1 5 10 15

Phe Gln Glu Phe Gly Gly Pro Ile Ala Pro Gln Thr Tyr Gln Leu Pro

20 25 30

Ala Pro Ala Ser Asp Glu Val Leu Leu Lys Val Asn Tyr Cys Gly Val

35 40 45

Cys His Ser Asp Val His Leu His Asp Gly Tyr Phe Glu Leu Gly Gly

50 55 60

Asp Lys Arg Leu Asn Phe Ala Met Pro Leu Pro Leu Thr Leu Gly His

65 70 75 80

Glu Val Ile Gly Thr Val Val Ala Val Gly Asp Gln Val Thr Gly Val

85 90 95

Lys Pro Gly Asp Gln Arg Leu Ile Tyr Pro Trp Ile Gly Cys Gly Lys

100 105 110

Cys Gly Ala Cys Gln Lys Gly Glu Glu Asn Leu Cys Val Thr Pro Ala

115 120 125

His Leu Gly Val Asn Lys Pro Gly Gly Tyr Ala Asp His Ile Val Val

130 135 140

Pro His Ser Arg Tyr Leu Leu Asp Ile Ser Gly Leu Asn Pro Gly Asp

145 150 155 160

Ala Ala Thr Leu Ala Cys Ser Gly Leu Thr Thr Phe Ser Ala Ile Asn

165 170 175

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

180 185 190

Gly Gly Leu Gly Gln Met Ala Leu Arg Ile Leu Gln Ala Met Gly Ile

195 200 205

Gly Asn Val Ile Gly Ile Asp Leu Ser Glu Glu Lys Arg Lys Leu Ala

210 215 220

His Glu Ser Gly Ala Arg His Ser Phe Asp Pro Asn Thr Pro Lys Leu

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

 290 295 300
 Ser Tyr Val Gly Thr Leu Lys Glu Leu Glu Asp Leu Val Ala Phe Ala
 305 310 315 320
 Lys Glu Lys Asn Leu Pro Pro Ile His Ile Glu His Arg Pro Leu Glu
 325 330 335
 Ser Ala Ala Gln Ala Val Glu Asp Leu Glu Lys Gly Gln Val Ala Gly
 340 345 350
 Arg Val Ile Leu Asp Ala Gly Asn
 355 360

<210> 25

<211> 711

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 25

atgaccgcac ttacggaagg ggcaaaactg ttgagaaag agataccgta tataaccgaa 60
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 accacgggga ccattaaagc gaaatacata tgcactacgg gcgacctgcc ggtaccgtgg 180
 gcaaccctgg tgagcaccct gagctacggg gtccagtgtt tcgccaagta cccgagccac 240
 ataaaggatt tctttaagag cgccatgccg gaagggtata cccaagagcg taccataagc 300
 ttcgaaggcg acggcgtgta caagacgcgt gctatggtca cctacgaacg cgggtctata 360

tacaatcgtg taacgtgac tggggagaac tttaagaaag acgggcacat tctgcgtaag 420
 aacgtcgcat tccaatgccc gccaaagcatt ctgtatatc tgcctgacac cgtcaacaat 480
 ggcatacgcg tcgagttcaa ccaggcgtac gatattgaag gggtgaccga aaaactggtc 540

accaaagca gccaaatgaa tcgtccgctt gcgggcagtg cggcagtgca tataccgct 600
tatcatcaca ttacctacca caccaaactg agcaaagacc gcgacgagcg ccgtgatcac 660
atgtgtctgg ttgaggtagt gaaagcggtc gatctggaca cgtatcagtg a 711

<210> 26

<211> 236

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 26

Met Thr Ala Leu Thr Glu Gly Ala Lys Leu Phe Glu Lys Glu Ile Pro

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Tyr Ile Thr Glu Leu Glu Gly Asp Val Glu Gly Met Lys Phe Ile Ile

20 25 30

Lys Gly Glu Gly Thr Gly Asp Ala Thr Thr Gly Thr Ile Lys Ala Lys

35 40 45

Tyr Ile Cys Thr Thr Gly Asp Leu Pro Val Pro Trp Ala Thr Leu Val

50 55 60

Ser Thr Leu Ser Tyr Gly Val Gln Cys Phe Ala Lys Tyr Pro Ser His

65 70 75 80

Ile Lys Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Thr Gln Glu

85 90 95

Arg Thr Ile Ser Phe Glu Gly Asp Gly Val Tyr Lys Thr Arg Ala Met

100 105 110

Val Thr Tyr Glu Arg Gly Ser Ile Tyr Asn Arg Val Thr Leu Thr Gly

115 120 125

Glu Asn Phe Lys Lys Asp Gly His Ile Leu Arg Lys Asn Val Ala Phe

130 135 140

Gln Cys Pro Pro Ser Ile Leu Tyr Ile Leu Pro Asp Thr Val Asn Asn

145 150 155 160

Gly Ile Arg Val Glu Phe Asn Gln Ala Tyr Asp Ile Glu Gly Val Thr

165 170 175

Glu Lys Leu Val Thr Lys Cys Ser Gln Met Asn Arg Pro Leu Ala Gly

180 185 190
Ser Ala Ala Val His Ile Pro Arg Tyr His His Ile Thr Tyr His Thr

195 200 205
Lys Leu Ser Lys Asp Arg Asp Glu Arg Arg Asp His Met Cys Leu Val

210 215 220
Glu Val Val Lys Ala Val Asp Leu Asp Thr Tyr Gln

225 230 235

<210> 27

<211> 366

<212> PRT

<213> Bacillus cereus

<400> 27

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala

20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

260 265 270

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

275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335

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

340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 28

<211> 1101

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 28

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gccttaggtg gcacccgtat gtggacgtac gactcggaag aagcggcaat tgaggatgcc 180

ttgaggttag ctaagggcat gacgtataaa aacgcggcag ccggtttgaa tctgggcggt 240

gcgaaaaccg tgattatcgg ggatccccgc aaagacaaat ctgaagcaat gtttcgggcg 300

ctgggccgat acatacaggg actaaatggt cgctatatca ccgctgaaga ttaggaact 360

accgtggatg atatggacat aattcacgaa gaaacggact tcgtcacggg cattagccct 420

agttttggta gtcccgggaa cccgtctccg gttaccgcct atggcgtgta ccgtggcatg 480

aaggcagcag cgaagaggc ctttggatca gacaacctgg aggggaaagt gatcgcggtt 540

caaggggtag gtaatgtggc gtatcatctg tgcaaacact tacatgccga gggcgccaag 600

ctgattgtca cggatatcaa caaagaagcg gtacagcgtg cagtcgaaga atttggcgct 660

tccgcccgtt agccgaatga aatctacggc gtggaatgcg atatttacgc gccgtgtgct 720

cttgggtcga cagtcaacga tgaaacgatc cctcagctga aagcaaaggt aattgcgggt 780

tcggctaata accagttaaa agaagacaga catggagaca taattcacga gatgggtatt 840

gtttatgcac cagattatgt aatcaatgcg ggccggcgtta ttaacgtcgc agatgaactg 900

tatggctaca accgcgaacg cgccctcaaa cgtgtggagt caatttatga caccattgcc 960

aaagtgatcg aaatcagcaa gcgcgatgga atcgccactt atgtggctgc cgatcgtctg 1020

gcggaagaac gcattgcaag tctcaaaaat agccgttcca cctaccttcg caatggccat 1080

gatattataa gtcggcgttg a 1101

<210> 29

<211> 548

<212> PRT

<213> Lactococcus lactis

<400> 29

Met Tyr Thr Val Gly Asp Tyr Leu Leu Asp Arg Leu His Glu Leu Gly

1 5 10 15

Ile Glu Glu Ile Phe Gly Val Pro Gly Asp Tyr Asn Leu Gln Phe Leu

20 25 30

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

35 40 45
 Glu Leu Asn Ala Ser Tyr Met Ala Asp Gly Tyr Ala Arg Thr Lys Lys
 50 55 60
 Ala Ala Ala Phe Leu Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Val
 65 70 75 80

 Asn Gly Leu Ala Gly Ser Tyr Ala Glu Asn Leu Pro Val Val Glu Ile
 85 90 95
 Val Gly Ser Pro Thr Ser Lys Val Gln Asn Glu Gly Lys Phe Val His
 100 105 110
 His Thr Leu Ala Asp Gly Asp Phe Lys His Phe Met Lys Met His Glu
 115 120 125
 Pro Val Thr Ala Ala Arg Thr Leu Leu Thr Ala Glu Asn Ala Thr Val
 130 135 140

 Glu Ile Asp Arg Val Leu Ser Ala Leu Leu Lys Glu Arg Lys Pro Val
 145 150 155 160
 Tyr Ile Asn Leu Pro Val Asp Val Ala Ala Ala Lys Ala Glu Lys Pro
 165 170 175
 Ser Leu Pro Leu Lys Lys Glu Asn Ser Thr Ser Asn Thr Ser Asp Gln
 180 185 190
 Glu Ile Leu Asn Lys Ile Gln Glu Ser Leu Lys Asn Ala Lys Lys Pro
 195 200 205

 Ile Val Ile Thr Gly His Glu Ile Ile Ser Phe Gly Leu Glu Lys Thr
 210 215 220
 Val Thr Gln Phe Ile Ser Lys Thr Lys Leu Pro Ile Thr Thr Leu Asn
 225 230 235 240
 Phe Gly Lys Ser Ser Val Asp Glu Ala Leu Pro Ser Phe Leu Gly Ile
 245 250 255
 Tyr Asn Gly Thr Leu Ser Glu Pro Asn Leu Lys Glu Phe Val Glu Ser
 260 265 270

 Ala Asp Phe Ile Leu Met Leu Gly Val Lys Leu Thr Asp Ser Ser Thr
 275 280 285

Gly Ala Phe Thr His His Leu Asn Glu Asn Lys Met Ile Ser Leu Asn
290 295 300

Ile Asp Glu Gly Lys Ile Phe Asn Glu Arg Ile Gln Asn Phe Asp Phe
305 310 315 320

Glu Ser Leu Ile Ser Ser Leu Leu Asp Leu Ser Glu Ile Glu Tyr Lys
325 330 335

Gly Lys Tyr Ile Asp Lys Lys Gln Glu Asp Phe Val Pro Ser Asn Ala
340 345 350

Leu Leu Ser Gln Asp Arg Leu Trp Gln Ala Val Glu Asn Leu Thr Gln
355 360 365

Ser Asn Glu Thr Ile Val Ala Glu Gln Gly Thr Ser Phe Phe Gly Ala
370 375 380

Ser Ser Ile Phe Leu Lys Ser Lys Ser His Phe Ile Gly Gln Pro Leu
385 390 395 400

Trp Gly Ser Ile Gly Tyr Thr Phe Pro Ala Ala Leu Gly Ser Gln Ile
405 410 415

Ala Asp Lys Glu Ser Arg His Leu Leu Phe Ile Gly Asp Gly Ser Leu
420 425 430

Gln Leu Thr Val Gln Glu Leu Gly Leu Ala Ile Arg Glu Lys Ile Asn
435 440 445

Pro Ile Cys Phe Ile Ile Asn Asn Asp Gly Tyr Thr Val Glu Arg Glu
450 455 460

Ile His Gly Pro Asn Gln Ser Tyr Asn Asp Ile Pro Met Trp Asn Tyr
465 470 475 480

Ser Lys Leu Pro Glu Ser Phe Gly Ala Thr Glu Asp Arg Val Val Ser
485 490 495

Lys Ile Val Arg Thr Glu Asn Glu Phe Val Ser Val Met Lys Glu Ala
500 505 510

Gln Ala Asp Pro Asn Arg Met Tyr Trp Ile Glu Leu Ile Leu Ala Lys
515 520 525

Glu Gly Ala Pro Lys Val Leu Lys Lys Met Gly Lys Leu Phe Ala Glu

530	535	540	
Gln Asn Lys Ser			
545			
<210>	30		
<211>	1647		
<212>	DNA		
<213>	Artificial Sequence		
<220><223>	Synthetic polynucleotide		
<400>	30		
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atgaaatggg	taggcaatgc	taacgaactg	aatgcgtctt acatggccga tggttatgca 180
cggacaaaa	aagcggcagc	ctttctgacg	actttcggcg ttggtgagtt aagcgcggtg 240
aacggccttg	cggggtcata	cgccgaaaat	ctaccagttg tcgaaatcgt gggctcgccg 300
accagcaaag	ttcagaacga	gggtaagttt	gtgcatcaca cccttctgta cggagatttt 360
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aagaaagaga	atagcacgtc	taacacgtct	gaccaagaaa ttctgaacaa aattcaggaa 600
tccctcaaaa	atgcgaaaaa	acctatcgtc	atcaccggtc atgaaataat ttcatttggg 660
ctggagaaaa	ccgttacaca	gttcattctc	aagacgaaac tgccaattac caccctaat 720
tttggcaaat	cgtccgtaga	cgaagccctg	ccgagcttct tggggatcta taacggcact 780
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gtggagcgcg aaatccatgg tccgaatcag agctataacg atataccgat gtggaattac 1440

agcaaaactcc ccgagagctt tggcgcaaca gaagataggg ttgtctcaa gatcgtgcgt 1500

acggaacacg aatttgtaag tgtaatgaaa gaagcgcaag cggaccctaa tcgaatgtac 1560

tggattgaac ttattctggc aaaagaaggg gccctaaag tcctcaagaa aatggggaag 1620

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<210> 31

<211> 348

<212> PRT

<213> Saccharomyces cerevisiae

<400> 31

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1 5 10 15

Gly Lys Leu Glu His Lys Asp Ile Pro Val Pro Lys Pro Lys Pro Asn

20 25 30

Glu Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu

35 40 45

His Ala Trp His Gly Asp Trp Pro Leu Pro Thr Lys Leu Pro Leu Val

50 55 60

Gly Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Glu Asn Val

65 70 75 80

Lys Gly Trp Lys Ile Gly Asp Tyr Ala Gly Ile Lys Trp Leu Asn Gly

85 90 95

Ser Cys Met Ala Cys Glu Tyr Cys Glu Leu Gly Asn Glu Ser Asn Cys

100 105 110

Pro His Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Gln Glu

115 120 125

Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala His Ile Pro Gln Gly Thr

130 135 140

Asp Leu Ala Glu Val Ala Pro Ile Leu Cys Ala Gly Ile Thr Val Tyr

145 150 155 160

Lys Ala Leu Lys Ser Ala Asn Leu Arg Ala Gly His Trp Ala Ala Ile

165 170 175
 Ser Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala Lys
 180 185 190
 Ala Met Gly Tyr Arg Val Leu Gly Ile Asp Gly Gly Pro Gly Lys Glu
 195 200 205

Glu Leu Phe Thr Ser Leu Gly Gly Glu Val Phe Ile Asp Phe Thr Lys
 210 215 220
 Glu Lys Asp Ile Val Ser Ala Val Val Lys Ala Thr Asn Gly Gly Ala
 225 230 235 240
 His Gly Ile Ile Asn Val Ser Val Ser Glu Ala Ala Ile Glu Ala Ser
 245 250 255
 Thr Arg Tyr Cys Arg Ala Asn Gly Thr Val Val Leu Val Gly Leu Pro
 260 265 270

Ala Gly Ala Lys Cys Ser Ser Asp Val Phe Asn His Val Val Lys Ser
 275 280 285
 Ile Ser Ile Val Gly Ser Tyr Val Gly Asn Arg Ala Asp Thr Arg Glu
 290 295 300
 Ala Leu Asp Phe Phe Ala Arg Gly Leu Val Lys Ser Pro Ile Lys Val
 305 310 315 320
 Val Gly Leu Ser Ser Leu Pro Glu Ile Tyr Glu Lys Met Glu Lys Gly
 325 330 335

Gln Ile Ala Gly Arg Tyr Val Val Asp Thr Ser Lys
 340 345

<210> 32

<211> 1047

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 32

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 agcggagtct gccacacgga tttgcatgcc tggcacgggg attggccgtt accgacaaaa 180

ctgcctctgg tgggtgggtca tgaggcgcg ggcgttggtg tgggtatggg agaaaatgtc 240

aaaggctgga aaatcggcga ctatgcaggg atcaagtggc tgaacgggtc ttgtatggcg 300

tgcgagtact gtgaattagg taatgaatcc aactgcccac acgcagatct gagtggttat 360

acccatgacg gcagcttcca agaatacgcc acagcggatg cctgcaggc agctcacatt 420

ccgcaaggaa ctgatcttgc ggaagtagcc ccaattctgt gcgcgggcat cacggtatat 480

aaagctctca aaagtgcaaa cttgcgcgcc ggtcattggg ctgcgatttc ggggtccgcg 540

ggcgggctgg gatcattagc tggtcagtagc gcaaggcaa tgggttatcg agttctgggc 600

atcgacggcg ggcccggtaa agaagagcta tttaccagcc tcggcgggtga ggtcttcac 660

gattttacca aagaaaaaga tatcgtgtcc gcagtcgtga aagcaaccaa tggcggcgct 720

cacggaatta taaatgtgtc tgtatcagaa gcggcgattg aagccagcac gcgttattgt 780

cgcgcaacg gcacagtggg tctggttagc ctgcccgcg gtgcgaaatg tagctcggac 840

gtgttcaatc atgtggtgaa gagtatttcc attgttggat cttacgtagg gaaccgtgcg 900

gatacgcggg aggcactgga tttttttgca aggggcttgg ttaaaagccc gatcaaagtc 960

gtgggtctgt cgtctctacc tgaaatatat gagaaaatgg aaaagggaca gatcgccgga 1020

cgctacgtcg tcgacacctc aaagtga 1047

<210> 33

<400> 33

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<210> 34

<400> 34

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<210> 35

<211> 439

<212> PRT

<213> Escherichia coli

<400> 35

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1 5 10 15

Thr Phe Ala Leu Phe Val Gly Ala Gly Asn Ile Ile Phe Pro Pro Met

20 25 30

Val Gly Leu Gln Ala Gly Glu His Val Trp Thr Ala Ala Phe Gly Phe

35 40 45
 Leu Ile Thr Ala Val Gly Leu Pro Val Leu Thr Val Val Ala Leu Ala
 50 55 60
 Lys Val Gly Gly Gly Val Asp Ser Leu Ser Thr Pro Ile Gly Lys Val
 65 70 75 80
 Ala Gly Val Leu Leu Ala Thr Val Cys Tyr Leu Ala Val Gly Pro Leu
 85 90 95
 Phe Ala Thr Pro Arg Thr Ala Thr Val Ser Phe Glu Val Gly Ile Ala
 100 105 110

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

 Ala Thr Glu Ala Tyr Gln Asn Ala Ala Phe Ser Asn Gly Phe Val Asn
 180 185 190
 Gly Tyr Leu Thr Met Asp Thr Leu Gly Ala Met Val Phe Gly Ile Val
 195 200 205
 Ile Val Asn Ala Ala Arg Ser Arg Gly Val Thr Glu Ala Arg Leu Leu
 210 215 220
 Thr Arg Tyr Thr Val Trp Ala Gly Leu Met Ala Gly Val Gly Leu Thr
 225 230 235 240

 Leu Leu Tyr Leu Ala Leu Phe Arg Leu Gly Ser Asp Ser Ala Ser Leu
 245 250 255
 Val Asp Gln Ser Ala Asn Gly Ala Ala Ile Leu His Ala Tyr Val Gln
 260 265 270
 His Thr Phe Gly Gly Gly Gly Ser Phe Leu Leu Ala Ala Leu Ile Phe
 275 280 285

Ile Ala Cys Leu Val Thr Ala Val Gly Leu Thr Cys Ala Cys Ala Glu
290 295 300

Phe Phe Ala Gln Tyr Val Pro Leu Ser Tyr Arg Thr Leu Val Phe Ile
305 310 315 320

Leu Gly Gly Phe Ser Met Val Val Ser Asn Leu Gly Leu Ser Gln Leu
325 330 335

Ile Gln Ile Ser Val Pro Val Leu Thr Ala Ile Tyr Pro Pro Cys Ile
340 345 350

Ala Leu Val Val Leu Ser Phe Thr Arg Ser Trp Trp His Asn Ser Ser
355 360 365

Arg Val Ile Ala Pro Pro Met Phe Ile Ser Leu Leu Phe Gly Ile Leu
370 375 380

Asp Gly Ile Lys Ala Ser Ala Phe Ser Asp Ile Leu Pro Ser Trp Ala
385 390 395 400

Gln Arg Leu Pro Leu Ala Glu Gln Gly Leu Ala Trp Leu Met Pro Thr
405 410 415

Val Val Met Val Val Leu Ala Ile Ile Trp Asp Arg Ala Ala Gly Arg
420 425 430

Gln Val Thr Ser Ser Ala His
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<210> 36

<211> 1320

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 36

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gtctggactg cggcattcgg cttcctcatt actgccgttg gcctaccggt attaacggta	180
gtggcgctgg caaaagttgg cggcgggtgtt gacagtctca gcacgccaat tggtaaagtc	240
gctggcgtag tgctggcaac agtttggttac ctggcggtgg ggccgctttt tgctacgccg	300

cgtaacagcta ccgtttcttt tgaagtgggc attgcgccgc tgacgggtga ttccgcgctg 360
ccgctgttta ttacagcct ggtctatttc gctatcgta ttctggttc gctctatccg 420
ggcaagctgc tggataccgt gggcaacttc cttgcgccgc tgaattat cgcgctggtc 480
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tatcaaacg ctgcgttttc taacggcttc gtcaacggct atctgacct ggatacgtg 600
ggcgcaatgg tgtttggat cgttatgtt aacgcggcgc gttctcgtgg cgttaccgaa 660
gcgcgtctgc tgaccgcta taccgtctgg gctggcctga tggcgggtgt tggctgact 720

ctgctgtacc tggcgtgtt ccgtctgggt tcagacagcg cgtcgtgtgt cgtacgtct 780
gcaaacgggt cggcgatcct gcatgcttac gttcagcata cctttggcgg cggcggtagc 840
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gcttgtgcag aattcttcgc ccagtacgta ccgctctctt atcgtacgt ggtgtttatc 960
ctcggcggct tctcgtggt ggtgtctaac ctcggcttga gccagctgat tcagatctct 1020
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cgctcatggt ggcataatc gtcgccgtg attgctccgc cgtgtttat cagcctgctt 1140

tttggtattc tcgacgggat caaggcatct gcattcagcg atatcttacc gtcctgggcg 1200
cagcgtttac cgtcggccga acaaggctcgc gcgtggttaa tgccaacagt ggtgatggtg 1260
gttctggcca ttatctggga tcgtcggcga ggtcgtcagg tgacctccag cgctcactaa 1320

<210> 37
<211> 1101
<212> DNA
<213> Artificial Sequence
<220><223> Synthetic polynucleotide
<400> 37

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gccttaggtg gcacccgtat gtggacgtac gactcggaag aagcggcaat tgaggatgcc 180

ttgaggttag ctaaggcat gacgtataaa aacgcggcag ccggtttgaa tctgggcggt 240
gcgaaaaccg tgattatcgg ggatccccgc aaagacaaat ctgaagcaat gtttcgggcg 300
ctgggccgat acatacaggg actaatggt cgctatatca ccgctgaaga ttaggaact 360
accgtggatg atatggacat aattcacgaa gaaacggact tcgtcacggg cattagccct 420
agttttggta gtcggggaa cccgtctccg gttaccgct atggcgtgta ccgtggcatg 480
aaggcagcag cgaaagaggc ctttgggtaca gacaacctgg aggggaaagt gatcgcggtt 540

caaggggtag gtaatgtggc gtatcatctg tgcaaacact tacatgccga gggcgccaag 600

ctgattgtca cggatatcaa caaagaagcg gtacagcgtg cagtcgaaga atttgcgct 660

tccgcggttg agccgaatga aatctacggc gtggaatgcg atatttacgc gccgtgtgct 720

cttggtgcga cagtcaacga tgaaacgatc cctcagctga aagcaaaggt aattgcgggt 780

tcggctaata accagttaaa agaagacaga catggagaca taattcacga gatgggtatt 840

gtttatgcac cagattatgt aatcaatgcg ggcggcggtta ttaacgtcgc agatgaactg 900

tatggctaca accgcgaacg cgccctcaaa cgtgtggagt caatttatga caccattgcc 960

aaagtgatcg aaatcagcaa gcgcgatgga atgccactt atgtggctgc cgatcgtctg 1020

gcggaagaac gcattgcaag tctcaaaaat agccgttcca cctaccttcg caatggccat 1080

gatattataa gtcggcgttg a 1101

<210> 38

<211> 1080

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 38

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ggcgggtacc gcctttggaa ctataactct gaggaagatg ccgttgaaga cgtaatccgt 180

ctggctcggg gcatgactta caaagcggct tgcgccggtc tgaatctggg cggcggtaaa 240

accgtgctga tcggtgatgc taaaaagatt aaatcagagt cctacttccg tggactgggg 300

cgctacgttc agtcgctgaa cggcagatat atcaccgcgg aagacgtaaa tactttctacg 360

aaggatatgg catacgttgc tatggaaact gactatgtgg taggcctggg aggtaatcc 420

ggcaacccta gtccagttac tgcttacggt gcatttatgg gtatcaaagc ggcgctgatg 480

aaaaaatthg aggatagctc tattgaaggc cgaaccttcg cagtgcaggg tgctgggcag 540

acgggttact atcttatcga ttacctcta ggcaacaaca agttcaaaga aaaggctaaa 600

aaaatttact tcaccgaaat taacgagagc tatatcgagc gtatgaacaa agaacatccg 660

gaagttgaat ttatttcccc ggacaaaatc tactcgctgg aagtagacgt cttcgtgccc 720

tgcgccctgg gcaaaatcgt taatgacaaa actatcgatg aatttaagt tccgatcatc 780

gcaggtaact caaacaacgt actggaaagg gaagcgcacg gcaacatgct taaagaacgt 840

ggcattcttt acgccccgga ctatgtgatc aatgctggtg ggctgatcaa cgtttaccac 900

gagctgaacg gttacaataa agagaacgct attctggaag tggaattaat ttatgatcgc 960
ctactggaaa tattcaacat cgctgattct ctgaacatca gcaccaatat cgctgccaac 1020
gagttcgcg aaaaacgtat caagcaaatt aagtccttga aaaacaactt cattaaacgc 1080

<210> 39

<211> 1038

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 39

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caggaatcgg gtctgaagcg catcattgct gtgcactcta cgaaattagg gccggcggtt 120
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gctgatgttg caataatgaa caaagagacc aactacgtac tgggactgga aggtaagtct 420
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caccagcatg gccaccagga cctggccggt gtgaaggttg ctgtgcaagg tttgggggct 540
gtagcttatt ctctgtgcaa atacctctat gaggccgtg cgagcttcta cgttactgac 600
attaatcagg catccattga tcgagtcgta aacgattca acgctacggc cgttggcatc 660
gacgaaatct acgatttaga cgttgatgtt tatagccgt gcgctctggg cgcaaccgtg 720
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ctggcagaat ctctgcacgg cgaactgctg cgccagaaag gcatcctata cgcgcccgat 840
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agtgcacagg cctcgaccaa gcatgttgag ggaatttttg gtactctgtc tgaattttc 960
gctcgctcgg tcaccgagca aaaatcaact cacctgatcg cagacgaact ggctcaggaa 1020
atcattgcca acggcctg 1038

<210> 40

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 40

atggagatca aggaattgga aaaagtagaa caggccggaa ttttcggcaa acttagccaa	60
ctgggtcacg aacaggctgt tttttgccat gacgaggcta cgggcttaaa agcgatcatt	120
gctatccaca acactgtgct ggggtccggca ctgggcggta cccgtatgtg gaattacgca	180
actgaacagg aagctctgac cgatgttcta cgcctgtcac gtggcatgac attcaaagcg	240
tcgatctctg gtctgaacct ggggtgggggc aaggccgtga tcattggaga cgcgaaaacc	300
atgaaaactg aggcttttat gcgtagattc ggtaaattcg tagattctct caacggcaag	360
tatataaccg cggaagacgt taacatgaaa actgctgata tggaatacat tggatatgga	420
acgaagcatg tcaccggcct gccagaatcc atgcgtggcg gtggcgaccc cagcccgggtg	480
actgcatatg gggtttacct tgggatgaaa gctgccgcta aaaaaaccta cggtaatgat	540
agtctgactg gcaaaactat cgcagttaaa ggtatcggtc aggtaggtac gtatcttaca	600
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gatatggaca tctacgccc ttgtgctctg ggcgccacac tgaatgacga taccatcccg	780
cgcctgaact gccaaagtcgt ggcaggtgctg gcaaacaacc agctgaaaga tgaatctaag	840
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ggtgggttaa tcaacgtata taacgaattt ctgggcaact acaatcgtgc ccgcgtattc	960
gaacaggctg aaggtattta cactacttgt atgaacatct tcaaaactggc cgctcaggag	1020
aaaatcaaca ctcaggagcg agcgattaaa ttagcagaaa aacgtatcgc tgacattgca	1080
caagttcgta cgcgacgc	1098

<210> 41

<211> 1089

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 41

atggtagaga tcaaggcttt gacggacact tccgtgtttg ggcaaattgc agaaccag	60
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cataacacag ttcttggccc cgccttaggt ggaactcgca tgtggcacta tgcttctgac	180
gcagaggcgc tgaatgatgt tctgcgtctg tcgcgcggta tgacctacaa agctgctata	240
agtggcctga acctgggtgg cggtaaagca gtgatcattg gggacgcaa aacctgaaa	300

accgaagcgc tgctgcggaa gttcggcaga ttcgtaaaaa acctgaatgg taaatacatc 360
 actgtctgaag atgtcaacat gactacaaaa gacatggagt acatcaggat ggaaaccaag 420
 cacgttgctg gcttacctga atcaatgggt ggaagcgggtg atccgtcccc ggtgactgca 480
 tttgggtacgt atatgggcat gaaagcggcg gccaaaaaag cgttcggctc tgactctctg 540

gctggcaaac gtatcgctgt tcagggtgta ggtcatgtcg gcacttacct gttggagtat 600
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 ccggccctcg tggagcggg gattgtgtac gctccggatt tcctgatcaa cgccggcggc 900
 ctgatcaacg ttactcgga agtagtgggt agtcccgctc aggtgtcttt gaaccagacc 960

gaaaaaatTT tcgacatcac cactcagggt ctaaacaag cggaacaaga gggttctcac 1020
 ccgcaggcgg cagctactaa gcagctgaa gagcgtattg caagcctggg caaagttaag 1080
 agcacctac 1089

<210> 42
 <211> 1047
 <212> DNA
 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 42

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 aagaccacgg gtctgaaaac tatcatcgct gtgcacaata caaacttagg gccgtccttg 120
 ggcggttgcc gcatgtggcc ctatgcatct gaacaggatg ctattcacga cgttcttcgt 180

ctatcacggg gcatgactta caaatctgca ctggctaacc tccactggg tggcggcaaa 240
 agcgtcatca tcggtgaccc tcgttcccag aaaaccccg aactgttccg cgcatggga 300
 cgtgcggttg aacagctggg tggcagatac atagtggctg aggatgtagg tacttctccg 360
 gaagatatgg gccacattgc tagtcagacc aagcatgtcg gaggcacaa cgacggtaaa 420
 gacccggaac gtaccggtga tcctagtccg ttacggcat atggcgTTTT catcgggctg 480
 aaagaagctg ttcgttttaa acacggtagc gacgacctga ctgggatgcg cgtcgcggta 540
 cagggtctgg gtcatgttgg ctaccacctc tgtcgtatgc tgcattgccg aggcgctaag 600

ctgattgtag cagatcttaa tgcggcctcc atgaaagcgg ctgctatgga gttcggcgcg 660

accgcagtac cggttgataa aatcctgtct gttgacgcag acattctggc cccatgcgcg 720
ctgggtggcg tgatcaacga taaaactatc gaagagctga aagtcggcgt tatcgctggc 780
gcagctaaca atcaactgga agatgaccgc cacggggaaa tgctgcgtga agccggtatt 840
ttgtacgcgc cggattacgt gatcaacgct ggaggtgtta ttgaagtga ttactgccgt 900
gagggcaaga ccgtagctga gactaacatg cacattgaag gtatcgggga aactgttcgc 960
gaaatctttg aacgcgcgaa acagcaaaac ttatccaccg gtttcgtggc tgataggttg 1020

gctgaagaac gggtcggctc gaaaaag 1047

<210> 43

<211> 1047

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 43

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accgcgtttt ggaattacct gaacgatcgt gaagctttaa tcgattgtct gcgattggct 180
cgcggtatga cgtataaagc agctgttcgc ggccctgaacc taggcggtgg aaagtcagtt 240
ataattgggtg acaacaaaat ccgtaatcgc gaaccaatct tcagggcaca tggccgtcac 300

gtaaaagctc tgggcggctc ttacatcact gcggaggacg taggcacctc tgttggatgat 360
atggaattta ttaaggccga aactgaccac gtgaccggac tgatcggtaa atccggcgat 420
ccgagcccgg ttaccgcttt cgggtgtctac cgtgggatta aagcatgcgc aaaacaccgc 480
tatggcgatg ccgaactcgc tggtaaaaag gtggcgatcc aggggtgcgg ccatgtgggt 540
tactatctgg ctgaactgct ctacaaagaa ggcgctgacc ttattgttac tgacatcgac 600
tccgctaaag tagagcgcgt tgtaaaagcg ttcgaagcga aggcgtgtggc cactgatgac 660
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cagaccattg cgcagctgga agttgatatc gttgcaggcg gtgccaacaa ccagttagct 780
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gcacggaaca aagcaggcga gatctatgac acattactga tgttgttcga aattgctggc 960
gaagagggtg tcccagcta ccgcgtgct gatgcctgg ccgaacggcg tatcgcggt 1020
attgctaaag tacggcaaaa ttttgc 1047

<210> 44

<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 44

atggagatct tcacatatat ggaaaagtac gactacgaac aactggtctt ttgtcaggat	60
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ggcggtagcc gcatgtggac ctataactct gaagaggaag caattgaaga cgctcttcgt	180
ctggcaaaag gcatgactta caaaaatgct gcggctggtc tgaacctggg cggcggtaaa	240
accgtaatca tcggtgacct taagaaagat aaaaaccggg aaatgttccg tgcatttggg	300
cgggtacattc agggcctgaa cggccgatat atcaccgcgg aggacgtggg tactactgtt	360
caggatatgg acctgatcca tatggaaaca gatttcgtta ccggaatcag cgctgaagcc	420
ggatcgtctg gtaatccctc cccagtaacc gcttacggcg tttaacaagg catgaaagcc	480
gcagcaaaag aggccttcaa cgacgatagt ctggaaggta aaacgattgc ggtccagggt	540
gtgggtaacg ttgcttatgc tctgtgcgaa tacctacaca aggaaggtgc aaaactcgtg	600
gttactgaca tcaacaaagg tgcggtagag cgcgctgtgg aagctttcaa cgctactgcg	660
gtagaccggg atgatattta cgacgttgat tgcgacatct acgtccgtg cgccctgggg	720
gccaccatta acgatgatac tatccctcgt atcaaggcaa aagtcatagc tggctctgcg	780
aacaatcaac ttaaaagctc cgaacacggc gatatcattt ttgagaaagg catcatctat	840
gccccggact acgttatcaa cagtgggggt gtgattaatg tcgctgacga gctggttgg	900
tacaacgaag aacgtgcact gaaaaaagtg gaaactatth atgatagctt gcagaaagtt	960
tttgagatct ctgcagggga ccatacceca tcttatgttg cagcggaccg tatggcggaa	1020
gaacgtattg aggcggaacg taattcgcgc tcccagttcc tgttaaacgg ccatacacatc	1080
ttaagcagac gc	1092

<210> 45

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 45

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aaaaattcag gcttgaaagc aattatagcc attcacgaca ccactcttgg tccagcgta 120
 gggggcaccc ggatgtggac gtatgattct gaagaggatg ctatcgaaga cgctctcgct 180
 ctggcaaaag gtatgactta caaaaacgct gccgcgggtc tgaacctggg cggcggtaaa 240
 accgttatca tcggagaccc cctgaaggat aaaaacgaag aaatgttccg agctttcggt 300
 cgttacatcc agggcctggc gggacgctat atcactgccg aagacgtagg taccactgtc 360

aaagatatgg acctgattca tgaggagacg gattacgtta ccggtatcag ccctgctttt 420
 ggctcctctg gcaacccgag cccggttact gcatacggcg tgtatcgtgg tattaaggct 480
 gcggcaaatg aagcgtacgg gtccgactcg ctggaaggta aaactatcgc tgtacagggt 540
 gtaggcaacg ttgctttcac cctatgtaga cacttacatg aagaagggtc taagctgac 600
 gtcactgaca ttaacaaaga gtctgttcag cgcgcgggtg atgaatttgg cgcaaaagcc 660
 gttgaaccga acgaaatcta cgggtgtcgac tgcgatattt tcgctccgtg tgccttggc 720
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aacaaccaac tgaaggaaac acgccacggt gatattctgc acgaacgtgg catagtgtat 840
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 tacaatcgtg agcgtgcgat gaaaaatgta gaaaaagttt atgacaacgt agcacgtgtt 960
 tttgaaattg ctaaaccgca tgggtgtcct agttacctgg cggcggaccg tatggcagaa 1020
 gaacgtatag ctctatggc aaaaagccgc tctcagttcc tgaggtccga gcataacatc 1080
 ttaagccgcc gtagc 1095

<210> 46

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 46

atggagatct tcaagtatat ggaaacctac gactacgaac aaatgggtcat ttgtcaggat 60
 aaacagagtg gtctgaaagc catcatcggt atacacgata cgactttagg gccggcattg 120
 ggcggtaccc gcatgtggac ttataaatct gaagaggacg cgcttgaaga cgctctccgt 180
 ctggctcggg gcatgacata caaaaatgca gctgcgggtc tgaacctggg cggcggtaaa 240
 accgtaatta tcggtgatcc taagaaagac aaaaacgaag aaatgtttcg tgccttcggg 300
 cgctacattc agggcctgaa cggcagatat atcaccgtg aggatgtggg tactactgta 360

gaagatatgg acatcattta ccaagaaaca ccatttgta ccggagttag ccccgattc 420

ggatcatccg gtaacccgtc tccagttacc gcttacggcg tttatcgtgg catgaaggca 480
gcbgctaagt aggccttcgg tactgacagc ctggaaggta aaatcatcgc ggttcagggt 540
gtgggtcatg ttgcttaca cctgtgccgt cacctgcatg aagaaggcgc aaagcttacc 600
gtaactgata ttaacaaaga agcgggtcgc cgcgttgtgg gcgaatttgg tgctacggcg 660
gtagatccgg atgaaattta cggcgttgaa tgcgacatat tcgcaccgtg tgctctgggt 720
gccatcatca atgatcagac cattggacag atcaaagcta aagtattgc aggtgcggca 780

aacaaccaat tacgtgagac tcgccacggc gacgtatcc acgaaatggg catcgtctat 840
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tacaaccgtg atcgtgcgat gaaaaagggtg gaaaccatct acgacaacat tgctaaagtt 960
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gaacgcatag agcgtatcgc taactcgcgt tctcagttct tactgaacga acgccacatt 1080
ctgagctcga ggacccga 1098

<210> 47

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 47

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aaacagagtgt gtctcaaagc catcattgct atacacgata cgactttagg gccggcgttg 120
ggcggtagcc gcatgtggac ttataacact gaagcagaag cttttgagga cgcacttcgt 180
ctggctaaag gcatgacctt caaaaatgcg gctgccggtc tgaacctggg cgggtggcaag 240
acagttatca tcggagacct tcgtaaagat aaaaacgaag agatgttcag agcattcggg 300
cggtagattc agggcctgaa tggccgttac atcactgccg aagacgttgg taccaccgta 360

ggcgatatgg acatcattca tgaagaaact gactatgtta ccggtatttc tcccgtttt 420
ggtagctcag gcaacccgtc cccggtgact gcgtatgggtg tttacgttgg catgaaagcg 480
gcagctaaag aagcgttcgg gaccgattct ctggaaggct tgacggctgc tgttcaaggt 540
gtgggcaacg tctcgtacac cctgtgcaag cacttacatg aggaagggtc taagctgatc 600
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gttgatatca gcgatatcta ctcagtggag tgcgacattt tcgctccatg tgctctagga 720
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aacaaccagc tgaaggaaac aaaacacggt gatcagataa gcgaactggg catcgtgtat 840
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 tttagaaattt ctaaacgcga caacatccct acttacatgg cggcagaccg tatggccgaa 1020
 gaacgtatag aaaacatgcg caaatcgcggt aaacagttcc tgacgaacga gcattctatc 1080
 ttaagccgcc gccga 1095

<210> 48

<211> 1074

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 48

atgatgagca tcgacatttt gaagaaaact gagacatcga tcccgggtcca ggatgacttc 60
 ctggattacg ctctggcaca tggctttggt gacctccact tcaaagttga tccagaaacc 120
 gggatgaaag cgattgtagc catccactct acgaagcttg gccctgctct ggggtggtgt 180
 cgttttatag aatatccaa tactgcatcc gctatcaacg atgcgatgcg cctggcccgt 240
 ggcatgtcat tcaaagcagc ttctgttaac ctgccgtgg gcggaggtaa agcgggtgatc 300
 attaaaccga acaaaccgtt cgacagggaa gcataacctgc atgcttttgg tcgctttgtg 360

aacgatttag gcggacgtta tatcaccgcg ctggacagcg gcaccaact gtccgacatg 420
 gacatcattg gtcagcacac ttcttacgta gctagcctat caagtcacaa tggcgatcca 480
 tccccgtcta ccgctaaggg tgttctgcga gggatccagg cagcggtcga gttcaaactt 540
 ggcaaagata acctgaacgg tctgcataat gcaatccagg gtctcgggtca cgttggttac 600
 ctggttagcca gccacattca tgctctgggc gccaaactga ctgttacgga cgtaaatccg 660
 cgcgcggtgc agcgtgctgt agaagaattt ggcgcaacag ctgtgtccac tgatatgatt 720
 caccgtgtgc cttgcgatgt ttctcgcccc tgcgcctcgc gcgcggttat caacgacatc 780

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 aatcagcaaa tcgacggcat tggctacttcg ctgctggaaa tctttattcg gtcccagaaa 1020
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<210> 49

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 49

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caggataaag aaagtggctt gaaagcaatt atagccatcc acgacactac gctgggtcct 120

gctttaaccg ggactcgcgt gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

ctacgtctgg cgaaggtat gacttacaaa aatgcagctg ccggcctcaa cctgggtggc 240

gcgaagaccg ttattatcgg tgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300

ctgggacgct acattcaggg cctgaacggt agatacatca ccgctgaaga tgtgggtacg 360

actgttgatg acatggacat tatccatgaa gaaaccgact tcgtgactgg gatctcacca 420

agctttggct ctcttggtaa cccgtccccg gttacggcat atggcgtata ccgcggcatg 480

aaagctgctg cgaagaggc ctctgggtacc gataacctgg aaggaaaggt aattgcggtt 540

cagggtgtcg gtaatgtggc ttatcacctc tgtaaaccatc tgcacgctga aggcgctaag 600

ctgattgtta ctgatatcaa caaagaggca gtccaaaggg ccgttgagga atttgccgcg 660

tcggcagtag aaccgaatga aatctacggt gttgaatgcg acatttacgc cccgtgtgcg 720

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agcgccaaca accagctgaa agaagaccgt catggggata tcatacacga gatgggtatc 840

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aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgcagc tgaccgcttg 1020

gctgaagagc ggatcgcac ctttaaagaac tcccgtagca cctatctgcg caacggccac 1080

gatatcatat cgcgacgt 1098

<210> 50

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 50

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ccggaaacgg gtctgcgcgc catcattgct atacacaaca catctcgtgg gccggcggtta 120

ggcgggtgcc ggatgtttcc atatgcatct gacgaagaag ctttgcgtga tgttcttcgt 180
ctatcacgcg gcatgactta caaaagtga ctggctaacc tcgacctggg tggcggcaag 240
agcgtcatca tcggtgatcc ccgtcagcat aaaaccgagg cgatgctgga agccatggga 300
cgctgtctgg agaaactggg tggccactac attgcggctg aagactccgg tacttctgtg 360
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ggattcgatg gtgctccatc tgacggcgat ccgtcacccg tcaccgcata cggcggtttc 480
gttggctctga aagccgccgt gcagcatggg ctgggtcgca cggacctgac tgggcttaag 540

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cacgaacgca ctgatcagga tctacaaaag gtctgtgccc atgtggacgc tattgcggat 960

accctaggcg aaatcttcac tcgttctcaa cgtgaccagc gcccgaccgg cgagattgct 1020
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aaagtagcaa gcgttggc 1098

<210> 51
<211> 1089
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<220><223> Synthetic polynucleotide
<400> 51

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gcaggcgcg cgtttggcgc acaggttggt ggcttgacg atatctacga tcaagaggtc 720

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ctgattaacg tgtatagcga agttacaggg tctaccgctc agggggcttt aactcagacc 960

gaaaaaatct atgactacac actccaagt ctggaaaaag ccgcggtga aggtctgcac 1020

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agcacctac 1089

<210> 52

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 52

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctcgcat cgaagatgct 180

ctacgtctgg cgaaaggtat gacctacaaa aatgcagctg ccggtctcaa cctgggcggt 240

gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300

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cagggtgtgg gtaatgtagc ttatcacctc tgtaaacatc tgcacgctga aggcgctaag 600

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gatatcatat cgcgacgt 1098

<210> 53

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 53

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 ggcaactcgca tgtggcccta cgctagcgaa gaggaagcac tgaaagatgt ccttcgttta 180
 tcccgtggga tgacctaaa agctcggtt tcaggtctaa acctgggcgg cggtaaagct 240
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<210> 54

<211> 1038

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 54

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ggtgggtgcc gcatgtggcc atacgcaact gacgaagaag ctcttcgtga tgttctccgt	180
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gaacgtttta accgtgcc	1038

<210> 55

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 55

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caggataaag aaagtggctt gaaagcaatt atagccatcc acgacactac gctgggtcct	120
gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
ctacgtctgg cgaaaggat gacctacaaa aatgcagctg ccggtttcaa cctgggcggt	240

gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gtttcgtgcg 300
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<210> 56
<211> 1098
<212> DNA
<213> Artificial Sequence
<220><223> Synthetic polynucleotide
<400> 56

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180
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gatatcatat cgaggcgt 1098

<210> 57

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 57

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

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aaagtaatcg aaatcagcaa acgtgatggg attgctacct acgtcgcggc tgaccgcttg 1020

gctgaagagc ggatcgcatc tttaaagaac tcccgtagca cctatctgcg caacggccac 1080

gatatcatat cgcgacgt 1098

<210> 58

<211> 1074

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 58

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<210> 59

<211> 1050

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 59

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<210> 60

<211> 1041

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 60

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ggaaacccgg ctccgtttac tgctctgggc acctatcgag gtatcaaagc agcggcaaaa 480

catcagtttg gctctgacga tctgcgcggt aagaccgttg ccgtgcaggg tcttgggtcc 540

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caacgtgctg atgccgaaca gcagccgacc tctgttgcg cagacctgat ggctcaggaa 1020

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<210> 61

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 61

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<210> 62
 <211> 1101
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 <400> 62

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 gaaatcgctg aacgtgacgg tgtaccgact taccaggccg cagatcgctt gggtagggaa 1020
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ggtcggatcc gcgggggcaa c 1101

<210> 63

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 63

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ggcggctactc gcatgtggat gtatgacact gaagcagatg cttttgaaga cgcacttcgt	180
ctggctaaag gcatgacctt caaaaatgcg gctgccggtc tgaacctggg cgggtggcaaa	240
acagttatca tcggagaccc tcgtaaggat aaaaacgagg aaatgttcag agcattcggg	300
cggtacattc agggcctgaa tggccgttac atcactgccg aagacgtagg taccaccgtg	360
caggatatgg acatcattta tgaagagact gactacgta cggcatttc tcccgtttt	420
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gcagctaaag aagcgttcgg gtctgacgat ctgggtggca aaaccatcgc tgttcaaggt	540
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tttgatatta gcaaacgcga ccaaatccct accttcaaag cggccgacgg tatggccgaa	1020
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<210> 64

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 64

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ggcgggtgtc gcatgttccc atatgcatct gacgaagaag ctgtttggga tgttttcgt 180
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acctgaatg aaatcttcac ccggtcggat cgttcaggcc gcccagacagg tgccatcgt 1020
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cgtatggcgc acgcgggc 1098

<210> 65

<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 65

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ggcggtagcc gcatgtggaa ctacgaatct gaggaagaag cgattgaaga cgctatccgt 180
ctaggcagag gtatgactta caaaaatgct gctgcgggcc tgaacctggg cgggtgtaaa 240
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cgttttatcc aggtgttgaa cggccgctat atcactgccg aagacgtggg taccaccgta 360

gctgatatgg acctgattca tgaggaaacg gatttcgtta ctggtatctc gccagcattt 420

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gttactgaca ttaaccagca ggctgttcag cgcgcagtgg acgaatttgg cgcaaccgct 660
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<210> 66

<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 66

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gctgttgggt gtactcgtat gtggaattat gcgagttccg ctgaagctct ggaagacgtc 180
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gagatcgttg ctccggacgc gatttatgac gtacggctg acatctatgc cccgtgtgcc 720
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gctcagaaag tt 1092

<210> 67

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 67

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ggcggtagcc gcatgtggac ttataaatct gaggaagacg catttgaaga cgctcttcgt 180
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cgcttcattc agggccctgaa cggcagatac atcacggcgg aagatgtggg tactactgta 360

gctgatatgg acctggttta tcaggaaacc gaatacgtga ccggaatcag cccagcattc 420
ggatcatccg gtaacccttc tccggttaca gcttacggcg tttatgtggg catgaaggcc 480
gcggctaag aggccttttg tgacgatagc ctggaaggtc gtacggctgc ggttcagggt 540
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<210> 68

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 68

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gcttttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct      180
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aaagctgctg cgaaagaggg cttcgggtact gataacctgg aagggaaggt tattgcggtt      540
caggggtgtgg gtaatgtagc ttatcacctc tgtaaacatc tgcacgctga aggcgctaag      600
ctgattgtca ccgatatcaa caaagaggca gttcaaaggg ccgttgagga atttggtgcg      660
tcggcagtag aaccgaatga aatctacggc gttgaatgcg acatttacgc cccgtgtgcg      720
ctgggtgcca cggtaaacga tgaaactatc cctcagctga aagctaaggt tatcgctggc      780
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tacggctata accgtgaacg cgctttgaaa cgggttgaat ctatttacga tactatcgca      960
aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgcagc tgaccgcttg      1020
gctgaagagc ggatcgcatc tttaaagaac tcccgtagca cctatctgcg caacggccac      1080
gatatcatat cgcgacgt                                     1098
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<210> 69

<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 69

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gaacgtattg agcgagttgc taaatcgcg ctcctcttcc tgcgtaacga acataacatc 1080
attagcaggc gc 1092

<210> 70

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 70

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ggcggtagcc gcatgtggac ctatgcatct gaagaggctg cgtttgaaga cgctcttcgt 180
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ctgggacacc gtaaa 1095

<210> 71

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 71

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctcgcat cgaagatgct 180
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accgttgatg acatggacat tatccatgaa gaaactgact tcgtgaccgg gatctcacca 420
agctttggct ctcttggtaa cccgtccccg gttacggcat atggcgata ccgcggcatg 480
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cagggtgtcg gtaatgtggc ttatcacctc tgtaaacatc tgcacgtga aggcgctaag 600
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<210> 72

<211> 1053

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 72

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ctgtctcggg gcatgacctt caaatccgct ctggctaata tgcctctggg cggcggtaaa 240
gcggtaatca ttggcgatcc acacaacggt aaaagtgaag cgctgtttca ggccatgggc 300
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gctgaaatgc agatcatggc tgagcgtagc cgccacgttg cgggcgcgaa ccagcgtgaa 420
gcattcgatg gtggtgttcg ttccggcgac ccgagccctt ctaccgtta cggcgctctt 480
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<210> 73

<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 73

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ggcggctctgc gcatgtggac ttatgcaact gaagaagaag ctatggagga cgcacttcgt 180

ctggctcggg gcatgacctc caaagcggct gccgcgggtc tgaacctggg cggcggtaaa 240

acagtcttga ttggagatcc caagaaagac aagtccgaag aactgtttag atcactgggt 300

cgttacatcg agggcctgaa cggacgctat atcactgccg aagatgtagg taccagcgtt 360

gaagatatgg acctaatcca tctggagacc aaatacgtta ctggtatctc gccagctttc 420

ggctcttctg gcaaccctag cccggttaaca gcatttggcg tgtataaagg tatgaaggct 480

gcggcaaaag aagcggttcgg gtctgacgct ctggatggtt tggttgtagc tgtccagggt 540

gtgggcaacg ttgcctactc catgtgcgag tacttacaca aagaaaatgt taaactgac 600

glaactgaca ttaacgaaga aaacgttcag cgcgcggtaa acgattttgg tgcaatccgt 660

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ggtatcatca atgacgacac tatcgaacgt ctgaaatgca aagttgtagc tggcagtgca 780

aacaaccaac tgcgtgaaga tcgccatggt gatattctgg aagaacgcgg aatgggtgat 840

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ttcgaaatcg ccaagcgaga tggatatcca tcttatcagg cggcagaccg tatggccgaa 1020

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ttaaaccagc gc 1092

<210> 74

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 74

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ggtgggtgcc gcatgtggga ctatggctct gaagaggaag cgctcgaaga tgttctgcgt 180
 ctgtcacggg gcatgaccta caaagctgct gtatccggtc tgaagtctggg aggtggcaaa 240
 agcgttatca ttggtgaccc taaaaaactg aagaatgagg cattcttccg tacctttggg 300
 cgcttcgtcg attctctgag cggcagatac atcaccgcgg aagacgtaaa cattcgtgtg 360
 aaagatatgg aatcggttgc tctggaaact ccatatgtaa ccggcatcaa ctctcgtgtt 420
 ggaggttccg gtgaccctc tccggttaca gccggggcg tgtttaacgg tatcaaagct 480
 agcgttaaac acaaactggg caaggattca gtgaacggtc taacggtagc ggttcagggt 540

 tgcgggtgcag ttggcacttt cctgactgaa tttctgacct aggaaggcgc aaaagtgttc 600
 gctgccgacc taaatcagga caaagtaaag aacgtggtcg aaagcttcgg tgctgaggcg 660
 gttgatctga ataaaattca ttcccttccg gtagacgtgt acgcgccgtg tgccctgggt 720
 ggcatcctga acgataacac tattccggaa ctgcaaacca cgatcgttcc tggaggcgcc 780
 aacaatcagc tgttagatga ggctaaacac gctgcgatgc ttaagaaaa aggtatcctc 840
 tacgcccctg actacgtgat aaacgcgggc ggtctgatta acgtatatca ggaactgcaa 900
 ggctacgatg cagatgtcgc gcgaactaaa gccgctggga tctttgatac ctttatcaac 960

 atctataagg agtcggacga acagggtatt accactatcc aggcaagcaa taaaattgcc 1020
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 ctgtggatca accaa 1095

 <210> 75
 <211> 1044
 <212> DNA
 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 75

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 ggcggttgc gcatgtggcc gtatgcatct gaagcggtg ctgttactga cgcactacgt 180

 ctttcgcgcg gcatgaccta caaatccgca ttggcgggtc tgcccctggg cggcggtaaa 240
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 cgtttcgtag acagtctggg tggccgttac atcgtgccg aagatgtagg taccggcgtg 360
 gcggacatcg aggcaatgag gcaggttact cggcacgtcg ctggcaccgc tgggtgcagc 420
 ggtgaccgt ctccggttac agcgtacggc gtatttcagg ggattcgcgc cgcagcaaaa 480
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gtgggcctgg atctggctcg ccagctctat gaagctggcg cagccctaat tgtcgccgac 600

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gatcgcatcc acgtgcgga cgttgatata ttgcaccgt gcgctctggg tgctattctg 720

aacgacgcaa ctatcccga aatcaaagcg ggaatcattg ctggtgcagc taacaaccaa 780

ctcgcggaag agcgccatgg agcagctctg atgaaacgag gcattctgta cgcgccggat 840

tatgcaatca atgctggggg catcattaac atccaccacg aatccgcggg taaatacgac 900

cgtgctgctg cactccgcca ggttgaaggg atctatgata ctttgctgga aattttcgcg 960

cgtgcccgcg ctgaaggtat cccgaccagc gatgctgcgg accgtgttgc ggagactcgt 1020

tttggcaagc atcgtcaggc ggca 1044

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<211> 1071

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 76

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ggtggtaact gcttctatcc ctacgcatct gaacaggatg ctcttaatga cgttctcgct 180

ctgtcgctg gcattgcata taaaaacgcg ctggctggtc tggatctggg cggcgcaaaa 240

gcggtcatca ttggtgacct tgccactgta aaaagcgaag ccctgctgcg tgcatacggg 300

cgcttcgttg aaacctggg tggccggtac atcacgctt gcgatgtcgg tacttatgtg 360

gcggatatgg acgttgttgc tcgtgagacc cgttacgtaa ccggccgcag ccgtgacgat 420

gggggtgccg gcgactcttc tgttctgaca gcttacggtg tctttcaggg catgcgcgca 480

tccgctgaac acgtttggg tactccggaa ctgcgtggtc gcagggtagg cgttgcgggt 540

gtgggtaaag ttggccattt gctggttggt cacctagtag aagctggcgc agaggctcgtg 600

gtcactgatg taagtgaagc tgcgatcgac cgtgttcggg cggtcaccc gtctgtggag 660

gtggtagcag aactgatac cctggtagcc tccgatatag acgtttacgc accgtgcgcg 720

cttggcggcg cgctcaacga tgctaccgtg gaagtctctg gtgccaaggt tgtatgtgga 780

gcagccaaca atcaactggc tcatccgggc gttgaaaaac tgctggatga acgcggtatt 840

cttttcgcgc cagattacct ggtgaacagc gggggcgtaa tcatggtgag cgacgaatta 900

cacggcttcc agtatgaac cgctcatcgc aaagtttctg cattatacga aactacaaa 960

aaagtatttg ctctggcgga ggaagaaggt gttccgcctg ccacggcggc tgatcgattg 1020

gctgaacgta ggatggccga agttagccgt ctccgtagca tcttgacacg t 1071

<210> 77

<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 77

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ggcgggtgcc ggatgtttcc atatgcgtct gacgatgaag cacttcgtga cgttctccgt 180

ctgtcccgcg gcatgactct gaaatcatct ctggctggtc tgaaactagg cggcggtaaa 240

gcggtcatca tcggtgatcc ccacaccgga aaaagccagg ctctgctgca cgccatgggg 300

gacttcgtcg actccctggg cggtagatac attacagcag ctgatagtgg tactggtgac 360

gcggaatgc aggcatcgc tcaacgtacc cgccatgtgg taggcgccac gccgcgtact 420

ctgtcggatg gctctgttgc ttctggcgac ccgagcccgt ccaccgcgta cggggatatat 480

gttggtttaa aggaagccgt tcgccagcgt ctgggccgtg atgagctgac cgggtctgaaa 540

gtggctatcc aggggtgtagg ccacgttggc ctgggccttg cccgccatct gaaagctgcg 600

ggtgctgaac tgtgggttgc tgacattttc gatgctaacg tcaaacaggc aatggaagag 660

gtgggagcaa atgttgttcg tccgcaggat atctacggcc tggatgtgga cgtctttgcg 720

ccttgcgcaa tgggtggcat cttgaacgaa caaactctgg aagtactgcg tgcaccagtg 780

atgcgccgcg ctgctaacaa tcagctggca tcagcgggta ttggagtga actacagcgc 840

cgcaaccagc tgiacgcgcc ggactacgt atcaacgctg gtggtatcat cgatgtatat 900

taccagcgt aacggcgtag cgccgctcag atagatgccc acgttaacgc tattgctggc 960

accctccgtg aaatcttga gcgagccgct gcttctgggtg aatgcacctc cgttatcgt 1020

gatcgtctgg cgctggaacg ttacaggca ggtgggtgcgc cgcaagtagc aactctgcaa 1080

cgtcaggcga gc 1092

<210> 78

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 78

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ggcgggtgcac gcatgtggac ctacgagtct gaagaagctg caattgaaga cgctctccgt	180
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acagttatca ttggagaccc ccgtactgat aagaacgacg agatgtttcg agccttcggt	300
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gaagatatgg acctgattca cctggagacg gactacgtta ccggtacgag cgcagctgat	420
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gcgaccgcca aggaagcgtt tggtagacgac tctactggtg ggaaaacat tgcagttcag	540
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gtcctgtctc gccgt	1095

<210> 79

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 79

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gctttagggg gactcgcgat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
ctacgtctgg cgaaaggat gacctacaaa actgccgcag ctggtctgaa tctgggcggt	240
gcgaaaaccg ttattatcgg cgaccaagg aaggacaaat ccgaggcaat gttccgagct	300

ctcggacgct acattcaggg gctgaacggt cgttatatca ctgcggaaga tgttggcacc	360
accgtggatg acatggacat catccatgag gaaacggatt ttgttacggg catttctccg	420
tctttcgggt cgagcggtaa cccgtccccg gtgactgcgt acggcgtata tcgtggtatg	480
aaagctgccg caaaggaagc ttctggcaca gacaaccttg agggtaaagt tatcgctgtc	540
cagggtgtag gcaatgtggc ctaccacctg tgtaaacacc tccatgctga aggcgcaaaa	600
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<400> 80	
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ggtggtaccc gcatgtggaa ctatgcatct agtgaagaag ctttgactga cgttcttcgt	180
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gccaaaaaac tggcgtcaaa aactgcg 1047

<210> 81
<211> 1104
<212> DNA
<213> Artificial Sequence
<220><223> Synthetic polynucleotide
<400> 81

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gccgcaaacg tggcgttcgg ttccgacgac ctgaacggta aaactgtggc tgttcaaggc 540
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ttccatttac gccgcggtcg tcac 1104

<210> 82

<211> 1041

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 82

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ggcgggtaccc gcatgtggaa ctatgcgtct agcgcagaag ctcttactga cgttctgcgt 180

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tccagcgccg aacacaggcc gaccggtgaa attgccgatc agatggcgcg tgaagtaatt 1020

gccaatgcaa aagcggcacg t 1041

<210> 83

<211> 1086

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 83

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ggtggtaccc gtatgtggaa ctatagtact gacgaagatg caattactga cgctcttcgt	180
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caggacatgg atacgatcca cgaagagact aactacgtta ccggcatttc tcccgtttc	420

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ttcgaattg ccgagcgaga tggcatccct tcctaccagg cggcggaccg tatggccgaa 1020
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<210> 85

<211> 1074

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 85

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gaagatatgg acttcgttca tatggaaacc acccacgtga cgggcatcgg atctaaatcc 420
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<211> 1047
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<213> Artificial Sequence
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<400> 86
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cagattgcgg aggaacgttt tagcaag 1047
<210> 87
<211> 1041
<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 87

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ggcgggtggc gcttgtggga ctatgcatcc gatgaagatg ctcttggtga cgtcctccgt	180
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cgcattggtcc accgtctggg cggcagctac tacagtgcgg aagacgttaa catcaccacc	360
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aacgcggccg agagcaccgc gaaagttagt cagatttatg atactctgtt gcgtattttc	960
gaacgcgctg atgccgagga caaaccaact tctaccgtcg cagaccagat ggctcaggaa	1020
attattgccc ggggaccgct a	1041

<210> 88

<211> 1065

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 88

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ggtggtaccg gcatgtggaa ctataagact gaagaggaag cgattgaaga cgctcttcgt	180
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ggcggttctg gcgaccctag cccgaaaact gcgtacggcg tctttcgtgg tattcaggca 480

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tacaacgaag aacgcgcgat gcagtcggtt agcaaaattt atgataatat caaaaaagtc 960

ttccagatcg caaaacgtga taatattccg acgtacaaag cggctgatcg tatggcggag 1020

gaacgcattg agaagttggg taggttacgt aacacttacc tgggt 1065

<210> 89

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 89

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gctcaggagg ggactcgcgt gtggacctat gatagcgaag aagctgcgat cgaggacgca 180

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tcattcggct cccttggtta cccagcccg gtcaccgcct acggcgata cgttggtatg 480

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aaagtcatcg aaatctctaa aagggacggc attgctacgt acgttgctgc ggaccgtctg 1020

gcagaagagc gtattgcgag cctgaagaac tcccggttcaa cctacctgcg caatggacac 1080

gatatcatct ctaggcgc 1098

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<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 90

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ggcggtactc gcatgtggac ctatgcatct gaggacgaag ctattgaaga cgcacttcgt 180

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catgatatgg acacgatcca cgaagagact gactatgtta ccggcatttc ccccgtttt 420

ggtagctcgg gtaaccgcgc accggtgact gcgtatggtg tataccgcgg catgaaagcg 480

gcagctatgg aagcgttcgg gaccgattct ctggaaggca aagtatcgc tgtccaaggt 540

gttggaatg tcgcttaca cctgtgcaag catttacag aggaaggtgc tcagctgac 600

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gttgaaaccg aggaaatcta ctccgttgac tgcgatattt acgtccatg tgccctcgga 720

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ctgagccgctc ga 1092
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<211> 1098
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide
<400> 91

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<210> 92
<211> 1101
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 92

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gctctgcgtc gcaactgaaa catttacaac accacactgg aaatattcaa ttctgcagag	1020
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aggaaaaaag aaaacgcgaa a	1101

<210> 93

<211> 1065

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 93

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cgcatatgg actgggttca tctgaaagc aactttgtga cgggagttag ctcttcgggt 420

gcgtccggcg atccctctcc tatgaccgca cgtggagtat ggaaaggcat gaaagccgt 480

gcaaaagaaa tgttcggtga cgatagccctg gagggcaaaa ctatcgctat ccaagggtt 540

ggccacgttg gttactacct ggcgaaacat ctgcgtgaag aaggtgctaa gctgattgtg 600

actgatatcc acgaggacgc tatcaaagc gttttaaacg aaatggacgc aactgtcgtg 660

gagccggaag agatTTTTGG cgttgatgcc gatatctacg cgccatgcgc aatgggtgcg 720

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gactaccagc gtgcactcca gaaagttagc acggtttatg acaacgtggc taaagtctg 960

caaatcgcta aacagatgaa catccaacc tacaagccg cagatcgaat ggccaggaa 1020

cgtattcaga ggctgggtcg tattcgctcg aattatctgc gaaa 1065

<210> 94

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 94

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caggataaag aaagtggctt gaaagcaatt atagccatcc acgacactac gctgggtcct 120

gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

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gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300

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agctttggct ctcttggtaa cccgtccccg gtcacggcat atggcgtata ccgcggcatg 480

aaagctgctg cgaaagaggc cttcgttact gataacctgg aagggaaggt tatcgcggtt 540

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<210> 95
 <211> 1068
 <212> DNA
 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 95

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<210> 96

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 96

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<210> 97

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 97

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aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgcggc tgaccgcttg 1020
gtgaagagc ggatcgcatc tttaaagaac tcccgtagca cctatctgcg caacggccac 1080
gatatcatat cgcgacgt 1098

<210> 98

<211> 1044

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 98

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ggtggttgcc gcatgtggcc ctatgcatct gaacaggaag caatccacga cgttcttcgt 180
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gacccggcac gtactggtag tcctagtcg tttacggcat atggcgtttt catcgactg 480
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<210> 99

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 99

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gctttagggg gcactcgcgt gtggacctat gatagcgaag aagctgcgat cgaagatgct 180
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aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgcggc tgaccgcttg 1020

gctgaagagc ggatcgcatc tttaagaac tcccgtagca cctatctgcg caacggccac 1080

gatatcatat cgcgacgt 1098

<210> 100

<211> 1065

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 100

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ggtagcaccg gtatgtggaa ttacgccagt gaagaagatg ctatcctgga tgcgttacgc 180

ctggcgcgag gtatgactta taaaaacgct gccgcaggct tgaacctggg cggcggtaaa 240

gctgttatta tggcgacag ccgtaccagc aaatcagagg aactgtttcg cgcgttcggt 300

cgttacgtgc aggcgtgaa cggccgttat atcaccgtg aggacgttgg tactaacgta 360

caagatatgg actggatata catggaacaa aagtttgtga cgggatctc ctcttcgtac 420

ggtgctagcg gagatccgtc cctctgacc gactgggagc ttaccgcgg tatgaaagcc 480

gccgcaaaag aagcgttcgg cagcgactct ttagagggtt aaactgttgc tattcagggt 540

cttgccacg tcggctatta cctggcaaaa cacctcactg atgaaggcgc taaactgac 600

gtgacggata tcaattctga agccgttaag agggtagcgc gtgagttcgt tgctaccgca 660

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tacaacgtg aacgtgctct gaaaaaagtt gagatggtat atgataatgt ggcacgcgtc 960

atcgctattg ccaagcgtga ccatatcccg acttataaag cagcggaccg aatggctgag 1020

gaacgtattg cgaatttgg caaagtttcc aacactttcc tgcgc 1065

<210> 101

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 101

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gctttagggg gcactcgcgt gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
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gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg	300
ctgggacgct acattcaggg tctgaacggc agatacatca ccgctgctga tgtgggtacc	360
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tcttttggtt ctcttgcaa cccgagcccg gtaactgcat atggggtgta tcgtggtatg	480
aaggctgccg ccaaagaagc gttcggcact gacaacctgg aaggtaaagt tatcgctgta	540
cagggtgtcg gcaatgttcg ttaccacctg tgtaaacatc tgcacgctga ggggtgctaaa	600
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gcggaggaaac gtattgcac ccttaaaaac agccgttcga catacctgcg caatggacac	1080
gacataatca gtcgtcgc	1098

<210> 102

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 102

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gctttagggg gcactcgcgt gtggacctat gatagcgaag aagctgcgat cgaagatgct	180

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aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgcagc tgaccgcttg 1020
gctgaagagc ggatcgcatc tttaagaac tcccgtagca cctatctgcg caacggccac 1080
gatatcatat cgcgacgt 1098

<210> 103

<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 103

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ggctgccgca tgttgaatta tgaaaccgaa gaggaagcta tcgaagatgt attgcgtctg 180
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ttaagccgac gt 1092

<210> 104

<211> 1122

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 104

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gcagaggaag cgtttggtgc cctggttgtt ggtccggacg aaatttacgg cgtcgaagcg 720
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taccgtgctg cggaaaaaat ggcggaagaa cgcacgcaa caatgggtag cgcgcggagc 1080
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<210> 105

<211> 1158

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 105

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gccgaccgtc tggcagaaaa acgcatgcgt gaaatctcca gcctaaggac catcctcctg 1140
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<210> 106

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 106

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gcttttagggg gcactcgcgt gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
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<210> 107

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 107

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ggcggtaacc gcatgtggac ctatgaatct gaggaagctg caattgaaga cgcactgcgt 180
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gctgacatgg acctgatcca tgaagaaact gatTTTgtta ccggcatttc ccccgcttc 420
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<210> 108

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 108

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<210> 109

<211> 1071

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 109

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gctccggact tcatcattaa cgcgggcggg gtaatcaatg ttagtgacga actgcgtgag 900

ggaggtctaca accgcgagcg tgctctgaag caggtagatg gtatatacga tattatggaa 960

caggtaatcg ccatctctaa acgtgatggt atccctactt acaaagctgc cgacattctg 1020

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<210> 110

<211> 1134

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 110

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gctactggcc tgaaggccgt gattgcagtt cattcgacag ctttgggtcc ggcacttggc 180

ggcactcgct tcttccata tgcttctgat gaagaagctg ttgacgatgc gctgaacctg 240

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atTTTTGCCA gagcgaagcg tgatggcgta ccacctgcgg tagctgccga tcgtctggcg 1080

gaacagcgca tggctgaacg cactccggca gcagactggc tgcgtgtcca aagc 1134

<210> 111

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 111

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gctactgggg gcacccgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
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<210> 112

<211> 1107

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 112

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gggtgtactc gcatgtggcc ctatgcatct gaagaggaag ctatcaacga cgttctccgt	180

ctgtccaaag gcatgactta caaagcagct gtatcaggtc tgaacctggg cggcggtaaa 240
gcggttatca ttggtgatcc tgaaaaagac aagagcgagg ccctgttccg aagttatggg 300
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ggaggtctcg gtaacccgtc tccatacact gctaagggcg ttttctgtgg tatcgaggca 480
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atcttcgcca tctccgatga acaggatata cccgtaata aagcggctga cgttctggcg 1020

gaatcgcgta ttgagaglat ccgtaacatc aacggcaaat atctgggtaa cctggggcac 1080
aggtttccgg gtcgcaagac tcgcaac 1107

<210> 113

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 113

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ggcggctactc gcatgtggac ctatgaatct gaggacgctg caatcgaaga cgcaactccgt 180
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gcggcgaaag aagcgtttgg gactgactct ctggaaggca aagttatcgc tgtccaaggt 540
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gttgacccaa acgaaatcta cgggtgttac tgcgatattt acgctccgtg cgccttcgga 720

gctacgatca atgattacac catccctcag ctgaaagcaa aagttatcgc cgggtgcgga 780

aacaaccagc tgaaggaaac ccgccacggt gatgctatac acgaaatggg catcgtgtat 840

gcgccggatt acgttatcaa cgcaggcgggt gtaatcaacg tagcagacga gctctatggg 900

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attgaaattg ccaaacgaga tggatatcca acctacatgg cggccgaccg tatggccgag 1020

gaacgtatag aaaaactgaa aaatagccgc tcccagttcc tgatgaacgg ccgtcatatc 1080

ttaaaccgcc gccgg 1095

<210> 114

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 114

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

ctacgtctgg cgaaaggtat gacctacaaa aatgcagctg ccggtctcaa cctgggcgggt 240

gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300

ctgggacgct acattcaggg tctgaacggc agatacatca ccgctgaaga tgtgggtaca 360

accgttgatg acatggacat tatccatgaa gaaactgact tcgtgaccgg gatctcacca 420

agctttggct ctcttggtaa cccgtccccg gttacggcat atggcgtata ccgcggcatg 480

aaagctgctg cgaaagaggc cttcgggtact gataacctgg aagggaaggt aattgcggtt 540

cagggtgtcg gtaatgtggc ttatcacctc tgtaaacatc tgcacgtga aggcgctaag 600

ctgattgtta ccgatatcaa caaagaggca gtccaaaggg ccgttgagga atttggtgcg 660

tcggcagtag aaccgaatga aatctacggc gttgaatgcg acatttacgc cccgtgtgcg 720

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<210> 115

<211> 1116

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 115

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gaggatattg aacacatctt tactgaaacc aacaacgtat gtggagttgc gatcccgcat 420
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gaaaacagga tcgaatctat tcgccgtatc ggtagccgtt atatgggcgt cagtcaacat 1080
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<210> 116

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 116

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<210> 117

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 117

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accgttgatg acatggacat tatccatgaa gaaactgact tcgtgtcagg gatctctcca 420
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<210> 118

<211> 1035

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 118

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<210> 119
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<400> 121

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<211> 1119

<212> DNA

<213> Artificial Sequence

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<400> 122

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atcaacatga ctctgcgt 1098

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<211> 1098

<212> DNA

<213> Artificial Sequence

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<400> 124

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<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 126

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<210> 127

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 127

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<211> 1032
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<400> 128

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<210> 130

<211> 1074

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 130

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<210> 131

<211> 1071

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 131

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 aaggtcatcg aaatcagcaa acgtgatggt atcgctacct acgtagctgc cgaccgtctg 1020
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<210> 133

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 133

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gcttttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180
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gatatcataat cgcgacgt 1098

<210> 134

<211> 1074

<212> DNA

<213> Artificial Sequence

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<400> 134

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gctgggtggct acataaccgc tgaagatgta ggcatcaccg cggcggacat ggaactgatt 420

gcatcgcaga ctggtcatgc tcgcggcacg gaagcgactg gtctggggga tccgtcacct 480

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<211> 1098

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<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 135

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gcttttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
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cagggtgtcg gtaatgtggc ttatcacctc tgtaaacatc tgcacgtga aggcgctaag	600
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<210> 136

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 136

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gcttttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
ctacgtctgg cgaaaggtat gacctacaaa aatgcagctg ccggtctcaa cctgggcggt	240

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<210> 137

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 137

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<210> 138

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 138

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<210> 139

<211> 1101

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 139

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<210> 140

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 140

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
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<211> 1098

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<220><223> Synthetic polynucleotide

<400> 141

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<400> 142

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<212> DNA

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<220><223> Synthetic polynucleotide

<400> 143

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aaggtcatcg aaatcagcaa acgtgatggt atcgctacct acgtagctgc cgaccgtctc 1020
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gacataatca gccgccgc 1098

<210> 144

<211> 1101

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 144

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atcattggca tccattctac gaccctgggt ccagcacttg gtggcactag aatgtggaac 180
tatgagaacg aagccgacgc tatccgtgat gcattgcgtc tgtcacgtgg catgacctac 240
aaagcttcta ttagtggctt ggacctcgga ggtggcaagg cggatgatcat cggcgacagc 300
cgcaaagata aaactgatgc actgatgcgt aaattcgggtg aatacgttaa ttccttaagc 360

ggacgtata taaccgctga agacgttgggt attaacaccc acgacatgga gatggtaaaa 420
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aaggcagagc tggcaaatgc c 1101

<210> 145

<211> 1059

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 145

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ggcgggttgcc ggatgtttcc atatgcatct gacgaagaag ctttgcgtga tgtttctcgt	180
ctgtcgcgcg gcatgactta caaaagtgcg ctggctaacc tggacctggg tggcggcaag	240
agcgtcatca ttggtgattc tcgtgagcac aaaaccgaag cgctgctgga aagcatggga	300
cgcttcctgg agcaactagg tggcctgtac atcgcggtg aagactcagg tactttctga	360
gcagatctta aaataatggg tcgtcagacc actcatgttg caggaatcag ggatcgcccc	420
ggattcgacg gcaaaccatc caacggtagc ccgagcccgg ctacagcctg gggcaccttt	480
gttggcattc aggtcgcgt gaagcacaaa ctgggtcgtt cggacctgga gggctctgaaa	540
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ggcgtgaac tctgggttta tgatatccac caggatcaga tggatagagc cgtcgtgag	660
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tatgagcgca ctggtccgga tccggaagct gtctgtcaac acgttaatac catcgccag	960
actttggaag aaatcttcca gcgctctgcc cgggatggtc ttccaacggg gcagattgct	1020
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<210> 146

<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 146

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ggtggcacac gtatgtggac ctacgctagt gaagaagccg ctattgagga tgcattacgc	180
ctagcgaaag gtatgactta taaaatgcc gctgctggtc tgaacctggg cggcggttaag	240

accgtaatca tcggagatcc tctcaaagac aaaaacgaag agatgttccg tgcgttcggt 300
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 gctgatatgg acctgattca cgaagaaacc aactacgtta ccggcataatc cccggctttc 420
 ggttcgtctg gcaatccctc cccggtgact gcgtatgggtg tataaccgtgg catgaaagcc 480

gcagctatgg aagcatttgg cagcgacagc ctggaaggta agcgcatcgc tgtgcagggg 540
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tacaatcgag aacgtgcatg gaaacgggtg gaaaccgtct acgacaatat tgctaaagtt 960
 atggaaatct ctcggaacca gggatttctt acttatgtcg ccgcagatcg tctggctgaa 1020
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 ctgagcggca ga 1092

<210> 147
 <211> 1092
 <212> DNA
 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 147

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 aaaaatagtg gtctcaaagc cattatcgct atacacgata cgactttagg gccggcgttg 120

ggcggtaacc gcatgtggac ctatgactct gaagaggaag caattgaaga cgctcttcgt 180
 ctggcaaaag gcatgactta caaaaacgct gcggctgggtc tgaacctggg cggcggtaaa 240
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 cgctacattc agggcctgaa cggcagatat atcaccgcgg aggatgtggg tactactgaa 360
 gaggatatgg acctgatcca tatggaaaca gacttcgtta ccggagttag cgaagaatcc 420
 ggatcgtctg gtaatccctc ccagtaacc gcttacggcg tttaacagg catgaaagcc 480
 agcgctaaag aggccttcgg ttacagatagc ctggaaggta aaaagggtggc ggttcagggt 540

gtgggtaacg ttgcttttac tctgtgcaaa tacctacacg aagaaggcgc aaaactcatc 600

gtcactgaca ttaacgaaga tgcggtaaag cgtgctgtgg acgctttcgg cgctgaagcg 660
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 aacaatcagc ttaaatcctc caaacacggt gaaataattc atgagaaagg catcgtttat 840
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ttcgaaatct ctgctcgtga taatattccg agctatgtcg cggctgatcg tatggcggag 1020
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 ctgagtcgtc gc 1092

<210> 148
 <211> 1098
 <212> DNA
 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 148

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 gctttagggg gcactcgcgt gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

ctacgtctgg cgaaaggatg gacctacaaa aatgcagctg ccggtgaaaa cctgggcggt 240
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 agctttggct ctcttggtaa cccgtccccg gttacggcat atggcgtata ccgcggcatg 480
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aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgcagc tgaccgcttg 1020

gctgaagagc ggatcgcatac tttaaagaac tcccgtagca cctatctgcg caacggccac 1080

gatatcatat cgcgacgt 1098

<210> 149

<211> 1104

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 149

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acgtccttcg atgaccacga gcagatcggt ttctgcaacg ataaagatac aggccttaaa 120

gctattatcg gtattcataa ctacgtgatg ggcccggctc tcggtggtac ccgtatgtat 180

aactactcga atgaatggga agccttgaac gacgttttac gcctgtctcg aggcattgact 240

tttaaagcag ctatcacggg tctgaacata ggccggaggta aagcgggtcat catcggcgac 300

cccaagactc agaaaacccc ggagctgatg agaaaattcg gcgaatttgt tcaactctctg 360

agcggtcgtt acattactgc tgaagatatg ggcatggaga cgcgcgacat ggatatcgta 420

agggacgtga ccccttatgt tactggtatc tccgaagaac gtggcggcgc aggaaacccg 480

tccccggtta cagcctacgg tgtattcatg gggatgaaag cggcggctaa gcgtcagttt 540

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accttagttg catacctagt taaggaaggc gctattgtga ctatcgcgga cattaacgag 660

cagaaactga acgaagttgc tgcaacctat aataccacca tattccgcgg cgaagatctg 720

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accgtataca aaattaaagc taaagtaatc gccggggctg cgaacaatca actggccgat 840

gaaaacatcc acggtgcgat cctgcaagag cgtggcatct tgtacgcgcc agacttcctg 900

atcaacgcag gcggtatcat taacgtgtac gctgaactgg ctactatga taaagcagaa 960

atcactcgtc gcacggaaaa catttatgat actactctgg aaatctttga tticgctatt 1020

gctaacaaga tgaccactca tacggcagct ttaacgatcg ctcaaacgg tatcaatcag 1080

cgcaagatcg agaacagccg tcgc 1104

<210> 150

<211> 1044

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 150

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gcggctacgg gtctgcaagc aatcggttgcg attcatgaca cccgtctggg gccagctctt	120
ggtggctgcc gtttcatcca ctaccctcac gaagaactgg ctttaataga tgcaactcca	180
ctggcacgcg gcatgactta caaagctgcc attactggta tccccatgg cggcggtaag	240
tccgtcatca ttcggccgcc gcgtgcgttt gaccgcggtg cgctgttccg tgctttcggc	300
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gaagatatgg aaaccattcg ttcggttaacc aaacacgtga ccggcgtgaa accggaacac	420
ggtggctctg gcgatccatc cccgtatact gcgctgggtg ttcgccgtgg gatcgaagct	480
tgtgttaagt tcgtctacaa acgcgacagc atcgaaggtc tgcatgttgc tgtgcaggga	540
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gttgccgaca tcgatcctct gaaagcagag cgtgcgcacc gtgagctagg tgctgaagta	660
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aacaaccagt tagccgaaac tcgacacggc gacgtctga tgcatcgcg catcctctac	840
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tacgatgaac agaaaagccg tgaacgcgtg ttaaaaattt acgacactat tttgaaatc	960
gcagaacgtg ctgagcgtgc catgcaacct acctatcgca tcgcagatac gatcgttgaa	1020
gaaaagctgg cgcgtgctgc tcgg	1044

<210> 151

<211> 1053

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 151

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ggcggttgcc gcatgtggcc ctacgcgtct agtcagaag ctcttactga tgttctccgt	180
ctgtctaaag gcatgtccta taaaagcgtc atggccaacc tgaagctggg tggcggcaaa	240
tcagttatca ttggtgaccc tcgtaaacac aaaagcgcgg atatgatgct ggcaatggga	300

gacttcgttc agtctctggg tggcaagtac atcagcgctg aagattccgg tatctctgta 360

agtgatctac aaacaatggc tcagcggtcg gactacatag cgggcacca ggccaaatat 420

aggtacgacg gtggcccagc tgatggcaac ccggcgccgt ctaccgcata cggagtattt 480

atgggtttta aggctagcgt tgcatatggg ctgaaatccg accigaacgg tgtagcgtc 540

gcgattcagg gtctgggcca tgtgggtttc cgctggccg aacacctcca caaagaagga 600

gctaaactgt tcgtactga tatctaccg gacaatctgg ataaagcgt tgagcaattc 660

ggcgcaaccg tggttactcc ggacgaaatc ttggcctgg acgttgacgt atttgctccg 720

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cagaagcagg gctcttccgc ggaagctctg cgaaacaca tcgaggggat tggatgatacc 960

cttacgaaa tctatcagaa agcagcccaa cagggcctcc caaccaacat cgaagcgaat 1020

cgtattgccg agcagcgttt cttagcaggt gct 1053

<210> 152

<211> 1128

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 152

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ctcggtcagg ccctgggcgg ttgtcgcatt tggcattatg cttctgacga agaagcactt 240

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gcataatggtt gtttcgttgg cctgaaagct gctgtcaaac accagtttgg ccgtgatgac 600

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cacctgcgcc aggctggatg agagctgttc gtcacagata tacatgagga acaagtgagg 720

ctggccgtta cggaactagg cgctactgcg gttgcgcagg aagaaatctt gggccttgac	780
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cagctgctgc aacagcgcgg tattctgtac gctccggatt atgtgattaa tgctggcgg	960
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gagggccgcc cggtatccga aaccaaccga cacattgaag gtattggggc tactgttcgc	960
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gcagaagaga gggtcggtaa aaaagca	1047

<210> 154

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 154

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caggataaag aaagtggctt gaaagcaatt atagccatcc acgacactac gctgggtcct 120

gcttttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

ctacgtctgg cgaaaggtat gacctacaaa aatgcagctg ccggtctcaa cctgggcggt 240

gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300

ctgggacgct acattcaggg tctgaacggc agatacatca ccgctgaaga tgtgggtaca 360

accgttgatg acatggacat tatccatgaa gaaactgact tcgtgaccgg gatctcacca 420

agctttggct cttctggtaa cccgtccccg gttacggcat atggcgtata ccgcggcatg 480

aaagctgctg cgaaagaggg cttcggctact gataacctgg aagggaaggt aattgcggtt 540

cagggtgtcg gtaatgtggc ttatcacctc tgtaaaccatc tgcacgctga aggcgctaag 600

ctgattgtta ccgatatcaa caaagaggca gtccaaaggg ccgttgagga atttggtgcg 660

tcggcagtag aaccgaatga aatctacggc gttgaatgcg acatttacgc cccgtgtgcg 720

ctgggtgccg cggtaacga tgaaactatc cctcagctga aagctaaggt tatcgtggc 780

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gtgtatgcgc cggattacgt gatcaacgca gggggcggtta ttaatgtgga cgacgaatta 900

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<210> 155

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 155

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gcttttaggg gactcgcgt gtggacctat gatagcgaag aagctgcgat cgaagatgct 180
ctacgtctgg cgaaaggat gacctacaaa aatgcagctg ccggtctcaa cctgggcggt 240
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ctgggacgct acattcaggg tctgaacggc agatacatca ccgctgaaga tgtgggtaca 360
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<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 156

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<220><223> Synthetic polynucleotide

<400> 157

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<220><223> Synthetic polynucleotide

<400> 158

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<220><223> Synthetic polynucleotide

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<220><223> Synthetic polynucleotide

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<211> 1098

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<220><223> Synthetic polynucleotide

<400> 161

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<210> 162

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 162

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<211> 1098

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<400> 166

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<210> 167

<211> 1044

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 167

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 ctgtcccggg gcatgacct acaatctgct atctccggc tgcctctggg cggcggtaaa 240
 gcggtaatca ttggtgacgc taaacagatc aagagcgcgg agctgttccg tgcctacggg 300
 cgctttgtta attctctgag cggcagatat atcaccgcag aagatgtaa cattcgtacc 360

tcagatatcg ctatcgttgc tgaagaaact aacttcgtgg cggaactga gggtaaagct 420
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 caccgtttag gctctgaaga cctgagcggc gtgaaaatcg cagtacaggg tcttggggct 540
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 <220><223> Synthetic polynucleotide
 <400> 168
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 gcttttagga tcaactcgat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180
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 gatcatctc cgcgacgt 1098
 <210> 169
 <211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 169

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ggtggcacac gtatgtggaa ttacgtacc gaagaagagg ccattgaaga tgctttacgc	180
ctagcgaaag gtatgactta taaaaacgca gctgccggtc tgaacctggg cggcggtaag	240
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gctccggact atgtcatcaa cagcggcggg gttattaatg ttgcggacga gctgtacgga	900
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ttcgaaatct ctaaacgtga tggcattcct acctacgttg ccgcagatcg tctggctgaa	1020
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<210> 170

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 170

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctcgat cgaagatgct 180

ctacgtctgg cgaaagggtc cacctacaaa aatgcagctg ccggtctcaa cctgggcggt 240

gcgaagactg ttattatcgg cgacccccga aaagacaaat ctgaggcaat gttccgtgcg 300

ctgggacgct acattcaggg tctgaacggc agatacatca ccgctgaaga tgtgggtaca 360

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agctttggct cttccggtaa cccgtctccg gttacggcat atggcgata cgcggcatg 480

aaagctgctg cgaaagaggg cttcggtact gataacctgg aagggaaggt aattgcggtt 540

cagggtgtcg gtaatgtggc ttatcacctc tgtaaacatc tgcacgctga aggcgctaag 600

ctgattgtta ccgatatcaa caaagaggca gtccaaaggg ccgttgagga atttggtgcg 660

agcgcagtag aaccgaatga aatctacggc gttgaatgcg acatttacgc cccgtgtgcg 720

ctgggtgccg cggtaacga tgaaactatc cctcagctga aagctaaggt tatcgtggc 780

tggccaaca accagctgaa agaagaccgt catggagata tcatcacga gatgggtatc 840

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aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgcagc tgaccgcttg 1020

gctgaagagc ggatcgcatc tttaaagaac tctcgtagca cctatctgcg caacggccac 1080

gatatcatat cgcgacgt 1098

<210> 171

<211> 1083

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 171

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gcggatcatg aacaagtagt cttttgctct gacgaaaaa gtggtttaaa ggcaattatc 120

gctgttcaca acttaacct ggggccagct ctgggcggtt gtcgtatgtg gccttatgcc 180

tcagaagagg aagcaattcg cgatgtgctt cgtttgtccc gaggtatgac gtacaaatcg 240

gcgatggcta acctgaaact gggcgggtggc aaaagcgtga tcataggaaa tccgcgcaca 300

gacaagacct cggaactgct gaaagcgttc gcacagctg tcgaacgtgt taacggtagg 360

tacatcgctg ccgaggactc tggcactggc gtagatgaca tgaaattcat gtcccagttt 420

accgacctg ttgccgglat tattgataag cccagcgaat acggcgtgcg cagtggcgat 480

ccgtctcctg cgactgctta tgggtacctic gtaggtatca aagcggcagt taaagagcgt 540
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gctctgaaat cgcatatcga aagcatctat gataacctaa tggaaatctt cgctcgggct 1020
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<210> 172
<211> 1098
<212> DNA
<213> Artificial Sequence
<220><223> Synthetic polynucleotide
<400> 172

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gctttagggg gcactcgcgt gtggacctat gatagcgaag aagctgcgat cgaagatgct 180
ctactcttgg cgaaaggtat gacctacaaa aatgcagctg ccggtctcaa cctgggcggt 240
gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300

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 aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgcagc tgaccgcttg 1020
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 gatatcatat cgcgacgt 1098

<210> 173

<211> 1080

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 173

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 caggttactc tggtagatga tgccgcgtg ctggttagtt ccgatattga cgtctacgca 720
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 actactcgtg aaattctgga actggccgat gcggaagggt ttccgccggc ggtagctgct 1020
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<210> 174

<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 174

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ggcgggtacc gcattgtggac ttacgcaact gaggaagacg ctattgttga cgcaactccgt 180

ctggctaaag gcatgacctt taaaaatgcg gctgccggtc tgaacctggg cgggtggcaag 240

acagtgatca tcggagatcc taaaaaagac aaaaacgaag cgatgtttcg ggccttcggt 300

agatacgtac agtcactgaa cggccgttac atcactgctg aagatgttgg taccaccgta 360

gaggacatgg aactgattca tactgaaact gacttcgtta ccggcatttc tgctgaaagc 420

ggtagctccg gcaacccgct cccagtgacc gcatatgggt tatacaaggg catcaaagcg 480

tcggcaaaag aggcgtttgg ggatgactct ctggaaggca aaacgatcgc tgttcaaggt 540

atcggcaatg tcgcttatgc actgtgagag cacttacatg cagaaggatg taagctgatc 600

gttactgata ttaacaaaga agctgtgcag aaggcggtag aggccttttg cgcaacagcc 660

gttgatccgg acgatatcta cgggtgtgag tgcgacattt tcgctccctg tgcccttgga 720

gctgtgatca acgatgacac tctgcgtgtg ctgaaagcaa aagtgttagc aggtgcggca 780

aataaccagc tgaaggaaga acaccatggt cagattctgt tcgaacgcgg aatcgtgtac 840

gcgccggatt acgttataaa cagcggcggg gtaatcaacg tcgaagatga gcttcacggc 900

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tttgaaattg ccaaacgcga cgagattcca acttctatcg cggctgatcg tatggcagaa 1020

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ctgtcccgcc ga 1092

<210> 175

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 175

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caggataaag aaagtggctt gaaagcaatt atagccatcc acgacactac gctgggtcct 120

gctttagggt acactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

ctacgtctgg cgaaaggtat gacctacaaa aatgcagctg ccggcctcaa cctgggtggc 240
gcgaagactg ttattatcgg tgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300
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cagggtgtcg gtaatgtggc ttaccacctc tgtaaacatc tgcacgtga aggcgctaag 600
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gatatcatat cgcgacgt 1098

<210> 176

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 176

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

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cagggtgtcg gtaatgtggc ttatcacctc tgtaaacatc tgcacgctga aggcgctaag 600

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aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgacg tgaccgcttg 1020

gctgaagagc ggatcgcatc tttaaagaac tcccgtagca cctatctgcg caacggccat 1080

gatatcatat cgcgacgt 1098

<210> 177

<211> 1101

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 177

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gggtcgggtg atccttctcc atttacgca ttcggcactc tgcaaggcct gatggctacc 480

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ggcctggacg atatctacga cgttgatgct gacgtgtata gcccggtgtc tctgggtggc 720

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ctggggcgta tgcgtggta g 1101

<210> 178

<211> 1104

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 178

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aacaactgta ctaaacatgt tgctggcatt tccgtggaac gtggtgggtc ggggaaccct 480
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cgtaagaacg aactgcaaaa taaa 1104

<210> 179

<211> 1047

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 179

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ggcgggttgc gcatgtatcc ctacgcatct gaagctgaag cattgaacga cgtttcttct	180
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gttgcggctg agcgtctggg tggccggtat atcgtggctg aagatagtgg tactttctgta	360
ccgcatatgc tgcgatgtc cgaacagaca cgtcacatta gcggcatcgc ggaaaaattt	420
gacgcagacg gtaaacgtcg ttctggcgac ccgagcccgga ttaccgctcg cggggttttc	480
gttgggtattc aggtgcccgt ccgctaccgc ctgggccgtg atgacctaca ggggtgtcgt	540
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ggcgctcgtc ttgggttttc tgatatcaac caggctgcgg tccaaagggc agttgatgag	660
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ccttgcgcca tgggtgccat cctcaacgac actaccatcc cagcctgca agctcgcac	780
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tacgaacgct ccgatatgga ccctcagcag gttatggaac aggttgatgg tatcggtgat	960
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<210> 180

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 180

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gcttttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
ctacgtctgg cgaaaggat gacctacaaa aatgcagctg ccggtctcaa ccatggcgg	240

gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300
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accgttgatg acatggacat tatccacgaa gaaactgact tcgtgaccgg gatctcacca 420
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gctgaagagc ggatcgcatc tttaaagaac tcccgtagca cctatctgcg caacggccat 1080
gatatcatat cgcgacgt 1098

<210> 181
<211> 1032
<212> DNA
<213> Artificial Sequence
<220><223> Synthetic polynucleotide
<400> 181

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ggtggttggc gcatgtgggc ttatccgat tcaacagttg cagctactga cgcgttacgt 180
ctcgccagag gcatgactta caaaaacgt atggccggcc ttccaattgg cgggtggcaaa 240
gcggtaatca tcggtgatgc tcgtacctcc aaaagcccgg aactgttccg cgcactgggg 300
cgtgcgattg accagctggg aggtcggtag atcaccgtg aagatgttgg tacttctccg 360
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ggaggcactg gtgacccttc tcccgtacg gctctgggtg ttttcgtagg catcgaggcc 480
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ctgggtcatg ttggctacga tctggctcgt cgcctgcacg aagctgggtc acgattgatc 600

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 <400> 182
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gatatcatat cgcgacgt 1098

<210> 183

<211> 1032

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 183

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gataaaacga attttaaagc aattatcgct gtacactcta cagaattagg gccggcgttg 120

gggtggttgc gcatgtggtt ctacaacaac gagaacgaag ctcttactga cgttctccgt 180

ctggcagaag gcatgactta taaaaattcc gctatgggtc tgaacctggg cggcggtaaa 240

gcggttatta tcggtgatcc tcgtaccgac aagtcaccgg aactgttcgc ccggtttgcg 300

gaggcagtca actctctggg aggcaatac tacaccgtg aagatgtagg tatctctcca 360

gctgatatgc tggaggttta taaacatacc ccgtacgtgg taggcctgcc ggctaagtcc 420

ggggacccca gtccgttcac tgettaccgc gtttacgtgg gtatgaaagc agcggtcgaa 480

gaagcctttg gtgataccag cctggaaggc aagaaagttg cagtgcaggg attggggcac 540

gtaggtatgt atctgctgga acatctctat aacgagggtg ccaaactaat cgttactgac 600

atTTTTaccg aacgcgttaa agaggtctgt gaacgtttcg gcgctctgcc agttgaaccg 660

gagaagatct acgaagtga agcggacatt ttcgcaccgt gtgctctggg cgccatcctg 720

aatgaaaaca cgattcctcg tcttaaagta aaagtgatcg ctggtgcggc taacaatcag 780

ctggcaaaac tttctgatgg ctctctgctg cgcgaccgtg gcatagttaa cgcgccagat 840

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gacaagaacc gagtctggga gaaagttgcg acaatttacc acaaagtga agaagttctg 960

actctggctc gtgaacagaa catcagtcct caagaagctg caatcagata tgctaagaaa 1020

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<210> 184

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 184

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
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ctgggtgccg cggtaacga tgaaactatc cctcagctga aagctaaggt tatcgtggc	780

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<210> 185

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 185

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
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<211> 1098
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<213> Artificial Sequence

<220><223> Synthetic polynucleotide
<400> 187

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<211> 1098
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<220><223> Synthetic polynucleotide
<400> 188

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<400> 189

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<211> 1077

<212> DNA

<213> Artificial Sequence

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<400> 191

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gctctacggc tggcacgtgg tatgacttac aaagctgctg cggcaggcct gaacctgggc 240

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<210> 192
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<213> Artificial Sequence

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<400> 193

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tgtctacgac tggcccggtg tatgacttat aaggctgcgg cagctgggct taacctgggc 240

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<400> 194

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<211> 1104

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<400> 196

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<211> 1059

<212> DNA

<213> Artificial Sequence

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<211> 1098

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<213> Artificial Sequence

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<400> 198

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<211> 1098

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<400> 204

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ctgaaaaatc ttgctatcgc ggcagatgaa ggtgttccgc cagccgtagc tgctgaccgt	1020
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<210> 214

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 214

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gggggcacta gaatgtggaa ttacgaaacc gaagaggaag cttttgaaga tgtcctgcgc	180
ctgtcccgtg gtatgactta caaaaacgct gctgcgggtc tgaacctggg cggcggtaaa	240
gcagttatca tcggagacgc ccgcaaggat aaaaaccagg aaatgttccg ggctttcgt	300

cgttacatcc agggcctgaa cggacgttat atcactgcgg aagatgtagg caccaccgtt 360

gaggacatgg acatcattca tgatgagacc gactacgtga cgggtatctc gcctgctttt 420

ggtgcatctg ggaaccccag cccggtcacc gcgtatgggtg tttatgtggg catgaaagcc 480

gctgcaaagg cgggcctggg gagtgaagat ctggctggca aaactattgc tgttcaaggt 540

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gttgctccgg acgagatcta ccaggttgat tgcgatatct tcgcgccgtg tgctctgggt 720

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gctccggact atgtaattaa cgcgggcggg gtcatcaacg tggccgacga actgaatggt 900

tacaaccgtg atcgcgcttt caaaaaagtt gaaggcatct atgaaaatgt gtctcgtgct 960

tttgaaattg ctaaagccca gaacatcccg actttccttg cagcggacaa aatggctgag 1020

gaacgcattg agcgtatgcg atacgtctgc ggtactttcc tgcaaacga acaccatc 1080

ctgtctcgta agaaa 1095

<210> 215

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 215

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gcttttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

ctacgtctgg cgaaggtat gacctacaaa aatgcagctg ccggtctcaa cctgggcgggt 240

gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300

ctgggacgct acattcaggg tctgaacggc agatacatca ccaggaaga tgtgggtaca 360

accgttgatg acatggacat tatccatgaa gaaactgact tcgtgaccgg gatctcacca 420

agctttggct ctcttggtaa cccgtccccg gttacggctt atggcgata cgcggcatg 480

aaagctgctg caaaagaggc cttcgggtact gataacctgg aagggaaggt aattgcggtt 540

cagggtgtcg gtaatgtggc ttatcacctc tgtaaacatc tgcacgtga aggcgctaag 600

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gctgaagagc ggatcgcatc ttttaagaac tcccgtagca cctatctgcg caacggccac 1080
gatatcatat cgcgacgt 1098

<210> 216
<211> 1086
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide
<400> 216

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ggtcctctgc tgggtggcac ccgcttctac ccgtacggtt ccgaagacga agctttgact 180
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cgggcgtacg gccgctttgt gcagagcctg aacgggcgtt actataccgc ttgcgatgta 360

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aatggc 1086

<210> 217
<211> 1098
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide
<400> 217

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gctttagggg gcaactcgat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180
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gcgaagactg ttattatcgg cgacccccga aaagacaagt ccgaggcaat gttccgtgcg 300
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accgttgatg acatggacat tatccatgaa gaaactgact tcgtgaccgg gatctcacca 420
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gatatcatat cgcgacgt 1098

<210> 218
<211> 1098
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 218

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
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agctttggct ctcttggtaa cccgtccccg gttacggcat atggcgtata ccgcggcatg	480
aaagctgctg cgaaaggagc cttcggctact gataacctgg aagggaaggt aattgcggtt	540
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<210> 219

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 219

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
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agctttggct ctcttggtaa cccgtccccg gttacggcat atggcgtata ccgcggcatg 480

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cagggtgtcg gtaatgtggc ttatcacctc tgtaaacatc tgcacgctga aggcgctaag 600

ctgattgtta ctgatatcaa caaagaggca gtccaaaggg ccgttgagga atttggtgcg 660

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aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgcagc tgaccgcttg 1020

gctgaagagc ggatcgcac tttaaagaac tcccgtagca cctatctgcg caacggccac 1080

gatatcatat cgcgacgt 1098

<210> 220

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 220

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gcttttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

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gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300

ctgggacgct acattcaggg tctgaacggc agatacatca ccgctctgga tgtgggtaca 360

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agctttggct ctcttggtaa cccgtccccg gttacggcat atggcgtata ccgcggcatg 480

aaagctgctg cgaaagaagc ctctgggtact gataacctgg aggggaaggt aattgcggtt 540

cagggtgtcg gtaatgtggc ttatcacctc tgtaaacatc tgcacgctga aggcgctaag 600

ctgattgtta ccgatatcaa caaagaagca gtccaaaggg ccgttgagga atttggtgcg 660

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<210> 221
<211> 1098
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 221

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<210> 222
<211> 1098
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide
<400> 222

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<220><223> Synthetic polynucleotide

<400> 223

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<210> 224

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 224

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
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<400> 227

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<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 248

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
ctacgtctgg cgaaaggatg gacctacaaa aatgcagctg ccggtctcaa cctgggcggt	240
gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg	300
ctgggacgct acattcaggg tctgaacggc agataccaga ccgctgaaga tgtgggtaca	360

accgttgatg acatggacat catccatgaa gaaactgact tcgtgaccgg gatttcacca	420
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aaagctgctg cgaaagggc cttcgttact gataacctgg aagggaaggt aatcgcggtt	540
cagggtgtcg gtaatgtggc ttatcacctc tgtaaaccatc tgcacgctga aggcgctaag	600
ctgattgtta ccgatatcaa caaagaggca gtccaaaggg ccgttgagga atttgggtgcg	660
tcggcagtag aaccgaatga aatctacggc gttgaatgcg acatttacgc cccgtgtgcg	720
ctgggtgccg cggtaacga tgaactatc cctcagctga aagctaaggt tatcgctggc	780

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<210> 249

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 249

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct	180
ctacgtctgg cgaaaggctg aacctacaaa aatgctgccg ccggtctcaa cctgggcggt	240
gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg	300

ctgggacgct acattcaggg tctgaacggc agatacatca ccgctgaaga tgtgggtaca 360

accgttgatg acatggacat tatccatgaa gaaactgact tcgtgaccgg gatctcacca 420

agctttggct ctcttggtaa cccgtccccg gttacggctt atggcgtata ccgcggcatg 480

aaagctgctg caaaagaggc attcgggtact gataacctgg aagggaaggt aattgcggtt 540

cagggtgtcg gtaatgtggc ttatcacctc tgtaaacatc tgcacgccga aggcgctaag 600

ctgattgtta ccgatatcaa caaagaggcg gtccaaaggg ccgttgagga atttggtgcg 660

tcggcagtag aaccgaatga aatctacggc gttgaatgcg acatttacgc cccgtgtgcg 720

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tacggctata accgtgaacg cgctttgaaa cgggttgaat ctatttacga tactatcgca 960

aaagtaatcg aaatcagcaa acgtgatggt attgctacct acgtcgcagc tgaccgcttg 1020

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<210> 250

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 250

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gctttagggg gcactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180

ctacgtctgg cgaaaggtat gacctacaaa aatgcagctg ccggtctcaa cctgggcggt 240

gcgaagactg ttattatcgg cgacccccga aaagacaaat ccgaggcaat gttccgtgcg 300

ctgggacgct acattcaggg tctgaacggc agatacatca ccgctgaaga tgtgggtaca 360

accgttgatg acatggacat tatccatgaa gaaactgact tcgtgaccgg gatctcacca 420

agctttggct ctcttggtaa cccgtccccg gttacggcat atggcgtata ccgcggcatg 480

aaagctgctg cgaaagaggc cttcgggtact gataacctgg aagggaaggt aattgcggtt 540

cagggtgtcg gtaatgtggc ttatcacctc tgtaaacatc tgcacgtga aggcgctaag 600

ctgattgtta ccgatatcaa caaagaggca gtccaaaggg ccgttgagga atttggtgcg 660

tcggcagtag aaccgaatga aatctacggc gttgaatgcg acatttacgc cccgtgtgcg 720
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gatatcatat cgcgacgt 1098

<210> 251
<211> 1098
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide
<400> 251

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ctactcttgg cgaaaggtat gacctacaaa aatgcagctg ccggtactaa cctgggcggt 240
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gctgaagagc ggatcgcatc tttaaagaac tcccgtagca cctatctgcg caacggccac 1080
gatatcatat cgcgacgt 1098
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<211> 1089
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide
<400> 252

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tcagaagaag atgcagttct ggatgccttg aatctgtctc gtggtatgag ctacaagaac 240
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aaccagtgga ccaccggtcg ttctcctgag aacggggggcg ctggcgattc cagcgtccta 480
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cgaagggca 1089

<210> 253
<211> 1062
<212> DNA
<213> Artificial Sequence

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<400> 253

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atcgctaata gggatgatat taccagccac gaagctgcta accgcatggc tgaggaacgt 1020
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<210> 254

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 254

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gctttagaag ggactcgcat gtggacctat gatagcgaag aagctgcgat cgaagatgct 180
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1089

<210> 257

<211> 366

<212> PRT

<213> Bacillus cereus

<400> 257

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20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
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Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
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Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
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<213> *Cetobacterium ceti*
<400> 258
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35 40 45

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

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

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

 Cys Ala Leu Gly Lys Ile Val Asn Asp Lys Thr Ile Asp Glu Phe Lys
 245 250 255
 Cys Pro Ile Ile Ala Gly Thr Ala Asn Asn Val Leu Glu Arg Glu Ala
 260 265 270
 His Gly Asn Met Leu Lys Glu Arg Gly Ile Leu Tyr Ala Pro Asp Tyr
 275 280 285
 Val Ile Asn Ala Gly Gly Leu Ile Asn Val Tyr His Glu Leu Asn Gly

290 295 300

Tyr Asn Lys Glu Asn Ala Ile Leu Glu Val Glu Leu Ile Tyr Asp Arg
305 310 315 320
Leu Leu Glu Ile Phe Asn Ile Ala Asp Ser Leu Asn Ile Ser Thr Asn
325 330 335
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340 345 350
Leu Lys Asn Asn Phe Ile Lys Arg
355 360
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<211> 346
<212> PRT
<213> Pseudoalteromonas tunicata

<400> 259

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Phe Cys Ser Asp Gln Glu Ser Gly Leu Lys Ala Ile Ile Ala Val His
20 25 30
Ser Thr Lys Leu Gly Pro Ala Val Gly Gly Cys Arg Leu Trp Asp Tyr
35 40 45
Val Ser Asp Glu Asp Ala Val Tyr Asp Val Leu Arg Leu Ser Lys Gly
50 55 60

Met Thr Tyr Lys Asn Ala Val Ala Arg Leu Pro Phe Gly Gly Gly Lys
65 70 75 80
Ser Val Ile Ile Gly Asn Ala Lys Glu Ile Lys Ser Glu Ala Leu Phe
85 90 95
Arg Ala Phe Gly Arg Lys Leu Glu Gly Leu Gly Gly Ala Tyr Tyr Ser
100 105 110
Ala Glu Asp Val Asn Ile Thr Cys Ala Asp Val Ala Ile Met Asn Lys
115 120 125

Glu Thr Asn Tyr Val Leu Gly Leu Glu Gly Lys Ser Gly Asn Pro Ser

130 135 140
 Pro Phe Thr Ala Leu Gly Thr Phe Leu Gly Ile Lys Ala Ala Tyr Gln
 145 150 155 160
 His Gln His Gly His Gln Asp Leu Ala Gly Val Lys Val Ala Val Gln
 165 170 175
 Gly Leu Gly Ala Val Ala Tyr Ser Leu Cys Lys Tyr Leu Tyr Glu Ala
 180 185 190

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

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

 Ala Arg Ser Val Thr Glu Gln Lys Ser Thr His Leu Ile Ala Asp Glu
 325 330 335
 Leu Ala Gln Glu Ile Ile Ala Asn Gly Leu
 340 345

 <210> 260
 <211> 366
 <212> PRT
 <213> Hassallia byssoidea
 <400> 260

Met Glu Ile Lys Glu Leu Glu Lys Val Glu Gln Ala Gly Ile Phe Gly
1 5 10 15
Lys Leu Ser Gln Leu Gly His Glu Gln Val Val Phe Cys His Asp Glu
20 25 30
Ala Thr Gly Leu Lys Ala Ile Ile Ala Ile His Asn Thr Val Leu Gly
35 40 45
Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr Ala Thr Glu Gln Glu
50 55 60
Ala Leu Thr Asp Val Leu Arg Leu Ser Arg Gly Met Thr Phe Lys Ala
65 70 75 80
Ser Ile Ser Gly Leu Asn Leu Gly Gly Gly Lys Ala Val Ile Ile Gly
85 90 95
Asp Ala Lys Thr Met Lys Thr Glu Ala Phe Met Arg Arg Phe Gly Lys
100 105 110
Phe Val Asp Ser Leu Asn Gly Lys Tyr Ile Thr Ala Glu Asp Val Asn
115 120 125
Met Lys Thr Ala Asp Met Glu Tyr Ile Gly Met Glu Thr Lys His Val
130 135 140
Thr Gly Leu Pro Glu Ser Met Arg Gly Gly Gly Asp Pro Ser Pro Val
145 150 155 160
Thr Ala Tyr Gly Val Tyr Leu Gly Met Lys Ala Ala Ala Lys Lys Thr
165 170 175
Tyr Gly Asn Asp Ser Leu Thr Gly Lys Thr Ile Ala Val Gln Gly Ile
180 185 190
Gly Gln Val Gly Thr Tyr Leu Thr Glu Tyr Leu Val Lys Glu Asn Ala
195 200 205
Asn Val Tyr Ile Thr Asp Ile Ala Glu Asp Lys Val Lys Ala Leu Ala
210 215 220
Gln Arg Leu Gly Val Lys Thr Val Ala Gln Asp Lys Ile Tyr Asp Leu
225 230 235 240
Asp Met Asp Ile Tyr Ala Pro Cys Ala Leu Gly Ala Thr Leu Asn Asp

245 250 255
 Asp Thr Ile Pro Arg Leu Asn Cys Gln Val Val Ala Gly Ala Ala Asn
 260 265 270
 Asn Gln Leu Lys Asp Glu Ser Lys His Gly Tyr Met Leu Ile Asp Lys
 275 280 285

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

Glu Lys Arg Ile Ala Asp Ile Ala Gln Val Arg Thr Arg Arg
 355 360 365

<210> 261

<211> 363

<212> PRT

<213> Hymenobacter daecheongensis

<400> 261

Met Val Glu Ile Lys Ala Leu Thr Asp Thr Ser Val Phe Gly Gln Ile
 1 5 10 15
 Ala Glu His Gln His Glu Gln Val Val Phe Cys His Asp His Glu Thr
 20 25 30
 Gly Leu Arg Ala Ile Ile Gly Ile His Asn Thr Val Leu Gly Pro Ala

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

Lys Thr Leu Lys Thr Glu Ala Leu Leu Arg Lys Phe Gly Arg Phe Val

100 105 110

Lys Asn Leu Asn Gly Lys Tyr Ile Thr Ala Glu Asp Val Asn Met Thr

115 120 125

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

130 135 140

Leu Pro Glu Ser Met Gly Gly Ser Gly Asp Pro Ser Pro Val Thr Ala

145 150 155 160

Phe Gly Thr Tyr Met Gly Met Lys Ala Ala Ala Lys Lys Ala Phe Gly

165 170 175

Ser Asp Ser Leu Ala Gly Lys Arg Ile Ala Val Gln Gly Val Gly His

180 185 190

Val Gly Thr Tyr Leu Leu Glu Tyr Leu Gln Lys Glu Gly Ala Lys Leu

195 200 205

Val Leu Thr Asp Tyr Tyr Glu Asp Arg Ala Leu Glu Ala Ala Thr Arg

210 215 220

Phe Gly Ala Lys Met Val Gly Leu Asp Glu Ile Tyr Asp Gln Asp Val

225 230 235 240

Asp Ile Tyr Ser Pro Cys Ala Leu Gly Ala Thr Ile Asn Asp Asp Thr

245 250 255

Ile Gly Arg Leu Lys Cys Gln Val Ile Ala Gly Cys Ala Asn Asn Gln

260 265 270

Leu Gln Asn Glu Asn Val His Gly Pro Ala Leu Val Glu Arg Gly Ile

275 280 285

Val Tyr Ala Pro Asp Phe Leu Ile Asn Ala Gly Gly Leu Ile Asn Val

290 295 300

Tyr Ser Glu Val Val Gly Ser Ser Arg Gln Gly Ala Leu Asn Gln Thr

305 310 315 320

Glu Lys Ile Phe Asp Ile Thr Thr Gln Val Leu Asn Lys Ala Glu Gln

325 330 335

Glu Gly Ser His Pro Gln Ala Ala Ala Thr Lys Gln Ala Glu Glu Arg

340 345 350
 Ile Ala Ser Leu Gly Lys Val Lys Ser Thr Tyr
 355 360

 <210> 262
 <211> 349
 <212> PRT
 <213> *Thalassospira profundimaris*
 <400> 262
 Met Asn Val Phe Ser Asp Ile Ala Phe Asp Asp His Glu Gln Val Val
 1 5 10 15
 Phe Ala Ser Asp Lys Thr Thr Gly Leu Lys Thr Ile Ile Ala Val His
 20 25 30
 Asn Thr Asn Leu Gly Pro Ser Leu Gly Gly Cys Arg Met Trp Pro Tyr
 35 40 45
 Ala Ser Glu Gln Asp Ala Ile His Asp Val Leu Arg Leu Ser Arg Gly

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

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

180 185 190
 Met Leu His Ala Ala Gly Ala Lys Leu Ile Val Ala Asp Leu Asn Ala
 195 200 205
 Ala Ser Met Lys Ala Ala Ala Met Glu Phe Gly Ala Thr Ala Val Pro
 210 215 220
 Val Asp Lys Ile Leu Ser Val Asp Ala Asp Ile Leu Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Gly Val Ile Asn Asp Lys Thr Ile Glu Glu Leu Lys Val Gly

 245 250 255
 Val Ile Ala Gly Ala Ala Asn Asn Gln Leu Glu Asp Asp Arg His Gly
 260 265 270
 Glu Met Leu Arg Glu Ala Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Glu Val Tyr Tyr Cys Arg Glu Gly Lys Thr
 290 295 300
 Val Ala Glu Thr Asn Met His Ile Glu Gly Ile Gly Glu Thr Val Arg

 305 310 315 320
 Glu Ile Phe Glu Arg Ala Lys Gln Gln Asn Leu Ser Thr Gly Phe Val
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Phe Gly Leu Lys Lys
 340 345
 <210> 263
 <211> 349
 <212> PRT
 <213> Gemmatimonadetes bacterium
 <400> 263
 Met Phe Ala Leu Leu Glu Glu His Glu His Glu Gln Val Ser Leu Val
 1 5 10 15

 Tyr Glu Pro Ser Ser Gly Tyr Arg Gly Ile Ile Ala Ile His Asp Thr
 20 25 30
 Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Phe Trp Asn Tyr Leu Asn
 35 40 45

Asp Arg Glu Ala Leu Ile Asp Cys Leu Arg Leu Ala Arg Gly Met Thr
 50 55 60
 Tyr Lys Ala Ala Val Ala Gly Leu Asn Leu Gly Gly Gly Lys Ser Val
 65 70 75 80

 Ile Ile Gly Asp Asn Lys Ile Arg Asn Arg Glu Pro Ile Phe Arg Ala
 85 90 95
 His Gly Arg His Val Lys Ala Leu Gly Gly Arg Tyr Ile Thr Ala Glu
 100 105 110
 Asp Val Gly Thr Ser Val Gly Asp Met Glu Phe Ile Lys Ala Glu Thr
 115 120 125
 Asp His Val Thr Gly Leu Ile Gly Lys Ser Gly Asp Pro Ser Pro Val
 130 135 140

 Thr Ala Phe Gly Val Tyr Arg Gly Ile Lys Ala Cys Ala Lys His Arg
 145 150 155 160
 Tyr Gly Asp Ala Glu Leu Arg Gly Lys Lys Val Ala Ile Gln Gly Cys
 165 170 175
 Gly His Val Gly Tyr Tyr Leu Ala Glu Leu Leu Tyr Lys Glu Gly Ala
 180 185 190
 Asp Leu Ile Val Thr Asp Ile Asp Ser Ala Lys Val Glu Arg Val Val
 195 200 205

 Lys Ala Phe Glu Ala Lys Ala Val Ala Thr Asp Asp Ile Tyr Gly Val
 210 215 220
 Pro Ala Ser Val Phe Ala Pro Cys Ala Leu Gly Gly Ile Ile Asn Asp
 225 230 235 240
 Gln Thr Ile Ala Gln Leu Glu Val Asp Ile Val Ala Gly Gly Ala Asn
 245 250 255
 Asn Gln Leu Ala Glu Glu Arg His Gly Asp Met Leu Glu Glu Arg Gly
 260 265 270

 Ile Thr Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly Leu Val Asn
 275 280 285
 Val Asn Ala Glu Leu Glu Gly Trp Thr Met Glu Arg Ala Arg Asn Lys

290 295 300
 Ala Gly Glu Ile Tyr Asp Thr Leu Leu Met Leu Phe Glu Ile Ala Gly
 305 310 315 320
 Glu Glu Gly Ile Pro Ser Tyr Arg Ala Ala Asp Arg Leu Ala Glu Arg
 325 330 335

 Arg Ile Ala Ala Ile Ala Lys Val Arg Gln Asn Phe Val
 340 345
 <210> 264
 <211> 364
 <212> PRT
 <213> Unknown
 <220><223> Virgibacillus sp. SK37
 <400> 264
 Met Glu Ile Phe Thr Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val
 1 5 10 15
 Phe Cys Gln Asp Lys Ser Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr

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

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

145 150 155 160
Ala Ala Lys Glu Ala Phe Asn Asp Asp Ser Leu Glu Gly Lys Thr Ile

 165 170 175
Ala Val Gln Gly Val Gly Asn Val Ala Tyr Ala Leu Cys Glu Tyr Leu

 180 185 190
His Lys Glu Gly Ala Lys Leu Val Val Thr Asp Ile Asn Lys Gly Ala

 195 200 205
Val Glu Arg Ala Val Glu Ala Phe Asn Ala Thr Ala Val Asp Pro Asp

 210 215 220
Asp Ile Tyr Asp Val Asp Cys Asp Ile Tyr Ala Pro Cys Ala Leu Gly

225 230 235 240
Ala Thr Ile Asn Asp Asp Thr Ile Pro Arg Ile Lys Ala Lys Val Ile

 245 250 255
Ala Gly Ser Ala Asn Asn Gln Leu Lys Ser Ser Glu His Gly Asp Ile

 260 265 270
Ile Phe Glu Lys Gly Ile Ile Tyr Ala Pro Asp Tyr Val Ile Asn Ser

 275 280 285
Gly Gly Val Ile Asn Val Ala Asp Glu Leu Val Gly Tyr Asn Glu Glu

 290 295 300
Arg Ala Leu Lys Lys Val Glu Thr Ile Tyr Asp Ser Leu Gln Lys Val

305 310 315 320
Phe Glu Ile Ser Arg Arg Asp His Ile Pro Ser Tyr Val Ala Ala Asp

 325 330 335
Arg Met Ala Glu Glu Arg Ile Glu Ala Glu Arg Asn Ser Arg Ser Gln

 340 345 350
Phe Leu Leu Asn Gly His His Ile Leu Ser Arg Arg

 355 360

<210> 265

<211> 365

<212> PRT

<213> Jeotgalibacillus malaysiensis

<400> 265

Met Glu Leu Phe Thr Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val
1 5 10 15

Phe Cys Gln Asp Lys Asn Ser Gly Leu Lys Ala Ile Ile Ala Ile His
20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
35 40 45

Asp Ser Glu Glu Asp Ala Ile Glu Asp Ala Leu Arg Leu Ala Lys Gly
50 55 60

Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
65 70 75 80

Thr Val Ile Ile Gly Asp Pro Leu Lys Asp Lys Asn Glu Glu Met Phe
85 90 95

Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Ala Gly Arg Tyr Ile Thr
100 105 110

Ala Glu Asp Val Gly Thr Thr Val Lys Asp Met Asp Leu Ile His Glu
115 120 125

Glu Thr Asp Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly
130 135 140

Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Ile Lys Ala
145 150 155 160

Ala Ala Asn Glu Ala Tyr Gly Ser Asp Ser Leu Glu Gly Lys Thr Ile
165 170 175

Ala Val Gln Gly Val Gly Asn Val Ala Phe Thr Leu Cys Arg His Leu
180 185 190

His Glu Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys Glu Ser
195 200 205

Val Gln Arg Ala Val Asp Glu Phe Gly Ala Lys Ala Val Glu Pro Asn
210 215 220

Glu Ile Tyr Gly Val Asp Cys Asp Ile Phe Ala Pro Cys Ala Leu Gly
225 230 235 240

Ala Ile Ile Asn Asp Asn Thr Leu Glu Val Leu Lys Ala Asp Val Ile
245 250 255

Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Thr Arg His Gly Asp Ile
260 265 270

Leu His Glu Arg Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala
275 280 285

Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Arg Glu
290 295 300

Arg Ala Met Lys Asn Val Glu Lys Val Tyr Asp Asn Val Ala Arg Val
305 310 315 320

Phe Glu Ile Ala Lys Arg Asp Gly Val Pro Ser Tyr Leu Ala Ala Asp
325 330 335

Arg Met Ala Glu Glu Arg Ile Ala Ser Met Ala Lys Ser Arg Ser Gln
340 345 350

Phe Leu Arg Ser Glu His Asn Ile Leu Ser Arg Arg Ser
355 360 365

<210> 266

<211> 366

<212> PRT

<213> Fictibacillus enclensis

<400> 266

Met Glu Ile Phe Lys Tyr Met Glu Thr Tyr Asp Tyr Glu Gln Met Val
1 5 10 15

Ile Cys Gln Asp Lys Gln Ser Gly Leu Lys Ala Ile Ile Val Ile His
20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
35 40 45

Lys Ser Glu Glu Asp Ala Leu Glu Asp Ala Leu Arg Leu Ala Arg Gly
50 55 60

Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
65 70 75 80

Thr Val Ile Ile Gly Asp Pro Lys Lys Asp Lys Asn Glu Glu Met Phe

85 90 95
 Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Ile Ile Tyr Gln

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

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

 245 250 255
 Ala Gly Ala Ala Asn Asn Gln Leu Arg Glu Thr Arg His Gly Asp Ala
 260 265 270
 Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala
 275 280 285
 Gly Gly Val Ile Asn Val Ala Asp Glu Leu Asn Gly Tyr Asn Arg Asp
 290 295 300
 Arg Ala Met Lys Lys Val Glu Thr Ile Tyr Asp Asn Ile Ala Lys Val

 305 310 315 320
 Ile Glu Ile Ser Lys Arg Asp His Ile Pro Thr Tyr Leu Ala Ala Asp
 325 330 335

Arg Leu Ala Glu Glu Arg Ile Glu Arg Met Arg Asn Ser Arg Ser Gln

340 345 350

Phe Leu Leu Asn Glu Arg His Ile Leu Ser Ser Arg Thr Arg

355 360 365

<210> 267

<211> 365

<212> PRT

<213> Anaerobacillus arseniciselenatis

<400> 267

Met Glu Leu Phe Lys Tyr Met Glu Thr Tyr Asp Tyr Glu Gln Val Val

1 5 10 15

Val Cys Gln Asp Lys Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His

20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr

35 40 45

Asn Thr Glu Ala Glu Ala Phe Glu Asp Ala Leu Arg Leu Ala Lys Gly

50 55 60

Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80

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

85 90 95

Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr

100 105 110

Ala Glu Asp Val Gly Thr Thr Val Gly Asp Met Asp Ile Ile His Glu

115 120 125

Glu Thr Asp Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly

130 135 140

Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Val Gly Met Lys Ala

145 150 155 160

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

165 170 175

Ala Val Gln Gly Val Gly Asn Val Ser Tyr Thr Leu Cys Lys His Leu

[illegible]

20 25 30
 His Phe Lys Val Asp Pro Glu Thr Gly Met Lys Ala Ile Val Ala Ile
 35 40 45
 His Ser Thr Lys Leu Gly Pro Ala Leu Gly Gly Cys Arg Phe Ile Glu
 50 55 60
 Tyr Pro Asn Thr Ala Ser Ala Ile Asn Asp Ala Met Arg Leu Ala Arg

 65 70 75 80
 Gly Met Ser Phe Lys Ala Ala Ser Val Asn Leu Pro Leu Gly Gly Gly
 85 90 95
 Lys Ala Val Ile Ile Lys Pro Asn Lys Pro Phe Asp Arg Glu Ala Tyr
 100 105 110
 Leu His Ala Phe Gly Arg Phe Val Asn Asp Leu Gly Gly Arg Tyr Ile
 115 120 125
 Thr Ala Leu Asp Ser Gly Thr Gln Leu Ser Asp Met Asp Ile Ile Gly

 130 135 140
 Gln His Thr Ser Tyr Val Ala Ser Leu Ser Ser His Asn Gly Asp Pro
 145 150 155 160
 Ser Pro Ser Thr Ala Lys Gly Val Leu Arg Gly Ile Gln Ala Ala Val
 165 170 175
 Glu Phe Lys Leu Gly Lys Asp Asn Leu Asn Gly Leu His Ile Ala Ile
 180 185 190
 Gln Gly Leu Gly His Val Gly Tyr Leu Leu Ala Ser His Leu His Ala

 195 200 205
 Leu Gly Ala Lys Leu Thr Val Thr Asp Val Asn Pro Arg Ala Val Gln
 210 215 220
 Arg Ala Val Glu Glu Phe Gly Ala Thr Ala Val Ser Thr Asp Met Ile
 225 230 235 240
 His Arg Val Pro Cys Asp Val Phe Ala Pro Cys Ala Leu Gly Ala Val
 245 250 255
 Ile Asn Asp Ile Thr Ile Ser Gln Leu Gln Thr Thr Ile Ile Ala Gly

 260 265 270

Ala Ala Asn Asn Gln Leu Ala His Thr Tyr His Gly Pro Ile Leu His
 275 280 285
 Glu Lys Gly Ile Leu Tyr Ala Ala Asp Tyr Val Ile Asn Ala Gly Gly
 290 295 300
 Leu Val Phe Ala Ala Ser Lys Tyr Phe Asn Thr Pro Gln Asp Gln Val
 305 310 315 320
 Asn Gln Gln Ile Asp Gly Ile Gly Thr Ser Leu Leu Glu Ile Phe Ile

325 330 335
 Arg Ser Gln Lys Glu Asn Arg Pro Ala Ser Glu Ile Ala Asp Thr Leu
 340 345 350
 Ala Gln Glu Lys Leu Ala

355

<210> 269

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 269

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala

20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Thr Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 270

<211> 366

<212> PRT

<213> Unknown

<220><223> Marinobacter sp. X15-166B

<400> 270

Met Asn Val Phe Ser His Pro Glu Phe Asp Asn His Glu Gln Val Ser

1 5 10 15

Phe Val Ser Asp Pro Glu Thr Gly Leu Arg Ala Ile Ile Ala Ile His

20 25 30

Asn Thr Ser Arg Gly Pro Ala Leu Gly Gly Cys Arg Met Phe Pro Tyr

35 40 45

Ala Ser Asp Glu Glu Ala Leu Arg Asp Val Leu Arg Leu Ser Arg Gly

50 55 60

Met Thr Tyr Lys Ser Ala Leu Ala Asn Leu Asp Leu Gly Gly Gly Lys

65 70 75 80

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

85 90 95

Glu Ala Met Gly Arg Cys Leu Glu Lys Leu Gly Gly His Tyr Ile Ala

100 105 110

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

115 120 125

His Thr Arg His Val Ala Gly Ile Thr Ser Arg Pro Gly Phe Asp Gly

130 135 140

Ala Pro Ser Asp Gly Asp Pro Ser Pro Val Thr Ala Tyr Gly Val Phe

145 150 155 160

Val Gly Leu Lys Ala Ala Val Gln His Gly Leu Gly Arg Thr Asp Leu

165 170 175

Thr Gly Leu Lys Val Ala Ile Gln Gly Ile Gly Asn Val Gly Tyr Arg

180 185 190

Leu Ala Arg His Leu Lys Asp Ala Gly Ala Glu Leu Trp Val Tyr Asp

195 200 205
 Ile His Gln Glu Gln Met Asp Arg Ala Val Ala Glu Leu Gly Ala Thr
 210 215 220

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

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

Arg Arg Ser Thr Ala Thr Ala Asn Lys Val Ala Ser Val Gly
 355 360 365

<210> 271

<211> 363

<212> PRT

<213> Unknown

<220><223> Hymenobacter sp. CRA2

<400> 271

Met Val Glu Ile Gln Ala Leu Pro Glu Thr Ser Ile Phe Gly Gln Ile
 1 5 10 15
 Ala Asp His Gln His Glu Gln Val Val Phe Cys His Asp His Glu Thr
 20 25 30

Gly Leu Arg Ala Ile Ile Gly Ile His Asn Thr Val Leu Gly Pro Ala

35 40 45

Leu Gly Gly Thr Arg Met Trp His Tyr Ala Thr Glu Ala Glu Ala Leu

50 55 60

Asn Asp Val Leu Arg Leu Ser Arg Gly Met Thr Tyr Lys Ala Ala Ile

65 70 75 80

Ser Gly Leu Asn Leu Gly Gly Gly Lys Ala Val Ile Ile Gly Asp Ala

85 90 95

Lys Thr Ile Lys Thr Glu Ala Leu Leu Arg Lys Phe Gly Arg Phe Val

100 105 110

Gln Asn Leu Asn Gly Lys Tyr Ile Thr Ala Glu Asp Val Asn Met Thr

115 120 125

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

130 135 140

Leu Pro Glu Ser Met Gly Gly Ser Gly Asp Pro Ser Pro Val Thr Ala

145 150 155 160

Tyr Gly Thr Tyr Met Gly Met Lys Ala Ala Ala Lys Lys Ala Phe Gly

165 170 175

Ser Asp Ser Leu Ala Gly Lys Arg Ile Ala Val Gln Gly Val Gly His

180 185 190

Val Gly Thr Tyr Leu Leu Glu His Leu Thr Lys Glu Gly Ala Gln Ile

195 200 205

Val Leu Thr Asp Tyr Tyr Lys Glu Arg Ala Glu Glu Ala Gly Ala Arg

210 215 220

Phe Gly Ala Gln Val Val Gly Leu Asp Asp Ile Tyr Asp Gln Glu Val

225 230 235 240

Asp Ile Tyr Ser Pro Cys Ala Leu Gly Ala Thr Ile Asn Asp Asp Thr

245 250 255

Ile Asp Arg Leu Arg Cys Ala Val Val Ala Gly Cys Ala Asn Asn Gln

260 265 270

Leu Lys Glu Glu Asn Val His Gly Pro Ala Leu Val Glu Arg Gly Ile

275 280 285
Val Tyr Ala Pro Asp Phe Leu Ile Asn Ala Gly Gly Leu Ile Asn Val

290 295 300
Tyr Ser Glu Val Thr Gly Ser Thr Arg Gln Gly Ala Leu Thr Gln Thr
305 310 315 320
Glu Lys Ile Tyr Asp Tyr Thr Leu Gln Val Leu Glu Lys Ala Ala Ala
325 330 335
Glu Gly Leu His Pro Gln Gln Ala Ala Ile Arg Gln Ala Glu Gln Arg
340 345 350
Ile Ala Ala Ile Gly Lys Val Lys Ser Thr Tyr
355 360

<210> 272

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 272

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

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

Ile Thr Ala Val Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

	355		360		365										
<210>	273														
<211>	366														
<212>	PRT														
<213>	Unknown														
<220><223>	Arenimonas sp. SCN 70-307														
<400>	273														
Met	Ile	Phe	Glu	Thr	Ile	Ser	Thr	Ser	Asn	His	Glu	Glu	Val	Val	Tyr
1			5					10					15		
Cys	His	Asn	Lys	Asp	Ala	Gly	Leu	Lys	Ala	Ile	Ile	Ala	Ile	His	Asn
			20					25					30		
Thr	Val	Leu	Gly	Pro	Ala	Leu	Gly	Gly	Thr	Arg	Met	Trp	Pro	Tyr	Ala
			35					40					45		
Ser	Glu	Glu	Glu	Ala	Leu	Lys	Asp	Val	Leu	Arg	Leu	Ser	Arg	Gly	Met
	50					55					60				
Thr	Tyr	Lys	Ala	Ala	Val	Ser	Gly	Leu	Asn	Leu	Gly	Gly	Gly	Lys	Ala
65					70					75				80	
Val	Ile	Trp	Gly	Asp	Pro	Asn	Lys	Asp	Lys	Ser	Glu	Ala	Leu	Phe	Arg
				85					90					95	
Ala	Phe	Gly	Arg	Phe	Val	Asn	Ser	Leu	Gly	Gly	Arg	Tyr	Ile	Thr	Ala
			100						105				110		
Glu	Asp	Val	Gly	Ile	Asp	Val	Asn	Asp	Met	Glu	Tyr	Val	Leu	Arg	Glu
	115						120					125			
Thr	Asp	Tyr	Val	Thr	Gly	Val	His	Gln	Val	His	Gly	Gly	Ser	Gly	Asp
	130						135				140				
Pro	Ser	Pro	Phe	Thr	Ala	Tyr	Gly	Thr	Leu	Gln	Gly	Leu	Met	Ala	Ala
145					150					155				160	
Leu	Gln	Val	Lys	Phe	Gly	Asn	Glu	Asp	Val	Gly	Asn	Tyr	Ser	Tyr	Ala
				165					170					175	
Val	Gln	Gly	Val	Gly	His	Val	Gly	Met	Glu	Phe	Val	Lys	Leu	Leu	Arg
	180						185						190		

Glu Arg Gly Ala Lys Val Phe Val Thr Asp Ile Asn Lys Asp Ala Val
 195 200 205
 Gln Arg Ala Val Asp Glu Phe Gly Cys Glu Ala Val Ala Leu Asp Glu
 210 215 220
 Ile Tyr Asp Val Asp Cys Asp Val Tyr Ser Pro Thr Ala Leu Gly Gly
 225 230 235 240
 Thr Val Asn Asp Lys Thr Leu Pro Arg Leu Lys Cys Lys Val Ile Cys
 245 250 255
 Gly Ala Ala Asn Asn Gln Leu Ala Asn Asp Glu Ile Gly Val Glu Leu
 260 265 270
 Glu Lys Lys Gly Ile Leu Tyr Ala Pro Asp Tyr Ala Val Asn Ala Gly
 275 280 285
 Gly Leu Met Asn Val Ser Leu Glu Ile Asp Gly Tyr Asn Arg Glu Arg
 290 295 300
 Ala Met Arg Met Met Arg Thr Ile Tyr Tyr Asn Leu Gly Arg Ile Phe
 305 310 315 320
 Glu Ile Ser Lys Arg Asp Gly Ile Pro Thr Phe Arg Ala Ala Asp Arg
 325 330 335
 Met Ala Glu Glu Arg Ile Thr Ala Ile Gly Lys Leu Arg Leu Pro His
 340 345 350
 Leu Gly Ala Ala Ala Pro Arg Phe Gln Gly Arg Arg Gly Asn
 355 360 365
 <210> 274
 <211> 346
 <212> PRT
 <213> Simiduia agarivorans
 <400> 274
 Met Ser Val Phe Ser His Pro Glu Phe Asp Gly His Glu His Val Ala
 1 5 10 15
 Phe Tyr His Asp Arg Lys Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asn Thr Asn Leu Gly Pro Ala Leu Gly Gly Cys Arg Met Trp Pro Tyr

35 40 45
 Ala Thr Asp Glu Glu Ala Leu Arg Asp Val Leu Arg Leu Ser Lys Gly
 50 55 60

 Met Thr Tyr Lys Ser Ala Val Ala Asn Ile Lys Leu Gly Gly Gly Lys
 65 70 75 80
 Ala Val Ile Leu Gly Asn His Arg Thr Glu Lys Thr Arg Asp Leu Leu
 85 90 95
 Leu Ala Met Gly Asp Phe Val Glu Ser Leu Gly Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Ser Gly Thr Ser Val Ala Asp Met Lys Val Ile Gly Glu
 115 120 125

 Arg Thr Arg Phe Ala Gly Gly Val Val Glu Gly Ser Glu His Gly Gly
 130 135 140
 Asp Pro Ser Pro Thr Thr Ala Tyr Gly Thr Tyr Val Gly Leu Lys Ala
 145 150 155 160
 Ala Ala Lys Phe Arg Leu Gly Val Asp Ser Leu Lys Gly Ile Arg Val
 165 170 175
 Ala Val Gln Gly Val Gly Asn Val Gly Tyr Arg Leu Ala Lys His Leu
 180 185 190

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

 Ala Gly Ala Ala Asn Asn Gln Leu Ala Glu Glu Arg His Gly Glu Leu
 260 265 270
 Leu Arg Ala Arg Glu Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala
 275 280 285

Gly Gly Ile Val Asp Val Tyr Tyr Gln Arg Thr Gly Glu Ser Ala Asp
290 295 300

Lys Leu Lys Ala His Val Glu Gly Ile Gly Asp Thr Leu Thr Glu Ile
305 310 315 320

Phe Thr Arg Ala Ala Glu Asn Gln Gln Pro Thr Gly Leu Val Ala Asn
325 330 335

Lys Ile Ala Glu Glu Arg Phe Asn Arg Ala
340 345

<210> 275

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 275

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Phe Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

260 265 270

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

275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335

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

340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 276

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 276

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Arg Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

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

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

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 277
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 277

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Cys Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

 355 360 365
 <210> 278
 <211> 358
 <212> PRT
 <213> Microbulbifer thermotolerans
 <400> 278
 Met Ser Ile Phe Ser His Pro Ala Tyr Asp Lys His Glu Gln Val Ala
 1 5 10 15
 Phe Cys Gln Asp Ala Lys Ser Gly Leu Lys Ala Ile Ile Ala Val His
 20 25 30
 Asn Thr Asn Leu Gly Pro Ser Leu Gly Gly Cys Arg Met Trp Pro Tyr
 35 40 45

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

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

Ala Val Glu His Arg Trp Gly Lys Ser Asp Leu Ser Gly Leu Lys Val
165 170 175

Ser Leu Gln Gly Val Gly Asn Val Gly Phe Arg Leu Ala Lys Leu Leu
180 185 190

Lys Asp Ala Gly Ala Glu Leu Phe Val Thr Asp Ile Phe Gln Asp Asn
195 200 205

Ile Asp Arg Ala Val Ser Glu Leu Gly Ala Thr Ala Val Ser Ala Asp
210 215 220

Glu Ile Phe Asp Leu Asp Val Asp Leu Phe Ala Pro Cys Ala Leu Gly
225 230 235 240

Ala Val Leu Asn Asp Asp Thr Ile Ala Arg Leu Lys Val Gly Ala Val
245 250 255

Ala Gly Ala Ala Asn Asn Gln Leu Thr Glu Met Arg His Ala Ala Ala
260 265 270

Leu Gly Glu Lys Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala
275 280 285

Gly Gly Ile Ile Asp Val Tyr Tyr Gln Gln Gln Gly Asp Tyr Asp Pro
290 295 300

Ala Arg Val Lys Ala His Ile Glu Thr Ile Gly Ser Thr Met Gln Glu
305 310 315 320

Ile Phe Gln Arg Ala Ala Glu Thr Gly Glu Thr Thr Ala His Val Ala
325 330 335

Asp Arg Ile Ala Glu Glu Arg Phe Gly His Glu Asp Ala Ser Lys Asn
340 345 350

Ile Asp Pro Ala Ala Ala
355

<210> 279

<211> 350

<212> PRT

<213> Pseudomonas alcaligenes

<400> 279

Met Pro Val Phe Thr His Ile Asp Phe Asp His His Glu Gln Val Val
1 5 10 15
Phe Gly His Asp Gln Ala Ser Gly Leu Lys Ala Ile Ile Ala Val His
20 25 30
Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Cys Arg Met Trp Asn Tyr
35 40 45
Ala Ser Asp Glu Glu Ala Leu Arg Asp Val Leu Arg Leu Ser Arg Gly
50 55 60

Met Thr Tyr Lys Ser Ala Leu Ala Arg Leu Pro Leu Gly Gly Gly Lys
65 70 75 80
Ala Val Ile Ile Gly Asp Pro Arg Ser Gly Lys Ser Glu Ala Leu Phe
85 90 95
Gln Ala Met Gly Asp Phe Val Asp Lys Leu Gly Gly Arg Tyr Ile Thr
100 105 110
Ala Ala Asp Ser Gly Thr Gly Val Ala Glu Met Gln Ile Met Ala Gln
115 120 125

Arg Thr Arg His Val Ala Gly Ala Gly Gln Arg Glu Ala Phe Asp Gly
130 135 140
Gly Ser Arg Asp Gly Asn Pro Ser Pro Ser Thr Ala Tyr Gly Val Phe
145 150 155 160
Val Gly Ile Arg Ala Ala Val Arg His Arg Leu Gly Arg Asp Asp Leu
165 170 175
Lys Gly Leu Lys Val Ala Ile Gln Gly Val Gly Glu Val Gly Phe Ser
180 185 190

Leu Ala Lys His Leu Lys Asp Ala Gly Ala Glu Leu Trp Val Thr Asp
195 200 205
Ile Phe Glu Ala Asn Gln Arg Arg Ala Val Glu Gln Leu Gly Ala Arg
210 215 220
Ala Val Gly Gln His Asp Ile Phe Gly Leu Asp Val Asp Val Phe Ala
225 230 235 240
Pro Cys Ala Leu Gly Ala Ile Val Asn Pro Gln Thr Leu Glu Ala Leu

245 250 255
 Arg Ala Pro Ile Ile Ala Gly Ala Ala Asn Asn Gln Leu Ala Ser Pro
 260 265 270
 Glu Leu Ala Glu Gln Leu Gln Arg Arg Gly Val Leu Tyr Ala Pro Asp
 275 280 285
 Tyr Ala Ile Asn Ala Gly Gly Ile Ile Asp Val Cys Tyr Glu Arg Thr
 290 295 300
 Gly Gly Ser Thr Ala Ala Leu Lys Ala His Ile Glu Gly Ile Glu Ala
 305 310 315 320

 Thr Leu Ala Glu Ile Phe Gln Arg Ala Ala Ala Glu Gly Ala Thr Thr
 325 330 335
 Thr Ala Ile Ala Asp Arg Met Ala Arg Glu Arg Leu Gly Arg
 340 345 350
 <210> 280
 <211> 347
 <212> PRT
 <213> Rheinheimera nanhaiensis
 <400> 280
 Met Ala Val Phe Asn His Ser Glu Phe Asp Asn His Glu Gln Val Val
 1 5 10 15
 Phe Cys Ser Asp Ala Glu Thr Gly Leu Lys Ala Ile Ile Ala Val His

 20 25 30
 Ser Thr Ala Leu Gly Pro Ala Val Gly Gly Cys Arg Leu Trp Asn Tyr
 35 40 45
 Ala Ser Asp Glu Asp Ala Ile Asn Asp Val Leu Arg Leu Ser Arg Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Met Ala Gly Leu Pro Leu Gly Gly Gly Lys
 65 70 75 80
 Ser Val Ile Ile Gly Asp Ala Lys Ser Ile Lys Ser Glu Ala Leu Phe

 85 90 95
 Arg Ala Phe Gly Arg Met Val His Arg Leu Ser Gly Ser Tyr Tyr Ser

100	105	110	
Ala Glu Asp Val Asn Ile Thr Thr Gly Asp Ile Met Ile Val Asn Lys			
115	120	125	
Glu Thr Pro Phe Val Ala Gly Leu Glu Gly Lys Ser Gly Asn Pro Ala			
130	135	140	
Pro Phe Thr Ala Leu Gly Thr Tyr Arg Gly Ile Lys Ala Ala Ala Lys			
145	150	155	160
His Gln Phe Gly Ser Asp Asp Leu Arg Gly Lys Thr Val Ala Val Gln			
165	170	175	
Gly Leu Gly Ser Val Gly Phe Tyr Leu Cys Glu His Leu His Arg Asp			
180	185	190	
Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Gln Asp Ala Val Lys Arg			
195	200	205	
Ala Val Glu Gln Phe Ala Ala Val Ala Val Gly Leu Asp Asp Ile Tyr			
210	215	220	
Arg Val Asp Ala Asp Ile Tyr Ala Pro Cys Ala Leu Gly Ala Thr Leu			
225	230	235	240
Asn Asp Asn Thr Ile Ser Gln Leu Lys Val Arg Ile Ile Ala Gly Cys			
245	250	255	
Ala Asn Asn Gln Leu Lys Glu Ala Arg His Gly Glu Val Leu Arg Gln			
260	265	270	
Lys Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly Ile			
275	280	285	
Ile Asn Val Ala Phe Glu Met Arg Pro Gln Gly Tyr Ser Glu Ala Glu			
290	295	300	
Ser Thr Ala Lys Val Met Ala Ile Tyr Asp Thr Leu Leu Asn Leu Phe			
305	310	315	320
Gln Arg Ala Asp Ala Glu Gln Gln Pro Thr Ser Val Val Ala Asp Leu			
325	330	335	
Met Ala Gln Glu Ile Ile Arg Arg Gly Lys Ala			
340	345		

<210> 281

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 281

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Tyr Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 282

<211> 367

<212> PRT

<213> Lysobacter daejeonensis

<400> 282

Met Ile Phe Glu Thr Leu Asp Thr Tyr Gly His Glu Gln Val Val Phe
1 5 10 15

Cys His Asn Lys Asp Ala Gly Leu Lys Ala Ile Ile Ala Ile His Asn
20 25 30

Thr Val Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Pro Tyr Lys
35 40 45

Ser Glu Gln Glu Ala Leu Asn Asp Val Leu Arg Leu Ser Arg Gly Met

50

55

60

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

65

70

75

80

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

85

90

95

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

100

105

110

Glu Asp Val Gly Ile Asp Val Asn Asp Met Glu Tyr Val Tyr Arg Glu

115

120

125

Thr Glu Phe Val Thr Gly Val His Gln Val His Gly Gly Ser Gly Asp

130

135

140

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

145

150

155

160

Leu Asn Lys Arg Phe Gly Asp Glu Glu Val Gly Lys Tyr Ser Tyr Ala

165

170

175

Val Gln Gly Leu Gly His Val Gly Met Glu Tyr Val Lys Leu Leu Lys

180

185

190

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

195

200

205

Asp Lys Ala Val Ser Glu Tyr Gly Ala Glu Ala Val Gly Leu Asp Glu

210

215

220

Ile Tyr Asp Val Pro Ala Asp Val Tyr Ser Pro Cys Ala Leu Gly Gly

225

230

235

240

Thr Val Asn Glu Gln Thr Leu Pro Arg Leu Lys Ala Lys Ile Ile Cys

245

250

255

Gly Ala Ala Asn Asn Gln Leu Ala Asn Asn Ala Ile Gly Asp Glu Val

260

265

270

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

275

280

285

Gly Val Met Asn Val Ala Leu Glu Leu Glu Gly Tyr Asn Arg Glu Arg

290 295 300
Ala Met Arg Met Met Arg Thr Ile Tyr His Asn Leu His Arg Ile Tyr

305 310 315 320
Glu Ile Ala Glu Arg Asp Gly Val Pro Thr Tyr Gln Ala Ala Asp Arg

325 330 335
Leu Gly Glu Glu Arg Ile Ala Ala Ile Gly Lys Leu Lys Leu Pro Leu

340 345 350
Ala Arg Gly Gln Thr Arg Phe Lys Gly Arg Ile Arg Gly Gly Asn

355 360 365
<210> 283
<211> 366
<212> PRT
<213> Bacillus wakoensis

<400> 283
Met Glu Leu Phe Ser Tyr Met Glu Asn Tyr Asp Tyr Glu Gln Val Val

1 5 10 15
Val Cys Gln Asp Lys Val Ser Gly Leu Lys Ala Ile Ile Ala Ile His

20 25 30
Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Met Tyr

35 40 45
Asp Thr Glu Ala Asp Ala Phe Glu Asp Ala Leu Arg Leu Ala Lys Gly

50 55 60
Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80
Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Asn Glu Glu Met Phe

85 90 95
Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr

100 105 110
Ala Glu Asp Val Gly Thr Thr Val Gln Asp Met Asp Ile Ile Tyr Glu

115 120 125
Glu Thr Glu Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly

130 135 140
 Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Val Gly Met Lys Ala
 145 150 155 160
 Ala Ala Lys Glu Ala Phe Gly Ser Asp Asp Leu Gly Gly Lys Thr Ile
 165 170 175
 Ala Val Gln Gly Val Gly Asn Val Ala Tyr Asn Leu Cys Lys His Leu
 180 185 190

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

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

 Phe Asp Ile Ser Lys Arg Asp Gln Ile Pro Thr Phe Lys Ala Ala Asp
 325 330 335
 Arg Met Ala Glu Glu Arg Ile Glu Arg Met Arg Arg Ser Arg Arg Gln
 340 345 350
 Phe Leu Gln Asn Gly Gln His Ile Leu Ser Arg Arg Glu Arg
 355 360 365

 <210> 284
 <211> 366
 <212> PRT

<213> Marinobacter lipolyticus

<400> 284

Met Asn Val Phe Ser His Pro Glu Phe Asp Asn His Glu His Leu Ser

1 5 10 15

Phe Phe Cys Asp Pro Glu Thr Gly Leu Lys Ala Ile Val Ala Ile His

20 25 30

Asn Thr Ser Arg Gly Pro Ala Leu Gly Gly Cys Arg Met Phe Pro Tyr

35 40 45

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

50 55 60

Met Thr Tyr Lys Ser Ala Leu Ala Asn Leu Asp Leu Gly Gly Gly Lys

65 70 75 80

Ser Val Ile Ile Gly Asp Pro Arg Lys Glu Lys Thr Glu Ala Leu Leu

85 90 95

Glu Ala Met Gly Arg His Leu Glu Ser Leu Gly Gly Gln Tyr Ile Ala

100 105 110

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

115 120 125

His Thr Arg His Val Ala Gly Ile Ser Gln His Ile Gly Phe Asp Gly

130 135 140

Lys Pro Ser Asn Gly Asp Pro Ser Pro Ala Thr Ala Tyr Gly Thr Phe

145 150 155 160

Ile Gly Leu Lys Ala Ala Val Ser His Lys Leu Gly Arg Ser Asp Leu

165 170 175

Asn Gly Leu Lys Val Ala Ile Gln Gly Ile Gly Asn Val Gly Phe Arg

180 185 190

Leu Ala Arg His Leu Lys Glu Ala Gly Ala Glu Leu Trp Val Tyr Asp

195 200 205

Ile His Ala Asp Asn Met Gln Arg Ala Ile Asp Glu Leu Gly Ala Lys

210 215 220

Pro Ala Ser Ala Glu Asp Ile Leu Phe Leu Pro Val Asp Val Ile Ala

225 230 235 240
 Pro Cys Ala Met Gly Ala Val Leu Asn Asp Glu Ser Ile Pro Gln Ile
 245 250 255
 Lys Ala Pro Val Val Ala Gly Ala Ala Asn Asn Leu Leu Glu Arg Pro

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

 325 330 335
 Gly Ala Ile Ala Asn Glu Leu Ala Glu Glu Arg Phe His Lys His Thr
 340 345 350
 Ala Arg Val Asp Ala Met Gln Glu Arg Met Ala His Ala Gly
 355 360 365
 <210> 285
 <211> 364
 <212> PRT
 <213> Unknown
 <220><223> Planococcus sp. Y42
 <400> 285
 Met Glu Ile Phe Lys Arg Met Glu Ser Gln Asp Tyr Glu Gln Leu Val
 1 5 10 15

 Phe Cys Gln Asp Lys Thr Ser Gly Leu Lys Ala Ile Ile Cys Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr
 35 40 45
 Glu Ser Glu Glu Glu Ala Ile Glu Asp Ala Ile Arg Leu Gly Arg Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65					70					75					80
Thr	Val	Ile	Ile	Gly	Asp	Pro	Leu	Lys	Asp	Lys	Asn	Glu	Glu	Met	Phe
				85						90					
Arg	Ala	Phe	Gly	Arg	Phe	Ile	Gln	Gly	Leu	Asn	Gly	Arg	Tyr	Ile	Thr
				100						105					
Ala	Glu	Asp	Val	Gly	Thr	Thr	Val	Ala	Asp	Met	Asp	Leu	Ile	His	Glu
				115						120					
Glu	Thr	Asp	Phe	Val	Thr	Gly	Ile	Ser	Pro	Ala	Phe	Gly	Ser	Ser	Gly
				130						135					
										140					
Asn	Pro	Ser	Pro	Val	Thr	Ala	Tyr	Gly	Cys	Tyr	Leu	Gly	Met	Lys	Ala
145				150				155				160			
Ala	Ala	Lys	Glu	Ala	Phe	Gly	Asp	Asp	Ser	Leu	Glu	Gly	Lys	Thr	Ile
				165						170					
Ala	Val	Gln	Gly	Val	Gly	Asn	Val	Ala	Phe	Thr	Leu	Cys	Arg	Tyr	Leu
				180						185					
His	Glu	Glu	Gly	Ala	Lys	Leu	Ile	Val	Thr	Asp	Ile	Asn	Gln	Gln	Ala
				195						200					
										205					
Val	Gln	Arg	Ala	Val	Asp	Glu	Phe	Gly	Ala	Thr	Ala	Val	Gly	Ile	Asn
210				215				220							
Glu	Ile	Tyr	Ser	Gln	Glu	Ala	Asp	Ile	Phe	Ala	Pro	Cys	Ala	Leu	Gly
225				230				235				240			
Ala	Ile	Ile	Asn	Asp	Glu	Thr	Ile	Pro	Gln	Leu	Lys	Val	Lys	Val	Val
				245						250					
Ala	Gly	Ser	Ala	Asn	Asn	Gln	Leu	Lys	Glu	Glu	Arg	His	Gly	Asp	Met
				260						265					
										270					
Leu	Glu	Glu	Arg	Gly	Ile	Val	Tyr	Ala	Pro	Asp	Phe	Val	Ile	Asn	Ala
275				280				285							
Gly	Gly	Val	Ile	Asn	Val	Ala	Asp	Glu	Leu	Asn	Gly	Tyr	Asn	Gln	Glu
290				295				300							
Arg	Ala	Met	Lys	Arg	Val	Glu	Thr	Ile	Tyr	Asp	Ser	Ile	Ser	Arg	Ile
305				310				315				320			

Phe Glu Ile Ala Lys Arg Asp Gly Ile Pro Ser Tyr Gln Ala Ala Asp
325 330 335

Arg Met Ala Glu Glu Arg Ile Asp Arg Val Cys Arg Ser Arg Ser Gln
340 345 350

Phe Leu Arg Asn Glu His Asn Ile Leu Ser Arg Arg
355 360

<210> 286

<211> 364

<212> PRT

<213> Brevundimonas diminuta

<400> 286

Met Gly Thr Thr Leu Phe Glu Ser Pro Ser Phe Ala Asn His Glu Gly
1 5 10 15

Val His Ala Phe Tyr Asp Glu Lys Thr Gly Leu Lys Ala Ile Val Ala

20 25 30

Val His Ser Thr Ala Arg Gly Pro Ala Val Gly Gly Thr Arg Met Trp
35 40 45

Asn Tyr Ala Ser Ser Ala Glu Ala Leu Glu Asp Val Leu Arg Leu Ser
50 55 60

Lys Gly Met Ser Tyr Lys Asn Ala Ile Ala Asp Leu Glu Met Gly Gly
65 70 75 80

Gly Lys Ser Val Ile Ile Gly Asp Ser Arg Thr Gln Lys Ser Pro Glu

85 90 95

Leu Phe His Ala Phe Gly Arg Tyr Leu Asn Gly Leu Gly Gly His Tyr
100 105 110

Tyr Ala Ala Glu Asp Val Gly Thr Ser Val Glu Asp Ile Ala Glu Ala
115 120 125

Arg Lys Val Thr Glu Phe Val Leu Gly Leu Lys Asp Gly Pro Glu Ala
130 135 140

Ser Gly Asp Pro Ser Pro Val Thr Ala Glu Gly Val Phe Arg Ser Ser

145 150 155 160

Leu Val Val Ala Arg Arg Leu Phe Asn Gln Asp Asp Met Thr Gly Leu
 165 170 175
 Thr Val Ala Leu Gln Gly Val Gly His Val Gly Ala Tyr Leu Ala Glu
 180 185 190
 Lys Leu His Lys Ala Gly Ala Lys Leu Ile Ile Thr Asp Val Asn Gln
 195 200 205
 Ala Asn Leu Glu Ala Val Ala Ala Lys Thr Gly Ala Glu Ile Val Ala
 210 215 220
 Pro Asp Ala Ile Tyr Asp Val Ala Ala Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Leu Asn Pro Gln Thr Leu Asp Arg Leu Lys Val Lys
 245 250 255
 Ala Val Cys Gly Ala Ala Asn Asn Gln Leu Ala Thr Ala Asp Ile Gly
 260 265 270
 Asp Glu Leu Phe Lys Arg Gly Ile Leu Tyr Ser Pro Asp Tyr Val Ile
 275 280 285
 Asn Gly Gly Gly Ile Ile Asn Val Ala Ser Glu Met Asn Ala Arg Gln
 290 295 300
 Thr Gly Gly Ala Tyr Asp Ala Ser Trp Val Glu Gly Lys Leu Ser Arg
 305 310 315 320
 Leu Met Glu Thr Phe Glu Glu Ile Leu Glu Arg Ser Val Ser Glu Asn
 325 330 335
 Lys Pro Thr His Leu Ile Ala Asp Ala Ile Ala Glu Ala Arg Ile Lys
 340 345 350
 Ala Ala Ala Asp Ala Lys Ala Glu Ala Gln Lys Val
 355 360
 <210> 287
 <211> 366
 <212> PRT
 <213> Bacillus selenitireducens
 <400> 287
 Met Glu Leu Phe Lys Tyr Met Glu Thr Tyr Asp Tyr Glu Gln Thr Val

1 5 10 15
 Val Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30

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

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

 Ala Ala Lys Glu Ala Phe Gly Asp Asp Ser Leu Glu Gly Arg Thr Val
 165 170 175
 Ala Val Gln Gly Val Gly Asn Val Ser Tyr Lys Leu Cys Asp Tyr Leu
 180 185 190
 His Lys Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys Asp Ala
 195 200 205
 Val Lys Arg Ala Val Glu Asp Phe Gly Ala Lys Ala Val Asp Val Asp
 210 215 220

 Asp Ile Tyr Ser Gln Asp Ala Asp Ile Tyr Ser Pro Cys Ala Leu Gly
 225 230 235 240
 Ala Thr Ile Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Arg Val Ile
 245 250 255

Ala Gly Ala Ala Asn Asn Gln Leu Arg Glu Ser Arg His Gly Asp Ile
260 265 270

Ile Gln Asp Lys Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ser
275 280 285

Gly Gly Val Ile Asn Val Ser Asp Glu Leu Ile Gly Tyr Asn Arg Glu
290 295 300

Arg Ala Leu Lys Lys Val Glu Thr Ile Tyr Asp Asn Ile Ser Lys Ile
305 310 315 320

Phe Glu Ile Ser Lys Arg Asp Gly Ile Ala Ser Tyr Lys Ala Ala Asp
325 330 335

Arg Met Ala Glu Glu Arg Ile Glu Thr Met Arg Lys Ser Arg Arg Gln
340 345 350

Phe Leu Gln Asn Gly Met His Ile Leu Ser Arg Gly Arg Thr
355 360 365

<210> 288
<211> 366
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 288

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Val Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

260 265 270

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

275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335

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

340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

 355 360 365
 <210> 289
 <211> 364
 <212> PRT
 <213> Planomicrobium glaciei
 <400> 289
 Met Ala Ile Phe Asp Lys Met Glu Gln His Asp Tyr Glu Gln Leu Val
 1 5 10 15
 Phe Cys Gln Asp Lys Thr Ser Gly Leu Lys Ala Ile Ile Cys Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr
 35 40 45

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

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

 Thr Val Gln Gly Val Gly Asn Val Ala Tyr Thr Leu Cys Lys His Leu

180 185 190
 His Glu Glu Gly Ala Lys Leu Ile Val Ser Asp Ile Asn Glu Glu Ala
 195 200 205
 Val Gln Arg Ala Val Asn Asp Phe Gly Ala Val Ala Val Ala Pro Asn
 210 215 220
 Asp Ile Tyr Ser Gln Glu Ala Asp Ile Phe Ala Pro Cys Ala Met Gly
 225 230 235 240

 Ala Ile Ile Asn Asp Glu Thr Ile Pro Gln Leu Lys Val Lys Leu Val
 245 250 255
 Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Glu Arg His Gly Asp Glu
 260 265 270
 Leu Glu Ala Arg Gly Ile Val Tyr Thr Pro Asp Phe Val Ile Asn Ser
 275 280 285
 Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Glu Glu
 290 295 300

 Arg Ala Leu Lys Arg Val Gly Thr Ile Tyr Asp Ser Ile Ser Lys Ile
 305 310 315 320
 Phe Glu Ile Ser Lys Arg Asp Gly Ile Pro Ser Tyr Lys Ala Ala Asp
 325 330 335
 Arg Leu Ala Glu Glu Arg Ile Glu Arg Val Ala Lys Ser Arg Ser Ser
 340 345 350
 Phe Leu Arg Asn Glu His Asn Ile Ile Ser Arg Arg
 355 360
 <210> 290
 <
 211> 365
 <212> PRT
 <213> Anaerobacillus macyae
 <400> 290
 Met Glu Leu Phe Thr Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Val Val
 1 5 10 15
 Val Cys Gln Asp Lys Ala Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
 35 40 45
 Ala Ser Glu Glu Ala Ala Phe Glu Asp Ala Leu Arg Leu Ala Lys Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
 65 70 75 80
 Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Asn Glu Ala Met Phe
 85 90 95
 Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Val Gly Thr Thr Val Gln Asp Met Asp Thr Ile His Glu
 115 120 125
 Glu Thr Glu Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly
 130 135 140
 Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Val Gly Met Lys Ala
 145 150 155 160
 Ala Ala Lys Glu Ala Phe Gly Thr Asp Ser Leu Glu Gly Lys Thr Val
 165 170 175
 Ala Val Gln Gly Val Gly Asn Val Ala Tyr Asn Leu Cys Lys His Leu
 180 185 190
 His Glu Glu Gly Ala Ser Leu Val Val Thr Asp Ile Asn Lys Glu Ser
 195 200 205
 Val Asp Arg Ala Val Ala Asp Phe Gly Ala Lys Ala Val Asp Pro Asp
 210 215 220
 Asp Ile Tyr Glu Val Asp Cys Asp Ile Phe Ala Pro Cys Ala Leu Gly
 225 230 235 240
 Ala Ile Ile Asn Asp Asp Thr Ile Gly Lys Ile Lys Ala Lys Val Ile
 245 250 255
 Ala Gly Ala Ala Asn Asn Gln Leu Arg Glu Thr Thr His Gly Asp Gln
 260 265 270
 Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala

275 280 285
Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Arg Asp
290 295 300
Arg Ala Met Lys Arg Val Asp Gly Ile Tyr Asp Thr Ile Ala Lys Val
305 310 315 320
Ile Glu Ile Ser Lys Arg Asp Gly Ile Pro Thr Tyr Ala Ala Ala Asp
325 330 335
Arg Leu Ala Glu Glu Arg Ile Ala Gln Met Lys His Ser Arg Ser Gln
340 345 350
Phe Leu Met Asn Ser Gln His Ile Leu Gly His Arg Lys
355 360 365
<210> 291
<211> 366
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic polypeptide
<400> 291
Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115	120	125
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser		
130	135	140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met		
145	150	155
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys		
165	170	175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys		
180	185	190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys		
195	200	205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu		
210	215	220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala		
225	230	235
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys		
245	250	255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly		
260	265	270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile		
275	280	285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Lys Tyr Gly Tyr Asn		
290	295	300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala		
305	310	315
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala		
325	330	335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg		
340	345	350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg		
355	360	365

<210> 292

<211> 351

<212> PRT

<213> *Pseudomonas alcaligenes*

<400> 292

Met Ser Val Phe Ser His Val Glu Phe Asp Gly His Glu Gln Val Val

1 5 10 15
Phe Gly His Asp Lys Ala Ser Gly Leu Lys Ala Ile Ile Ala Ile His

20 25 30
Asn Thr Asn Leu Gly Pro Ala Leu Gly Gly Cys Arg Met Trp Asn Tyr

35 40 45
Ala Asn Asp Glu Gln Ala Leu Arg Asp Val Leu Arg Leu Ser Arg Gly

50 55 60
Met Thr Tyr Lys Ser Ala Leu Ala Asn Leu Pro Leu Gly Gly Gly Lys

65 70 75 80
Ala Val Ile Ile Gly Asp Pro His Asn Gly Lys Ser Glu Ala Leu Phe

85 90 95
Gln Ala Met Gly Asp Phe Val Asp Thr Leu Gly Gly Arg Tyr Ile Thr

100 105 110
Ala Ala Asp Ser Gly Thr Gly Pro Ala Glu Met Gln Ile Met Ala Glu

115 120 125
Arg Ser Arg His Val Ala Gly Ala Asn Gln Arg Glu Ala Phe Asp Gly

130 135 140
Gly Val Arg Ser Gly Asp Pro Ser Pro Ser Thr Ala Tyr Gly Val Phe

145 150 155 160
Ile Gly Ile Gln Val Ala Val Lys His Arg Leu Arg Arg Asp Asp Leu

165 170 175
Lys Gly Leu Arg Val Ala Ile Gln Gly Val Gly Gln Val Gly Phe His

180 185 190
Leu Ala Arg Leu Leu Arg Asp Ala Gly Ala Glu Leu Trp Val Thr Asp

195 200 205

Ile Val Asp Ala Asn Val Arg Arg Ala Val Glu Gln Leu Gly Ala Lys
210 215 220
Ala Val Leu Gln His Glu Ile Tyr Gly Leu Asn Val Asp Val Phe Ala
225 230 235 240
Pro Cys Ala Met Gly Gly Ile Ile Asn Pro Gln Ser Leu Glu Ala Leu
245 250 255
Arg Val Pro Ile Ile Ala Gly Gly Ala Asn Asn Gln Leu Ala Asp Ala
260 265 270
Gln Leu Ala Glu Glu Leu Lys Arg Asn Gly Cys Leu Tyr Ala Pro Asp
275 280 285
Tyr Ala Ile Asn Ala Gly Gly Ile Ile Asp Val Tyr Phe Glu Arg Ser
290 295 300
Gly Gly Ser Ala Ala Glu Leu Lys Ala His Ile Glu Gly Ile Gly Asn
305 310 315 320
Thr Leu Arg Gln Ile Phe Ile Arg Ala Asp Glu Glu Gly Arg Thr Thr
325 330 335
Thr Glu Val Ala Asp Arg Leu Ala Glu Glu Arg Phe Gly Arg Val
340 345 350
<210> 293
<211> 364
<212> PRT
<213> Unknown
<220><223> Thermoactinomyces sp. DSM 45891
<400> 293
Met Lys Leu Phe Asp Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Val Val
1 5 10 15
Ile Cys Gln Asp Lys Asn Ser Gly Leu Lys Ala Ile Ile Ala Ile His
20 25 30
Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Leu Arg Met Trp Thr Tyr
35 40 45
Ala Thr Glu Glu Glu Ala Met Glu Asp Ala Leu Arg Leu Ala Arg Gly
50 55 60

Met Thr Tyr Lys Ala Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
65 70 75 80
Thr Val Leu Ile Gly Asp Pro Lys Lys Asp Lys Ser Glu Glu Leu Phe
85 90 95

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

Ala Ala Lys Glu Ala Phe Gly Ser Asp Ala Leu Asp Gly Leu Val Val
165 170 175
Ala Val Gln Gly Val Gly Asn Val Ala Tyr Ser Met Cys Glu Tyr Leu
180 185 190
His Lys Glu Asn Val Lys Leu Ile Val Thr Asp Ile Asn Glu Glu Asn
195 200 205
Val Gln Arg Ala Val Asn Asp Phe Gly Ala Ile Arg Val Ser Pro Glu
210 215 220

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

Gly Gly Leu Ile Asn Val Ala Asp Glu Leu Val Gly Tyr Asn Pro Glu
290 295 300
Arg Ala Met Lys Lys Val Glu Gly Ile Tyr Asp Asn Ile Leu Arg Val

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

 Phe Val Gln Thr Glu Arg His Ser Leu Asn Gln Arg
 355 360
 <210> 294
 <211> 365
 <212> PRT
 <213> Pseudobacteriovorax antillogorgiicola
 <400> 294

 Met Ala Ile Phe Glu Thr Leu Ala Gly Thr Gly His Glu Gln Val Val
 1 5 10 15
 Phe Cys Asn Asp Glu Ala Thr Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Cys Arg Met Trp Asp Tyr

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

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

Ser Val Lys His Lys Leu Gly Lys Asp Ser Val Asn Gly Leu Thr Val

165 170 175

Ala Val Gln Gly Cys Gly Ala Val Gly Thr Phe Leu Thr Glu Phe Leu

180 185 190

Thr Gln Glu Gly Ala Lys Val Phe Ala Ala Asp Leu Asn Gln Asp Lys

195 200 205

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

210 215 220

Lys Ile His Ser Leu Pro Val Asp Val Tyr Ala Pro Cys Ala Leu Gly

225 230 235 240

Gly Ile Leu Asn Asp Asn Thr Ile Pro Glu Leu Gln Thr Thr Ile Val

245 250 255

Ser Gly Gly Ala Asn Asn Gln Leu Leu Asp Glu Ala Lys His Ala Ala

260 265 270

Met Leu Lys Glu Lys Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn

275 280 285

Ala Gly Gly Leu Ile Asn Val Tyr Gln Glu Leu Gln Gly Tyr Asp Ala

290 295 300

Asp Ala Ala Arg Thr Lys Ala Ala Gly Ile Phe Asp Thr Leu Ile Asn

305 310 315 320

Ile Tyr Lys Glu Ser Asp Glu Gln Gly Ile Thr Thr Ile Gln Ala Ser

325 330 335

Asn Lys Ile Ala Glu Asp Arg Ile Asn Ser Val Arg Asn Met Lys Asp

340 345 350

Leu Arg Asn Asn Phe Glu Gly Gln Leu Trp Ile Asn Gln

355 360 365

<210> 295

<211> 348

<212> PRT

<213> Oceanibaculum pacificum

<400> 295

Met Pro Ile Phe Thr Ala Pro Asp Phe Asp Asn His Glu Gln Val Val
1 5 10 15
Phe Cys Asn Asp Ala Glu Thr Gly Leu Lys Ala Ile Ile Ala Ile His
20 25 30
Asp Thr Thr Arg Gly Pro Ser Leu Gly Gly Cys Arg Met Trp Pro Tyr
35 40 45
Ala Ser Glu Ala Ala Ala Val Thr Asp Ala Leu Arg Leu Ser Arg Gly
50 55 60
Met Thr Tyr Lys Ser Ala Leu Ala Gly Leu Pro Leu Gly Gly Gly Lys
65 70 75 80
Ser Val Ile Ile Gly Asp Ala Lys Thr Gln Lys Ser Pro Ala Leu Phe
85 90 95
Arg Ala Phe Gly Arg Phe Val Asp Ser Leu Gly Gly Arg Tyr Ile Ala
100 105 110
Ala Glu Asp Val Gly Thr Gly Val Ala Asp Ile Glu Ala Met Arg Gln
115 120 125
Val Thr Arg His Val Ala Gly Thr Ala Gly Gly Ser Gly Asp Pro Ser
130 135 140
Pro Val Thr Ala Tyr Gly Val Phe Gln Gly Ile Arg Ala Ala Ala Lys
145 150 155 160
Ala Lys Leu Gly Arg Asp Asp Leu Ala Gly Leu Arg Val Ala Val Gln
165 170 175
Gly Leu Gly His Val Gly Leu Asp Leu Ala Arg Gln Leu Tyr Glu Ala
180 185 190
Gly Ala Ala Leu Ile Val Ala Asp Ile Asp Leu Asp Arg Ile Ala Arg
195 200 205
Ala Thr Thr Ala Tyr Arg Ala Glu Ala Met Pro Ala Asp Arg Ile His
210 215 220
Ala Ala Asp Val Asp Ile Phe Ala Pro Cys Ala Leu Gly Ala Ile Leu
225 230 235 240
Asn Asp Ala Thr Ile Pro Glu Ile Lys Ala Gly Ile Ile Ala Gly Ala

245 250 255
Ala Asn Asn Gln Leu Ala Glu Glu Arg His Gly Ala Ala Leu Met Lys
260 265 270
Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Ala Ile Asn Ala Gly Gly Ile
275 280 285
Ile Asn Ile His His Glu Ser Ala Gly Lys Tyr Asp Arg Ala Ala Ala
290 295 300

Leu Arg Gln Val Glu Gly Ile Tyr Asp Thr Leu Leu Glu Ile Phe Ala
305 310 315 320
Arg Ala Ala Ala Glu Gly Ile Pro Thr Ser Asp Ala Ala Asp Arg Val
325 330 335
Ala Glu Thr Arg Phe Gly Lys His Arg Gln Ala Ala
340 345

<210> 296

<211> 357

<212> PRT

<213> Saccharomonospora glauca

<400> 296

Met Thr Asp Gly Val Phe Gly Arg Asp Gly Gly His Glu Gln Val Val

1 5 10 15
Tyr Cys Gln Asp Pro Gln Thr Gly Leu Lys Ala Ile Ile Ala Val His
20 25 30
Ser Thr Ala Leu Gly Pro Ala Leu Gly Gly Thr Arg Phe Tyr Pro Tyr
35 40 45
Ala Ser Glu Gln Asp Ala Leu Asn Asp Val Leu Ala Leu Ser Arg Gly
50 55 60
Met Ser Tyr Lys Asn Ala Leu Ala Gly Leu Asp Leu Gly Gly Gly Lys

65 70 75 80
Ala Val Ile Ile Gly Asp Pro Ala Thr Val Lys Ser Glu Ala Leu Leu
85 90 95
Arg Ala Tyr Gly Arg Phe Val Glu Thr Leu Gly Gly Arg Tyr Ile Thr
100 105 110

Ala Cys Asp Val Gly Thr Tyr Val Ala Asp Met Asp Val Val Ala Arg
115 120 125
Glu Thr Arg Tyr Val Thr Gly Arg Ser Arg Asp Asp Gly Gly Ala Gly
130 135 140
Asp Ser Ser Val Leu Thr Ala Tyr Gly Val Phe Gln Gly Met Arg Ala
145 150 155 160
Ser Ala Glu His Val Trp Gly Thr Pro Glu Leu Arg Gly Arg Arg Val
165 170 175
Gly Val Ala Gly Val Gly Lys Val Gly His Leu Leu Val Gly His Leu
180 185 190
Val Glu Ala Gly Ala Glu Val Val Val Thr Asp Val Ser Glu Ala Ala
195 200 205
Ile Asp Arg Val Arg Ser Ala His Pro Ser Val Glu Val Val Ala Asp
210 215 220
Thr Asp Thr Leu Val Ala Ser Asp Ile Asp Val Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Gly Ala Leu Asn Asp Ala Thr Val Glu Val Leu Arg Ala Lys
245 250 255
Val Val Cys Gly Ala Ala Asn Asn Gln Leu Ala His Pro Gly Val Glu
260 265 270
Lys Leu Leu Asp Glu Arg Gly Ile Leu Phe Ala Pro Asp Tyr Leu Val
275 280 285
Asn Ser Gly Gly Val Ile Met Val Ser Asp Glu Leu His Gly Phe Gln
290 295 300
Tyr Glu Arg Ala His Arg Lys Val Ser Ala Leu Tyr Glu Thr Thr Lys
305 310 315 320
Lys Val Phe Ala Leu Ala Glu Glu Glu Gly Val Pro Pro Ala Thr Ala
325 330 335
Ala Asp Arg Leu Ala Glu Arg Arg Met Ala Glu Val Ser Arg Leu Arg
340 345 350
Ser Ile Leu Thr Arg

355

<210> 297

<211> 364

<212> PRT

<213> *Pseudomonas stutzeri*

<400> 297

Met Ser Val Phe Ala His Pro Asp Phe Asp Arg His Glu Gln Val Val

1 5 10 15

Phe Cys His Asp Gln Ala Ser Gly Leu Lys Ala Ile Ile Ala Ile His

20 25 30

Asp Thr Arg Leu Gly Pro Ala Leu Gly Gly Cys Arg Met Phe Pro Tyr

35 40 45

Ala Ser Asp Asp Glu Ala Leu Arg Asp Val Leu Arg Leu Ser Arg Gly

50 55 60

Met Thr Leu Lys Ser Ser Leu Ala Gly Leu Lys Leu Gly Gly Gly Lys

65 70 75 80

Ala Val Ile Ile Gly Asp Pro His Thr Gly Lys Ser Gln Ala Leu Leu

85 90 95

His Ala Met Gly Asp Phe Val Asp Ser Leu Gly Gly Arg Tyr Ile Thr

100 105 110

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

115 120 125

Arg Thr Arg His Val Val Gly Ala Thr Pro Arg Thr Leu Leu Asp Gly

130 135 140

Ser Val Ala Ser Gly Asp Pro Ser Pro Ser Thr Ala Tyr Gly Val Tyr

145 150 155 160

Val Gly Leu Lys Glu Ala Val Arg Gln Arg Leu Gly Arg Asp Glu Leu

165 170 175

Thr Gly Leu Lys Val Ala Ile Gln Gly Val Gly His Val Gly Leu Gly

180 185 190

Leu Ala Arg His Leu Lys Ala Ala Gly Ala Glu Leu Trp Val Ala Asp

195 200 205

Ile Phe Asp Ala Asn Val Lys Gln Ala Met Glu Glu Val Gly Ala Asn

210 215 220

Val Val Arg Pro Gln Asp Ile Tyr Gly Leu Asp Val Asp Val Phe Ala

225 230 235 240

Pro Cys Ala Met Gly Gly Ile Leu Asn Glu Gln Thr Leu Glu Val Leu

245 250 255

Arg Ala Pro Val Ile Ala Gly Ala Ala Asn Asn Gln Leu Ala Ser Ala

260 265 270

Gly Ile Gly Val Glu Leu Gln Arg Arg Asn Gln Leu Tyr Ala Pro Asp

275 280 285

Tyr Ala Ile Asn Ala Gly Gly Ile Ile Asp Val Tyr Tyr Gln Arg Asn

290 295 300

Gly Gly Ser Ala Ala Gln Ile Asp Ala His Val Asn Ala Ile Ala Gly

305 310 315 320

Thr Leu Arg Glu Ile Phe Glu Arg Ala Ala Ala Ser Gly Glu Cys Thr

325 330 335

Ser Val Ile Ala Asp Arg Leu Ala Leu Glu Arg Leu Gln Ala Gly Gly

340 345 350

Ala Pro Gln Val Ala Thr Leu Gln Arg Gln Ala Ser

355 360

<210> 298

<211> 365

<212> PRT

<213> Unknown

<220><223> Bacillus sp.

<400> 298

Met Glu Ile Phe Lys Lys Leu Glu Glu His Asp Tyr Glu Gln Leu Val

1 5 10 15

Ile Cys Gln Asp Lys Thr Ser Gly Leu Lys Ala Ile Ile Ala Ile His

20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Ala Arg Met Trp Thr Tyr

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

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

 Ala Thr Ala Lys Glu Ala Phe Gly Asp Asp Ser Leu Ala Gly Lys Thr
 165 170 175
 Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr Ser Leu Cys Glu Tyr
 180 185 190
 Leu His Glu Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Glu Glu
 195 200 205
 Ala Val Gln Arg Ala Val Glu Ala Phe Gly Ala Thr Ala Val Gly Ile
 210 215 220

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

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

Gln Phe Leu Gln Asn Glu Lys Ser Val Leu Ser Arg Arg
 355 360 365

<210> 299

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 299

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

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

100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365
<210> 300

<211> 349

<212> PRT

<213> Unknown

<220><223> Idiomarina sp. A28L

<400> 300

Met Ala Leu Phe Glu His Thr Glu Tyr Asp Gly His Glu Gln Val Val

1 5 10 15

Phe Cys His Asp Lys Val Thr Gly Leu Lys Ala Ile Ile Ala Val His

20 25 30

Asp Thr Thr Met Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr

35 40 45

Ala Ser Ser Glu Glu Ala Leu Thr Asp Val Leu Arg Leu Ser Arg Gly

50 55 60

Met Thr Tyr Lys Ser Ala Leu Ala Gly Leu Pro Leu Gly Gly Gly Lys

65 70 75 80

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

85 90 95

Lys Ala Tyr Gly Arg Phe Val Asn Ser Leu Gly Gly Lys Tyr Ile Thr

100 105 110

Ala Glu Asp Val Asn Ile Arg Thr Ala Asp Ile Asp Ile Val Ala Thr

115 120 125

Glu Thr Ser Phe Val Ala Gly Thr Ala Ser Lys Ala Gly Asp Pro Ser

130 135 140

Pro His Thr Ala Glu Gly Thr Tyr Leu Gly Leu Lys Ala Ala Ala Lys

145 150 155 160

His Ala Phe Gly Asn Glu Asp Leu Lys Gly Val Arg Ile Ala Ile Gln

165 170 175

Gly Leu Gly Ala Val Gly Tyr Asp Phe Ala Glu Tyr Cys Ala Lys Glu

180 185 190

Gly Ala Lys Leu Ile Val Ala Asp Val Asn Glu Glu Ala Val Glu Arg

195 200 205

Ala Val Lys Glu Leu Gly Ala Glu Ala Val Ser Ile His Asp Ile Tyr

210 215 220
 Ser Val Asp Cys Asp Val Tyr Ala Pro Cys Ala Leu Gly Ala Thr Ile
 225 230 235 240

 Asn Asp Asp Thr Leu Lys Leu Ile Lys Ala Lys Val Ile Ala Gly Ser
 245 250 255
 Ala Asn Asn Gln Leu Ala Thr Pro Ala His Asp Lys Ile Val Lys Asp
 260 265 270
 Met Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly Val
 275 280 285
 Ile His Val Cys Ser Glu Ala Ala Asn Phe Ser Leu Glu Asp Thr Ala
 290 295 300

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

 <210> 301
 <211> 368
 <212> PRT
 <213> Novibacillus thermophilus
 <400> 301
 Met Glu Ile Phe Ala Gln Leu Ser Gln Tyr Asp Tyr Glu Glu Leu Val

 1 5 10 15
 Phe Cys His Asp Glu Asn Ser Gly Leu Arg Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Val Arg Met Trp Thr Tyr
 35 40 45
 Glu Ser Glu Gln Glu Ala Val Gln Asp Val Leu Arg Leu Ala Arg Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Val Ala Gly Leu Asn Leu Gly Gly Gly Lys

65						70						75						80
Ala	Val	Ile	Ile	Gly	Asp	Pro	Asn	Lys	Asp	Lys	Ser	Glu	Glu	Leu	Phe			
					85						90						95	
Arg	Ala	Phe	Gly	Arg	Tyr	Val	Gln	Gly	Leu	Asn	Gly	Arg	Tyr	Ile	Thr			
					100						105						110	
Ala	Glu	Asp	Val	Gly	Thr	Thr	Glu	Glu	Asp	Met	Asp	Thr	Ile	Tyr	Glu			
					115						120						125	
Glu	Thr	Asp	Tyr	Val	Thr	Gly	Val	Ser	Pro	Ala	Phe	Gly	Ser	Gly	Gly			
					130						135						140	
Asn	Pro	Ser	Pro	Val	Thr	Ala	Tyr	Gly	Val	Tyr	Gln	Gly	Met	Lys	Ala			
					145						150						155	160
Ala	Ala	Asn	Val	Ala	Phe	Gly	Ser	Asp	Asp	Leu	Asn	Gly	Lys	Thr	Val			
					165						170						175	
Ala	Val	Gln	Gly	Leu	Gly	Asn	Val	Ala	Phe	Asn	Leu	Cys	Arg	His	Leu			
					180						185						190	
Ser	Glu	Glu	Gly	Ala	Lys	Leu	Val	Val	Thr	Asp	Leu	Asn	Glu	Glu	Arg			
					195						200						205	
Val	Gln	Arg	Ala	Val	Glu	Gln	Phe	Gly	Ala	Glu	Ala	Val	Gly	Val	Gln			
					210						215						220	
Asp	Ile	Tyr	Gly	Val	Ala	Cys	Asp	Ile	Phe	Ser	Pro	Asn	Ala	Leu	Gly			
					225						230						235	240
Gly	Val	Leu	Asn	Asp	Glu	Thr	Ile	Pro	Met	Leu	Asn	Cys	Arg	Val	Val			
					245						250						255	
Ala	Gly	Ala	Ala	Asn	Asn	Gln	Leu	Lys	Glu	Glu	Arg	His	Gly	Lys	Met			
					260						265						270	
Leu	Glu	Glu	Arg	Gly	Ile	Val	Tyr	Ala	Pro	Asp	Tyr	Val	Ile	Asn	Ala			
					275						280						285	
Gly	Gly	Val	Ile	Asn	Ile	Ala	Asp	Glu	Leu	Ile	Gly	Tyr	Asn	Arg	Glu			
					290						295						300	
Arg	Ala	Met	Lys	Lys	Val	Glu	Ser	Ile	Tyr	Asp	Thr	Val	Leu	Asn	Val			
					305						310						315	320

Phe Ala Ile Ala Glu Arg Asp Gly Ile Pro Ser Tyr Gln Ala Ala Asp

325

330

335

Arg Met Ala Glu Glu Arg Ile Gln Ser Ile Arg Arg Ser Arg Asn Pro

340

345

350

Phe Val Arg Asp Glu Lys Asn Val Phe His Leu Arg Arg Gly Arg His

355

360

365

<210> 302

<211> 347

<212> PRT

<213> Idiomarina woesei

<400> 302

Met Ser Leu Phe Glu His Lys Glu Phe Asp Gln His Glu Gln Val Val

1

5

10

15

Phe Cys His Asp Lys Glu Thr Gly Leu Lys Ala Ile Ile Ala Ile His

20

25

30

Asp Thr Thr Leu Gly Pro Ser Leu Gly Gly Thr Arg Met Trp Asn Tyr

35

40

45

Ala Ser Ser Ala Glu Ala Leu Thr Asp Val Leu Arg Leu Ser Arg Gly

50

55

60

Met Thr Tyr Lys Ser Ala Leu Ala Gly Leu Pro Leu Gly Gly Gly Lys

65

70

75

80

Ala Val Ile Ile Gly Asp Ala Lys Ala Ile Lys Thr Pro Asp Leu Met

85

90

95

Arg Ala Tyr Gly Arg Phe Val Asn Ser Leu Ser Gly Arg Tyr Ile Thr

100

105

110

Ala Glu Asp Val Asn Ile Arg Thr Ser Asp Ile Ala His Val Ala Glu

115

120

125

Glu Thr Ser Phe Val Ala Gly Thr Ala Glu Lys Ala Gly Asp Pro Ser

130

135

140

Pro His Thr Ala Leu Gly Thr Tyr Leu Gly Leu Lys Ala Ala Ala Lys

145

150

155

160

His Lys Phe Gly Asn Asp Asn Leu Asn Gly Leu Lys Ile Ala Val Gln
165 170 175

Gly Leu Gly Ala Val Gly Tyr Asp Phe Ala Glu Tyr Cys Ala Lys Glu
180 185 190

Gly Ala Gln Leu Phe Val Thr Asp Ile Asn Glu Asp Ala Cys Asn Lys
195 200 205

Ala Ala Thr Glu Leu Asn Ala Thr Ile Val Gly Leu Asp Asp Ile Tyr
210 215 220

Gly Leu Asp Val Asp Val Tyr Ala Pro Cys Ala Leu Gly Ala Thr Ile
225 230 235 240

Asn Asp Glu Thr Leu Lys Gln Ile Lys Ala Lys Ile Ile Ala Gly Ser
245 250 255

Ala Asn Asn Gln Leu Ala Thr Pro Pro His Asp Lys Ile Val Met Asp
260 265 270

Met Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly Val
275 280 285

Ile His Val Cys Ser Glu Ala Ala Asn Met Ser Arg Glu Glu Thr Asp
290 295 300

Lys Arg Val Arg Asp Ile Tyr Asp Thr Leu Asp Lys Ile Phe Ala Arg
305 310 315 320

Ser Ser Ala Glu His Arg Pro Thr Gly Glu Ile Ala Asp Gln Met Ala
325 330 335

Arg Glu Val Ile Ala Asn Ala Lys Ala Ala Arg
340 345

<210> 303

<211> 362

<212> PRT

<213> Chlorobi bacterium

<400> 303

Met Lys Leu Phe Asp Thr Leu Gln Thr Met Gly His Glu Gln Val Val
1 5 10 15

Leu Cys Ser Asp Pro Val Thr Gly Leu Arg Ala Val Ile Ala Ile His

20 25 30
 Asp Thr Ser Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr
 35 40 45

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

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

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

 Val Leu Asn Asn Glu Thr Ile Ala Gln Leu Ser Cys Ser Val Val Cys
 245 250 255
 Gly Ala Ala Asn Asn Gln Leu Gln Asn Glu Asp Val His Ala Ala Ala
 260 265 270

Leu Gln Lys Gln Asn Ile Ile Tyr Ala Pro Asp Tyr Val Val Asn Ser
 275 280 285
 Gly Gly Leu Met Asn Val Ala Ser Glu Val Thr Gly Tyr Asp Arg Asp
 290 295 300

 Ser Val Met Arg Gln Ala Glu Gly Ile Tyr Asp Ile Thr Met Asn Ile
 305 310 315 320
 Leu Thr Thr Ala Arg Asp Lys Asn Ile Leu Thr Ile Glu Ala Ser Asn
 325 330 335
 Ala Ile Ala Glu Glu Arg Ile Lys Lys Val Arg His Val His Gly Met
 340 345 350
 Phe Thr Gly Thr Pro Ser Ile Arg Gly Leu
 355 360
 <210> 304
 <211> 364
 <212>
 > PRT
 <213> Pontibacillus halophilus
 <400> 304
 Met Glu Ile Phe Lys Tyr Leu Asn Glu Tyr Asp Tyr Glu Gln Leu Leu
 1 5 10 15
 Phe Cys His Asp Glu Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
 35 40 45
 Ala Thr Glu Glu Glu Ala Ile Val Asp Ala Leu Arg Leu Ala Arg Gly

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

Ala Glu Asp Val Gly Thr Thr Val Gln Asp Met Asp Thr Ile His Glu

115 120 125

Glu Thr Asn Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly

130 135 140

Asn Pro Ser Pro Val Thr Ala Phe Gly Val Tyr Arg Gly Met Lys Ala

145 150 155 160

Ala Ala Lys Ala Ala Phe Gly Thr Asp Ser Leu Glu Gly Arg Thr Ile

165 170 175

Ala Val Gln Gly Val Gly Ser Val Ala Tyr Asn Leu Cys Lys Tyr Leu

180 185 190

His Glu Glu Gly Ala Asn Leu Val Val Thr Asp Ile Asn Lys Glu Ala

195 200 205

Val Gln Arg Ala Val Asp Glu Phe Gly Ala Thr Ala Val Glu Thr Asp

210 215 220

Glu Ile Tyr Gly Val Asp Cys Asp Ile Tyr Ala Pro Cys Ala Leu Gly

225 230 235 240

Ala Thr Ile Asn Asp Asp Thr Ile Ser Gln Leu Lys Ala Lys Val Ile

245 250 255

Ala Gly Ala Ala Asn Asn Gln Leu Lys Asp Thr Thr His Gly Asp Ala

260 265 270

Ile His Glu Met Gly Ile Tyr Tyr Ala Pro Asp Tyr Val Ile Asn Ala

275 280 285

Gly Gly Val Met Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Gln Glu

290 295 300

Arg Ala Leu Lys Arg Val Glu Gly Ile Tyr Asp Asn Val Ala Arg Val

305 310 315 320

Phe Glu Ile Ala Glu Arg Asp Gly Ile Pro Ser Tyr Gln Ala Ala Asp

325 330 335

Arg Met Ala Glu Glu Arg Ile Glu Arg Met Arg Lys Ser Arg Ser Thr

340 345 350

Phe Leu Gln Asn Glu Lys Ser Ile Leu Asn Arg Arg

355 360

<210> 305

<211> 358

<212> PRT

<213> Gemmatimonas phototrophica

<400>

305

Met His Tyr Phe Asp Thr Ile Ala Glu Met Gly His Glu Gln Val Val

1 5 10 15

Phe Cys His Asp Lys Ala Ser Gly Tyr Arg Gly Ile Ile Ala Ile His

20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Cys Arg Phe Trp Asn Tyr

35 40 45

Ala Ser Asp Glu Glu Ala Val Ile Asp Ala Leu Arg Leu Ser Arg Gly

50 55 60

Met Thr Tyr Lys Asn Ala Val Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80

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

85 90 95

Arg Ala His Gly Arg Phe Val Asp Ser Leu Gly Gly Arg Tyr Val Thr

100 105 110

Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Phe Val His Met

115 120 125

Glu Thr Thr His Val Thr Gly Ile Gly Ser Lys Ser Gly Asp Pro Ser

130 135 140

Ser Val Thr Ala Arg Gly Val Phe Arg Ala Ile Gln Ala Ser Ala Phe

145 150 155 160

Gln Lys Trp Gly Ser Lys Glu Leu Thr Gly Arg Thr Val Ala Ile Gln

165 170 175

Gly Leu Gly His Val Gly Tyr Tyr Leu Ala Arg Glu Leu His Val Ala

180 185 190

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

195 200 205
 Val Val Gln Glu Phe Gly Ala Thr Ser Val Ala Leu Ala Asp Ile Tyr
 210 215 220
 Ala Ala Lys Ala Asp Ile Phe Ala Pro Cys Ala Leu Gly Gly Ile Leu
 225 230 235 240
 Asn Asp Asp Thr Ile Pro Gln Leu Ser Val Glu Ile Val Ser Gly Ala
 245 250 255

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

 Ala Lys Ser Thr Gly Ile Pro Thr Tyr Lys Ala Ala Asp Arg Val Ala
 325 330 335
 Glu Gln Arg Ile Ala Ala Val Arg Gly Met Met Arg Thr Trp Pro Gln
 340 345 350
 Tyr Pro Asn Lys Glu Ala
 355
 <210> 306
 <211> 349
 <212> PRT
 <213> Paraglaciecola arctica
 <400> 306
 Met Ser Val Phe Glu His Ser Glu Phe Asp Gly His Glu His Val Ala
 1 5 10 15

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

Ser Ser Asp Glu Glu Ala Leu Arg Asp Val Leu Arg Leu Ser Lys Gly
50 55 60
Met Thr Tyr Lys Ala Ala Met Ala Gly Leu Lys Gln Gly Gly Gly Lys
65 70 75 80

Ala Val Ile Leu Gly Asn Pro Arg Thr Glu Lys Thr Pro Glu Lys Met
85 90 95
Leu Ala Met Gly Lys Phe Ile Asn Ser Leu Ser Gly Gln Tyr Ile Ser
100 105 110
Ala Glu Asp Ser Gly Leu Thr Val Asp Asp Leu Lys Leu Met Ala Lys
115 120 125
Glu Thr Ala Tyr Val Ser Gly Ile Gln Ala Lys Tyr His Ile Asn Ser
130 135 140

Glu Ser Ala Asp Gly Asn Pro Ala Pro Ser Thr Ala Tyr Gly Val Phe
145 150 155 160
Val Gly Leu Arg Thr Ser Val Glu His Thr Met Asn Ser Asp Leu Lys
165 170 175
Asn Val Lys Val Ala Ile Gln Gly Leu Gly His Val Gly Met Arg Leu
180 185 190
Ala Lys His Leu Cys Asn Gln Gly Ala Lys Leu Tyr Val Thr Asp Ile
195 200 205

His Pro Glu Asn Ile Glu Lys Ala Val Asn Glu Phe Ser Ala Ile Ala
210 215 220
Val Asn Pro Asn Asp Ile Tyr Asp Leu Asp Val Asp Val Phe Ala Pro
225 230 235 240
Cys Ala Met Gly Ala Ile Leu Asp Ala Glu Asn Ile Gly Arg Leu Arg
245 250 255
Val Lys Val Ile Ala Gly Ala Ala Asn Asn Gln Leu Ala Lys Glu Val
260 265 270

Phe Gly Gln Leu Leu Val Asp Lys Gly Ile Leu Tyr Ala Pro Asp Tyr
275 280 285
Val Ile Asn Ala Gly Gly Val Ile Asp Ile Tyr His Gln Ser Ile Ala

290 295 300
 Ser Ser Asp Lys Gly Leu Arg Asp His Ile Glu Lys Ile Ser Asp Thr
 305 310 315 320
 Leu Leu Glu Ile Tyr Arg Arg Ala Glu Ala Gln Gly Ile Ala Thr Asn
 325 330 335

 Ile Val Ala Asn Gln Ile Ala Glu Glu Arg Phe Ser Lys
 340 345
 <210> 307
 <211> 347
 <212> PRT
 <213> Unknown
 <220><223> Alishewanella sp. WH16-1
 <400> 307
 Met Ala Val Phe Asn His Pro Glu Phe Asp Gln His Glu Gln Val Val
 1 5 10 15
 Phe Cys Ser Asp Gln Glu Thr Gly Leu Lys Ala Ile Ile Ala Val His
 20 25 30
 Ser Thr Arg Leu Gly Pro Ala Val Gly Gly Cys Arg Leu Trp Asp Tyr

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

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

145 150 155 160
His Gln Phe Gly Ser Ala Asp Leu Ala Gly Lys Thr Val Ala Val Gln

 165 170 175
Gly Leu Gly Ser Val Gly Phe Tyr Leu Cys Glu His Leu His Lys Glu

 180 185 190
Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Gln Asp Ala Val Asn Arg

 195 200 205
Ala Val Ala Gln Phe Gly Ala Thr Ala Val Gly Leu Asn Asp Ile Tyr

 210 215 220
Gly Val Ala Ala Asp Ile Tyr Ala Pro Cys Ala Leu Gly Ala Thr Ile

225 230 235 240
Asn Asp Asp Thr Ile Pro Gln Leu Lys Ala Lys Val Val Ala Gly Cys

 245 250 255
Ala Asn Asn Gln Leu Lys Arg Pro Glu His Gly Gln Lys Leu Arg Asp

 260 265 270
Ser Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Gly Gly Gly Ile

 275 280 285
Ile Asn Val Ala Phe Glu Met Arg Pro Gln Gly Tyr Asn Ala Ala Glu

 290 295 300
Ser Thr Ala Lys Val Met Gln Ile Tyr Asp Thr Leu Leu Arg Ile Phe

305 310 315 320
Glu Arg Ala Asp Ala Glu Asp Lys Pro Thr Ser Thr Val Ala Asp Gln

 325 330 335
Met Ala Gln Glu Ile Ile Ala Arg Gly Pro Leu

 340 345

<210> 308

<211> 355

<212> PRT

<213> Anaerobranca californiensis

<400> 308

Met Glu Ile Phe Lys Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val

1 5 10 15
 Ile Cys His Asp Lys Thr Ser Gly Leu Lys Ala Ile Ile Gly Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr
 35 40 45
 Lys Thr Glu Glu Glu Ala Ile Glu Asp Ala Leu Arg Leu Ser Arg Gly
 50 55 60

 Met Thr Tyr Lys Ala Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
 65 70 75 80
 Thr Val Ile Trp Gly Asp Pro Lys Thr Gln Lys Ser Glu Glu Leu Trp
 85 90 95
 Arg Ala Phe Gly Arg Phe Val Gln Ser Leu Asn Gly Arg Tyr Ile Thr
 100 105 110
 Ala Ala Asp Val Gly Thr Val Val Asp Asp Met Asp Tyr Ile Arg Gln
 115 120 125

 Glu Thr Lys His Val Val Gly Val Ser Lys Thr Leu Gly Gly Ser Gly
 130 135 140
 Asp Pro Ser Pro Lys Thr Ala Tyr Gly Val Phe Arg Gly Ile Gln Ala
 145 150 155 160
 Cys Ala Asn Glu Val Trp Gly Ser Asp Asp Ile Thr Gly Arg Val Val
 165 170 175
 Ala Val Gln Gly Val Gly Lys Val Gly Tyr Tyr Leu Cys Glu Tyr Leu
 180 185 190

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

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

Phe Gln Ile Ala Lys Arg Asp Asn Ile Pro Thr Tyr Lys Ala Ala Asp
325 330 335
Arg Met Ala Glu Glu Arg Ile Glu Lys Leu Gly Arg Val Arg Asn Thr
340 345 350

Tyr Leu Gly
355

<210> 309

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 309

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Gln Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

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

340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 310
 <211> 364
 <212> PRT
 <213> Pontibacillus yanchengensis
 <400> 310
 Met Glu Ile Phe Lys Tyr Met Lys Glu Tyr Asp Tyr Glu Gln Leu Val
 1 5 10 15
 Phe Cys Gln Asp Glu Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
 35 40 45
 Ala Ser Glu Asp Glu Ala Ile Glu Asp Ala Leu Arg Leu Ala Lys Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
 65 70 75 80
 Thr Val Ile Ile Gly Asp Pro Lys Thr Glu Lys Asn Glu Glu Met Phe
 85 90 95
 Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Val Gly Thr Thr Val His Asp Met Asp Thr Ile His Glu
 115 120 125
 Glu Thr Asp Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly
 130 135 140
 Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys Ala
 145 150 155 160
 Ala Ala Met Glu Ala Phe Gly Thr Asp Ser Leu Glu Gly Lys Val Ile
 165 170 175
 Ala Val Gln Gly Val Gly Asn Val Ala Tyr Asn Leu Cys Lys His Leu
 180 185 190

His Glu Glu Gly Ala Gln Leu Ile Val Thr Asp Ile Asn Lys Glu Ala
195 200 205
Val Asn Arg Ala Val Glu Asn Phe Gly Ala Lys Ala Val Glu Thr Glu
210 215 220
Glu Ile Tyr Ser Val Asp Cys Asp Ile Tyr Ala Pro Cys Ala Leu Gly
225 230 235 240
Ala Val Ile Asn Asp Glu Thr Ile Pro Gln Ile Lys Ala Lys Val Ile
245 250 255
Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Ser Arg His Gly Asp Leu
260 265 270
Ile His Glu Met Gly Ile Val Tyr Thr Pro Asp Tyr Val Ile Asn Ala
275 280 285
Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Tyr Asp
290 295 300
Arg Ala Met Lys Arg Val Glu Gly Leu Tyr Asp Thr Cys Thr Arg Ile
305 310 315 320
Phe Glu Ile Ala Arg Arg Asp Asn Ile Pro Thr Tyr Met Ala Ala Asp
325 330 335
Arg Met Ala Glu Glu Arg Ile Glu Lys Met Arg Lys Thr Lys Ser Thr
340 345 350
Phe Leu Gln Asn Glu His His Ile Leu Ser Arg Arg
355 360
<210> 311
<211> 366
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 311
Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala

20				25				30							
Ile	His	Asp	Thr	Thr	Leu	Gly	Pro	Ala	Leu	Gly	Gly	Thr	Arg	Met	Trp
35				40				45							
Thr	Tyr	Asp	Ser	Glu	Glu	Ala	Ala	Ile	Glu	Asp	Ala	Leu	Arg	Leu	Ala
50				55				60							
Lys	Gly	Met	Thr	Tyr	Lys	Asn	Ala	Ala	Ala	Gly	Leu	Asn	Leu	Gly	Gly
65				70				75				80			
Ala	Lys	Thr	Val	Ile	Ile	Gly	Asp	Pro	Arg	Lys	Asp	Lys	Ser	Glu	Ala
85				90				95							
Met	Phe	Arg	Ala	Leu	Gly	Arg	Tyr	Ile	Gln	Gly	Leu	Asn	Gly	Arg	Tyr
100				105				110							
Ile	Thr	Ala	Glu	Asp	Val	Gly	Thr	Thr	Val	Asp	Asp	Met	Asp	Ile	Ile
115				120				125							
His	Glu	Glu	Thr	Asp	Phe	Val	Thr	Gly	Ile	Ser	Pro	Ser	Phe	Gly	Ser
130				135				140							
Ser	Gly	Asn	Pro	Ser	Pro	Val	Thr	Ala	Tyr	Gly	Val	Tyr	Arg	Gly	Met
145				150				155				160			
Lys	Ala	Ala	Ala	Lys	Glu	Ala	Phe	Gly	Thr	Asp	Asn	Leu	Glu	Gly	Lys
165				170				175							
Val	Ile	Ala	Val	Gln	Gly	Val	Gly	Asn	Val	Ala	Tyr	His	Leu	Cys	Lys
180				185				190							
His	Leu	His	Ala	Glu	Gly	Ala	Lys	Leu	Ile	Val	Thr	Asp	Ile	Asn	Lys
195				200				205							
Glu	Ala	Val	Gln	Arg	Ala	Val	Glu	Glu	Phe	Gly	Ala	Ser	Ala	Val	Glu
210				215				220							
Pro	Asn	Glu	Ile	Tyr	Gly	Val	Glu	Cys	Asp	Ile	Tyr	Ala	Pro	Cys	Ala
225				230				235				240			
Leu	Gly	Ala	Thr	Val	Asn	Asp	Glu	Thr	Ile	Pro	Gln	Leu	Lys	Ala	Lys
245				250				255							
Val	Ile	Ala	Gly	Ser	Ala	Asn	Asn	Gln	Leu	Lys	Glu	Asp	Arg	His	Gly
260				265				270							

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val His Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 312

<211> 367

<212> PRT

<213> Unknown

<220><223> Flavobacterium sp. Leaf359

<400> 312

Met Ile Thr Glu Val Ala Lys Ala Ser Glu Leu His Lys Ile Asp Pro
1 5 10 15

Val Phe Gly Gln Leu Ser Phe Asp Asn His Glu Gln Ile Val Phe Cys
20 25 30

Asn Asp Lys Asp Thr Gly Leu Lys Ala Ile Ile Gly Ile His Asn Thr

35 40 45

Val Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Lys Tyr Thr Asn
50 55 60

Glu Trp Glu Ala Leu Asn Asp Val Leu Arg Leu Ser Arg Gly Met Thr
65 70 75 80

Phe Lys Ser Ala Ile Ser Gly Leu Asn Leu Gly Gly Gly Lys Ala Val
85 90 95

Ile Ile Gly Asp Ser Lys Val Asp Lys Thr Pro Glu Met Met Ile Lys

100	105	110	
Phe Gly Glu Phe Ile Asn Ser Leu Ser Gly Lys Tyr Ile Thr Ala Glu			
115	120	125	
Asp Val Gly Thr Thr Thr Pro Asp Met Asp Leu Ile Arg Asp Val Thr			
130	135	140	
Pro Tyr Val Thr Gly Ile Ser Gln Ser Arg Gly Gly Ser Gly Asn Pro			
145	150	155	160
Ser Pro Val Thr Ala Tyr Gly Val Tyr Met Gly Met Lys Ala Ala Ala			
165	170	175	
Lys Tyr Gln Phe Gly Ser Asp Asn Leu Glu Gly Lys Lys Ile Leu Val			
180	185	190	
Gln Gly Thr Gly Asn Val Gly Glu Thr Leu Ile Asp His Leu Thr Lys			
195	200	205	
Glu Gly Ala Leu Val Gln Ile Thr Asp Ile Asn Glu Ala Lys Leu Lys			
210	215	220	
Glu Ile Ser Gln Lys Tyr Gly Ala Gln Ile Phe Thr Gly Glu Asp Ile			
225	230	235	240
Tyr Ser Ala Pro Val Asp Ile Tyr Ala Pro Cys Ala Leu Gly Ala Thr			
245	250	255	
Ile Asn Asp Thr Thr Val Asn Lys Ile Gln Ala Lys Val Ile Ala Gly			
260	265	270	
Ala Ala Asn Asn Gln Leu Ala Asn Glu Glu Ile His Gly Lys Ile Leu			
275	280	285	
Lys Asp Arg Gly Ile Ala Tyr Ala Pro Asp Phe Leu Ile Asn Ala Gly			
290	295	300	
Gly Ile Ile Asn Val Tyr Ala Glu Ile Val Gly Tyr Asp Ser Ala Glu			
305	310	315	320
Ala Leu Arg Arg Thr Glu Asn Ile Tyr Asn Thr Thr Leu Glu Ile Phe			
325	330	335	
Asn Phe Ala Glu Thr Asn Ser Ile Thr Thr His Gln Ala Ala Leu Ser			
340	345	350	

Ile Ala Gln Lys Arg Ile Asp Asp Arg Lys Lys Glu Asn Ala Lys

355 360 365

<210> 313

<211> 355

<212> PRT

<213> Desulfosporosinus acidiphilus

<400> 313

Met Lys Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln Leu Val

1 5 10 15

Ile Cys Gln Asp Glu Thr Ser Gly Leu Lys Ala Ile Ile Cys Ile His

20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr

35 40 45

Glu Cys Glu Glu Asp Ala Ile Leu Asp Ala Leu Arg Leu Ala Arg Gly

50 55 60

Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80

Thr Val Ile Ile Gly Asp Ser Arg Thr Gln Lys Ser Glu Glu Leu Phe

85 90 95

Arg Ala Phe Gly Arg Tyr Val Gln Ser Leu Asn Gly Arg Tyr Ile Thr

100 105 110

Ala Glu Asp Val Gly Thr Thr Val Arg Asp Met Asp Trp Val His Leu

115 120 125

Glu Ser Asn Phe Val Thr Gly Val Ser Ser Ser Gly Ala Ser Gly Asp

130 135 140

Pro Ser Pro Met Thr Ala Arg Gly Val Trp Lys Gly Met Lys Ala Ala

145 150 155 160

Ala Lys Glu Met Phe Gly Asp Asp Ser Leu Glu Gly Lys Thr Ile Ala

165 170 175

Ile Gln Gly Leu Gly His Val Gly Tyr Tyr Leu Ala Lys His Leu Arg

180 185 190

Glu Glu Gly Ala Lys Leu Ile Val Thr Asp Ile His Glu Asp Ala Ile
 195 200 205
 Lys Arg Val Leu Asn Glu Met Asp Ala Thr Val Val Glu Pro Glu Glu
 210 215 220
 Ile Phe Gly Val Asp Ala Asp Ile Tyr Ala Pro Cys Ala Met Gly Ala
 225 230 235 240

Val Ile Asn Asp Lys Thr Ile Pro Gln Phe Lys Phe Lys Val Ile Ala
 245 250 255
 Gly Ala Ala Asn Asn Val Leu Leu Glu Asp Arg His Gly Asp Lys Leu
 260 265 270
 His Glu Leu Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly
 275 280 285
 Gly Val Ile Asn Val Ala Asp Glu Leu Glu Gly Tyr Asp Tyr Gln Arg
 290 295 300

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

Leu Arg Lys
 355

<210> 314

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 314

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Val Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

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

275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 315

<211> 356

<212> PRT

<213> Tenericutes bacterium

<400> 315

Met Asn Lys Phe Asp Tyr Met Glu Lys His Gly Tyr Glu Gln Met Val

1 5 10 15
 Tyr Phe Tyr Asp Lys Thr Thr Gly Leu Lys Gly Ile Thr Cys Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Ile Leu Asn Tyr
 35 40 45
 Ala Ser Glu Glu Asp Ala Val Leu Asp Cys Leu Arg Leu Ala Arg Gly
 50 55 60
 Met Thr Tyr Lys Ser Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80
 Thr Val Leu Ile Gly Asp Pro Asn Val Val Lys Asn Glu Ala Tyr Phe
 85 90 95
 Arg Ala Leu Gly Arg Phe Ile Gln Ser Leu Asn Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Val Asn Thr Asn Thr Lys Asp Met Asp Phe Val Ala Met
 115 120 125

Glu Thr Asp His Val Val Gly Leu Glu Ser Lys Ser Gly Asn Pro Ser

130

135

140

Pro Ile Thr Ala Leu Gly Ala Tyr His Gly Ile Arg Ala Ala Ile Lys

145

150

155

160

Phe Ala Phe Gly Asp Asp Asp Val Thr Lys Arg Thr Phe Ala Val Gln

165

170

175

Gly Ala Gly Gln Thr Gly Tyr Tyr Leu Ile Asn Phe Leu Val Glu Asn

180

185

190

Lys Ala Lys Lys Ile Tyr Phe Ser Glu Ile Asn Pro Lys His Val Glu

195

200

205

Arg Met Gln Lys Glu His Pro Glu Val Glu Phe Val Lys Pro Glu Asn

210

215

220

Phe Phe Glu Cys Asp Val Asp Val Ile Cys Pro Cys Ala Leu Gly Ala

225

230

235

240

Val Leu Asn Asp Glu Thr Ile Pro Lys Ile Lys Ala Lys Val Ile Ala

245

250

255

Gly Thr Ala Asn Asn Val Leu Leu Asp Glu Asp Arg His Gly Asn Met

260

265

270

Ile Lys Glu Lys Gly Ile Leu Tyr Ala Pro Asp Phe Val Ile Asn Ala

275

280

285

Gly Gly Val Ile Asn Val Phe Asn Glu Leu Gly Thr Tyr Asn Arg Asp

290

295

300

Lys Val Gln Arg Asp Val Glu Lys Ile Tyr Asp Arg Leu Ile Asp Ile

305

310

315

320

Phe Thr Ile Ala Lys Glu Asp Asn Ile His Thr Gln Glu Ala Ala Lys

325

330

335

Arg Phe Ala Lys Met Arg Met Glu Thr Ile Gly Arg Val Arg Ser Asn

340

345

350

Tyr Val Pro Arg

355

<210> 316

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 316

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210

215

220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

225

230

235

240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

245

250

255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

260

265

270

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

275

280

285

Asn Ala Gly Gly Val Ile Asn Val Asn Asp Glu Leu Tyr Gly Tyr Asn

290

295

300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305

310

315

320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325

330

335

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

340

345

350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355

360

365

<210> 317

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 317

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1

5

10

15

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

20

25

30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35	40	45	
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala			
50	55	60	
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly			
65	70	75	80
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala			
85	90	95	
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr			
100	105	110	
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile			
115	120	125	
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser			
130	135	140	
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met			
145	150	155	160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys			
165	170	175	
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys			
180	185	190	
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys			
195	200	205	
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu			
210	215	220	
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala			
225	230	235	240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys			
245	250	255	
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly			
260	265	270	
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile			
275	280	285	

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

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 318

<211> 348

<212> PRT

<213> Unknown

<220><223> Thalassospira sp. MCCC 1A03138

<400> 318

Met Asn Val Phe Ser Asp Thr Ala Phe Asp Gly His Glu Glu Val Val
 1 5 10 15
 Phe Ala Ser Asp Pro Asp Thr Gly Leu Lys Ala Ile Ile Ala Val His
 20 25 30
 Asn Thr Asn Leu Gly Pro Ser Leu Gly Gly Cys Arg Met Trp Pro Tyr

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

100 105 110
 Ala Glu Asp Val Gly Thr Ser Pro Glu Asp Met Glu Gln Ile Ala Ser
 115 120 125

Gln Thr Lys His Val Gly Gly Ile Asn Asp Gly Lys Asp Pro Ala Arg
130 135 140

Thr Gly Asp Pro Ser Pro Phe Thr Ala Tyr Gly Val Phe Ile Gly Leu
145 150 155 160

Lys Glu Ala Val Arg Phe Lys Asn Gly His Asp Asp Leu Ala Gly Leu
165 170 175

Arg Val Ala Val Gln Gly Leu Gly Asn Val Gly Tyr His Leu Cys Arg
180 185 190

Met Leu His Ser Ala Gly Ala Arg Leu Val Val Ser Asp Leu Asn Ala
195 200 205

Asn Ser Val Asn Arg Ala Val Glu Glu Phe Gly Ala Thr Ala Val Ser
210 215 220

Thr Asp Glu Ile Leu Phe Ile Asp Ala Asp Ile Leu Ala Pro Cys Ala
225 230 235 240

Leu Gly Gly Val Val Asn Asp Arg Ser Ile Asp Lys Ile Arg Ala Arg
245 250 255

Ile Ile Ala Gly Ala Ala Asn Asn Gln Leu Glu Ala Asp Arg His Gly
260 265 270

Glu Met Leu Arg Glu Ala Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Val Glu Val Tyr Tyr Cys Arg Glu Gly Arg Pro
290 295 300

Val Ser Glu Thr Asn Lys His Ile Glu Gly Ile Ala Ala Thr Val Arg
305 310 315 320

Glu Ile Phe Glu Arg Ala Asp Arg Gln Asn Leu Ser Thr Gly Phe Val
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Phe Gly Lys Arg
340 345

<210> 319
<211> 366
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 319

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255

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

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 320

<211> 355

<212> PRT

<213> Peptococcaceae bacterium

<400> 320

Met Thr Thr Phe Glu Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val

1 5 10 15
 Leu Cys Gln Asp Asn Thr Ser Gly Leu Lys Ala Val Ile Cys Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr
 35 40 45
 Ala Ser Glu Glu Asp Ala Ile Leu Asp Ala Leu Arg Leu Ala Arg Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65					70				75				80			
Ala	Val	Ile	Met	Gly	Asp	Ser	Arg	Thr	Gln	Lys	Ser	Glu	Glu	Leu	Phe	
				85				90				95				
Arg	Ala	Phe	Gly	Arg	Tyr	Val	Gln	Ala	Leu	Asn	Gly	Arg	Tyr	Ile	Thr	
				100				105				110				
Ala	Glu	Asp	Val	Gly	Thr	Asn	Val	Gln	Asp	Met	Asp	Trp	Ile	His	Met	
				115				120				125				
Glu	Thr	Lys	Phe	Val	Thr	Gly	Ile	Ser	Ser	Ser	Tyr	Gly	Ala	Ser	Gly	
				130				135				140				
Asp	Pro	Ser	Pro	Leu	Thr	Ala	Leu	Gly	Val	Tyr	Arg	Gly	Met	Lys	Ala	
145				150				155				160				
Ala	Ala	Lys	Glu	Ala	Phe	Gly	Ser	Asp	Ser	Leu	Glu	Gly	Lys	Thr	Val	
				165				170				175				
Ala	Ile	Gln	Gly	Leu	Gly	His	Val	Gly	Tyr	Tyr	Leu	Ala	Lys	His	Leu	
				180				185				190				
Thr	Asp	Glu	Gly	Ala	Lys	Leu	Ile	Val	Thr	Asp	Ile	Asn	Ser	Glu	Ala	
				195				200				205				
Val	Lys	Arg	Val	Ala	Arg	Glu	Phe	Val	Ala	Thr	Ala	Val	Arg	Thr	Glu	
210				215				220								
Glu	Ile	Phe	Gly	Val	Lys	Cys	Asp	Ile	Phe	Ala	Pro	Cys	Ala	Leu	Gly	
225				230				235				240				
Ala	Val	Ile	Asn	Asp	Glu	Thr	Ile	Pro	Gln	Leu	Lys	Cys	Gln	Val	Val	
				245				250				255				
Ala	Gly	Ala	Ala	Asn	Asn	Val	Leu	Lys	Glu	Asp	Arg	His	Gly	Asp	Glu	
				260				265				270				
Leu	Tyr	Glu	Lys	Gly	Ile	Leu	Tyr	Ala	Pro	Asp	Tyr	Val	Ile	Asn	Ala	
275				280				285								
Gly	Gly	Val	Ile	Asn	Val	Ala	Asp	Glu	Leu	Glu	Gly	Tyr	Asn	Ala	Glu	
290				295				300								
Arg	Ala	Leu	Lys	Lys	Val	Glu	Met	Val	Tyr	Asp	Asn	Val	Ala	Arg	Val	
305				310				315				320				

Ile Ala Ile Ala Lys Arg Asp His Ile Pro Thr Tyr Lys Ala Ala Asp

325 330 335

Arg Met Ala Glu Glu Arg Ile Ala Lys Ile Gly Lys Val Ser Asn Thr

340 345 350

Phe Leu Arg

355

<210> 321

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 321

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Ala Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile

 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg

 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 322
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide

<400> 322

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Thr Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285

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

 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 323
 <211> 364
 <212> PRT
 <213> *Salinicoccus halodurans*
 <400> 323
 Met Ile Phe Asp Lys Met Val Glu Phe Asp Tyr Glu Gln Leu Val Phe
 1 5 10 15
 Cys His Asp Glu Thr Ser Gly Leu Lys Ala Ile Ile Cys Ile His Asp
 20 25 30
 Thr Thr Leu Gly Pro Ala Leu Gly Gly Cys Arg Met Trp Asn Tyr Glu
 35 40 45
 Thr Glu Glu Glu Ala Ile Glu Asp Val Leu Arg Leu Ala Arg Gly Met
 50 55 60
 Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys Thr
 65 70 75 80
 Val Val Ile Gly Asp Ala Lys Lys Asp Lys Ser Glu Ala Phe Phe Arg

85 90 95
Ala Leu Gly Arg Tyr Val Asn Ser Leu Asn Gly Arg Tyr Ile Thr Ala

100 105 110
Glu Asp Val Gly Thr Thr Val Ala Asp Met Asp Leu Ile Tyr Gln Glu

115 120 125
Thr Pro Tyr Val Cys Gly Met Ser Glu Ser Tyr Gly Thr Gly Gly Asn

130 135 140
Pro Ser Pro Met Thr Ala Phe Gly Val Tyr Met Ala Met Lys Arg Thr

145 150 155 160
Ala Lys Glu Ala Phe Asp Asp Asp Ser Leu Glu Gly Arg Thr Ile Ala

165 170 175
Val Gln Gly Val Gly Asn Val Ser Tyr Ser Leu Cys Arg His Leu His

180 185 190
Glu Glu Gly Ala Lys Leu Val Val Thr Asp Ile Ser Gln Glu Ala Ile

195 200 205
Asp Arg Ala Val Asn Asp Phe Gly Ala Lys Ala Val Gly Ile Glu Glu

210 215 220
Ile Tyr Asp Val Glu Ala Asp Ile Phe Ala Pro Cys Ala Leu Gly Gly

225 230 235 240
Val Leu Asn Asp Glu Thr Ile Pro Ala Leu Lys Val Lys Ala Val Cys

245 250 255
Gly Ser Ala Asn Asn Gln Leu Leu Glu Glu Asp Lys His Gly Glu Leu

260 265 270
Leu Gln Gln Arg Gly Ile Val Tyr Ala Pro Asp Tyr Val Val Asn Cys

275 280 285
Gly Gly Val Ile Asn Val Ala Asp Glu Leu Gln Gly Tyr Asn Lys Glu

290 295 300
Arg Ala Lys Ser Lys Val Glu Gly Ile Tyr Asp Gln Met Asp Lys Ile

305 310 315 320
Phe Asn Ile Ala Arg Arg Asp Arg Ile Thr Pro Ala Val Ala Ala Asp

325 330 335

Arg Leu Ala Glu Glu Arg Ile Glu Ser Met Met Arg Val Lys Ser Thr
340 345 350

Phe Ser Gln Asn Glu Ile Thr Pro Leu Ser Arg Arg

355 360

<210> 324

<211> 374

<212> PRT

<213> *Exiguobacterium antarcticum*

<400> 324

Met Val Glu Thr Asn Val Glu Ala Arg Phe Ser Ile Phe Glu Thr Met
1 5 10 15

Ala Met Glu Asp Tyr Glu Gln Val Val Phe Cys His Asp Lys Val Ser
20 25 30

Gly Leu Lys Ala Ile Ile Ala Ile His Asp Thr Thr Leu Gly Pro Ala
35 40 45

Leu Gly Gly Leu Arg Met Trp Asn Tyr Ala Ser Asp Glu Glu Ala Leu
50 55 60

Ile Asp Ala Leu Arg Leu Ala Lys Gly Met Thr Tyr Lys Asn Ala Ala
65 70 75 80

Ala Gly Leu Asn Leu Gly Gly Gly Lys Ala Val Ile Ile Gly Asp Ala
85 90 95

Lys Thr Gln Lys Ser Glu Ala Leu Phe Arg Ala Phe Gly Arg Tyr Val
100 105 110

Gln Ser Leu Asn Gly Arg Tyr Ile Thr Ala Glu Asp Val Asn Thr Thr
115 120 125

Val Ala Asp Met Asp Tyr Ile His Met Glu Thr Asp Phe Val Thr Gly
130 135 140

Val Ser Pro Ala Phe Gly Ser Ser Gly Asn Pro Ser Pro Val Thr Ala
145 150 155 160

Tyr Gly Val Tyr Arg Gly Met Lys Ala Ala Ala Lys Glu Val Tyr Gly
165 170 175

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

Asp Ile Phe Ala Pro Cys Ala Leu Gly Ala Thr Leu Asn Asp Glu Thr
245 250 255
Ile Pro Gln Leu Lys Val Lys Ile Ile Ala Gly Ala Ala Asn Asn Gln
260 265 270
Leu Lys Glu Asp Arg His Gly Asp Met Leu Gln Glu Arg Gly Ile Leu
275 280 285
Tyr Ala Pro Asp Phe Val Ile Asn Ala Gly Gly Val Ile Asn Val Ala
290 295 300

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

Ile Leu Gly Ser Arg Gly
370

<210> 325

<211> 386

<212> PRT

<213> Unknown

<220><223> Streptomyces sp. CB03911

<400> 325

Met Thr Asp Val Gln Thr Ala Ser Ala Thr His Pro Ala Pro Gly Val
1 5 10 15
Leu Ser Arg Ile Phe Arg Thr Glu Gln Asp Gly Ala Pro Gly Asp Gly
20 25 30
His Glu Gln Val Val Leu Cys His Asp Arg Ser Ser Gly Leu Lys Ala
35 40 45
Ile Ile Ala Ile His Ser Thr Ala Leu Gly Pro Ala Leu Gly Gly Thr
50 55 60
Arg Phe Phe Pro Tyr Leu Thr Glu Glu Glu Ala Leu Glu Asp Ala Leu
65 70 75 80
Arg Leu Ser Arg Gly Met Ser Tyr Lys Asn Ala Leu Ala Gly Leu Asp
85 90 95
Leu Gly Gly Gly Lys Ala Val Ile Ile Gly Asp Pro Gly Lys Asp Lys
100 105 110
Asn Glu Ala Met Leu Arg Ala Tyr Gly Arg Phe Val Glu Ser Leu Arg
115 120 125
Gly Arg Tyr Val Thr Ala Cys Asp Val Gly Thr Tyr Val Gln Asp Met
130 135 140
Asp Val Ile Ala Arg Glu Thr Thr Phe Val Thr Gly Arg Ser Pro Glu
145 150 155 160
His Gly Gly Ala Gly Asp Ser Ser Ile Leu Thr Ala Phe Gly Val Phe
165 170 175
Gln Gly Met Arg Ala Ser Ala Gln Ala Arg Trp Gly Gln Pro Thr Leu
180 185 190
Arg Gly Arg Arg Val Gly Val Ser Gly Val Gly Lys Val Gly His Tyr
195 200 205
Leu Val Gly His Leu Val Ala Asp Gly Ala His Val Val Val Thr Asp
210 215 220
Val Ser Glu Ala Ala Val Asn Arg Val Arg Ala Ala His Pro Asp Val
225 230 235 240
Glu Val Val Ala Asp Thr Ala Ala Leu Leu Ala Ala Ala Leu Asp Val

245 250 255
Tyr Ala Pro Cys Ala Leu Gly Gly Ala Leu Asp Asp His Thr Val Gly
260 265 270
Ala Leu Gly Ala Ala Gly Thr Ser Leu Val Cys Gly Ala Ala Asn Asn
275 280 285
Gln Leu Ala His Pro Gly Val Glu Lys Asp Leu Ala Asp Arg Gly Ile
290 295 300

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

Met Arg Glu Ile Ser Ser Leu Arg Thr Ile Leu Leu Pro Gly Ala Arg
370 375 380

Gly Asn

385

<210> 326

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 326

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95

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

 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220

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

 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Asn Tyr Gly Tyr Asn
 290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 327

<211> 365

<212> PRT

<213> Bacillus loiseleuriae

<400> 327

Met Glu Ile Phe Thr Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln Leu Leu
 1 5 10 15
 Phe Cys Gln Asp Lys Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr

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

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

145 150 155 160
Ala Ala Lys Glu Ala Phe Gly Thr Asp Ser Leu Glu Gly Lys Thr Val

 165 170 175
Ala Val Gln Gly Ile Gly Asn Val Ala Phe Thr Leu Leu Gln Tyr Leu

 180 185 190
His Glu Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys Glu Ala

 195 200 205
Val Gln Arg Ala Val Glu Lys Phe Gly Ala Arg Ala Val Asn Thr Asp

 210 215 220
Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala Leu Gly

225 230 235 240
Ala Val Ile Asn Asp Gln Thr Ile Ser Gln Ile Lys Ala Lys Val Ile

 245 250 255
Ala Gly Ser Ala Asn Asn Gln Leu Lys Asp Pro Arg His Gly Asp Gln

 260 265 270
Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala

 275 280 285
Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Arg Glu

 290 295 300
Arg Ala Met Lys Lys Val Glu Gly Val Tyr Asn Thr Ile Glu Lys Val

305 310 315 320
Ile Glu Ile Ala Lys Arg Asp Gly Ile Pro Thr Tyr Leu Ala Ala Asp

 325 330 335
Arg Met Ala Glu Glu Arg Ile Lys Arg Met Arg Asn Ser Arg Ser Gln

 340 345 350
Phe Leu Gln Asn Glu Lys His Ile Leu Asn Arg Arg Lys

 355 360 365

<210> 328

<211> 365

<212> PRT

<213> Brochothrix campestris

<400> 328

Met Leu Phe Glu Thr Met Val Gln Asp Gly Tyr Glu Gln Val Val Phe
1 5 10 15

Cys His Asp Lys Ala Ser Gly Leu Lys Ala Ile Ile Ala Ile His Asp
20 25 30

Thr Thr Leu Gly Pro Ala Leu Gly Gly Cys Arg Met Trp Pro Tyr Ala
35 40 45

Thr Glu Glu Glu Ala Leu His Asp Val Leu Arg Leu Ser Arg Gly Met
50 55 60

Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Ile Gly Gly Gly Lys Thr
65 70 75 80

Val Ile Ile Gly Asp Pro Arg Thr Asp Lys Ser Glu Thr Leu Phe Arg
85 90 95

Ala Leu Gly Arg Tyr Val Glu Ser Leu Asn Gly Arg Tyr Ile Ile Ala
100 105 110

Glu Asp Val Gly Thr Thr Glu Asp Asp Met Asn Phe Ile Tyr Asn Glu
115 120 125

Thr Asn Tyr Val Thr Gly Ser Thr Ala Gly Ala Gly Ser Ser Gly Asn
130 135 140

Pro Ser Pro Lys Thr Ala Leu Gly Ile Tyr Tyr Ala Met Lys Arg Thr
145 150 155 160

Ala Lys Glu Val Phe Gly Ser Asp Ser Leu Ala Asp Lys Lys Val Ser
165 170 175

Val Gln Gly Val Gly Asn Val Ser Tyr Thr Leu Cys Glu Leu Leu His
180 185 190

Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Glu Val Ala Val
195 200 205

Ala Arg Ala Val Thr Asn Leu Asn Ala Thr Ala Val Gly Ile Asp Glu
210 215 220

Ile Tyr Asp Val Asp Ala Asp Ile Phe Ala Pro Cys Ala Leu Gly Ala
225 230 235 240

Ile Leu Asn Asp Asp Thr Ile Gln Arg Leu Arg Val Lys Ala Ile Cys
245 250 255

Gly Ser Ala Asn Asn Gln Leu Met Asp Leu Glu Lys His Gly Gln Met
260 265 270

Leu Glu Ala Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Ile Val Asn Ser
275 280 285

Gly Gly Val Ile Asn Val Ala Asp Glu Leu Ser Gly Tyr Asn Glu Ala
290 295 300

Arg Ala Ile Lys Gln Val Lys Glu Ile Tyr Asn Gln Ile Gly Lys Val
305 310 315 320

Phe Glu Ile Ala Lys Thr Lys Asn Ile Ile Pro Ala Ile Ala Ala Asp
325 330 335

Glu Leu Ala Glu Gln Arg Ile Ala Gln Val Lys Ala Met Arg Ser Asn
340 345 350

Phe Leu Gln Thr Glu His Ser Ser Ile Ser Arg Lys Ser
355 360 365

<210> 329

<211> 357

<212> PRT

<213> Acetonema longum

<400> 329

Met Gly Ile Phe Glu Lys Met Glu Gln His Gly Tyr Glu Gln Leu Val
1 5 10 15

Phe Cys His Asp Pro Ala Ser Gly Leu Lys Ala Ile Ile Cys Ile His
20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Pro Tyr
35 40 45

Glu Cys Glu Glu Asp Ala Ile Thr Asp Val Val Arg Leu Ala Arg Gly
50 55 60

Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
65 70 75 80

Ala Val Ile Ile Gly Asn Ser Arg Thr Asp Lys Ser Glu Ala Leu Phe

85 90 95
 Arg Ala Phe Gly Arg Phe Val Gln Ser Leu Asn Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Glu His Ile Arg Met

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

 180 185 190
 Tyr Glu Glu Gly Ala Asn Leu Ile Val Thr Asp Ile Asn Glu Glu Asn
 195 200 205
 Val Arg Arg Val Val Ala Glu Phe Gly Ala Arg Ser Ala Ala Pro Asp
 210 215 220
 Glu Ile Tyr Gly Val Glu Cys Asp Ile Phe Ala Pro Cys Ala Leu Gly
 225 230 235 240
 Ala Ile Ile Asn Asp Ala Thr Leu Pro Arg Leu Lys Cys Arg Ile Val

 245 250 255
 Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Ala Arg His Gly Glu Leu
 260 265 270
 Leu Arg Asp Lys Lys Ile Leu Tyr Ala Pro Asp Phe Ile Ile Asn Ala
 275 280 285
 Gly Gly Val Ile Asn Val Ser Asp Glu Leu Arg Glu Gly Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Gln Val Asp Gly Ile Tyr Asp Ile Met Glu

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

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

340

345

350

Lys Thr Leu Leu Pro

355

<210> 330

<211> 378

<212> PRT

<213> Streptomyces rubidus

<400> 330

Met Gly Val Thr Thr Val Thr Asp Val Arg Gln Thr Ser Pro Ser Asn

1

5

10

15

Glu Gly Val Leu Ala Lys Leu Phe Arg Ser Glu Gln Gly Gly His Glu

20

25

30

Gln Val Val Leu Cys Gln Asp Arg Ala Thr Gly Leu Lys Ala Val Ile

35

40

45

Ala Val His Ser Thr Ala Leu Gly Pro Ala Leu Gly Gly Thr Arg Phe

50

55

60

Phe Pro Tyr Ala Ser Asp Glu Glu Ala Val Asp Asp Ala Leu Asn Leu

65

70

75

80

Ala Arg Gly Met Ser Tyr Lys Asn Ala Leu Ala Gly Leu Asp Leu Gly

85

90

95

Gly Gly Lys Ala Val Ile Ile Gly Asp Pro Asp Thr Leu Lys Ser Glu

100

105

110

Glu Leu Leu Leu Ala Tyr Gly Arg Phe Val Ala Ser Leu Gly Gly Arg

115

120

125

Tyr Val Thr Ala Cys Asp Val Gly Thr Tyr Val Ser Asp Met Asp Val

130

135

140

Ile Ala Arg Glu Asn Arg Trp Thr Thr Gly Arg Ser Pro Gln Asn Gly

145

150

155

160

Gly Ala Gly Asp Ser Ser Val Leu Thr Ala Phe Gly Val Phe Gln Gly

165

170

175

Met Arg Ala Ala Ala Gln Ala Gln Trp Gly Glu Ser Thr Leu Lys Gly

180 185 190
Arg Arg Val Gly Val Ala Gly Val Gly Lys Val Gly His His Leu Val

195 200 205
Glu His Leu Val Glu Asp Gly Ala Glu Val Val Ile Thr Asp Val Arg

210 215 220
Ala Glu Ala Val Glu Arg Ile Ile Ala Arg His Pro Asp Val Thr Ala

225 230 235 240
Val His Asp Ala Glu Val Leu Val Arg Ser Pro Leu Asp Val Tyr Ala

245 250 255
Pro Cys Ala Leu Gly His Ala Leu Asp Asp Ala Thr Val Gly Ala Leu

260 265 270
Thr Ala Thr Val Val Cys Gly Ala Ala Asn Asn Gln Leu Ala His Pro

275 280 285
Gly Val Glu Lys Asp Leu Ala Asp Arg Gly Ile Leu Tyr Ala Pro Asp

290 295 300
Tyr Val Val Asn Ala Gly Gly Val Ile Gln Val Ala Asp Glu Leu His

305 310 315 320
Gly Phe Asp Phe Asp Arg Ala Lys Ala Lys Ala Thr Lys Ile Phe Asp

325 330 335
Thr Thr Leu Ala Ile Phe Ala Arg Ala Lys Ala Asp Gly Val Pro Pro

340 345 350
Ala Val Ala Ala Asp Arg Leu Ala Glu Gln Arg Met Ala Glu Arg Thr

355 360 365
Pro Ala Ala Asp Trp Leu Arg Val Gln Ser

370 375

<210> 331

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 331

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Thr Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

260 265 270

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

275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335

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

340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 332

<211> 369

<212> PRT

<213> Halobacteriovorax marinus

<400> 332

Met Met Ser Phe Glu Arg Leu Tyr Lys Asp Gly His Glu Glu Val Ile

1 5 10 15

Phe Phe Ser Asp Pro Ser Cys Asn Leu Lys Ala Ile Val Ala Ile His

20 25 30

Asn Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Pro Tyr

35 40 45

Ala Ser Glu Glu Glu Ala Ile Asn Asp Val Leu Arg Leu Ser Lys Gly

50 55 60

Met Thr Tyr Lys Ala Ala Val Ser Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80

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

85 90 95
 Arg Ser Tyr Gly Arg Phe Leu Glu Ser Leu Asn Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Val Asn Ile Gly Val Gln Asp Ile Glu His Val Phe Thr
 115 120 125
 Glu Thr Gly Asn Val Cys Gly Val Ala Lys Ile His Gly Gly Ser Gly

 130 135 140
 Asn Pro Ser Pro Tyr Thr Ala Lys Gly Val Phe Arg Gly Ile Glu Ala
 145 150 155 160
 Ala Cys Met Lys Val Tyr Gly Asp Arg Ser Pro Lys Gly Lys Thr Val
 165 170 175
 Ala Leu Gln Gly Ala Gly Ser Val Gly Arg Tyr Leu Ala Lys Phe Leu
 180 185 190
 Asp Glu Ala Gly Ala Lys Val Val Val Cys Asp Ile Asn Glu Arg Asn

 195 200 205
 Ile Gln Leu Leu Lys Glu Ala Val Pro Ala Val Glu Val Val Gly Val
 210 215 220
 Asn Asp Ile Tyr Asp Val Asp Cys Asp Ile Tyr Ala Pro Cys Ala Leu
 225 230 235 240
 Gly Ala Thr Val Asn Asp Asp Thr Ile Asp Arg Leu Lys Cys Lys Ile
 245 250 255
 Val Ala Gly Ala Ala Asn Asn Gln Leu Ala Glu Asp Arg His Gly Glu

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

 325 330 335

Asp Val Leu Ala Glu Ser Arg Ile Glu Ser Ile Arg Asn Ile Asn Gly
340 345 350

Lys Tyr Leu Gly Asn Leu Gly His Arg Phe Pro Gly Arg Lys Thr Arg
355 360 365

Asn

<210> 333

<211> 365

<212> PRT

<213> Unknown

<220><223> Bacillus sp. FJAT-27916

<400> 333

Met Glu Leu Phe Lys Tyr Met Glu Gln Tyr Asp Tyr Glu Gln Leu Leu

1 5 10 15
Phe Val Gln Asp Arg Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His

20 25 30
Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr

35 40 45
Glu Ser Glu Asp Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala Lys Gly

50 55 60
Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80
Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Asn Glu Glu Met Phe

85 90 95
Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr

100 105 110
Ala Glu Asp Val Gly Thr Thr Val Ala Asp Met Asp Ile Ile His Glu

115 120 125
Glu Thr Asp Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly

130 135 140
Asn Pro Ser Pro Val Thr Ala Phe Gly Val Tyr Arg Gly Met Lys Ala

145 150 155 160

Ala Ala Lys Glu Ala Phe Gly Thr Asp Ser Leu Glu Gly Lys Val Ile
165 170 175

Ala Val Gln Gly Val Gly Asn Val Ala Phe Asn Leu Cys Lys His Leu
180 185 190

His Glu Glu Gly Ala Gln Leu Ile Val Thr Asp Ile Asn Lys Asp Ser
195 200 205

Val Gln Met Ala Val Glu Gln Phe Gly Ala Lys Ala Val Asp Pro Asn
210 215 220

Glu Ile Tyr Gly Val Asp Cys Asp Ile Tyr Ala Pro Cys Ala Leu Gly
225 230 235 240

Ala Thr Ile Asn Asp Tyr Thr Ile Pro Gln Leu Lys Ala Lys Val Ile
245 250 255

Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Thr Arg His Gly Asp Ala
260 265 270

Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala
275 280 285

Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Gln Glu
290 295 300

Arg Ala Leu Lys Lys Val Glu Leu Ile Tyr Asn Asn Ile Glu Arg Val
305 310 315 320

Ile Glu Ile Ala Lys Arg Asp Gly Ile Pro Thr Tyr Met Ala Ala Asp
325 330 335

Arg Met Ala Glu Glu Arg Ile Glu Lys Leu Lys Asn Ser Arg Ser Gln
340 345 350

Phe Leu Met Asn Gly Arg His Ile Leu Asn Arg Arg Arg
355 360 365

<210> 334

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 334

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Asn Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 335

<211> 372

<212> PRT

<213> Bdellovibrionales bacterium

<400> 335

Met Pro Thr Leu Glu Lys Met Tyr Ser Met Gly His Glu Glu Val Val
1 5 10 15

Phe Tyr Ala Asp Pro Thr Cys Asn Leu Arg Ala Ile Val Ala Ile His

20 25 30
Asn Thr Ile Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Pro Tyr

35 40 45
Lys Ser Glu Asp Glu Ala Leu Glu Asp Val Leu Arg Leu Ser Lys Gly

50 55 60
Met Thr Tyr Lys Ala Ser Val Ser Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80
Ala Val Ile Ile Gly Asp Pro Glu Lys Asp Lys Ser Glu Ala Leu Phe

85	90	95	
Arg Ser Phe Gly Arg Leu Val Glu Ser Leu Asn Gly Arg Tyr Ile Thr			
100	105	110	
Ala Glu Asp Val Asn Ile Lys Val Glu Asp Ile Glu His Ile Phe Thr			
115	120	125	
Glu Thr Asn Asn Val Cys Gly Val Ala Ile Pro His Gly Gly Ser Gly			
130	135	140	
Asn Pro Ala Pro Tyr Thr Ala Leu Gly Val Phe Lys Gly Ile Glu Ala			
145	150	155	160
Ser Cys Leu Lys Leu Tyr Gly Asp Arg Ser Val Lys Gly Lys Val Val			
165	170	175	
Ala Leu Gln Gly Ala Gly Phe Val Gly Arg His Leu Gly Glu Leu Leu			
180	185	190	
Ser Gln Ala Gly Ala Lys Val Tyr Val Ala Asp Ile Asn Glu Lys Asn			
195	200	205	
Ile Lys Leu Phe Leu Glu Met Val Pro Asn Ala Glu Val Val Ala Ala			
210	215	220	
Asp Ala Ile Tyr Gly Val Lys Cys Asp Ile Tyr Ala Pro Cys Ala Leu			
225	230	235	240
Gly Ala Thr Val Asn Asp Gln Thr Val Glu Lys Leu Lys Cys Lys Ile			
245	250	255	
Val Ala Gly Ala Ala Asn Asn Gln Leu Ala Glu Pro Arg His Gly Asp			
260	265	270	
Ile Leu Arg Ser Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Leu Ile Asn			
275	280	285	
Ala Gly Gly Leu Met Asn Val Ser Ile Glu Phe Glu Gly Trp Ser Asp			
290	295	300	
Ser Lys Ala Arg Arg Met Val Asp Thr Ile Tyr Asp Thr Thr Leu Glu			
305	310	315	320
Ile Phe Arg Ile Ala Asp Lys Asn Asn Ile Thr Thr Tyr Lys Ala Ala			
325	330	335	

Asp Met Trp Ala Glu Asn Arg Ile Glu Ser Ile Arg Arg Ile Gly Ser

340 345 350

Arg Tyr Met Gly Val Ser Gln His Arg Phe Pro Gly Arg Lys Arg Arg

355 360 365

Asn Pro Asn Gly

370

<210> 336

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 336

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Lys Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile

 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg

 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 337
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide

<400> 337

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Ser Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285

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

 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 338
 <211> 345
 <212> PRT
 <213> Colwellia psychrerythraea
 <400> 338
 Met Ala Leu Phe Asp Leu Pro Asp Phe Asp Asp His Glu Gln Val Val
 1 5 10 15
 Tyr Cys Ser Asp Glu Ala Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Ser Thr Lys Leu Gly Ala Ala Val Gly Gly Cys Arg Met Trp Asp Tyr
 35 40 45
 Ala Asp Asp Asp Glu Ala Leu Val Asp Val Leu Arg Leu Ser Lys Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Met Ala Gly Leu Ser Met Gly Gly Gly Lys
 65 70 75 80
 Ser Val Ile Ile Gly Asp Ala Lys Lys Leu Lys Ser Lys Ala Leu Phe

85 90 95
Lys Ala Phe Gly Glu Ala Leu Asn Arg Leu Asn Gly Arg Tyr Leu Ser

100 105 110
Ala Glu Asp Val Asn Ile Thr Thr Ser Asp Ile Asp Ile Thr Asn Ser

115 120 125
Val Thr Pro Phe Val Thr Gly Thr Glu Gly Lys Ser Gly Asn Pro Ala

130 135 140
Pro Phe Thr Ala Leu Gly Thr Phe Leu Gly Ile Lys Ala Ser Val Lys

145 150 155 160
His Lys Leu Asn Arg Asp Asp Leu Thr Gly Leu Lys Val Ala Ile Gln

165 170 175
Gly Leu Gly Ser Val Gly Tyr Gln Leu Cys Asp His Leu His Gln Ala

180 185 190
Gly Ala Glu Leu Val Ile Thr Asp Ile Asn Gln Thr Ala Leu Asp Met

195 200 205
Ala Ala Thr Glu Phe Asn Ala Thr Ile Val Gly Leu Asp Glu Ile Tyr

210 215 220
Asp Gln Glu Val Asp Ile Tyr Ala Pro Cys Ala Leu Gly Ala Thr Ile

225 230 235 240
Asn Asp Asp Thr Leu Asn Arg Leu Lys Ala Ser Ile Ile Ala Gly Cys

245 250 255
Ala Asn Asn Gln Leu Ala Glu Pro Arg His Asp Gln Ala Leu Val Glu

260 265 270
Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly Ile

275 280 285
Ile Asn Ile Ser Phe Glu His Asn Tyr Asp Cys Glu Lys Ala Thr Glu

290 295 300
Lys Val Gly Asp Ile Tyr His Thr Leu Leu Asp Ile Tyr Ala Lys Ala

305 310 315 320
Asp Ala Gln Asn Arg Pro Thr Gly Ile Ile Ala Asp Glu Met Ala Arg

325 330 335

Glu Ile Ile Lys Asn Gly Gly Lys Ala

340

345

<210> 339

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<

400> 339

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1

5

10

15

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

20

25

30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35

40

45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50

55

60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65

70

75

80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85

90

95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100

105

110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115

120

125

His Glu Glu Thr Asp Phe Val Phe Gly Ile Ser Pro Ser Phe Gly Ser

130

135

140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145

150

155

160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165

170

175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

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

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

 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 340
 <211> 364
 <212> PRT
 <213> Unknown
 <220><223> Bacillus sp. 1NLA3E
 <400> 340
 Met Gly Ile Phe Glu Asn Leu Glu Ile Tyr Asp Tyr Glu Gln Leu Val

Phe Cys Gln Asp Lys Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
 35 40 45
 Ser Ser Glu Asp Asp Ala Ile Glu Asp Ala Leu Arg Leu Ala Arg Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

 65 70 75 80
 Thr Val Ile Ile Gly Asp Pro Arg Arg Asp Lys Asn Glu Glu Met Phe
 85 90 95
 Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Val Gly Thr Thr Val Ala Asp Met Asp Leu Ile His Glu
 115 120 125
 Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly

 130 135 140
 Asn Pro Ser Pro Ala Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys Ala
 145 150 155 160
 Ala Ala Lys Glu Ala Phe Gly Thr Asp Ser Leu Glu Gly Lys Val Val
 165 170 175
 Ala Ile Gln Gly Val Gly Asn Val Ala Ile Asn Leu Cys Lys His Leu
 180 185 190
 Arg Gly Glu Gly Ala Glu Leu Ile Val Thr Asp Ile His Lys Glu Ser

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

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

325 330 335
 Arg Leu Ala Glu Glu Arg Ile Ala Arg Ile Arg Asn Ser Arg Ser Gln
 340 345 350
 Phe Leu Leu Asn Gly His His Ile Leu Ser Arg Arg

355 360
 <210> 341
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 341

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Gln Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100	105	110
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile		
115	120	125
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser		
130	135	140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met		
145	150	155
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys		
165	170	175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys		
180	185	190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys		
195	200	205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu		
210	215	220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala		
225	230	235
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys		
245	250	255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly		
260	265	270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile		
275	280	285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn		
290	295	300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala		
305	310	315
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala		
325	330	335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg		
340	345	350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 342
<211> 373
<212> PRT
<213> Unknown
<220><223> Exiguobacterium sp.
<400> 342

Met Met Glu Thr Asn Thr Glu Pro Arg Phe Arg Ile Phe Asp Val Leu
1 5 10 15
Gln Ser Glu Asp Tyr Glu Gln Ile Val Phe Cys Gln Asp Gln Ala Ser
20 25 30
Gly Leu Lys Ala Ile Ile Ala Ile His Asp Thr Thr Leu Gly Pro Ala
35 40 45
Leu Gly Gly Leu Arg Met Trp Asn Tyr Glu Ser Glu Gln Glu Ala Leu
50 55 60
Thr Asp Val Leu Arg Leu Ala Lys Gly Met Thr Tyr Lys Asn Ala Ala
65 70 75 80
Ala Gly Leu Asn Leu Gly Gly Gly Lys Ala Val Ile Ile Gly Asn Ala
85 90 95
Lys Thr Asp Lys Ser Glu Ala Leu Phe Arg Ala Phe Gly Arg Tyr Val
100 105 110
Gln Ser Leu Ser Gly Arg Tyr Ile Thr Ala Glu Asp Val Asn Thr Thr
115 120 125
Val Ala Asp Met Asp Phe Ile His Met Glu Thr Asp Tyr Val Thr Gly
130 135 140
Val Ser Pro Ala Phe Gly Ser Ser Gly Asn Pro Ser Pro Val Thr Ala
145 150 155 160
Tyr Gly Val Tyr Arg Gly Met Lys Ala Ala Ala Lys Trp Lys Phe Gly
165 170 175
Thr Asp Ser Leu Ala Gly Lys Thr Val Ala Val Gln Gly Val Gly Asn
180 185 190

Val Ala Tyr Asn Leu Cys Arg His Leu His Glu Glu Gly Ala His Leu
195 200 205

Ile Val Thr Asp Ile Asn Glu Glu Ala Leu Lys Arg Ala Glu Ala Asp
210 215 220

Phe Gly Ala Thr Val Val Lys Pro Asp Glu Ile Tyr Ala Val Glu Cys
225 230 235 240

Asp Ile Phe Ala Pro Cys Ala Leu Gly Ala Val Ile Asn Asp Lys Thr
245 250 255

Ile Pro Gln Leu Lys Ala Gln Ile Val Ala Gly Ala Ala Asn Asn Gln
260 265 270

Leu Ala Glu Asp Arg His Gly Asp Val Leu Asp Glu Asn Gly Ile Leu
275 280 285

Tyr Ala Pro Asp Phe Val Ile Asn Ala Gly Gly Val Ile Asn Val Ala
290 295 300

Asp Glu Leu Glu Gly Tyr Asn Arg Glu Arg Ala Met Lys Lys Val Glu
305 310 315 320

Leu Ile Tyr Asp Asn Met Met Arg Val Phe Glu Ile Ala Glu Arg Asp
325 330 335

Gly Val Pro Thr His Val Ala Ala Asp Lys Met Ala Glu Glu Arg Ile
340 345 350

His Met Met Ser Arg Ser Arg Ser Gln Phe Leu Lys Val Glu Lys Ser
355 360 365

Ile Leu Gly Arg Arg
370

<210> 343
<211> 366
<212> PRT
<213> Marininema halotolerans
<400> 343

Met Gln Leu Phe Asp Tyr Leu Ser Lys Tyr Asp Tyr Glu Gln Leu Ile
1 5 10 15

Phe Cys Gln Asp Glu Asn Ser Gly Leu Lys Ala Ile Ile Ala Ile His

20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr

35 40 45

Ala Ser Glu Glu Asp Ala Ile Val Asp Ala Leu Arg Leu Ala Arg Gly

50 55 60

Met Thr Tyr Lys Asn Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80

Thr Val Ile Ile Gly Asp Pro Lys Thr Asp Lys Asn Glu Ala Met Phe

85 90 95

Arg Ala Phe Gly Arg Phe Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr

100 105 110

Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Leu Ile His Glu

115 120 125

Glu Thr Arg Phe Val Thr Gly Ile Ser Pro Glu Phe Gly Ser Ser Gly

130 135 140

Asn Pro Ser Pro Val Thr Ala Tyr Gly Cys Tyr Met Gly Met Lys Ala

145 150 155 160

Ala Ala Lys Glu Ala Phe Gly Asp Asp Ser Leu Glu Gly Arg Thr Val

165 170 175

Ala Val Gln Gly Val Gly Ser Val Ala Tyr His Leu Cys Lys Tyr Leu

180 185 190

His Asp Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Gln Glu Asn

195 200 205

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

210 215 220

Ser Ile Tyr Asp Val Asp Cys Asp Ile Phe Ser Pro Cys Ala Leu Gly

225 230 235 240

Ala Val Ile Asn Asp Asp Thr Val Asn Arg Leu Lys Cys Lys Val Ile

245 250 255

Ala Gly Ser Ala Asn Asn Gln Leu Lys Asp Asn Glu His Gly Asp Ile

260 265 270
Leu Gln Glu Lys Gly Ile Phe Tyr Ala Pro Asp Tyr Val Ile Asn Ser

275 280 285
Gly Gly Val Ile Asn Val Ala Asp Glu Leu Ile Gly Tyr Asn Arg Glu

290 295 300
Arg Ala Met Arg Arg Val Glu Gly Ile Tyr Gly Thr Ile Leu Arg Val

305 310 315 320
Phe Glu Ile Ala Lys Arg Asp Arg Ile Pro Ser Tyr Leu Ala Ala Asp

325 330 335
Arg Met Ala Glu Glu Arg Ile Ala Ser Ile Arg Gln Ser Arg Ser Pro

340 345 350
Phe Leu Gln Asn Glu Arg Asn Ile Ile Asn Met Thr Leu Arg

355 360 365

<210> 344

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 344

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Arg Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

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

340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 345
 <211> 375
 <212> PRT
 <213> Streptacidiphilus jiangxiensis
 <400> 345
 Met Thr Asp Val Ser Glu Arg Ser Gly Val Leu Ser Arg Ile Phe Ala
 1 5 10 15
 Thr Asp Pro Asn Ala Ala Pro Gly Asp Ser His Glu Gln Val Val Leu
 20 25 30
 Cys His Asp Arg Asp Thr Gly Leu Lys Ala Val Ile Ala Ile His Ser
 35 40 45
 Thr Ala Leu Gly Pro Ala Leu Gly Gly Thr Arg Phe His Pro Tyr Ala
 50 55 60
 Thr Glu Glu Glu Ala Val Gln Asp Ala Leu Asn Leu Ser Arg Gly Met
 65 70 75 80
 Ser Tyr Lys Asn Ala Met Ala Gly Leu Asp Leu Gly Gly Gly Lys Ala
 85 90 95
 Val Ile Ile Gly Asp Pro Thr Lys Ile Lys Thr Glu Ala Leu Leu Arg
 100 105 110
 Ala Tyr Gly Arg Phe Val Gln Ser Leu Asn Gly Arg Tyr Val Thr Ala
 115 120 125
 Cys Asp Val Gly Thr Tyr Val Ala Asp Met Asp Val Ile Ala Arg Glu
 130 135 140
 Cys Asp Phe Val Thr Gly Arg Ser Pro Glu Tyr Gly Gly Ala Gly Asp
 145 150 155 160
 Ser Ser Val Leu Thr Ser Phe Gly Val Phe Gln Gly Met Arg Ala Ala
 165 170 175
 Ala Gln His Lys Trp Gly Ser Pro Ser Leu Glu Gly Arg Arg Val Gly

180 185 190
 Val Ala Gly Ile Gly Lys Val Gly His Tyr Leu Val Glu His Leu Ile
 195 200 205
 Glu Asp Gly Ala Gln Val Val Ile Thr Asp Val Arg Glu Asp Ala Val
 210 215 220
 Asn Arg Val Arg Ala Ala His Pro Gly Val Glu Val Ala Ala Asp Thr

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

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

 355 360 365
 Ile Leu Leu Pro Arg Ser Arg
 370 375
 <210> 346
 <211> 353
 <212> PRT
 <213> Tissierella creatinophila
 <400> 346
 Met Asn Ile Phe Asp Tyr Leu Lys Glu Tyr Asp Tyr Glu Gln Val Val
 1 5 10 15

Phe Cys Gln Asp Lys His Ser Gly Leu Lys Ala Ile Ile Gly Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Ile Trp Asp Tyr
 35 40 45
 Lys Ser Glu Glu Glu Ala Ile Ile Asp Val Leu Arg Leu Ala Arg Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
 65 70 75 80
 Ala Val Ile Ile Gly Asp Pro Glu Lys Ile Lys Ser Glu Glu Leu Phe
 85 90 95
 Arg Thr Phe Gly Arg Phe Val Glu Ser Leu Gly Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Met Asn Ala Gly Thr Lys Asp Met Ala Tyr Ile Asn Glu
 115 120 125
 Glu Thr Asn Tyr Val Val Gly Leu Glu Gly Lys Ser Gly Asn Pro Ser
 130 135 140
 Pro Val Thr Ala Phe Gly Val Phe Lys Gly Ile Leu Ala Ala Val Asp
 145 150 155 160
 Glu Val Tyr Gly Ser Glu Gly Leu Lys Gly Lys Thr Val Ala Val Gln
 165 170 175
 Gly Leu Gly Ala Val Gly Tyr Gly Leu Cys Glu Tyr Leu His Lys Ala
 180 185 190
 Gly Ala Lys Leu Leu Val Thr Asp Ile Arg Lys Asp Ser Ile Glu Lys
 195 200 205
 Ile Val Asn Glu Phe Gly Ala Lys Ser Val Asn Pro Asp Asp Ile Tyr
 210 215 220
 Gly Val Asp Cys Asp Ile Phe Ala Pro Cys Ala Met Gly Ala Ile Ile
 225 230 235 240
 Asn Asp Phe Thr Ile Asp Lys Leu Lys Cys Lys Ile Val Ala Gly Cys
 245 250 255
 Ala Asn Asn Gln Leu Ala Glu Glu Lys His Gly Asp Met Leu Met Glu

260 265 270
Lys Glu Ile Leu Tyr Ile Pro Asp Tyr Val Ile Asn Ser Gly Gly Val
275 280 285
Ile Asn Val Tyr Glu Glu Leu Lys Gly Tyr Asn Lys Glu Arg Ala Met

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

<210> 347

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 347

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

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

100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

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

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

 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Gln Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 348

<211> 344

<212> PRT

<213> *Shewanella amazonensis*

<400> 348

Met Ala Val Phe Asn His Val Ser Tyr Asp Glu His Glu Gln Val Val

1 5 10 15

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

20 25 30

Asn Thr Asn Leu Gly Pro Ala Val Gly Gly Cys Arg Met Trp Asn Tyr

35 40 45

Gln Ser Asp Glu Glu Ala Leu Asn Asp Val Leu Arg Leu Ser Arg Gly

50 55 60

Met Thr Tyr Lys Asn Ala Leu Ala Gly Leu Thr Met Gly Gly Gly Lys

65 70 75 80

Ser Val Ile Ile Ala Asp Pro Lys Thr Gln Asp Arg Glu Ala Leu Phe

85 90 95

Arg Ala Phe Gly Arg Phe Ile Asn Thr Leu Gly Gly Lys Tyr Tyr Ser

100 105 110

Ala Glu Asp Val Gly Thr Thr Thr Ala Asp Ile Met Ile Ala His Gln

115 120 125

Glu Thr Pro Tyr Met Ala Gly Leu Glu Gly Lys Ser Gly Asp Pro Ser

130 135 140

Pro Phe Thr Ala Leu Gly Thr Phe Leu Gly Ile Lys Ala Ala Val Lys

145 150 155 160

His Gln Arg Gly Leu Asp Ser Leu Lys Gly Leu Lys Ile Ala Val Gln

165 170 175

Gly Val Gly His Val Gly Tyr Tyr Leu Cys Lys His Leu His Glu Glu

180 185 190

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

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

Asp Glu Gln Asn Arg Thr Thr Gly Ala Val Ala Asp Glu Met Ala Arg
325 330 335

Ala Ile Ile Asp Ala Ala Arg Lys
340

<210> 349

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 349

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Ser Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg

340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 350

<211> 358

<212> PRT

<213> Gemmatimonas aurantiaca

<400> 350

Met Gln His Phe Glu Val Ile Ala Glu Met Gly His Glu Gln Val Val

1 5 10 15

Phe Cys His Asp Lys Ala Ser Gly Tyr Arg Gly Ile Ile Ala Ile His

20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Phe Trp Asn Tyr

35 40 45

Ala Thr Asp Glu Asp Ala Phe Ile Asp Ala Leu Arg Leu Ser Arg Gly

50 55 60

Met Thr Tyr Lys Asn Ala Val Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80

Ala Val Ile Ile Gly Asp Asn Lys Thr Pro His Arg Glu Met Leu Phe

85 90 95

Arg Ala His Gly Arg Phe Cys Asp Ser Leu Gly Gly Arg Tyr Val Thr

100 105 110

Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Phe Val His Met

115 120 125

Glu Thr Thr His Val Ala Gly Ile Gly Ser Lys Ser Gly Asp Pro Ser

130 135 140

Ser Val Thr Ala His Gly Val Phe Arg Ala Ile Glu Ala Ser Ala His
145 150 155 160

Ala Arg Trp Gly Ser Asn Ser Leu Glu Gly Arg Thr Ile Ala Leu Gln
165 170 175

Gly Leu Gly His Val Gly Thr His Leu Ala Lys Glu Leu His Ala Ala
180 185 190

Gly Ala Gln Leu Val Val Thr Asp Ile Asp Ala Gly Arg Ile Ala His
195 200 205

Val Val Asp Thr Cys Gly Ala Arg Ala Val Ala Leu Asn Glu Ile Tyr
210 215 220

Gly Val Lys Ala Asp Ile Phe Thr Pro Cys Ala Leu Gly Gly Val Ile
225 230 235 240

Asn Asp Asp Thr Ile Pro Gln Leu Gln Val Glu Ile Val Ala Gly Ala
245 250 255

Ala Asn Asn Gln Leu Leu Glu Asp Arg His Gly Asp Glu Leu Glu Arg
260 265 270

Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ala Asn Ala Gly Gly Val
275 280 285

Ile Asn Val Tyr Ser Glu Leu Thr Gly Trp Ser Arg Asp Arg Ala Leu
290 295 300

Arg Lys Ala Asp Glu Ile Tyr Glu Thr Val Leu Ser Val Phe Arg Met
305 310 315 320

Ala Lys Ser Thr Gly Ile Pro Thr Tyr Gln Ala Ala Asp Arg Val Ala
325 330 335

Glu Gln Arg Ile Asn Ala Val Arg Gly Met Ile Arg Thr Trp Pro Gln
340 345 350

Tyr Pro Asn Lys Glu Thr
355

<210> 351

<211> 357

<212> PRT

<213> Legionella erythra

<400> 351

Met Met Ser Val Asp Thr Met Lys Ile Asn Glu Pro Thr Thr Arg Gln

1 5 10 15

Asp Asp Phe Leu Asp Tyr Ala Leu Ser His Gly Phe Gly Asp Ile His

20 25 30

Phe Lys Val Asp Ser Lys Thr Gly Met Lys Ala Ile Ile Ala Ile His

35 40 45

Ser Thr Lys Leu Gly Pro Ala Leu Gly Gly Cys Arg Phe Ile Glu Tyr

50 55 60

Pro Ser Thr Glu Asn Ala Ile Asn Asp Ala Met Arg Leu Ala Arg Gly

65 70 75 80

Met Ser Tyr Lys Ala Ala Ser Val Asn Leu Pro Leu Gly Gly Gly Lys

85 90 95

Ala Val Val Ile Lys Pro His Gly Pro Tyr Asp His Glu Ala Tyr Phe

100 105 110

His Ala Phe Gly Glu Phe Val Asn Asp Leu Gly Gly Arg Tyr Ile Thr

115 120 125

Ala Leu Asp Ser Gly Thr Gln Leu Ser Asp Met Asp Ile Ile Ala Gln

130 135 140

His Thr Pro Tyr Val Ala Ser Leu Ser Ser His Asn Gly Asp Pro Ser

145 150 155 160

Pro Ser Thr Ala Lys Gly Val Phe Lys Gly Ile Glu Ala Ala Val His

165 170 175

Phe Lys Leu Gly Lys Asp Asn Leu Lys Gly Leu His Ile Ala Ile Gln

180 185 190

Gly Leu Gly His Val Gly Tyr Leu Leu Ala Arg His Leu His Glu Ala

195 200 205

Gly Ala Arg Leu Thr Val Ala Asp Val Asn Lys Glu Ala Val Glu Arg

210 215 220

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

225 230 235 240
 Lys Val Pro Cys Asp Val Phe Ser Pro Cys Ala Leu Gly Ala Ile Leu
 245 250 255
 Asn Asp Met Thr Ile Asn Gln Leu Gln Thr Thr Ile Val Ala Gly Ala
 260 265 270
 Ala Asn Asn Gln Leu Ala His Thr Tyr His Gly Lys Ile Leu His Asp
 275 280 285
 Lys Gly Ile Val Tyr Ala Ala Asp Tyr Val Ile Asn Ala Gly Gly Leu
 290 295 300

 Ile Phe Ala Ala Ser Lys Tyr Leu Asn Thr Pro Glu Glu Gln Val Val
 305 310 315 320
 Lys Gln Ile Asn Ser Ile Gly Thr Ser Leu Met Glu Ile Phe Val Arg
 325 330 335
 Ser Gln Lys Glu Asn Arg Pro Ala Ser Glu Ile Ala Asp Thr Leu Ala
 340 345 350
 Gln Glu Lys Leu Ala
 355
 <210> 352
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220
 ><223> Synthetic polypeptide
 <400> 352
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Phe Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125

 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190

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

 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335

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

340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 353

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 353

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Glu Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365
<210> 354
<211> 358
<212> PRT
<213> Nesiotobacter exalbescens

<400> 354

Met Asn Ala Pro Leu Ala Gln Ala Val Ala Leu Glu Asp Thr Ser Thr
1 5 10 15

Ala Phe Asp His Pro Glu Phe Ser Gly His Glu Gln Val Val Phe Ala
20 25 30

His Asp Pro Ala Ser Gly Leu Arg Ala Ile Ile Ala Ile His Asn Thr
35 40 45

Arg Leu Gly Pro Ala Leu Gly Gly Cys Arg Met Trp Gly Tyr Arg Thr
50 55 60

Ser Arg Glu Ala Leu Thr Asp Ala Leu Arg Leu Ser Lys Gly Met Thr
65 70 75 80

Tyr Lys Asn Ala Leu Ala Gly Leu Pro Leu Gly Gly Gly Lys Ser Val
85 90 95

Ile Ile Ala Asp Pro Lys Thr Glu Lys Thr Pro Glu Leu Leu Lys Ala
100 105 110

Phe Gly Arg His Val Glu Arg Leu Ala Gly Gly Tyr Ile Thr Ala Glu
115 120 125

Asp Val Gly Ile Thr Ala Ala Asp Met Glu Leu Ile Ala Ser Gln Thr
130 135 140

Gly His Ala Arg Gly Thr Glu Ala Thr Gly Leu Gly Asp Pro Ser Pro
145 150 155 160

Tyr Thr Ala Leu Gly Val Phe Thr Gly Ile Gln Ala Ala Val Ala His
165 170 175

Lys Phe Gly Thr Ser His Leu Thr Gly Ile Thr Val Ser Val Gln Gly
180 185 190

Leu Gly Asn Val Gly Tyr Gly Val Cys Arg Tyr Leu His Ala His Gly
195 200 205

Ala Lys Leu Val Val Ser Asp Ile His Glu Pro Asn Val Lys Arg Ala
210 215 220

Val Ala Glu Phe Gly Ala Gln Pro Ile Asp Pro His Gln Ala His Ala
225 230 235 240

Ala Asp Val Asp Val Tyr Ala Pro Cys Ala Leu Gly Ala Thr Ile Asn
245 250 255
Ala Ala Thr Ile Pro Gln Ile Lys Ala Lys Ile Ile Ala Gly Ala Ala
260 265 270

Asn Asn Gln Leu Gln Thr Pro Glu Asp Gly Val Lys Leu Met Gln Arg
275 280 285
Gly Ile Leu Tyr Ala Pro Asp Tyr Ala Leu Asn Ala Gly Gly Val Ile
290 295 300
Ser Val Ala Leu Ala Thr Ser Ser Lys Asp Asp Ala Met Val Arg Glu
305 310 315 320
Lys Thr Leu Ala Ile Gly Asp Thr Leu Thr Ala Ile Phe Lys Arg Ala
325 330 335

Asp Leu Glu Gly Leu Pro Thr Ser Val Val Ala Asp Lys Leu Ala Glu
340 345 350
Glu Arg Leu Met Ala Gly
355

<210> 355

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 355

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Ala Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 356

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 356

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110
Ile Thr Ala Ser Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

260 265 270

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

275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335

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

340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 357

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 357

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Phe Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

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

<210> 358

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 358

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Phe Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 359

<211> 367

<212> PRT

<213> Anoxybacillus flavithermus

<400> 359

Met Glu Ile Phe Lys Tyr Met Glu Gln Tyr Asp Tyr Glu Gln Leu Val
1 5 10 15
Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala Ile His
20 25 30
Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Met Tyr
35 40 45
Glu Ser Glu Asp Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala Arg Gly

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

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

Ala Val Gln Gly Val Gly Asn Val Ala Tyr Asn Leu Cys Arg His Leu

180 185 190
His Glu Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys Glu Ala

195 200 205
Val Gln Arg Val Val Glu Gln Phe Gly Ala Thr Ala Val Asp Pro Asn

210 215 220
Asp Ile Tyr Gly Val Asp Cys Asp Ile Phe Ala Pro Cys Ala Leu Gly

225 230 235 240
Gly Ile Ile Asn Asp Gln Thr Ile Pro Gln Leu Lys Ala Lys Val Ile

245 250 255
Ala Gly Ala Ala Asn Asn Gln Leu Arg Glu Ala Arg His Gly Asp Ile

260 265 270
Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala

275 280 285
Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Arg Glu

290 295 300
Arg Ala Met Lys Lys Val Glu Gln Ile Tyr Asn Asn Ile Glu Lys Val

305 310 315 320
Ile Glu Ile Ala Lys Arg Asp Gly Ile Pro Thr Tyr Gln Ala Ala Asp

325 330 335
Arg Leu Ala Glu Glu Arg Ile Ala Lys Met Arg Gln Ser Arg Ser Gln

340 345 350
Phe Leu Gln Asn Gly Gln His Ile Leu Ser Arg Arg Arg Thr Arg

355 360 365

<210> 360

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 360

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

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

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

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

 245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Cys Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 361

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 361

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Phe Tyr Gly Tyr Asn
290 295 300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg

340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 362
 <211> 367
 <212> PRT
 <213> *Xanthomarina gelatinilytica*

 <400> 362
 Met Val Thr Asp Val Ile Asn Ala Asn Glu Leu His Lys Ala Asp Pro
 1 5 10 15
 Val Phe Gly Gln Leu Ser Phe Asp Asn His Glu Gln Val Val Phe Cys
 20 25 30
 Asn Asp Lys Asp Thr Gly Leu Lys Ala Ile Ile Gly Ile His Asn Thr
 35 40 45
 Val Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr Thr Asn
 50 55 60

 Glu Trp Glu Ala Leu Asn Asp Val Leu Arg Leu Ser Arg Gly Met Thr
 65 70 75 80
 Tyr Lys Ser Ala Ile Thr Gly Leu Asn Leu Gly Gly Gly Lys Ala Val
 85 90 95
 Ile Ile Gly Asp Ala Lys Thr Gln Lys Thr Pro Glu Leu Met Lys Lys
 100 105 110
 Phe Gly Glu Phe Val His Ser Leu Ser Gly Arg Tyr Ile Thr Ala Glu
 115 120 125

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

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

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

 Ile Met Arg Lys Thr Glu Asn Ile Tyr Asn Thr Thr Leu Glu Ile Leu
 325 330 335
 Ser Asn Ala Lys Thr His Asn Ile Thr Thr Asn His Ala Ala Leu Asn
 340 345 350
 Ile Ala Gln Asn Arg Ile Asp Thr Arg Lys Lys Glu Asn Lys Arg
 355 360 365
 <210> 363
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 363
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Phe Gly Gly
65 70 75 80
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

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

325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 364

<211> 367

<212> PRT

<213> Owenweeksia hongkongensis

<400> 364

Met Ser Asp Leu Thr Ile Leu Asn Lys Ser Ile Asp Arg Gly Pro Val
 1 5 10 15

Phe Asn Ser Glu Ala Phe Lys Gly His Glu Gln Leu Val Phe Cys Gln
 20 25 30

Asp Glu Glu Thr Gly Leu Lys Ala Ile Ile Gly Ile His Ser Thr Thr
 35 40 45

Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr Glu Asn Glu
 50 55 60

Ala Asp Ala Ile Arg Asp Ala Leu Arg Leu Ser Arg Gly Met Thr Tyr
 65 70 75 80

Lys Ala Ser Ile Ser Gly Leu Asp Leu Gly Gly Gly Lys Ala Val Ile
 85 90 95

Ile Gly Asp Ser Arg Lys Asp Lys Thr Asp Ala Leu Met Arg Lys Phe
 100 105 110

Gly Glu Tyr Val Asn Ser Leu Ser Gly Arg Tyr Ile Thr Ala Glu Asp
115 120 125

Val Gly Ile Asn Thr His Asp Met Glu Met Val Lys Leu Glu Thr Asn
130 135 140

His Val Thr Gly Ile Pro Glu His Met Gly Gly Ser Gly Asp Pro Ser
145 150 155 160

Pro Val Thr Ala Tyr Gly Val Phe Met Gly Met Lys Ala Ser Ala Gln
165 170 175

Gln Lys Trp Gly Ser Asp Asn Leu Ala Gly Lys Lys Val Leu Val Gln
180 185 190

Gly Ile Gly His Val Gly Glu Thr Leu Val Lys Tyr Leu Thr Asp Glu
195 200 205

Gly Ala Ile Val Thr Ile Asn Asp Ile His Glu Asp Arg Ile Val Glu
210 215 220

Ile Ser Ala Lys Tyr Asn Thr Gln Val Tyr Arg Gly Asn Asn Leu Phe
225 230 235 240

Glu Val Glu Met Asp Ile Tyr Ala Pro Cys Ala Leu Gly Ala Thr Val
245 250 255

Asn Ser Lys Thr Ile Glu Met Met Lys Cys Asp Ile Ile Ala Gly Ala
260 265 270

Ala Asn Asn Gln Leu Glu Asp Glu Val Val His Gly Gln Met Val Lys
275 280 285

Asp Lys Gly Ile Leu Tyr Ala Pro Asp Phe Leu Ile Asn Ala Gly Gly
290 295 300

Leu Ile Asn Val Tyr Arg Glu Ile Ala Gly Tyr Asp Gln Ala Glu Ala
305 310 315 320

Met Arg Arg Thr Glu Asn Ile Tyr Asp Thr Thr Leu Arg Ile Phe Lys
325 330 335

Leu Ser Gln Glu Arg Asn Ile Ser Thr His Glu Ala Ala Leu Lys Ile
340 345 350

Ala Glu Glu Arg Val Ala Leu Lys Lys Ala Glu Leu Ala Asn Ala

355 360 365

<210> 365

<211> 353

<212> PRT

<213> Unknown

<220><223> Marinobacter sp. HL-58

<400> 365

Met Thr Val Phe Thr His Pro Glu Phe Asp His His Glu His Leu Thr

1 5 10 15

Phe Cys Cys Asp Pro Glu Thr Gly Leu Arg Ala Ile Ile Ala Val His

20 25 30

Asn Thr Ser Arg Gly Pro Ala Leu Gly Gly Cys Arg Met Phe Pro Tyr

35 40 45

Ala Ser Asp Glu Glu Ala Leu Arg Asp Val Leu Arg Leu Ser Arg Gly

50 55 60

Met Thr Tyr Lys Ser Ala Leu Ala Asn Leu Asp Leu Gly Gly Gly Lys

65 70 75 80

Ser Val Ile Ile Gly Asp Ser Arg Glu His Lys Thr Glu Ala Leu Leu

85 90 95

Glu Ser Met Gly Arg Phe Leu Glu Gln Leu Gly Gly Leu Tyr Ile Ala

100 105 110

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

115 120 125

Gln Thr Thr His Val Ala Gly Ile Arg Asp Arg Pro Gly Phe Asp Gly

130 135 140

Lys Pro Ser Asn Gly Asp Pro Ser Pro Ala Thr Ala Trp Gly Thr Phe

145 150 155 160

Val Gly Ile Gln Ala Ala Val Lys His Lys Leu Gly Arg Ser Asp Leu

165 170 175

Glu Gly Leu Lys Val Ala Val Gln Gly Ile Gly Asn Val Gly Tyr Arg

180 185 190

Leu Ala Arg His Leu Arg Glu Ala Gly Ala Glu Leu Trp Val Tyr Asp

195 200 205
Ile His Gln Asp Gln Met Asp Arg Ala Val Ala Glu Phe Gly Ala Thr

210 215 220
Pro Ala Ser Ala Glu Asp Ile Leu Phe Leu Pro Val Asp Val Val Ala
225 230 235 240
Pro Cys Ala Met Gly Ala Val Leu Asn Asp Ala Ser Ile Ala Arg Leu
245 250 255
Gln Ala Pro Ile Val Ala Gly Ala Ala Asn Asn Gln Leu Ala Ser Pro
260 265 270
Ala His Asp Glu Val Leu Trp Lys His Gly Val Leu Tyr Ala Pro Asp

275 280 285
Phe Val Ile Asn Ala Gly Gly Ile Ile Asp Val Phe Tyr Glu Arg Thr
290 295 300
Gly Pro Asp Pro Glu Ala Val Arg Gln His Val Asn Thr Ile Gly Gln
305 310 315 320
Thr Leu Glu Glu Ile Phe Gln Arg Ser Ala Arg Asp Gly Leu Pro Thr
325 330 335
Gly Gln Ile Ala Asp Gln Leu Ala Glu Glu Arg Phe Arg His Ile Pro

340 345 350
Arg

<210> 366

<211> 364

<212> PRT

<213> Unknown

<220><223> Paenisporosarcina sp. HGH0030

<400> 366

Met Glu Ile Phe Lys Tyr Met Glu Thr Tyr Asp Tyr Glu Gln Leu Val
1 5 10 15
Phe Cys Gln Asp Lys Thr Ser Gly Leu Lys Ala Ile Ile Ala Ile His
20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr

35 40 45

Ala Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala Lys Gly

50 55 60

Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80

Thr Val Ile Ile Gly Asp Pro Leu Lys Asp Lys Asn Glu Glu Met Phe

85 90 95

Arg Ala Phe Gly Arg Phe Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr

100 105 110

Ala Glu Asp Val Gly Thr Thr Val Ala Asp Met Asp Leu Ile His Glu

115 120 125

Glu Thr Asn Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly

130 135 140

Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys Ala

145 150 155 160

Ala Ala Met Glu Ala Phe Gly Ser Asp Ser Leu Glu Gly Lys Arg Ile

165 170 175

Ala Val Gln Gly Val Gly Asn Val Ala Tyr Asn Leu Cys Arg His Leu

180 185 190

His Glu Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys Ala Ala

195 200 205

Val Asp Arg Val Val Glu Glu Phe Gly Ala Thr Ala Val Asn Thr Asp

210 215 220

Glu Ile Tyr Ser Gln Asp Val Asp Ile Phe Ala Pro Cys Ala Leu Gly

225 230 235 240

Ala Ile Ile Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys Val Val

245 250 255

Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Thr Lys His Gly Asp Gln

260 265 270

Leu His Glu Leu Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala

275 280 285
Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Arg Glu

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

355 360
<210> 367
<211> 364
<212> PRT
<213> Ornithinibacillus halophilus
<400> 367

Met Glu Ile Phe Thr Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val
1 5 10 15
Phe Cys Gln Asp Lys Asn Ser Gly Leu Lys Ala Ile Ile Ala Ile His
20 25 30
Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
35 40 45

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

Ala Glu Asp Val Gly Thr Thr Glu Glu Asp Met Asp Leu Ile His Met

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

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

 Ala Thr Ile Asn Asp Glu Thr Ile Pro Arg Ile Lys Ala Lys Val Ile
 245 250 255
 Ala Gly Ser Ala Asn Asn Gln Leu Lys Ser Ser Lys His Gly Glu Ile
 260 265 270
 Ile His Glu Lys Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala
 275 280 285
 Gly Gly Val Ile Asn Val Ala Asp Glu Leu Asn Gly Tyr Asn Gln Glu
 290 295 300

 Arg Ala Met Lys Lys Val Glu Thr Ile Tyr Asp Ser Leu Ser Lys Val
 305 310 315 320
 Phe Glu Ile Ser Arg Arg Asp Asn Ile Pro Ser Tyr Val Ala Ala Asp
 325 330 335
 Arg Met Ala Glu Glu Arg Ile Glu Thr Met Lys Lys Ser Arg Asn Gln
 340 345 350
 Phe Leu Leu Asn Glu His His Ile Leu Ser Arg Arg
 355 360
 <210> 368

<

211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 368

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Glu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365
<210> 369
<211> 368
<212> PRT
<213> Flavobacterium micromati
<400> 369
Met Asn Ala Ala Phe Thr Thr Ser Asn Glu Leu Gln Lys Met Asp Pro
1 5 10 15
Val Phe Gly Gln Thr Ser Phe Asp Asp His Glu Gln Ile Val Phe Cys
20 25 30
Asn Asp Lys Asp Thr Gly Leu Lys Ala Ile Ile Gly Ile His Asn Ser
35 40 45
Val Met Gly Pro Ala Leu Gly Gly Thr Arg Met Tyr Asn Tyr Ser Asn

50 55 60
 Glu Trp Glu Ala Leu Asn Asp Val Leu Arg Leu Ser Arg Gly Met Thr
 65 70 75 80
 Phe Lys Ala Ala Ile Thr Gly Leu Asn Ile Gly Gly Gly Lys Ala Val
 85 90 95
 Ile Ile Gly Asp Pro Lys Thr Gln Lys Thr Pro Glu Leu Met Arg Lys
 100 105 110
 Phe Gly Glu Phe Val His Ser Leu Ser Gly Arg Tyr Ile Thr Ala Glu
 115 120 125

 Asp Met Gly Met Glu Thr Arg Asp Met Asp Ile Val Arg Asp Val Thr
 130 135 140
 Pro Tyr Val Thr Gly Ile Ser Glu Glu Arg Gly Gly Ala Gly Asn Pro
 145 150 155 160
 Ser Pro Val Thr Ala Tyr Gly Val Phe Met Gly Met Lys Ala Ala Ala
 165 170 175
 Lys Arg Gln Phe Gly Ser Asp Asn Leu Ser Gly Lys Lys Val Leu Val
 180 185 190

 Glu Gly Ile Gly His Val Gly Glu Thr Leu Val Ala Tyr Leu Val Lys
 195 200 205
 Glu Gly Ala Ile Val Thr Ile Ala Asp Ile Asn Glu Gln Lys Leu Asn
 210 215 220
 Glu Val Ala Ala Thr Tyr Asn Thr Thr Ile Phe Arg Gly Glu Asp Leu
 225 230 235 240
 Tyr Ala Ala Asp Val Asp Ile Tyr Ala Pro Cys Ala Met Gly Ala Thr
 245 250 255

 Ile Asn Asn Asp Thr Val Tyr Lys Ile Lys Ala Lys Val Ile Ala Gly
 260 265 270
 Ala Ala Asn Asn Gln Leu Ala Asp Glu Asn Ile His Gly Ala Ile Leu
 275 280 285
 Gln Glu Arg Gly Ile Leu Tyr Ala Pro Asp Phe Leu Ile Asn Ala Gly
 290 295 300

Gly Ile Ile Asn Val Tyr Ala Glu Leu Ala His Tyr Asp Lys Ala Glu
305 310 315 320

Ile Thr Arg Arg Thr Glu Asn Ile Tyr Asp Thr Thr Leu Glu Ile Phe
325 330 335

Asp Phe Ala Ile Ala Asn Lys Met Thr Thr His Thr Ala Ala Leu Thr
340 345 350

Ile Ala Gln Asn Arg Ile Asn Gln Arg Lys Ile Glu Asn Ser Arg Arg
355 360 365

<210> 370

<211> 348

<212> PRT

<213> Sandaracinus amylolyticus

<400> 370

Met Asn Val Phe Glu His Leu Gln Gln His Asp Tyr Gly Glu Val His

1 5 10 15
Phe Ala Arg Asp Ala Ala Thr Gly Leu Gln Ala Ile Val Ala Ile His
20 25 30

Asp Thr Arg Leu Gly Pro Ala Leu Gly Gly Cys Arg Phe Ile His Tyr
35 40 45

Pro His Glu Glu Leu Ala Leu Ile Asp Ala Leu Arg Leu Ala Arg Gly
50 55 60

Met Thr Tyr Lys Ala Ala Ile Thr Gly Ile Pro His Gly Gly Gly Lys

65 70 75 80
Ser Val Ile Ile Arg Pro Pro Arg Ala Phe Asp Arg Gly Ala Leu Phe
85 90 95

Arg Ala Phe Gly Arg Phe Val Asp Gly Leu Gly Gly Arg Tyr Ile Thr
100 105 110

Ala Glu Asp Ser Gly Thr Ser Met Glu Asp Met Glu Thr Ile Arg Ser
115 120 125

Val Thr Lys His Val Thr Gly Val Lys Pro Glu His Gly Gly Ser Gly

130 135 140

Asp Pro Ser Pro Tyr Thr Ala Leu Gly Val Arg Arg Gly Ile Glu Ala
 145 150 155 160
 Cys Val Lys Phe Val Tyr Lys Arg Asp Ser Ile Glu Gly Leu His Val
 165 170 175
 Ala Val Gln Gly Val Gly His Val Gly Tyr Trp Leu Cys Lys Gln Leu
 180 185 190
 His Asp Leu Gly Ala Lys Leu Thr Val Ala Asp Ile Asp Pro Leu Lys
 195 200 205
 Ala Glu Arg Ala His Arg Glu Leu Gly Ala Glu Val Val Pro Leu Asp
 210 215 220
 Gln Ile Phe Ser Val Asp Cys Glu Val Phe Ala Pro Cys Ala Leu Gly
 225 230 235 240
 Ser Ala Leu Asn Asp Asp Ser Ile Pro Lys Leu Lys Cys Lys Ile Val
 245 250 255
 Ala Gly Ala Ala Asn Asn Gln Leu Ala Glu Thr Arg His Gly Asp Ala
 260 265 270
 Leu Met His Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Ala Ile Asn Ala
 275 280 285
 Gly Gly Leu Val Asn Val Ala Gln Glu His Ala Gly Tyr Asp Glu Gln
 290 295 300
 Lys Ser Arg Glu Arg Val Leu Lys Ile Tyr Asp Thr Ile Leu Glu Ile
 305 310 315 320
 Ala Glu Arg Ala Glu Arg Ala Met Gln Pro Thr Tyr Arg Ile Ala Asp
 325 330 335
 Thr Ile Val Glu Glu Lys Leu Ala Arg Ala Ala Arg
 340 345
 <210> 371
 <211> 351
 <212> PRT
 <213> Lacimicrobium alkaliphilum
 <400> 371
 Met Ser Val Phe Asp His Ala Ala Tyr Asp Lys His Glu His Val Ala

1 5 10 15
 Phe Tyr His Asp Val Lys Ser Gly Leu Lys Ala Ile Ile Ala Val His
 20 25 30

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

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

 Met Gly Leu Lys Ala Ser Val Ala Tyr Gly Leu Lys Ser Asp Leu Asn
 165 170 175
 Gly Val Ser Val Ala Ile Gln Gly Leu Gly His Val Gly Phe Arg Leu
 180 185 190
 Ala Glu His Leu His Lys Glu Gly Ala Lys Leu Phe Val Thr Asp Ile
 195 200 205
 Tyr Pro Asp Asn Leu Asp Lys Ala Val Glu Gln Phe Gly Ala Thr Val
 210 215 220

 Val Thr Pro Asp Glu Ile Phe Gly Leu Asp Val Asp Val Phe Ala Pro
 225 230 235 240
 Cys Ala Leu Gly Ala Ala Ile Asn Asp Gln Thr Ile Asp Gln Ile Lys
 245 250 255

Ala Arg Val Ile Ala Gly Ala Ala Asn Asn Gln Leu Ala Glu Glu Arg
260 265 270
His Gly Gln Met Leu Met Asp Lys Gly Ile Leu Tyr Ala Pro Asp Tyr
275 280 285
Val Ile Asn Ala Gly Gly Val Ile Asp Ile Tyr His Gln Lys Gln Gly
290 295 300
Ser Ser Ala Glu Ala Leu Arg Lys His Ile Glu Gly Ile Gly Asp Thr
305 310 315 320
Leu Thr Glu Ile Tyr Gln Lys Ala Ala Gln Gln Gly Leu Pro Thr Asn
325 330 335
Ile Glu Ala Asn Arg Ile Ala Glu Gln Arg Phe Leu Ala Gly Ala
340 345 350

<210> 372

<211> 376

<212> PRT

<213> Unknown

<220><223> Marinobacterium sp. AK27

<400> 372

Met Asn Ala Pro Ile Asn Ser Thr Ile Asn Gln Pro Leu Thr Asp Thr
1 5 10 15
Asn Glu Gln Asn Lys Glu Pro Met Asn Met Ser Val Phe Ser His Pro
20 25 30
Glu Phe Asp Asn His Glu Gln Leu Thr Phe Phe Ser Asp Glu Lys Ser
35 40 45
Gly Leu Lys Ala Ile Ile Ala Val His Asn Thr Asn Leu Gly Pro Ala
50 55 60
Leu Gly Gly Cys Arg Met Trp His Tyr Ala Ser Asp Glu Glu Ala Leu
65 70 75 80
Arg Asp Val Leu Arg Leu Ser Arg Gly Met Thr Tyr Lys Ser Ala Leu
85 90 95
Ala Asn Leu Lys Leu Gly Gly Gly Lys Ser Val Ile Ile Gly Asp Pro
100 105 110

Arg Gln His Lys Ser Glu Ala Leu Leu Glu Met Met Gly Arg Cys Leu

115 120 125
Glu Arg Thr Gly Gly Gln Tyr Ile Ala Ala Glu Asp Ser Gly Thr Ser

130 135 140
Val Pro Asp Leu Gln Val Met Ser Arg Phe Thr Asn Asn Val Ala Gly

145 150 155 160
Ile Thr Glu Arg Thr Gly Ile Asp Gly Leu Pro Cys Asn Gly Asp Pro

165 170 175
Ser Pro Ala Thr Ala Tyr Gly Cys Phe Val Gly Leu Lys Ala Ala Val

180 185 190
Lys His Gln Phe Gly Arg Asp Asp Leu Ser Gly Leu Lys Val Ala Ile

195 200 205
Gln Gly Val Gly Asn Val Gly Tyr Arg Leu Ala Lys His Leu Arg Gln

210 215 220
Ala Gly Ala Glu Leu Phe Val Thr Asp Ile His Glu Glu Gln Val Arg

225 230 235 240
Leu Ala Val Thr Glu Leu Gly Ala Thr Ala Val Ala Gln Glu Glu Ile

245 250 255
Leu Gly Leu Asp Val Asp Val Leu Ser Pro Cys Ala Leu Gly Ala Val

260 265 270
Leu Asn Asp Phe Ser Ile Pro Gln Ile Lys Ala Lys Val Ile Ala Gly

275 280 285
Ala Ala Asn Asn Gln Leu Ala Leu Ala Lys His Asp Gln Leu Leu Gln

290 295 300
Gln Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly

305 310 315 320
Ile Ile Asp Ile Tyr Tyr Glu Arg Val Gly His Glu His Thr Lys Val

325 330 335
Arg Ala His Ile Asp Thr Ile Ala Asp Thr Leu Gln Glu Ile Phe Arg

340 345 350
Arg Ala Asp Asp Ser Gly Arg Pro Thr Gly Glu Ile Ala Asn Thr Leu

355 360 365
Ala Glu Glu Arg Phe Met Thr Arg
370 375

<210> 373
<211> 349
<212> PRT
<213> Unknown
<220><223> Thalassospira sp. TSL5-1
<400> 373

Met Ser Ile Phe Ser Asp Pro Ala Phe Asp Asn His Glu Gln Val Val
1 5 10 15
Phe Ala Ser Asp Arg Glu Thr Gly Leu Lys Ala Ile Ile Ala Val His
20 25 30
Asn Thr His Leu Gly Pro Ser Leu Gly Gly Cys Arg Met Trp Pro Tyr
35 40 45
Ala Ser Glu Gln Asp Ala Ile His Asp Val Leu Arg Leu Ser Arg Gly

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

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

Arg Val Ala Val Gln Gly Leu Gly Asn Val Gly Phe His Leu Cys Glu

180 185 190
 Leu Leu His Asn Ala Gly Ala Glu Leu Ile Val Ala Asp Ile Asn Ala
 195 200 205
 Ser Ala Val Asp Arg Ala Val Asp Arg Phe Gly Ala Lys Ala Val Ser
 210 215 220
 Val Asp Glu Ile Leu Ser Val Asn Ala Asp Val Leu Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Gly Ile Ile Asn Asp Thr Ser Ile Ala Ser Leu Lys Ala Gly

245 250 255
 Ile Ile Ala Gly Ala Ala Asn Asn Gln Leu Glu Ala Asp Arg His Gly
 260 265 270
 Asp Ile Leu Arg Glu Met Gly Val Leu Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Val Glu Val His Tyr Cys Arg Glu Gly Arg Pro
 290 295 300
 Val Ser Glu Thr Asn Arg His Ile Glu Gly Ile Gly Ala Thr Val Arg

305 310 315 320
 Glu Ile Phe Glu Arg Ala Asp Arg Glu Asn Lys Ser Thr Ser Phe Ile
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Phe Gly Lys Lys Ala
 340 345

<210> 374

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 374

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15

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

20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Asp Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335

 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 375
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 375
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile

 275 280 285
 Asn Ala Gly Gly Gln Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg

 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 376

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 376

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Glu Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220

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

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

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 377

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 377

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

260 265 270

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

275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Asp Tyr Gly Tyr Asn

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

355 360 365

<210> 378

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 378

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Thr Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

	355		360		365										
<210>	379														
<211>	366														
<212>	PRT														
<213>	Artificial Sequence														
<220><223>	Synthetic polypeptide														
<400>	379														
Met	Thr	Leu	Glu	Ile	Phe	Glu	Tyr	Leu	Glu	Lys	Tyr	Asp	Tyr	Glu	Gln
1				5					10					15	
Val	Val	Phe	Cys	Gln	Asp	Lys	Glu	Ser	Gly	Leu	Lys	Ala	Ile	Ile	Ala
			20					25					30		
Ile	His	Asp	Thr	Thr	Leu	Gly	Pro	Ala	Leu	Gly	Gly	Thr	Arg	Met	Trp
		35					40						45		
Thr	Tyr	Asp	Ser	Glu	Glu	Ala	Ala	Ile	Glu	Asp	Ala	Leu	Arg	Leu	Ala
	50					55					60				
Lys	Gly	Met	Thr	Tyr	Lys	Asn	Ala	Ala	Ala	Gly	His	Asn	Leu	Gly	Gly
65					70					75				80	
Ala	Lys	Thr	Val	Ile	Ile	Gly	Asp	Pro	Arg	Lys	Asp	Lys	Ser	Glu	Ala
				85					90					95	
Met	Phe	Arg	Ala	Leu	Gly	Arg	Tyr	Ile	Gln	Gly	Leu	Asn	Gly	Arg	Tyr
		100						105					110		
Ile	Thr	Ala	Glu	Asp	Val	Gly	Thr	Thr	Val	Asp	Asp	Met	Asp	Ile	Ile
		115						120				125			
His	Glu	Glu	Thr	Asp	Phe	Val	Thr	Gly	Ile	Ser	Pro	Ser	Phe	Gly	Ser
	130					135					140				
Ser	Gly	Asn	Pro	Ser	Pro	Val	Thr	Ala	Tyr	Gly	Val	Tyr	Arg	Gly	Met
145				150						155				160	
Lys	Ala	Ala	Ala	Lys	Glu	Ala	Phe	Gly	Thr	Asp	Asn	Leu	Glu	Gly	Lys
			165						170					175	
Val	Ile	Ala	Val	Gln	Gly	Val	Gly	Asn	Val	Ala	Tyr	His	Leu	Cys	Lys
		180						185						190	

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300

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

<210> 380

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 380

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Trp Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

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

275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

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

<210> 381

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 381

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

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

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

	355		360		365
<210>	382				
<211>	366				
<212>	PRT				
<213>	Artificial Sequence				
<220><223>	Synthetic polypeptide				
<400>	382				
Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln					
1 5 10 15					
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala					
20 25 30					
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp					
35 40 45					
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala					
50 55 60					
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly					
65 70 75 80					
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala					
85 90 95					
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr					
100 105 110					
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile					
115 120 125					
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser					
130 135 140					
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met					
145 150 155 160					
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys					
165 170 175					
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys					
180 185 190					

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Met Tyr Gly Tyr Asn
 290 295 300

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

<210> 383

<211> 368

<212> PRT

<213> Unknown

<220><223> Bacteriovorax sp. BAL6_X

<400> 383

Met Pro Ser Phe Glu Arg Leu Tyr Lys Asp Gly His Glu Glu Val Ile
 1 5 10 15
 Phe Phe Ser Asp Pro Ser Cys Asn Leu Lys Ala Ile Val Ala Ile His
 20 25 30

Asn Thr Val Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Pro Tyr
 35 40 45
 Glu Ser Glu Glu Glu Ala Leu Asn Asp Val Leu Arg Leu Ser Arg Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Val Ala Gly Leu Asn Leu Gly Gly Gly Lys
 65 70 75 80
 Ala Val Ile Ile Gly Asp Pro Glu Lys Asp Lys Ser Glu Ala Leu Phe
 85 90 95
 Arg Ser Tyr Gly Arg Phe Met Glu Ser Leu Asn Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Val Asn Ile Ser Val Asp Asp Ile Glu His Val Phe Thr
 115 120 125
 Glu Thr Asn Asn Val Ala Gly Val Ala Glu Ile His Gly Gly Ser Gly
 130 135 140
 Asn Pro Ser Pro Trp Thr Ala Arg Gly Val Phe Arg Gly Ile Glu Ala
 145 150 155 160
 Ala Cys Met Lys Val Tyr Gly Asn Arg Ser Pro Lys Gly Lys Val Val
 165 170 175
 Ala Leu Gln Gly Ala Gly Ser Val Gly Arg Tyr Leu Gly Glu Tyr Leu
 180 185 190
 Tyr Asn Glu Gly Ala Glu Val Tyr Val Cys Asp Ile Asn Glu Lys Asn
 195 200 205
 Leu Glu Leu Phe Lys Glu Lys Val Pro Asn Ala Lys Val Val Gly Ile
 210 215 220
 Asp Glu Ile Tyr Asp Val Lys Met Asp Ile Tyr Ala Pro Cys Ala Leu
 225 230 235 240
 Gly Ala Thr Ile Asn Asp Asp Thr Ile Asp Arg Leu Gln Cys Lys Ile
 245 250 255
 Val Ala Gly Ala Ala Asn Asn Gln Leu Ala Glu Asn Arg His Gly Lys
 260 265 270
 Ile Leu Lys Glu Arg Gly Val Leu Tyr Ala Pro Asp Tyr Leu Ile Asn

275 280 285
 Ala Gly Gly Val Met Asn Val Ser Ile Glu Phe Glu Gly Trp Ser Glu
 290 295 300
 Asp Lys Ala Ile Arg Met Val Asp Ser Ile Tyr Asp Thr Thr Leu Glu

 305 310 315 320
 Val Phe Asn Ile Ser Glu Glu Gln Asp Ile Pro Val Tyr Gln Ala Thr
 325 330 335
 Asp Ile Leu Ala Glu Ser Arg Ile Glu Ser Ile Lys Asn Ile Gln Gly
 340 345 350
 Lys Phe Leu Gly His Val Gly His Arg Phe Pro Gly Arg Lys Lys Arg
 355 360 365
 <210> 384
 <211> 368
 <212> PRT
 <213> *Pseudoalteromonas luteoviolacea*

 <400> 384
 Met Ile Glu Ser Gly Gln Phe Gln Arg Tyr Leu Thr Arg Ser Asp Asn
 1 5 10 15
 Asn Arg Arg Ile Ile Lys Val Ala Val Phe Asn Gln Val Glu Phe Asp
 20 25 30
 Asn His Glu Gln Val Val Phe Cys Ser Asp Glu Lys Ser Gly Leu Lys
 35 40 45
 Ala Ile Ile Ala Val His Ser Thr Lys Leu Gly Pro Ala Val Gly Gly
 50 55 60

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

115	120	125	
Gly Gly Ser Tyr Tyr Ser Ala Glu Asp Val Asn Ile Thr Thr Gly Asp			
130	135	140	
Val Met Val Met His Lys Glu Thr Asn Tyr Val Leu Gly Leu Glu Gly			
145	150	155	160
Lys Ser Gly Asn Pro Ser Pro Phe Thr Ala Leu Gly Thr Phe Leu Gly			
	165	170	175
Ile Lys Ala Ala Tyr Gln His Lys Phe Gly His Gln Asp Leu Thr Gly			
180	185	190	
Val Lys Val Ala Val Gln Gly Leu Gly Ala Val Ala Tyr Gly Leu Cys			
195	200	205	
Lys His Leu His Glu Ala Gly Ala Lys Leu Phe Val Thr Asp Ile Asn			
210	215	220	
Gln Ala Ser Ile Asp Arg Val Val Thr Asp Phe Gly Ala Val Ala Val			
225	230	235	240
Asp Ile Asp Glu Ile Tyr Asp Leu Asp Val Asp Val Tyr Ala Pro Cys			
	245	250	255
Ala Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Arg Ile Lys Ala			
260	265	270	
Thr Ile Ile Ala Gly Cys Ala Asn Asn Gln Leu Ala Glu Pro Arg His			
275	280	285	
Gly Asp Val Leu Arg Glu Lys Gly Val Leu Tyr Ala Pro Asp Tyr Val			
290	295	300	
Ile Asn Ala Gly Gly Ile Ile Asn Val Tyr Tyr Glu Thr Lys Pro Glu			
305	310	315	320
Gly Tyr Asn Glu Ala Leu Ala Thr Lys His Val Glu Gly Ile Phe Asp			
325	330	335	
Thr Leu Ala Glu Ile Phe Lys Arg Ser Asp Glu Glu Gln Lys Ser Thr			
340	345	350	
His Val Ile Ala Asp Glu Leu Ala Gln Glu Ile Ile Glu Asn Gly Leu			
355	360	365	

<210> 385

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 385

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

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

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

 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

 <210> 386
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 386

 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

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

 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285

Asn Ala Gly Gly Val Ile Asn Val Glu Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 387
 <211> 348
 <212> PRT
 <213> *Idiomarina xiamenensis*
 <400> 387
 Met Ser Leu Phe Glu His Lys Glu Phe Asp Gln His Glu Gln Val Val
 1 5 10 15
 Phe Cys His Asp Lys Ala Thr Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Met Gly Pro Ala Leu Gly Gly Thr Arg Leu Trp Asn Tyr
 35 40 45
 Ala Ser Ser Ser Glu Ala Leu Thr Asp Val Leu Arg Leu Ser Arg Gly
 50 55 60
 Met Thr Tyr Lys Ser Ala Ile Ser Gly Leu Pro Leu Gly Gly Gly Lys
 65 70 75 80
 Ala Val Ile Ile Gly Asp Ala Lys Gln Ile Lys Ser Ala Glu Leu Phe
 85 90 95
 Arg Ala Tyr Gly Arg Phe Val Asn Ser Leu Ser Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Val Asn Ile Arg Thr Ser Asp Ile Ala Ile Val Ala Glu
 115 120 125
 Glu Thr Asn Phe Val Ala Gly Thr Glu Gly Lys Ala Gly Asp Pro Ser

130 135 140
 Pro His Thr Ala Leu Gly Thr Tyr Leu Gly Leu Lys Ile Ala Ala Lys
 145 150 155 160
 His Arg Leu Gly Ser Glu Asp Leu Ser Gly Val Lys Ile Ala Val Gln
 165 170 175
 Gly Leu Gly Ala Val Gly Tyr Ala Phe Ala Glu Tyr Leu Ala Lys Asp
 180 185 190
 Gly Ala Glu Leu Phe Val Thr Asp Ile Asn Glu Glu Ala Val Asn Lys
 195 200 205

 Ala Val Asn Glu Leu Gly Ala Thr Ala Val Gly Leu Asp Asp Ile Tyr
 210 215 220
 Gly Leu Asp Val Asp Ile Tyr Ala Pro Cys Ala Leu Gly Ala Thr Ile
 225 230 235 240
 Asn Asp Asp Thr Leu Gln Gln Leu Lys Ala Lys Val Ile Ala Gly Ser
 245 250 255
 Ala Asn Asn Gln Leu Ala Thr Pro Lys His Asp Gln Leu Val Lys Asp
 260 265 270

 Gln Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly Val
 275 280 285
 Ile His Ile Cys Ser Glu Ala Ala Asn Phe Thr Val Glu Glu Thr Glu
 290 295 300
 Lys Arg Val Arg Gly Ile Tyr Asp Thr Leu Asp Asn Val Phe Thr Arg
 305 310 315 320
 Ala Ala Glu Gln Asn Arg Pro Thr Gly Glu Ile Ala Asp Ala Met Ala
 325 330 335

 Arg Glu Ile Ile Ala Asn Glu Lys Lys Lys Lys Ala
 340 345
 <210> 388
 <211> 366
 <212> PRT
 <213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 388

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Ile Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

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

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

 355 360 365
 <210> 389
 <211> 364
 <212> PRT
 <213> Unknown
 <220><223> Bacillus sp. FJAT-22090
 <400> 389
 Met Glu Ile Phe Lys Tyr Met Glu Thr Tyr Asp Tyr Glu Gln Leu Val
 1 5 10 15
 Phe Cys Gln Asp Lys Thr Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr
 35 40 45

 Ala Thr Glu Glu Glu Ala Ile Glu Asp Ala Leu Arg Leu Ala Lys Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65						70						75						80
Thr	Val	Ile	Ile	Gly	Asp	Pro	Leu	Lys	Asp	Lys	Asn	Glu	Glu	Met	Phe			
				85							90						95	
Arg	Ala	Phe	Gly	Arg	Phe	Ile	Gln	Gly	Leu	Asn	Gly	Arg	Tyr	Ile	Thr			
				100							105						110	
Ala	Glu	Asp	Val	Gly	Thr	Thr	Val	Ala	Asp	Met	Asp	Leu	Ile	His	Glu			
				115							120						125	
Glu	Thr	Asn	Tyr	Val	Thr	Gly	Ile	Ser	Glu	Ala	Phe	Gly	Ser	Ser	Gly			
				130							135						140	
Asn	Pro	Ser	Pro	Val	Thr	Ala	Tyr	Gly	Val	Tyr	Val	Gly	Met	Lys	Ala			
				145							150						155	
											155						160	
Ala	Ala	Lys	Glu	Ala	Phe	Gly	Ser	Asp	Ser	Leu	Ala	Gly	Lys	Thr	Val			
				165							170						175	
Ala	Val	Gln	Gly	Val	Gly	Asn	Val	Ala	Tyr	Thr	Leu	Cys	Glu	Tyr	Leu			
				180							185						190	
His	Asn	Glu	Gly	Ala	Lys	Leu	Ile	Ile	Ala	Asp	Ile	Asn	Gln	Ala	Ser			
				195							200						205	
Val	Asp	Arg	Ala	Val	Asn	Ala	Phe	Gly	Ala	Val	Gln	Val	Gly	Val	Asp			
				210							215						220	
Glu	Ile	Tyr	Ser	Gln	Glu	Ala	Asp	Ile	Phe	Ala	Pro	Cys	Ala	Leu	Gly			
				225							230						235	
											235						240	
Ala	Ile	Ile	Asn	Asp	Ser	Thr	Ile	Pro	Gln	Leu	Lys	Ala	Lys	Val	Ile			
				245							250						255	
Ala	Gly	Ser	Ala	Asn	Asn	Gln	Leu	Lys	Asp	Thr	Lys	His	Gly	Asp	Leu			
				260							265						270	
Ile	His	Glu	Met	Gly	Ile	Ala	Tyr	Ala	Pro	Asp	Tyr	Val	Ile	Asn	Ser			
				275							280						285	
Gly	Gly	Val	Ile	Asn	Val	Ala	Asp	Glu	Leu	Tyr	Gly	Tyr	Asn	His	Asp			
				290							295						300	
Arg	Ala	Met	Asn	Arg	Val	Ala	Gly	Ile	Tyr	Asp	Lys	Ile	Glu	Arg	Ile			
				305							310						315	
											315						320	

Phe Glu Ile Ser Lys Arg Asp Gly Ile Pro Thr Tyr Val Ala Ala Asp
325 330 335

Arg Leu Ala Glu Glu Arg Ile Ala Arg Val Ser Lys Ser Arg Ser Gln
340 345 350

Phe Leu Gln Asn Gly Lys His Ile Ile Thr Gly Arg
355 360

<210> 390

<

211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 390

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Ser Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 391
 <211> 361
 <212> PRT
 <213> Unknown
 <220><223
 > Azoarcus sp. CIB

<400> 391

Met His Pro Phe Gln Thr Asn Glu Gly Asp Ile Met Ser Val Phe Asn
1 5 10 15

Leu Ser Asp Phe Ala Asp His Glu Gln Val Val Phe Cys Ser Asp Glu
20 25 30

Lys Ser Gly Leu Lys Ala Ile Ile Ala Val His Asn Ser Asn Leu Gly
35 40 45

Pro Ala Leu Gly Gly Cys Arg Met Trp Pro Tyr Ala Ser Glu Glu Glu
50 55 60

Ala Ile Arg Asp Val Leu Arg Leu Ser Arg Gly Met Thr Tyr Lys Ser
65 70 75 80

Ala Met Ala Asn Leu Lys Leu Gly Gly Gly Lys Ser Val Ile Ile Gly
85 90 95

Asn Pro Arg Thr Asp Lys Thr Pro Glu Leu Leu Lys Ala Phe Ala Gln
100 105 110

Ala Val Glu Arg Val Asn Gly Arg Tyr Ile Ala Ala Glu Asp Ser Gly
115 120 125

Thr Gly Val Asp Asp Met Lys Phe Met Ser Gln Phe Thr Asp His Val
130 135 140

Ala Gly Ile Ile Asp Lys Pro Ser Glu Asn Gly Val Arg Ser Gly Asp
145 150 155 160

Pro Ser Pro Ala Thr Ala Tyr Gly Thr Phe Val Gly Ile Lys Ala Ala
165 170 175

Val Lys Glu Arg Leu Gly Arg Asp Ser Leu Ala Gly Leu Lys Ile Ala
180 185 190

Val Gln Gly Leu Gly Asn Val Gly Phe Asp Leu Ala Arg Gln Leu Lys
195 200 205

Glu Ala Gly Ala Gln Leu Trp Val Thr Asp Ile His Arg Glu Pro Leu
210 215 220

Ile Arg Ala Gly Lys Glu Leu Asp Ala Thr Val Val Ala Pro Asp Glu
225 230 235 240

Ile Phe Gly Leu Asp Val Asp Val Phe Ala Pro Cys Ala Met Gly Ala

245 250 255

Ile Ile Asn Asp Gln Thr Leu Pro Gln Leu Lys Ala Lys Ile Val Ala

260 265 270

Gly Ala Ala Asn Asn Gln Leu Ala Glu Pro Arg His Gly Leu Ala Leu

275 280 285

Met Asn Lys Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly

290 295 300

Gly Ile Ile Asp Val Tyr Tyr Glu Arg Thr Gly Asn Phe Asp Arg Ala

305 310 315 320

Ala Leu Lys Ser His Ile Glu Ser Ile Tyr Asp Asn Leu Met Glu Ile
325 330 335

Phe Ala Arg Ala Arg Lys Glu Glu Arg Pro Thr Gly Glu Val Ala Asp
340 345 350

Ala Ile Ala Glu Glu Arg Phe Lys Arg
355 360

<210> 392

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 392

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Thr Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 393
 <211> 360
 <212> PRT
 <213> Micromonospora avicenniae
 <400> 393
 Met Gly Val Phe Thr Ser Thr Asp Asp Pro Gly Ser Thr Gly His Glu
 1 5 10 15

 Gln Val Val Phe Cys Gln Asp Lys Gln Thr Gly Leu Lys Ala Ile Ile
 20 25 30
 Gly Ile Tyr Ser Thr Ala Leu Gly Pro Ala Leu Gly Gly Thr Arg Phe
 35 40 45
 Tyr Pro Tyr Asp Ser Glu Glu Ala Ala Leu Ala Asp Val Leu Asp Leu
 50 55 60
 Ser Arg Gly Met Ala Tyr Lys Asn Ala Leu Ala Gly Leu Asp Leu Gly
 65 70 75 80

 Gly Gly Lys Ala Val Ile Trp Gly Asp Pro Glu Lys Ile Lys Ser Glu
 85 90 95
 Ala Leu Leu Arg Ala Tyr Gly Arg Phe Val Glu Ser Leu Gly Gly Arg
 100 105 110
 Tyr Tyr Thr Ala Cys Asp Val Gly Thr Tyr Val Pro Asp Met Asp Val
 115 120 125
 Ile Ala Arg Glu Thr Arg Tyr Val Thr Gly Arg Ser Val Glu His Gly
 130 135 140

 Gly Ala Gly Asp Ser Ser Ile Leu Thr Ala Trp Gly Val Phe Gln Gly
 145 150 155 160
 Met Arg Ala Ala Ala Glu His Val Trp Gly Glu Pro Thr Leu Arg Gly
 165 170 175

Arg Arg Val Gly Val Thr Gly Leu Gly Lys Val Gly Lys Tyr Leu Val
180 185 190

Gly His Leu Leu Asp Asp Gly Ala Glu Val Val Ala Ser Asp Val Asn
195 200 205

Pro Arg Ala Leu Glu Trp Ala Arg Thr Asn His Pro Gln Val Thr Leu
210 215 220

Val Asp Asp Ala Ala Leu Leu Val Ser Ser Asp Ile Asp Val Tyr Ala
225 230 235 240

Pro Cys Ala Leu Gly Gly Ala Leu Asn Asp Glu Thr Val Pro Ala Leu
245 250 255

Arg Ala Lys Val Val Ala Gly Ala Ala Asn Asn Gln Leu Ala His Ser
260 265 270

Gly Ile Glu Lys Leu Leu Ala Asp Arg Gly Ile Leu Tyr Ala Pro Asp
275 280 285

Tyr Val Val Asn Ala Gly Gly Val Ile Gln Val Ala Asp Glu Ile Glu
290 295 300

Gly Phe Asn Phe Glu Arg Ala Lys Leu Arg Ala Thr Arg Ile Tyr Asp
305 310 315 320

Thr Thr Arg Glu Ile Leu Glu Leu Ala Asp Ala Glu Gly Val Pro Pro
325 330 335

Ala Val Ala Ala Asp Arg Leu Ala Glu Arg Arg Met Ala Glu Val Gly
340 345 350

Arg Leu Arg Thr Ile His Leu Pro
355 360

<210> 394

<211> 364

<212> PRT

<213> *Terribacillus goriensis*

<400> 394

Met Lys Ile Phe Glu Thr Leu Glu Gln Tyr Asp Tyr Glu Gln Leu Val
1 5 10 15

Leu Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala Ile His

				20				25				30			
Asp	Thr	Thr	Leu	Gly	Pro	Ala	Leu	Gly	Gly	Thr	Arg	Met	Trp	Thr	Tyr
35				40				45							
Ala	Thr	Glu	Glu	Asp	Ala	Ile	Val	Asp	Ala	Leu	Arg	Leu	Ala	Lys	Gly
50				55				60							
Met	Thr	Tyr	Lys	Asn	Ala	Ala	Ala	Gly	Leu	Asn	Leu	Gly	Gly	Gly	Lys
65				70				75				80			
Thr	Val	Ile	Ile	Gly	Asp	Pro	Lys	Lys	Asp	Lys	Asn	Glu	Ala	Met	Phe
85				90				95							
Arg	Ala	Phe	Gly	Arg	Tyr	Val	Gln	Ser	Leu	Asn	Gly	Arg	Tyr	Ile	Thr
100				105				110							
Ala	Glu	Asp	Val	Gly	Thr	Thr	Val	Glu	Asp	Met	Glu	Leu	Ile	His	Thr
115				120				125							
Glu	Thr	Asp	Phe	Val	Thr	Gly	Ile	Ser	Ala	Glu	Ser	Gly	Ser	Ser	Gly
130				135				140							
Asn	Pro	Ser	Pro	Val	Thr	Ala	Tyr	Gly	Val	Tyr	Lys	Gly	Ile	Lys	Ala
145				150				155				160			
Ser	Ala	Lys	Glu	Ala	Phe	Gly	Asp	Asp	Ser	Leu	Glu	Gly	Lys	Thr	Ile
165				170				175							
Ala	Val	Gln	Gly	Ile	Gly	Asn	Val	Ala	Tyr	Ala	Leu	Cys	Glu	His	Leu
180				185				190							
His	Ala	Glu	Gly	Ala	Lys	Leu	Ile	Val	Thr	Asp	Ile	Asn	Lys	Glu	Ala
195				200				205							
Val	Gln	Lys	Ala	Val	Glu	Ala	Phe	Gly	Ala	Thr	Ala	Val	Asp	Pro	Asp
210				215				220							
Asp	Ile	Tyr	Gly	Val	Glu	Cys	Asp	Ile	Phe	Ala	Pro	Cys	Ala	Leu	Gly
225				230				235				240			
Ala	Val	Ile	Asn	Asp	Asp	Thr	Leu	Arg	Val	Leu	Lys	Ala	Lys	Val	Val
245				250				255							
Ala	Gly	Ala	Ala	Asn	Asn	Gln	Leu	Lys	Glu	Glu	His	His	Gly	Gln	Ile
260				265				270							

Leu Phe Glu Arg Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ser
275 280 285

Gly Gly Val Ile Asn Val Glu Asp Glu Leu His Gly Tyr Asn Arg Glu
290 295 300

Arg Ala Leu Arg Lys Val Glu Thr Ile Tyr Asp Ser Leu Gln Arg Val
305 310 315 320

Phe Glu Ile Ala Lys Arg Asp Glu Ile Pro Thr Ser Ile Ala Ala Asp
325 330 335

Arg Met Ala Glu Glu Arg Ile Glu Thr Met Arg Lys Ser Arg Ser Gln
340 345 350

Phe Leu Arg Asn Gly His His Thr Leu Ser Arg Arg
355 360

<210> 395

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 395

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Tyr Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100	105	110	
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile			
115	120	125	
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser			
130	135	140	
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met			
145	150	155	160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys			
	165	170	175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys			
	180	185	190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys			
	195	200	205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu			
	210	215	220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala			
225	230	235	240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys			
	245	250	255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly			
	260	265	270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile			
	275	280	285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn			
290	295	300	
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala			
305	310	315	320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala			
	325	330	335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg			
	340	345	350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 396

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 396

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

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

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu His Tyr Gly Tyr Asn
290 295 300

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

<210> 397

<211> 367

<212> PRT

<213> Mizugakiibacter sediminis

<400> 397

Met Ile Phe Glu Thr Ile Ala Thr Ser Gly His Glu Glu Val Val Phe
1 5 10 15
Cys His Asn Lys Asp Ala Gly Leu Lys Ala Ile Ile Ala Val His Asn
20 25 30

Thr Val Leu Gly Pro Ala Leu Gly Gly Leu Arg Met Trp Pro Tyr Lys
35 40 45

Thr Glu Gln Glu Ala Leu Asn Asp Val Leu Arg Leu Ser Arg Gly Met
50 55 60

Thr Tyr Lys Asn Ala Val Ala Gly Leu Asn Leu Gly Gly Gly Lys Ala
65 70 75 80

Val Ile Ile Gly Asp Pro Ser Lys Asp Lys Ser Glu Ala Leu Phe Arg
85 90 95

Ala Phe Gly Arg Phe Val Asn Ser Leu Asn Gly Arg Tyr Ile Thr Ala
100 105 110

Glu Asp Val Gly Ile Asp Val Asn Asp Met Glu Trp Val Phe Arg Glu
115 120 125

Thr Glu Phe Val Thr Gly Val His Gln Val His Gly Gly Ser Gly Asp
130 135 140

Pro Ser Pro Phe Thr Ala Phe Gly Thr Leu Gln Gly Leu Met Ala Thr
145 150 155 160

Leu Ser Ala Arg Phe Gly Asn Glu Asp Val Gly Lys Tyr Ser Tyr Ala
165 170 175

Val Gln Gly Val Gly His Val Gly Met Glu Phe Val Lys Leu Leu Arg
180 185 190

Glu Gln Gly Ala Lys Val Phe Val Thr Asp Ile Asn Lys Glu Ala Val
195 200 205

Gln Arg Cys Val Asp Glu Leu Gly Cys Glu Ala Val Gly Leu Asp Asp
210 215 220

Ile Tyr Asp Val Asp Ala Asp Val Tyr Ser Pro Cys Ala Leu Gly Gly
225 230 235 240

Thr Val Asn Glu Lys Thr Leu Pro Arg Leu Lys Met Lys Ile Ile Cys
245 250 255

Gly Ala Ala Asn Asn Gln Leu Ala Asn Asp Ala Ile Gly Asp Glu Val
260 265 270

Glu Lys Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Ala Val Asn Ala Gly

275 280 285
 Gly Val Met Asn Val Ser Leu Glu Ile Asp Gly Tyr Asn Arg Glu Arg
 290 295 300
 Ala Met Arg Met Met Arg Thr Ile Tyr Tyr Asn Leu Ser Arg Ile Phe

 305 310 315 320
 Gln Ile Ala Lys Arg Asp Gly Ile Pro Thr Tyr Lys Ala Ala Asp Arg
 325 330 335
 Met Ala Glu Glu Arg Ile Ser Ala Ile Gly Lys Ile Lys Leu Pro Thr
 340 345 350
 Met Gly Asn His Gly Pro Arg Phe Leu Gly Arg Met Arg Gly Gln
 355 360 365
 <210> 398
 <211> 368
 <212> PRT
 <213> Flavobacterium haorani i

 <400> 398
 Met Thr Ala Asp Leu Leu Thr Thr Ser Glu Leu His Lys Val Asp Pro
 1 5 10 15
 Val Phe Gly Gln Val Ser Phe Asp Gly His Glu Gln Val Val Phe Cys
 20 25 30
 Tyr Asp Lys Asp Thr Gly Leu Lys Ala Ile Ile Gly Ile His Asn Thr
 35 40 45
 Val Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Lys Tyr Thr Asn
 50 55 60

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

115 120 125
 Asp Val Gly Met Glu Thr Lys Asp Met Asp Ile Val Asn Asn Val Thr
 130 135 140
 Lys His Val Ala Gly Ile Ser Val Glu Arg Gly Gly Ser Gly Asn Pro
 145 150 155 160
 Ser Pro Val Thr Ala Tyr Gly Val Phe Met Gly Met Lys Ala Ala Ala
 165 170 175
 Lys Tyr Lys Phe Gly Ser Asp Asn Leu Glu Gly Lys Ser Val Leu Val
 180 185 190

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

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

 Val Met Glu Lys Thr Glu Asn Ile Tyr Asn Thr Ala Leu Glu Ile Phe
 325 330 335
 Asp Phe Ala Asp Lys Asn Asn Val Thr Thr His Ala Ala Ala Leu Ser
 340 345 350
 Ile Ala Gln Lys Arg Ile Glu Asp Arg Lys Asn Glu Leu Gln Asn Lys
 355 360 365

<210> 399

<211> 349

<212> PRT

<213> *Sedimenticola thiotaurini*

<400> 399

Met Lys Leu Phe Ser His His Glu Phe Asp Asn His Glu Gln Val Val

1 5 10 15
Phe Cys His Asp Lys Thr Ser Gly Leu Lys Ala Ile Ile Ala Ile His

20 25 30
Asn Thr His Arg Gly Pro Ala Leu Gly Gly Cys Arg Met Tyr Pro Tyr

35 40 45
Ala Ser Glu Ala Glu Ala Leu Asn Asp Val Leu Arg Leu Ser Arg Gly

50 55 60
Met Thr Tyr Lys Ser Ala Ile Ala Asn Leu Pro Leu Gly Gly Gly Lys

65 70 75 80
Ser Val Ile Ile Gly Asp Pro His Ser Asp Lys Thr Pro Gln Leu Ile

85 90 95
Arg Ala Met Gly Val Ala Val Glu Arg Leu Gly Gly Arg Tyr Ile Val

100 105 110
Ala Glu Asp Ser Gly Thr Ser Val Pro Asp Met Leu Leu Met Ser Glu

115 120 125
Gln Thr Arg His Ile Ser Gly Ile Ala Glu Lys Phe Asp Ala Asp Gly

130 135 140
Lys Arg Arg Ser Gly Asp Pro Ser Pro Ile Thr Ala Arg Gly Val Phe

145 150 155 160
Val Gly Ile Gln Ala Ala Val Arg Tyr Arg Leu Gly Arg Asp Asp Leu

165 170 175
Gln Gly Val Arg Val Ala Ile Gln Gly Leu Gly Asn Val Gly Tyr His

180 185 190
Leu Ala Ser Gln Leu Arg Ala Ala Gly Ala Arg Leu Trp Val Ser Asp

195 200 205

Ile Asn Gln Ala Ala Val Gln Arg Ala Val Asp Glu Leu Gly Ala Val
210 215 220
Ala Val Ala Asn Gly Glu Ile Tyr Asp Gln Ala Val Asp Leu Phe Ala
225 230 235 240
Pro Cys Ala Met Gly Ala Ile Leu Asn Asp Thr Thr Ile Pro Arg Leu
245 250 255
Gln Ala Arg Ile Val Ala Gly Ala Ala Asn Asn Gln Leu Ala Asp Lys
260 265 270
Arg His Gly Gln Ala Leu Met Glu Arg Gly Ile Leu Tyr Ala Pro Asp
275 280 285
Tyr Val Ile Asn Ala Gly Gly Val Ile Asp Val Cys Tyr Glu Arg Ser
290 295 300
Asp Met Asp Pro Gln Gln Val Met Glu Gln Val Asp Gly Ile Gly Asp
305 310 315 320
Thr Leu Thr Glu Ile Phe Ser Arg Ala Glu Gln Gln His Lys Pro Thr
325 330 335
Asp Val Leu Ala Asp Gln Leu Ala Glu Glu Arg Phe Ser
340 345
<210> 400
<211> 366
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 400
Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn His Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95

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

 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220

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

 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350

 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 401
 <211> 344
 <212> PRT
 <213> Pseudogulbenkiania subflava
 <400> 401
 Met Ser Ile Phe Glu Leu Pro Asp Phe Asp Gly His Glu Gln Val Val
 1 5 10 15
 Phe Ala Ser Asp Ser Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asn Thr His Arg Gly Pro Ala Met Gly Gly Cys Arg Met Trp Ala Tyr

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

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

Ala Val Arg His Arg Leu Gly Val Asp Ser Val Asn Gly Leu Thr Val

165 170 175

Ala Val Gln Gly Leu Gly His Val Gly Tyr Asp Leu Ala Arg Arg Leu

180 185 190

His Glu Ala Gly Ala Arg Leu Ile Val Ala Asp Ile Asp Arg Ala Asn

195 200 205

Gly Glu Arg Ala Ala Ala Glu Phe Gly Ala Ser Val Val Ser Pro Asp

210 215 220

Glu Ile Val Asp Ala Gln Ala Asp Val Phe Ala Pro Cys Ala Leu Gly

225 230 235 240

Ala Val Leu Asn Arg Gln Thr Leu Pro Arg Leu Lys Cys Ser Val Val

245 250 255

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

260 265 270

Leu Arg Asp Ala Gly Val Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala

275 280 285

Gly Gly Ile Ile Lys Val Cys Ala Glu Tyr Leu Gln Glu Pro Val Asp

290 295 300

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

305 310 315 320

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

325 330 335

Thr Leu Ala Arg Thr Arg Phe Ala

340

<210> 402

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 402

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60

 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125

 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190

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

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

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 403

<211> 344

<212> PRT

<213> Carboxydotherrnus pertinax

<400> 403

Met Glu Ile Ser Lys Lys Glu Asn Tyr Gln Gly Tyr Glu Trp Val Val

1 5 10 15
 Phe Ala Ser Asp Asp Lys Thr Asn Phe Lys Ala Ile Ile Ala Val His
 20 25 30
 Ser Thr Glu Leu Gly Pro Ala Leu Gly Gly Cys Arg Met Trp Phe Tyr
 35 40 45
 Asn Asn Glu Asn Glu Ala Leu Thr Asp Val Leu Arg Leu Ala Glu Gly
 50 55 60
 Met Thr Tyr Lys Asn Ser Ala Met Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80
 Ala Val Ile Ile Gly Asp Pro Arg Thr Asp Lys Ser Pro Glu Leu Phe
 85 90 95
 Ala Arg Phe Ala Glu Ala Val Asn Ser Leu Gly Gly Lys Tyr Tyr Thr

100 105 110
 Ala Glu Asp Val Gly Ile Ser Pro Ala Asp Met Leu Glu Val Tyr Lys
 115 120 125
 His Thr Pro Tyr Val Val Gly Leu Pro Ala Lys Ser Gly Asp Pro Ser

 130 135 140
 Pro Phe Thr Ala Tyr Gly Val Tyr Val Gly Met Lys Ala Ala Val Glu
 145 150 155 160
 Glu Ala Phe Gly Asp Thr Ser Leu Glu Gly Lys Lys Val Ala Val Gln
 165 170 175
 Gly Leu Gly His Val Gly Met Tyr Leu Leu Glu His Leu Tyr Asn Glu
 180 185 190
 Gly Ala Lys Leu Ile Val Thr Asp Ile Phe Thr Glu Arg Val Lys Glu

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

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

 325 330 335
 Tyr Ala Lys Lys Arg Leu Asn Arg
 340

<210> 404

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 404

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Tyr Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 405

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 405

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

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

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

 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

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

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290

295

300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305

310

315

320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325

330

335

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

340

345

350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355

360

365

<210> 406

<211> 371

<212> PRT

<213> Planomonospora sphaerica

<400> 406

Met Thr Asp Val Phe Gly Leu Ser His Lys Asp Ser Ser Pro Val Ser

1

5

10

15

Thr Pro Met Ser Gly Gln Ala Gly His Glu Gln Val Val Phe Cys Ser

20

25

30

Asp Glu Arg Ser Gly Leu Arg Ala Ile Ile Ala Ile His Asn Thr Ala

35

40

45

Leu Gly Pro Ala Leu Gly Gly Thr Arg Phe Tyr Pro Tyr Glu Ser Glu

50

55

60

Gln Ala Ala Leu Ala Asp Val Leu Asn Leu Ser Arg Ala Met Ala Tyr

65

70

75

80

Lys Asn Ala Leu Ala Gly Leu Asp Leu Gly Gly Gly Lys Ala Val Ile

85

90

95

Ile Gly His Pro Glu Thr Asp Lys Asn Glu Ala Met Leu Arg Ala Tyr

100

105

110

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

115

120

125

Val Gly Thr Tyr Ser Glu Asp Met Asp Leu Ile Ala Arg Glu Thr Ser
130 135 140

Tyr Val Thr Gly Arg Thr Leu Ala Gln Gly Gly Ala Gly Asp Ser Ser
145 150 155 160

Ile Leu Thr Ala Phe Gly Val Phe Gln Gly Met Arg Ala Ala Ser Glu
165 170 175

His Val Phe Gly Thr Ser Ser Leu Arg Gly Arg Arg Val Gly Val Glu
180 185 190

Gly Val Gly Lys Val Gly His Arg Leu Val Asp His Leu Val Glu Asp
195 200 205

Gly Ala Glu Val Val Val Cys Asp Val Ser Glu Arg Ala Val Glu Leu
210 215 220

Val Arg Arg Arg His Pro Gln Val Glu Val Val Ala Asp Gln Ser Ala
225 230 235 240

Leu Thr Ala Ala Asp Ile Asp Val Tyr Ala Pro Cys Ala Leu Gly Gly
245 250 255

Ala Leu Asp Asp Gly Thr Val Ala Arg Leu Arg Ala Ser Ile Val Cys
260 265 270

Gly Gly Ala Asn Asn Gln Leu Ala His Pro Gly Val Glu Lys Gln Leu
275 280 285

Ala Asp Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Val Val Asn Ser Gly
290 295 300

Gly Val Ile Gln Val Ala Asp Glu Ile Gln Gly Phe Asp Met Asp Arg
305 310 315 320

Ala Arg Ala Lys Ala Glu Lys Ile Tyr Ala Thr Thr Leu Lys Ile Phe
325 330 335

Thr Thr Ala Ala Glu Asp Gly Val Pro Pro Ala Val Ala Ala Asp Arg
340 345 350

Leu Ala Glu Arg Arg Met Ser Glu Val Gly Arg Ile Arg Gly Ile Trp
355 360 365

Leu Gly Arg

370

<210> 407

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 407

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Lys Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300

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

<210> 408

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 408

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Tyr Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110

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

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

 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 409

<211> 366

<212> PRT

<213> Bacillus cellulosilyticus

<400> 409

Met Glu Leu Phe Lys Tyr Met Glu Thr Tyr Asp Tyr Glu Gln Val Val
1 5 10 15

Val Cys Gln Asp Lys Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His
20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
35 40 45

Glu Ser Glu Glu Ala Ala Phe Glu Asp Ala Leu Arg Leu Ala Lys Gly

50 55 60

Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
65 70 75 80

Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Asn Glu Ala Met Phe
85 90 95

Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr
100 105 110

Ala Glu Asp Val Gly Thr Ser Val Glu Asp Met Asp Ile Val Tyr Gln

115 120 125

Glu Thr Asp Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly
 130 135 140
 Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Phe Val Gly Met Lys Ala
 145 150 155 160
 Ala Ala Lys Glu Ala Phe Gly Thr Asp Ser Leu Glu Gly Lys Lys Val
 165 170 175
 Ala Val Gln Gly Val Gly Asn Val Ala Phe Thr Leu Cys Lys Tyr Leu
 180 185 190
 His Glu Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys Asp Ala
 195 200 205
 Val Lys Arg Ala Val Glu Glu Phe Asp Ala Glu Ala Val Asp Pro Glu
 210 215 220
 Asp Ile Tyr Ser Val Gln Cys Asp Ile Tyr Ser Pro Cys Ala Leu Gly
 225 230 235 240
 Ala Thr Ile Asn Asp Asn Thr Ile Pro Lys Leu Lys Ala Lys Val Ile
 245 250 255
 Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Thr Arg His Gly Asp Ile
 260 265 270
 Leu Gln Glu Ile Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ser
 275 280 285
 Gly Gly Val Ile Asn Val Ala Asp Glu Leu Leu Gly Tyr Asn Arg Asp
 290 295 300
 Arg Ala Phe Lys Lys Val Glu Thr Ile Tyr Asp Ser Ile Ser Thr Ile
 305 310 315 320
 Phe Lys Ile Ala Lys Arg Asp Ser Ile Pro Thr Tyr Ala Ala Ala Asp
 325 330 335
 Arg Met Ala Glu Glu Arg Ile Glu Asn Met Arg Arg Ser Arg Lys Gln
 340 345 350
 Phe Leu Arg Ser Asp Val Asn Ile Ile Ser Arg Gly Arg Arg
 355 360 365
 <210> 410
 <211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 410

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys His Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 411
 <211> 359
 <212> PRT
 <213> Tenericutes bacterium

 <400> 411
 Met Ser Asp Phe Lys His Phe Glu Tyr Met Ala Lys His Arg Tyr Glu
 1 5 10 15
 Gln Val Val Tyr Phe Tyr Asp Lys Thr Thr Gly Leu Lys Gly Ile Thr
 20 25 30
 Cys Ile His Asn Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Leu
 35 40 45
 Trp Asn Tyr Ala Ser Glu Glu Asp Ala Val Ile Asp Ala Leu Arg Leu

50 55 60
 Ala Arg Gly Met Thr Tyr Lys Ala Ala Ala Ala Gly Leu Asn Leu Gly
 65 70 75 80
 Gly Gly Lys Thr Val Leu Ile Gly Asp Pro Glu Thr Val Lys Ser Glu
 85 90 95
 Gly Tyr Phe Arg Ala Leu Gly Arg Tyr Val Gln Ser Leu Asn Gly Arg
 100 105 110
 Tyr Ile Thr Ala Glu Asp Val Asn Thr Ser Thr Lys Asp Met Asp Phe
 115 120 125

 Val Ala Met Glu Thr Asp Tyr Val Val Gly Leu Glu Gly Lys Ser Gly
 130 135 140
 Asn Pro Ser Pro Met Thr Ala Leu Gly Ala Phe His Gly Ile Arg Ala
 145 150 155 160
 Ala Leu Gln Tyr Lys Phe Gly Asn Glu Glu Phe Ser Lys Tyr Thr Phe
 165 170 175
 Ala Val Gln Gly Ala Gly Gln Thr Gly Tyr Tyr Leu Ile Lys Lys Leu
 180 185 190

 Val Glu Ala Lys Ala Lys Lys Ile Tyr Phe Ser Glu Ile Asn Pro Lys
 195 200 205
 His Ile Glu Arg Met Lys Arg Glu His Pro Asp Val Glu Phe Val Glu
 210 215 220
 Pro Lys Asn Tyr Phe Gly Leu Asn Val Asp Val Ile Val Pro Cys Ala
 225 230 235 240
 Leu Gly Gly Val Leu Asn Asp Glu Ser Ile Pro Gln Ile Lys Ala Lys
 245 250 255

 Val Ile Ala Gly Thr Ala Asn Asn Val Leu Leu Asp Glu Asp Ile His
 260 265 270
 Gly Thr Met Ile Lys Glu Lys Gly Ile Leu Tyr Ala Pro Asp Phe Val
 275 280 285
 Ile Asn Ala Gly Gly Leu Ile Asn Val Tyr His Glu Leu Lys Glu Tyr
 290 295 300

Asn Val Gly Arg Ala Thr Arg Asp Ile Glu Lys Ile Tyr Asp Arg Leu
305 310 315 320

Leu Glu Ile Phe Lys Ile Ala Asp Thr Glu Asn Ile His Thr Gln Gln
325 330 335

Ala Ala Lys Val Phe Ala Lys Lys Arg Ile Glu Thr Ile Asn Asn Val
340 345 350

Gln Asp Asn Tyr Ile Lys Arg
355

<210> 412

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 412

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Trp Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130	135	140	
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met			
145	150	155	160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys			
	165	170	175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys			
	180	185	190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys			
195	200	205	
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu			
210	215	220	
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala			
225	230	235	240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys			
	245	250	255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly			
260	265	270	
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile			
275	280	285	
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn			
290	295	300	
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala			
305	310	315	320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala			
	325	330	335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg			
340	345	350	
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg			
355	360	365	
<210> 413			
<211> 359			

<212> PRT

<213> *Acholeplasma brassicae*

<400> 413

Met Asn Asp Val Lys Val Phe Asp Leu Met Glu Lys Asp Lys Tyr Glu

1 5 10 15

Gln Val Val Tyr Phe Tyr Asp Lys Ser Thr Gly Leu Lys Gly Ile Thr

20 25 30

Val Ile His Asn Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Ile

35 40 45

Trp Asn Tyr Glu Ser Glu Asp Asp Ala Leu Lys Asp Cys Leu Arg Leu

50 55 60

Ala Arg Gly Met Thr Tyr Lys Ala Ala Ala Ala Gly Leu Asn Leu Gly

65 70 75 80

Gly Gly Lys Thr Val Leu Ile Gly Asp Pro Lys Ile Val Lys Ser Glu

85 90 95

Ala Tyr Phe Arg Gly Leu Gly Arg Tyr Val Gln Ser Leu Asn Gly Arg

100 105 110

Tyr Ile Thr Ala Glu Asp Val Asn Thr Ser Thr Lys Asp Met Ser Tyr

115 120 125

Val His Met Glu Thr Asp Tyr Val Val Gly Leu Glu Gly Lys Ser Gly

130 135 140

Asn Pro Ser Pro Phe Thr Ala Leu Gly Ala Phe Tyr Gly Ile Lys Ala

145 150 155 160

Ala Leu Lys Tyr Arg Phe Asn Asn Glu Ser Ile Glu Asn Tyr Thr Phe

165 170 175

Ala Val Gln Gly Ala Gly Gln Thr Gly Tyr Tyr Leu Ile Asn Tyr Leu

180 185 190

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

195 200 205

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

210 215 220

Pro Lys Asp Ile Phe Thr Leu Asp Val Asp Val Phe Cys Pro Cys Ala
 225 230 235 240
 Leu Gly Gly Val Leu Asn Asp Glu Thr Ile Lys Val Leu Lys Ala Pro
 245 250 255
 Ile Ile Ala Gly Thr Ala Asn Asn Val Leu Leu Asp Glu Gln Thr His
 260 265 270
 Gly Asn Ala Leu Leu Asp Lys Gly Ile Leu Tyr Ala Pro Asp Phe Val
 275 280 285
 Ile Asn Ala Gly Gly Leu Ile Asn Val Tyr Tyr Glu Leu Asn Asp Tyr
 290 295 300
 Thr Lys Glu Lys Val Glu His Asp Ile Lys Leu Ile Tyr Asp Arg Leu
 305 310 315 320
 Ile Gln Val Phe Asp Ile Ser Lys Asn Gln Asn Ile Pro Thr Gln Leu
 325 330 335
 Ala Ala Lys Val Phe Ala Lys Asn Arg Ile Glu Ser Val Arg Asn Leu
 340 345 350
 His Asp Asn Tyr Ile Lys Arg
 355
 <210> 414
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 414
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Arg Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

 355 360 365
 <210> 415
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 415
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45

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

 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175

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

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300

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

<210> 416

<211> 368

<212> PRT

<213> Flavobacteria bacterium7

<400> 416

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Met Thr Thr Asp Ile Ile Asn Ser Asn Glu Leu His Lys Val Asp Pro
1           5           10           15
Val Phe Gly Gln Ile Ser Phe Asp Gly His Glu Gln Val Val Phe Cys
           20           25           30
Asn Asp Lys Asp Thr Gly Leu Lys Ala Ile Ile Gly Ile His Asn Thr
           35           40           45
Val Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Lys Tyr Ser Asn

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

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

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

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Tyr Ser Leu Asp Val Asp Ile Tyr Ala Pro Cys Ala Leu Gly Ala Thr

245 250 255

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

260 265 270

Ala Ala Asn Asn Gln Leu Ala Asn Glu Val Ile His Gly Lys Leu Leu

275 280 285

Lys Glu Lys Gly Ile Leu Tyr Ala Pro Asp Phe Leu Ile Asn Ala Gly

290 295 300

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

305 310 315 320

Val Met Glu Lys Thr Glu Asn Ile Tyr Asn Thr Ala Met Asp Ile Phe

325 330 335

Asn Leu Ser Asp Val Gln Asn Ile Thr Thr His Gln Ala Ala Leu Asn

340 345 350

Ile Ala Gln Lys Arg Ile Asp Asp Arg Lys Lys Glu Leu Gln Asn Lys

355 360 365

<210> 417

<211> 353

<212> PRT

<213> *Thalassospira alkalitolerans*

<400> 417

Met Asn Val Phe Ser Asp Thr Ala Phe Asp Gly His Glu Gln Val Val

1 5 10 15

Phe Ala Ser Asp Pro Asp Thr Gly Leu Lys Ser Ile Ile Ala Val His

20 25 30

Asn Thr Asn Leu Gly Pro Ser Leu Gly Gly Cys Arg Met Trp Pro Tyr

35 40 45

Ala Thr Glu Gln Glu Ala Ile His Asp Val Leu Arg Leu Ser Arg Gly

50 55 60

Met Thr Tyr Lys Ser Ala Leu Ala Asn Leu Pro Leu Gly Gly Gly Lys

65 70 75 80

Ser Val Ile Ile Gly Asp Pro Arg Ser Gln Lys Thr Pro Gln Leu Phe
85 90 95

Arg Ala Met Gly Arg Ala Ile Glu Gln Val Gly Gly Arg Tyr Ile Val
100 105 110

Ala Glu Asp Val Gly Thr Thr Pro Ala Asp Met Val Gln Ile Ala Ser
115 120 125

Gln Thr Lys His Val Gly Gly Ile Asn Asp Gly Lys Asp Pro Ala Arg
130 135 140

Thr Gly Asp Pro Ser Pro Phe Thr Ala Tyr Gly Val Phe Met Gly Leu
145 150 155 160

Lys Glu Ala Val Arg Phe Lys Asn Gly His Asp Asp Leu Gly Gly Leu
165 170 175

Arg Val Ala Val Gln Gly Leu Gly Asn Val Gly Tyr His Leu Cys Arg
180 185 190

Met Leu His Lys Ala Gly Ala Gln Leu Val Val Ala Asp Leu Asn Ala
195 200 205

Asn Asn Val Asn Asn Ala Val Thr Glu Phe Gly Ala Thr Thr Val Pro
210 215 220

Ala Asp Glu Ile Leu Tyr Ala Asp Val Asp Ile Leu Ala Pro Cys Ala
225 230 235 240

Leu Gly Gly Val Ile Asn Asp His Ser Ile Asn Lys Ile Arg Ala Arg
245 250 255

Ile Ile Ala Gly Ala Ala Asn Asn Gln Leu Glu Ser Asp Arg His Gly
260 265 270

Asp Met Leu Arg Glu Ala Asp Ile Leu Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Val Glu Val Tyr Tyr Cys Arg Glu Gly Lys Pro
290 295 300

Val Thr Glu Thr Asn Lys His Ile Glu Gly Ile Gly Ala Thr Val Arg
305 310 315 320

Glu Ile Phe Glu Arg Ala Lys Gln Gln Asn Leu Ser Thr Gly Phe Val

325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Phe Gly Ser Lys Ala Lys Thr Val
340 345 350
Thr

<210> 418

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 418

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

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

 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270

 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Thr Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335

 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

 <210> 419
 <211> 367
 <212> PRT
 <213> Staphylococcus schleiferi
 <400> 419
 Met Ile Phe Glu Lys Met Ala Gln Ala Asp Tyr Glu Gln Leu Val Phe
 1 5 10 15

Cys His Asp Glu Thr Thr Gly Leu Lys Ala Ile Ile Cys Ile His Asp

20 25 30

Thr Thr Leu Gly Pro Ala Leu Gly Gly Cys Arg Phe Trp Asn Tyr Glu

35 40 45

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

50 55 60

Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Ala Lys Thr

65 70 75 80

Val Val Ile Gly Asp Pro Lys Lys Asp Lys Ser Glu Ala Phe Phe Arg

85 90 95

Ala Leu Gly Arg Tyr Ile His Ser Leu Asp Gly Arg Tyr Ile Thr Ala

100 105 110

Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Met Ile His Leu Glu

115 120 125

Thr Pro His Val Cys Gly Ile Ser Glu Ser Tyr Gly Ser Gly Gly Asn

130 135 140

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

145 150 155 160

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

165 170 175

Val Gln Gly Val Gly Asn Val Ala Phe His Met Cys Gln Tyr Leu His

180 185 190

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

195 200 205

Gln Asn Ala Val Glu Ala Phe Asp Ala Gln Ala Val Gly Ile Asp Glu

210 215 220

Ile Tyr Ser Val Asp Ala Asp Ile Phe Ala Pro Cys Ala Leu Gly Gly

225 230 235 240

Val Leu Asn Asp Glu Thr Ile Pro Ser Leu Lys Ala Lys Met Val Cys

245 250 255

Gly Ser Ala Asn Asn Gln Leu Leu Glu Glu Asn Arg His Gly Gln Met

260 265 270
Leu Glu Lys Arg Gly Ile Ile Tyr Ala Pro Asp Phe Val Val Asn Ser

275 280 285
Gly Gly Val Ile Asn Val Ala Asp Glu Leu Asn Gly Tyr His Arg Glu

290 295 300
Arg Ala Glu Lys Lys Val Lys Ala Val Tyr Asp Gln Met Asp Lys Ile

305 310 315 320
Phe Thr Ile Ala Lys Glu Thr His Val Leu Pro Leu Gln Ala Ala Glu

325 330 335
His Leu Ala Glu Ser Arg Ile Asn Thr Met Met Arg Val His Ser Lys

340 345 350
Tyr Ser Ser Lys Pro Asn Asn Gln Leu Arg Asp Thr Arg Thr His

355 360 365

<210> 420

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 420

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Trp Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

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

340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 421
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 421
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Cys Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365
<210> 422
<211> 355
<212> PRT
<213> Aeromicrobium marinum
<400> 422
Met Thr Val Phe Ser His Pro His Glu Gln Val Val Phe Cys His Asp
1 5 10 15
Pro Ala Ser Gly Leu Arg Ala Ile Ile Gly Leu Tyr Ser Thr Ala Leu

20 25 30
 Gly Pro Gly Leu Gly Gly Thr Arg Phe His Pro Tyr Ala Ser Glu Ala
 35 40 45

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

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

 Val Gly Lys Val Gly Arg His Leu Val Ser His Leu Val Glu Glu Asp
 180 185 190
 Ala Arg Val Val Val Thr Asp Pro Val Asp Ala Ala Val Ser His Val
 195 200 205
 Leu Ser Leu Ser Ser Asp Val Arg Ser Val Ala Ser Thr Glu Ala Leu
 210 215 220
 Leu Ala Glu Pro Leu Asp Val Tyr Ala Pro Cys Ala Leu Gly Gly Ala
 225 230 235 240

 Leu Thr Asp Ala Val Val Gln Thr Leu Ser Ala Gly Ile Val Cys Gly
 245 250 255
 Gly Ala Asn Asn Gln Leu Ala His Pro Gly Val Ala Lys Leu Leu Asp
 260 265 270

Glu Ala Gly Ile Thr Tyr Ala Pro Asp Tyr Cys Val Asn Ala Gly Gly
275 280 285

Val Ile Gln Val Ala Asp Glu Leu Asp Gly Phe Asp Phe Asp Arg Ala
290 295 300

Lys Arg Arg Ala Thr Gly Ile Phe Asp Thr Thr Leu Ala Val Leu Glu
305 310 315 320

Arg Ala Ala Ser Asp Gly Thr Thr Thr Ala Asp Ala Ala Asp Arg Gln
325 330 335

Ala Glu Gln Arg Met Arg Glu Ile Gly Arg Leu Gly Gln Val Trp Leu
340 345 350

Pro Thr Arg
355

<210> 423

<211> 367

<212> PRT

<213> Sinomicrobium oceanii

<400> 423

Met Asn Thr Asp Ile Leu His Ala Gly Glu Leu Lys Lys Ala Asp Pro

1 5 10 15
Val Phe Gly Gln Leu Ser Phe Asp Asp His Glu Gln Ile Val Phe Cys
20 25 30

Asn Asp Lys Asp Thr Gly Leu Lys Ala Ile Ile Gly Ile His Asn Thr
35 40 45

Val Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr Asn Ser
50 55 60

Glu Trp Glu Ala Leu Asn Asp Val Leu Arg Leu Ser Arg Gly Met Thr

65 70 75 80
Phe Lys Ser Ala Ile Thr Gly Leu Asn Leu Gly Gly Gly Lys Ala Val
85 90 95

Ile Ile Gly Asp Ala Lys Thr Arg Lys Thr Pro Glu Leu Met Arg Arg
100 105 110

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

115 120 125
Asp Val Gly Met Glu Thr Ser Asp Met Asp Leu Val Arg Asp Val Thr

130 135 140
Pro Tyr Val Thr Gly Val Ser Glu Ser Arg Gly Gly Ala Gly Asn Pro

145 150 155 160
Ser Pro Ile Thr Ala Tyr Gly Val Tyr Met Gly Met Lys Ala Ala Ala

165 170 175
Ala His Arg Phe Gly Thr Asp Lys Leu Glu Gly Lys Gln Val Leu Val

180 185 190
Gln Gly Ile Gly His Val Gly Glu Ser Leu Val Glu His Leu Thr Lys

195 200 205
Glu Gly Ala Arg Val Phe Ile Thr Asp Ile Asn Glu Asp Arg Leu Gln

210 215 220
Glu Val Ser Lys Lys Tyr Gly Ala Val Ile Tyr Ala Gly Asp Asp Leu

225 230 235 240
Tyr Thr Ala Ala Val Asp Ile Tyr Ala Pro Cys Ala Leu Gly Ala Thr

245 250 255
Ile Asn Asp Asp Thr Val Tyr Lys Ile Lys Ala Gly Val Val Ala Gly

260 265 270
Ala Ala Asn Asn Gln Leu Ala Asp Glu Asn Arg His Gly Lys Ile Leu

275 280 285
Met Glu Arg Gly Ile Ala Tyr Ala Pro Asp Phe Leu Ile Asn Ala Gly

290 295 300
Gly Ile Ile Asn Val Tyr Ala Glu Leu Glu Gly Tyr Gly Lys Asp Glu

305 310 315 320
Ile Ile Arg Lys Thr Glu Asn Ile Tyr Thr Thr Thr Leu Glu Ile Phe

325 330 335
Ala His Ser Ala Lys Asn Gly Cys Ser Thr His Gln Ser Ala Leu Arg

340 345 350
Val Ala Gln Gly Arg Ile Asp Ala Arg Lys Gln Gly Lys Gly Ala

355 360 365

<210> 424

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 424

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Lys Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270

 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335

 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 425
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 425
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ser Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile

275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg

340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 426

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 426

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30

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

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115	120	125	
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser			
130	135	140	
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met			
145	150	155	160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys			
165	170	175	
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys			
180	185	190	
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys			
195	200	205	
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu			
210	215	220	
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala			
225	230	235	240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys			
245	250	255	
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly			
260	265	270	
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile			
275	280	285	
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Ser Tyr Gly Tyr Asn			
290	295	300	
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala			
305	310	315	320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala			
325	330	335	
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg			
340	345	350	
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg			
355	360	365	

<210> 427

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 427

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Trp Tyr Gly Tyr Asn
290 295 300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365
<210> 428
<211> 367
<212> PRT
<213> Flavobacteria bacterium
<400> 428
Met Thr Ala Glu Leu Leu Lys Ala Asn Glu Leu His Lys Val Asp Pro
1 5 10 15
Val Phe Gly Gln Val Ser Phe Asp Gly His Glu Gln Val Val Phe Cys
20 25 30
His Asp Lys Asp Thr Gly Leu Lys Ala Ile Ile Gly Ile His Asn Thr
35 40 45

Val Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr Thr Asn
50 55 60
Glu Trp Glu Ala Leu Asn Asp Val Leu Arg Leu Ser Arg Gly Met Thr
65 70 75 80
Phe Lys Asn Ser Ile Ser Gly Leu Asn Leu Gly Gly Gly Lys Ala Val
85 90 95
Ile Ile Gly Asp Ala Lys Thr Gln Lys Ser Pro Glu Leu Met Arg Arg
100 105 110
Phe Gly Gln Phe Val Asp Ser Leu Ser Gly Lys Tyr Ile Thr Ala Glu
115 120 125
Asp Val Gly Met Glu Thr Lys Asp Met Asp Thr Val Asn Glu Val Thr
130 135 140
Lys His Val Ala Gly Ile Ser Val Glu Arg Gly Gly Ser Gly Asn Pro
145 150 155 160
Ser Pro Val Thr Ala Tyr Gly Val Phe Met Gly Met Lys Ala Ala Ala
165 170 175
Lys Tyr Lys Tyr Gly Ser Asp Ser Leu Glu Gly Lys Lys Val Leu Val
180 185 190
Gln Gly Ile Gly His Val Gly Glu Val Leu Val Gln His Leu Thr Glu
195 200 205
Ser Gly Ala Leu Val Thr Ile Thr Asp Ile Asn Glu Asp Arg Val Asn
210 215 220
Gln Val Gly Ala Lys Tyr Gly Ala Lys Ile Tyr Thr Gly Ala Asp Leu
225 230 235 240
Tyr Ser Ala Asp Val Asp Ile Tyr Ala Pro Cys Ala Leu Gly Ala Thr
245 250 255
Ile Asn Asp Ala Thr Ile Asn Asn Ile Lys Ala Ser Ile Ile Ala Gly
260 265 270
Ala Ala Asn Asn Gln Leu Ala Asn Glu Ala Val His Gly Lys Ile Leu
275 280 285
Lys Glu Lys Gly Ile Leu Tyr Ala Pro Asp Phe Leu Ile Asn Ala Gly

290 295 300

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

<210> 429
<211> 360
<212> PRT
<213> Streptomyces silvensis
<400> 429

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

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

180 185 190
 Gly His Ile Leu Val Glu His Leu Leu Glu Asp Gly Ala Glu Val Val
 195 200 205
 Ile Thr Asp Val Arg Glu Asp Ser Leu Leu Arg Ile Thr Ser Lys His
 210 215 220
 Pro Glu Val Thr Ala Val Ala Asp Thr Asp Thr Leu Ile Arg Thr Glu
 225 230 235 240
 Gly Leu Asp Val Tyr Ala Pro Cys Ala Leu Gly Gly Ala Leu Asp Asp

245 250 255
 Asp Thr Val Pro Val Leu Thr Ala Arg Val Val Cys Gly Ala Ala Asn
 260 265 270
 Asn Gln Leu Ala His Pro Gly Val Glu Lys Asp Leu Ala Asp Arg Gly
 275 280 285
 Ile Leu Tyr Ala Pro Asp Tyr Val Val Asn Ala Gly Gly Val Ile Gln
 290 295 300
 Val Ala Asp Glu Leu His Gly Phe Asp Phe Asp Arg Cys Lys Glu Lys

305 310 315 320
 Ala Ser Lys Ile Phe Asp Thr Thr Val Ala Ile Phe Ala Arg Ala Lys
 325 330 335
 Gln Asp Gly Ile Pro Pro Ala Ala Ala Ala Asp Arg Ile Ala Glu Gln
 340 345 350
 Arg Ile Ala Glu Ala Arg Gly Arg

355 360

<210> 430

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 430

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255

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

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 431

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 431

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Tyr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

260 265 270

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

275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg

340 345 350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 432

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 432

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Val Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205

 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270

 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335

 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

 <210> 433
 <211> 359
 <212> PRT
 <213> Unknown

<220><223> Nonomuraea sp. ATCC 55076

<400> 433

Met Thr Asp Val Phe Gly Ala Ser His Lys Asp Val His Glu Gln Val

1 5 10 15

Val Phe Cys Ala Asp Glu Gln Ser Gly Leu Arg Ala Ile Ile Ala Ile

20 25 30

His Asn Thr Ala Leu Gly Pro Ala Leu Gly Gly Thr Arg Phe Tyr Pro

35 40 45

Tyr Glu Ser Glu Ser Ala Ala Leu Ala Asp Val Leu Asn Leu Ala Lys

50 55 60

Gly Met Ala Tyr Lys Asn Ala Leu Ala Gly Leu Asp Leu Gly Gly Gly

65 70 75 80

Lys Ala Val Ile Ile Gly Asp Pro Ala Arg Asp Lys Ser Glu Ala Leu

85 90 95

Leu Arg Ala Tyr Gly Arg Phe Val Glu Ser Leu Gly Gly Arg Tyr Ile

100 105 110

Thr Ala Cys Asp Val Gly Thr Tyr Ser Glu Asp Met Asp Val Val Ala

115 120 125

Arg Glu Ser Arg Phe Val Thr Gly Arg Thr Thr Ala Asn Gly Gly Ala

130 135 140

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

145 150 155 160

Ala Ser Ala Glu Arg Val Tyr Gly Thr Pro Ser Leu His Gly Arg Arg

165 170 175

Val Gly Val Glu Gly Val Gly Lys Val Gly His Arg Leu Val Glu Leu

180 185 190

Leu Arg Glu Asp Gly Ala Glu Val Val Ile Cys Asp Val Asp Pro Lys

195 200 205

Ala Val Glu Arg Val Arg Leu Arg His Pro Glu Val Asp Val Val Ala

210 215 220

Asp Ala Arg Thr Leu Met Ala Ser Asp Leu Asp Val Phe Ala Pro Cys

225 230 235 240
 Ala Leu Gly Gly Ala Leu Asp Asp Glu Thr Val Thr Thr Leu Arg Ala
 245 250 255
 Lys Ile Val Cys Gly Ala Ala Asn Asn Gln Leu Ala His Pro Gly Val
 260 265 270
 Glu Lys Gln Leu Ala Glu Arg Gly Ile Leu Tyr Ala Pro Asp Tyr Val

 275 280 285
 Val Asn Ser Gly Gly Val Ile Gln Val Ala Asp Glu Ile Gly Gly Phe
 290 295 300
 Asp Met Glu Arg Ala Arg Ser Lys Ala Ala Gln Ile Tyr Asp Thr Thr
 305 310 315 320
 Leu Lys Ile Phe Ala Ile Ala Ala Asp Glu Gly Val Pro Pro Ala Val
 325 330 335
 Ala Ala Asp Arg Leu Ala Glu Arg Arg Met Ser Glu Val Gly Arg Ile

 340 345 350
 Arg Ala Ile Trp Leu Gly His
 355
 <210> 434
 <211> 365
 <212> PRT
 <213> Unknown
 <220><223> Bacillus sp. JCM 19045
 <400> 434
 Met Asn Leu Phe Thr Lys Met Val Glu Arg Asp Tyr Glu Gln Leu Val
 1 5 10 15
 Val Cys Gln Asp Lys Thr Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Asn Tyr

 35 40 45
 Glu Thr Glu Glu Glu Ala Phe Glu Asp Val Leu Arg Leu Ser Arg Gly
 50 55 60
 Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65						70						75						80
Ala	Val	Ile	Ile	Gly	Asp	Ala	Arg	Lys	Asp	Lys	Asn	Gln	Glu	Met	Phe			
					85						90						95	
Arg	Ala	Phe	Gly	Arg	Tyr	Ile	Gln	Gly	Leu	Asn	Gly	Arg	Tyr	Ile	Thr			
					100						105						110	
Ala	Glu	Asp	Val	Gly	Thr	Thr	Val	Glu	Asp	Met	Asp	Ile	Ile	His	Asp			
					115						120						125	
Glu	Thr	Asp	Tyr	Val	Thr	Gly	Ile	Ser	Pro	Ala	Phe	Gly	Ala	Ser	Gly			
					130						135						140	
Asn	Pro	Ser	Pro	Val	Thr	Ala	Tyr	Gly	Val	Tyr	Val	Gly	Met	Lys	Ala			
					145						150						155	160
Ala	Ala	Lys	Ala	Gly	Leu	Gly	Ser	Glu	Asp	Leu	Ala	Gly	Lys	Thr	Ile			
					165						170						175	
Ala	Val	Gln	Gly	Val	Gly	Asn	Val	Ala	Tyr	His	Leu	Cys	Lys	Tyr	Leu			
					180						185						190	
His	Lys	Glu	Gly	Ala	Asn	Leu	Ile	Val	Thr	Asp	Ile	Tyr	Lys	Pro	Ser			
					195						200						205	
Val	Asp	Arg	Ala	Val	Thr	Glu	Phe	Gly	Ala	Lys	Ala	Val	Ala	Pro	Asp			
					210						215						220	
Glu	Ile	Tyr	Gln	Val	Asp	Cys	Asp	Ile	Phe	Ala	Pro	Cys	Ala	Leu	Gly			
					225						230						235	240
Gly	Val	Ile	Asn	Asp	Glu	Thr	Leu	Thr	Gln	Ile	Lys	Ala	Lys	Val	Ile			
					245						250						255	
Ala	Gly	Ala	Ala	Asn	Asn	Gln	Leu	Lys	Glu	Glu	Lys	His	Gly	Glu	Arg			
					260						265						270	
Leu	Gln	Glu	Met	Gly	Ile	Ala	Tyr	Ala	Pro	Asp	Tyr	Val	Ile	Asn	Ala			
					275						280						285	
Gly	Gly	Val	Ile	Asn	Val	Ala	Asp	Glu	Leu	Asn	Gly	Tyr	Asn	Arg	Asp			
					290						295						300	
Arg	Ala	Phe	Lys	Lys	Val	Glu	Gly	Ile	Tyr	Glu	Asn	Val	Ser	Arg	Val			
					305						310						315	320

Phe Glu Ile Ala Lys Ala Gln Asn Ile Pro Thr Phe Leu Ala Ala Asp
325 330 335
Lys Met Ala Glu Glu Arg Ile Glu Arg Met Arg Tyr Ala Arg Gly Thr
340 345 350
Phe Leu Gln Asn Glu His His Ile Leu Ser Arg Lys Lys

355 360 365

<210> 435

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 435

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

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

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

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 436

<211> 362

<212> PRT

<213> Actinomadura echinospora

<400> 436

Met Thr Asn Val Phe Gly Ser Pro His Lys Gly Ser Gly Pro Ser His
1 5 10 15
Glu Gln Val Val Phe Cys Gln Asp Glu Ala Ser Gly Leu Arg Ala Ile
20 25 30
Ile Ala Ile Tyr Ser Thr Ala Leu Gly Pro Ser Leu Gly Gly Thr Arg
35 40 45
Phe Tyr Pro Tyr Gly Ser Glu Asp Glu Ala Leu Thr Asp Val Leu Asn
50 55 60
Leu Ser Arg Ala Met Ala Tyr Lys Asn Ala Leu Ala Gly Leu Asp Leu
65 70 75 80
Gly Gly Gly Lys Ala Val Ile Ile Gly Asp Pro Glu Leu Asp Lys Ser
85 90 95
Glu Ala Leu Leu Arg Ala Tyr Gly Arg Phe Val Gln Ser Leu Asn Gly
100 105 110
Arg Tyr Tyr Thr Ala Cys Asp Val Gly Thr Tyr Ser Glu Asp Met Asp
115 120 125
Val Ile Ala Arg Glu Ser Thr Tyr Val Thr Gly Arg Thr Val Ala His
130 135 140
Gly Gly Ala Gly Asp Ser Ser Val Leu Thr Ala Tyr Gly Val Phe Gln
145 150 155 160
Gly Met Arg Ala Ala Ala Gln Ala Leu Trp Gly Ser Pro Thr Leu Arg
165 170 175
Gly Arg Arg Val Gly Ile Glu Gly Val Gly Lys Val Gly His Arg Leu
180 185 190
Val Glu His Leu Arg Glu Asp Gly Ala Glu Val Val Ile Cys Asp Val
195 200 205
Ser Glu Ala Ala Val Asp Arg Val Arg Arg Leu His Pro Glu Val Glu
210 215 220
Val Val Ala Asp Gly Asp Ala Leu Val Lys Thr Asp Leu Asp Val Tyr
225 230 235 240
Ser Pro Cys Ala Leu Gly Gly Ser Leu Asn Asp Glu Thr Val Pro Leu

245 250 255
 Leu Arg Ala Arg Ile Val Cys Gly Gly Ala Asn Asn Gln Leu Ala His
 260 265 270
 Pro Gly Val Glu Lys Arg Leu Ala Asp Arg Gly Ile Leu Tyr Ala Pro
 275 280 285
 Asp Tyr Val Val Asn Ala Gly Gly Val Ile Gln Val Ala Asp Glu Ile
 290 295 300
 Glu Gly Phe Ser Phe Glu Arg Ala Lys Ala Lys Ala Thr Gln Ile Phe

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

<210> 437

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 437

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60

Lys Gly Lys Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85	90	95	
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr			
100	105	110	
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile			
115	120	125	
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser			
130	135	140	
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met			
145	150	155	160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys			
165	170	175	
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys			
180	185	190	
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys			
195	200	205	
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu			
210	215	220	
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala			
225	230	235	240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys			
245	250	255	
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly			
260	265	270	
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile			
275	280	285	
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn			
290	295	300	
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala			
305	310	315	320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala			
325	330	335	

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 438
<211> 366
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 438

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Gln Gly Gly

65 70 75 80
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365
<210> 439
<211> 366
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 439
Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80

 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Leu Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140

 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205

 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 440

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 440

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Leu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile

 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335

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

340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 441

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 441

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Met Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220

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

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

 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 442
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 442
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Tyr Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 443
<211> 366
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 443

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Ala Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

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

			340					345					350			
Ser	Thr	Tyr	Leu	Arg	Asn	Gly	His	Asp	Ile	Ile	Ser	Arg	Arg			
		355					360					365				
<210>	444															
<211>	366															
<212>	PRT															
<213>	Artificial Sequence															
<220><223>	Synthetic polypeptide															
<400>	444															
Met	Thr	Leu	Glu	Ile	Phe	Glu	Tyr	Leu	Glu	Lys	Tyr	Asp	Tyr	Glu	Gln	
1				5					10					15		
Val	Val	Phe	Cys	Gln	Asp	Lys	Glu	Ser	Gly	Leu	Lys	Ala	Ile	Ile	Ala	
			20					25					30			
Ile	His	Asp	Thr	Thr	Leu	Gly	Pro	Ala	Leu	Gly	Gly	Thr	Arg	Met	Trp	
		35					40					45				
Thr	Tyr	Asp	Ser	Glu	Glu	Ala	Ala	Ile	Glu	Asp	Ala	Leu	Arg	Leu	Ala	
	50					55				60						
Lys	Gly	Met	Thr	Tyr	Lys	Asn	Ala	Ala	Ala	Gly	Leu	Asn	Leu	Gly	Gly	
65				70						75				80		
Ala	Lys	Thr	Val	Ile	Ile	Gly	Asp	Pro	Arg	Lys	Asp	Lys	Ser	Glu	Ala	
			85					90					95			
Met	Phe	Arg	Ala	Leu	Gly	Arg	Tyr	Ile	Gln	Gly	Leu	Asn	Gly	Arg	Tyr	
		100						105					110			
Ile	Thr	Ala	Glu	Asp	Val	Gly	Thr	Thr	Val	Asp	Asp	Met	Asp	Ile	Ile	
		115					120					125				
His	Glu	Glu	Thr	Asp	Phe	Val	Thr	Gly	Ile	Ser	Pro	Ser	Phe	Gly	Ser	
	130						135				140					
Ser	Gly	Asn	Pro	Ser	Pro	Val	Thr	Ala	Tyr	Gly	Val	Tyr	Arg	Gly	Met	
145				150						155				160		
Lys	Ala	Ala	Ala	Lys	Glu	Ala	Phe	Gly	Thr	Asp	Asn	Leu	Glu	Gly	Lys	
			165					170					175			

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

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Lys Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

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

<210> 445

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 445

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Arg Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300

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

<210> 446

<211> 364

<212> PRT

<213> Bacillus subtilis

<400> 446

Met Glu Leu Phe Lys Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val
 1 5 10 15
 Phe Cys Gln Asp Glu Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
 35 40 45
 Glu Asn Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala Arg Gly

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

Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Ile Ile His Asp

115 120 125

Glu Thr Asp Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly

130 135 140

Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys Ala

145 150 155 160

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

165 170 175

Ala Val Gln Gly Val Gly Asn Val Ala Tyr Asn Leu Cys Arg His Leu

180 185 190

His Glu Glu Gly Ala Asn Leu Ile Val Thr Asp Ile Asn Lys Gln Ser

195 200 205

Val Gln Arg Ala Val Glu Asp Phe Gly Ala Arg Ala Val Asp Pro Asp

210 215 220

Asp Ile Tyr Ser Gln Asp Cys Asp Ile Tyr Ala Pro Cys Ala Leu Gly

225 230 235 240

Ala Thr Ile Asn Asp Asp Thr Ile Lys Gln Leu Lys Ala Lys Val Ile

245 250 255

Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Thr Arg His Gly Asp Gln

260 265 270

Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala

275 280 285

Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Ala Glu

290 295 300

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

305 310 315 320

Leu Glu Ile Ser Gln Arg Asp Gly Ile Pro Ala Tyr Leu Ala Ala Asp

325 330 335

Arg Leu Ala Glu Glu Arg Ile Glu Arg Met Arg Arg Ser Arg Ser Gln

340 345 350

Phe Leu Gln Asn Gly His Ser Val Leu Ser Arg Arg

355 360

<210> 447

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 447

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110
Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

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

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

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 448

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 448

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60
 Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile

275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Arg Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 449

<211> 363

<212> PRT

<213> *Staphylococcus massiliensis*

<400> 449

Met Ile Phe Glu Lys Met Glu Gln Tyr Asp Tyr Glu Gln Leu Val Phe
 1 5 10 15

Cys His Asp Lys Thr Ser Gly Leu Lys Ala Ile Ile Cys Ile His Asp
 20 25 30
 Ser Thr Leu Gly Pro Ala Leu Gly Gly Cys Arg Phe Trp Asn Tyr Glu
 35 40 45
 Thr Glu Glu Glu Ala Ile Glu Asp Val Met Arg Leu Ala Lys Gly Met
 50 55 60
 Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Ala Lys Thr
 65 70 75 80

Val Val Met Gly Asp Pro Lys Lys Asp Lys Ser Glu Ala Phe Phe Arg
 85 90 95
 Ala Leu Gly Arg Tyr Ile Asn Ser Leu Asp Gly Arg Tyr Ile Thr Ala
 100 105 110
 Glu Asp Val Asn Thr Thr Val Glu Asp Met Asp Phe Ile Tyr Gln Glu
 115 120 125

Thr Pro Tyr Val Thr Gly Ile Ser Glu Ser Tyr Gly Ser Ser Gly Asn
130 135 140

Pro Ser Pro Lys Thr Ala Leu Gly Val Phe Tyr Ala Met Lys Arg Thr
145 150 155 160

Ala Lys Glu Ala Phe Gly Thr Asp Asp Leu Glu Gly Lys Thr Val Ser
165 170 175

Val Gln Gly Leu Gly Asn Val Ala Tyr Thr Leu Cys Glu Tyr Leu His
180 185 190

Glu Ala Gly Ala Lys Leu Val Val Thr Asp Ile Asn Asp Glu Ala Val
195 200 205

Glu Arg Val Val Asn Asp Phe Asn Ala Glu Lys Val Gly Val Asp Asp
210 215 220

Ile Tyr Ser Val Glu Ala Asp Ile Phe Ala Pro Cys Ala Leu Gly Ala
225 230 235 240

Ile Leu Asn Asp Asp Thr Ile Pro Gln Leu Lys Val Lys Ala Val Cys
245 250 255

Gly Ser Ser Asn Asn Gln Leu Leu Asp Thr Glu Lys His Gly Lys Met
260 265 270

Leu Glu Asp Lys Gly Ile Val Tyr Ala Pro Asp Phe Val Val Asn Ala
275 280 285

Gly Gly Val Ile Asn Val Ala Asp Glu Leu Gln Gly Tyr Asn Glu Asp
290 295 300

Arg Ala Ile Ala Lys Val Lys Gly Ile Tyr Asn Gln Met Asp Lys Ile
305 310 315 320

Phe Asn Ile Ala Lys Glu Gln Asp Ile Leu Pro Val Ser Ala Ala Glu
325 330 335

His Leu Ala Glu Lys Arg Ile Lys Asp Met Met Val Val His Ser Lys
340 345 350

Phe Ser Ala Lys Ser Asn Asn Gln Ile Asn Arg
355 360

<210> 450

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 450

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Ser Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala

225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys

245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly

260 265 270

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

275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala

325 330 335

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

340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg

355 360 365

<210> 451

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 451

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35	40	45	
Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala			
50	55	60	
Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly			
65	70	75	80
Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala			
85	90	95	
Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr			
100	105	110	
Trp Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile			
115	120	125	
His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser			
130	135	140	
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met			
145	150	155	160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys			
165	170	175	
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys			
180	185	190	
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys			
195	200	205	
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu			
210	215	220	
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala			
225	230	235	240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys			
245	250	255	
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly			
260	265	270	
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile			
275	280	285	

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

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 452

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 452

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

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

100 105 110
 Ile Thr Asn Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140
Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160
Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175
Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190
His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205
Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240
Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300
Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320
Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335
Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350
Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365
<210> 453

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 453

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Ser Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300

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

<210> 454

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 454

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45

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

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

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

 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

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

<210> 455

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 455

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Ala Gly Gly Thr Arg Met Trp
 35 40 45

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

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 456

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 456

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240

 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Cys Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300

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

 <210> 457
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 457
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45

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

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

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

 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

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

<210> 458

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 458

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45

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

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Ala Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 459

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 459

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Trp Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240

 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300

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

 <210> 460
 <211> 366
 <212> PRT
 <213> Artificial Sequence
 <220><223> Synthetic polypeptide
 <400> 460
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45

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

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

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

 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Gln Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

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

<210> 461

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 461

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45

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

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Thr Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 462

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 462

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Tyr Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

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

<210> 463

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 463

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

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

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

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

 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

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

<210> 464

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 464

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly His Thr Arg Met Trp
 35 40 45

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

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 465

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 465

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Lys Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300

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

<210> 466

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 466

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Tyr Gly Thr Arg Met Trp
 35 40 45

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

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

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

 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

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

<210> 467

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 467

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45

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

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 468

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 468

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Gln Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

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

<210> 469

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 469

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15
Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30
Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

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

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

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

 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn

290 295 300

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

<210> 470

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 470

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
 1 5 10 15
 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45

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

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285

Asn Ala Gly Gly Val Ile Asn Thr Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
355 360 365

<210> 471

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 471

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Thr Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220
Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255
Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
260 265 270
Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
275 280 285
Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
290 295 300

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

<210> 472

<211> 363

<212> PRT

<213> Unknown

<220><223> Streptomyces sp. CB02923

<400> 472

Met Gln Gly Ala Pro Ser Ala Asp Gly Ser Val Leu His Thr Leu Phe
1 5 10 15
Arg Ser Glu Gln Gly Gly His Glu Gln Val Val Leu Cys Gln Asp Arg
20 25 30
Ala Ser Gly Leu Arg Ala Val Ile Ala Ile His Asp Thr Ala Leu Gly
35 40 45

Pro Ala Leu Gly Gly Thr Arg Phe His Ala Tyr Ala Ser Glu Glu Asp

50 55 60

Ala Val Leu Asp Ala Leu Asn Leu Ser Arg Gly Met Ser Tyr Lys Asn

65 70 75 80

Ala Leu Ala Gly Leu Asp His Gly Gly Gly Lys Ala Val Ile Ile Gly

85 90 95

Asp Pro Glu Leu Ile Lys Thr Glu Glu Leu Leu Leu Ala Tyr Gly Arg

100 105 110

Phe Val Ala Ser Leu Gly Gly Arg Tyr Val Thr Ala Cys Asp Val Gly

115 120 125

Thr Tyr Val Ala Asp Met Asp Val Val Ala Arg Thr Asn Gln Trp Thr

130 135 140

Thr Gly Arg Ser Pro Glu Asn Gly Gly Ala Gly Asp Ser Ser Val Leu

145 150 155 160

Thr Ala Phe Gly Val Phe Gln Gly Met Arg Ala Ser Ala Gln His Leu

165 170 175

Trp Gly Asp Pro Thr Leu Arg Gly Arg Lys Val Gly Val Ala Gly Val

180 185 190

Gly Lys Val Gly His His Leu Val Glu His Leu Leu Gln Asp Gly Ala

195 200 205

Glu Val Val Ile Thr Asp Val Arg Ala Glu Ser Ile Glu Arg Val Arg

210 215 220

Ser Arg His Pro Gln Val Gly Val Ala Ala Asp Thr Gly Ser Leu Ile

225 230 235 240

Arg Thr Ala Gly Leu Asp Val Tyr Ala Pro Cys Ala Leu Gly Gly Ala

245 250 255

Leu Asn Asp Glu Ser Val Pro Ala Leu Thr Ala Lys Val Val Cys Gly

260 265 270

Ala Ala Asn Asn Gln Leu Ala His Pro Gly Val Glu Lys Asp Leu Ser

275 280 285

Asp Arg Gly Val Leu Tyr Ala Pro Asp Tyr Val Val Asn Ala Gly Gly

290 295 300
Val Ile Gln Val Ala Asp Glu Leu His Gly Phe Asp Phe Asp Arg Cys

305 310 315 320
Lys Thr Lys Ala Ala Lys Ile Phe Asp Thr Thr Leu Ala Ile Phe Ala

325 330 335
Arg Ala Lys Glu Asp Gly Ile Pro Pro Ala Ala Ala Ala Asp Arg Leu

340 345 350
Ala Glu Gln Arg Met Ala Asp Ala Arg Arg Ala

355 360

<210> 473

<211> 354

<212> PRT

<213> Natranaerobius thermophilus

<400> 473

Met Lys Ile Leu Glu Thr Met Lys Ala Ser Asp Tyr Glu Gln Leu Val

1 5 10 15

Phe Cys Gln Asp Glu Lys Thr Gly Leu Lys Gly Ile Ile Ala Ile His

20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr

35 40 45

Asp Asn Glu Glu Glu Ala Ile Glu Asp Val Leu Arg Leu Ala Arg Gly

50 55 60

Met Thr Tyr Lys Ser Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys

65 70 75 80

Gly Val Ile Ile Gly Asp Pro Lys Lys Asp Lys Ser Glu Glu Met Trp

85 90 95

Arg Ala Phe Gly Arg Phe Val Gln Ser Leu Asn Gly Arg Tyr Ile Thr

100 105 110

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

115 120 125

Glu Thr Asp Phe Ala Val Gly Leu Pro Gly Lys Ser Gly Asn Pro Ser

130 135 140
 Pro Ala Thr Ala Tyr Gly Val Tyr Ser Gly Ile Lys Ala Val Ala Asp
 145 150 155 160
 Glu Ile Trp Gly Ser Ala Asp Leu Asn Gly Lys Thr Ile Ala Ile Gln
 165 170 175
 Gly Ala Gly Ser Val Gly Tyr Tyr Leu Ser Glu Leu Leu His Lys Asp
 180 185 190

 Gly Ala Lys Leu Ile Val Thr Asp Ile Asp Lys Glu Ala Val Asp Lys
 195 200 205
 Leu Val Ser Asp Phe Gly Ala Thr Ala Val Glu Thr Asp Glu Ile Tyr
 210 215 220
 Glu Gln Glu Ala Asp Ile Phe Ala Pro Cys Ala Leu Gly Ala Ile Leu
 225 230 235 240
 Asn Asp Glu Thr Ile Pro Lys Leu Lys Val Lys Ala Val Ala Gly Ala
 245 250 255

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

 Ile Ala Asn Arg Asp Asp Ile Thr Ser His Glu Ala Ala Asn Arg Met
 325 330 335
 Ala Glu Glu Arg Ile Glu Ala Ile Lys His Val Lys Thr Ser Tyr Ile
 340 345 350
 Asn Lys

<210> 474

<211> 366

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 474

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln

1 5 10 15

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

20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Glu Gly Thr Arg Met Trp

35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala

50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly

65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr

100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile

115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser

130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys

165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys

180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys

195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 475
 <211> 366
 <212> PRT
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 <220><223> Synthetic polypeptide
 <400> 475
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 Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
 20 25 30
 Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
 35 40 45
 Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
 50 55 60

Lys Gly Met Thr Tyr Lys Lys Ala Ala Ala Gly Leu Asn Leu Gly Gly
 65 70 75 80
 Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala

 85 90 95
 Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
 100 105 110
 Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
 115 120 125
 His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
 130 135 140
 Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met

 145 150 155 160
 Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu

 210 215 220
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile

 275 280 285
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala

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

 340 345 350
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365
 <210> 476
 <211> 362
 <212> PRT
 <213> Unknown
 <220><223> 'Candidatus Kapabacteria' thiocyanatum
 <400> 476
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 20 25 30

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

 Arg Ala Tyr Gly Arg Met Val Glu Ser Gln Arg Gly Arg Tyr Ile Thr
 100 105 110
 Ala Glu Asp Val Gly Thr Ser Val Arg Asp Met Glu Trp Ile Arg Met
 115 120 125
 Glu Thr Lys Tyr Val Thr Gly Val Gly Gly Asn Gly Gly Ser Gly Asp
 130 135 140
 Pro Ser Pro Val Thr Ala Leu Gly Val Tyr Ser Gly Met Lys Ala Cys

145 150 155 160

Ala Lys Ser Val Tyr Gly Thr Asp Ala Leu Ser Gly Lys Arg Ile Val

165 170 175

Val Gln Gly Ala Gly Asn Val Ala Ser His Leu Val His Ser Leu Val

180 185 190

Lys Glu Gly Ala Val Val Phe Val Thr Asp Ile Tyr Glu Glu Lys Ala

195 200 205

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

210 215 220

Val Phe Thr Thr Gln Cys Asp Ile Phe Ser Pro Asn Ala Leu Gly Ala

225 230 235 240

Val Leu Asn Asp Glu Thr Ile Pro Gln Leu Thr Cys Ala Ile Val Ala

245 250 255

Gly Gly Ala Asn Asn Gln Leu Lys Ile Glu Gln Arg His Ala Thr Ala

260 265 270

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

275 280 285

Gly Gly Leu Met Asn Val Ala Ser Glu Val Asp Gly Tyr Asn Arg Glu

290 295 300

Lys Val Met Arg Gln Ala Glu Gly Ile Tyr Asp Ile Thr Met Asn Ile

305 310 315 320

Leu Asn Thr Ala Arg Glu Arg Asn Ile Leu Thr Ile Glu Ala Ser Asn

325 330 335

Ala Ile Ala Glu Glu Arg Ile Asn Lys Val Arg His Val His Gly Asn

340 345 350

Phe Ile Gly Ser Pro Ser Ile Arg Gly Val

355 360

<210> 477

<211> 1647

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 477

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atgaaatggg taggcaatgc taacgaactg aatgcgtctt acatggccga tggttatgca	180
cggacaaaa aagcggcagc ctttctgacg actttcggcg ttggtgagtt aagcgcggtg	240

aacggcctgg cggggtcata cgccgaaaat ctaccagtgt tcgaaatcgt gggctcgccg	300
accagcaaag ttcagaacga gggtaagttt gtgcatcaca cccttgctga cggagatatt	360
aaacatttca tgaaaatgca cgaacctgta acggcagcgc gcacactgtt gactgcggag	420
aacgccaccg tcgaaattga tcgctgtctg agtgcctctt tgaaggaacg taaaccggtg	480
tatatcaatc tcccgttga cgtggcggca gctaaagccg aaaaaccgag ttgcccctta	540
aagaaagaga atagcacgtc taacacgtct gaccaagaaa ttctgaacaa aattcaggaa	600
tccctcaaaa atgcgaaaaa acctatcgtc atcaccgtgc atgaataat ttcatttga	660

ctggagaaaa ccgttacaca gttcatctca aagacgaaac tgccaattac caccctaaat	720
tttggcaaat cgtccgtaga cgaagccctg ccgagcttct tggggatcta taacggcact	780
ttaagcgaac cgaatttaaa ggaatttgtg gagagcgcg atttcattct catgctgggt	840
gttaagctga cagattccag tacgggcgcg ttactcatc acctgaacga gaacaaaatg	900
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acggaacacg aatttgtaag tgtaatgaaa gaagcgcaag cggaccctaa tcgaatgtac	1560
tggattgaac ttattctggc aaaagaaggg gccctaaag tcctcaagaa aatggggaag	1620
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<210> 478

<211> 1638

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 478

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aaattagaat gggttggtaa taccaacgaa ctgaacgtg cctatgctgc ggatggctac	180
gctcgtctga aaggctcttc ggccatggta actactttcg gcgtaggatga gctgagtga	240
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gagaacgccc tgaccgaaat tccacgtgtg atccaggtg ctctggacga aaagcggccg	480
gttcatattc acctaccgat cgacacagca atgggtgaaa tcgacgtacc ggatacgaa	540
cagccttcaa aagaagagga aatcactgct accgagtggc tgactgttct ggagcacaaa	600
ctgcaacagg caaaacaacc caccctgac gtcggtcacg aaattaactc ttttcgtctg	660
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ggcaagagcg cttttgatga aactcaccg aattatatgg gcatttatga cggttccatc	780
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 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 479
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 atggcaagcc tgtacaaggc c 1641

<210> 480
 <211> 1650
 <212> DNA
 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 480

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cgcattagcg aaactgttca gctgactgct ctgatggctc agctgacca acagaccgt 1560

ctgtctttta tcgaggttgt aatgcaaaaa gatgaccttc cccctctgct gcgcaaagtt 1620

agcgcgtgtt tatcgacg cgaaatgggtggc 1650

<210> 481

<211> 1650

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 481

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gatatcggtt ggatcggttg cactaacgaa ctgaacgtg catatgctgc ggatggctac 180

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tctatcaaaa cttatacgc gagcgccaaa 1650

<210> 482

<211> 1641

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 482

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cccaccagg ccgttgaaca ggctggaaaa tacgtgcacc attccctggg tgagggtaac 360
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gttcacattc acttaccgat cgacgtagca gcgaaggaaa tcgaggttaa agaagactat 540
cattataaaa tgctaaacc agctgatgtt agccagtaca ttgatatggt acaggctaag 600
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<210> 483
<211> 1761
<212> DNA
<213> Artificial Sequence
<220><223> Synthetic polynucleotide
<400> 483

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aatgtttcgg gtctgaaatg gattggatgc tgcaacgaac tgaacggtgc ctacgtgct 180
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<210> 484

<211> 1785

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 484

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ctgcggatgg tggaatcgt tctggaccgt gaagatgtcc tcgagggccc gctgctggac 1740

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<210> 485

<211> 1662

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 485

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cacaaagaac tggaatggat cggtaatgtt aacgaattaa acgtgcata cgctgcggac 180

ggttatgcgc gcctgaatgg cattggcgct gttatgacca cattcggtgt aggagagcta 240

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aaacctgttc acattgttct gccgatcgac gtatataata agccggctaa caaacgaaa 540

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aacttactga tgaaaattaa taaggccaaa aaacctgtga tccttgcgga ctatgaagta 660

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<210> 486

<211> 1680

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 486

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cacatcgtgg cacaccccg tctgagatgg gttggcaacg ccaacgaact gaatgctggt	180
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<210> 487

<211> 1641

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 487

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gcgcgtatta agcccatggg tgctctgcta actaccttcg gcgtaggtga actgtccgca	240
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ttcagcgcac agaatagtta c 1641

<210> 488

<211> 1686

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 488

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 gaaaac 1686

<210> 489

<211> 1653

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 489

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<210> 490

<211> 1698

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 490

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tataacttca ctttactgga cgccctgcaa gaatacaacg gtattcggtt ctataacggc 180
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gaattggatg aagcgatcac acaggctgag caagagtacg ccgaaaaact gtgcctgac 1620

gagatgattg ctgctgatcc aatggacgca ccggaatata tgcaccgtat ccgtaacat 1680

aagcaggaac agaaaaag 1698

<210> 491

<211> 1641

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 491

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<211> 1656

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 493

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<211> 1644

<212> DNA

<213> Artificial Sequence

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<400> 494

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 <211> 1644
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<220><223> Synthetic polynucleotide

<400> 496

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<210> 499

<211> 1656

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 499

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<211> 1695

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 500

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<210> 501

<211> 1638

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 501

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<210> 503

<211> 1695

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 503

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<210> 504

<211> 1647

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 504

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<211> 1671

<212> DNA

<213> Artificial Sequence

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<400> 505

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<210> 506

<211> 1641

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 506

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<211> 1653

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 507

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<210> 508

<211> 1692

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 508

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gaaggtctgc gttagggccgg caacgcgaac gagctgaact ccgcttacgc agctgatggt 180

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ccagtattcg tgactccgat gggtaaaggc gttgtggacg aacagcacc cgcgtttggt 780

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gttaaaaact acatcccagt tcctgtgccg tctttaagc tgactaactc gccggccggt 1080

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<210> 509

<211> 1653

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 509

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<210> 510

<211> 1647

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 510

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 ggccglatca aaggcatggc agctatcgca actactttcg gtgtgggtga gctgtctgct 240
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aaaactgaga ttgagctgat gaacgcttta aaggaagctg acaacaacaa agacaaactg 1560

acctttattg aagtgtgtat ggacaaaatg gatagccccc agttactgaa ggacctgggc 1620

gagctgttct ctaaacagaa cagctat 1647

<210> 511

<211> 1719

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 511

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cctgctggtc tgcattgggt aggtaatgt aacgagctga acgcagctta cgcggctgat 180

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<210> 512
<211> 1653
<212> DNA
<213> Artificial Sequence
<220><223> Synthetic polynucleotide
<400> 512

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<210> 513

<211> 1674

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 513

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<210> 514

<211> 1653

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 514

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caccgggaaa tcaattggat tggttgctgt aacgaattga acgctgccta cgcagctgat 180
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<400> 516

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<211> 1647

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 517

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<210> 518

<211> 1683

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 518

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<210> 519

<211> 1644

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 519

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<210> 520

<211> 1650

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 520

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<211> 1662

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 521

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<400> 522

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<211> 1644

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 530

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 gcgaccgtta ctgaaagctc cgatccgggt gtacttaccc aagttgttga catcctcgcg 600
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ccggaacagc gaactgtgct gatcaccgga gagggttctc accaactgac cgctcaggaa 1320

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tggaaatatg aaaaactgcc ggaagcgatg ggctgcgaaa actggttcac ggctcgtgtt 1500

actacctgtg aggaactgga cgcagccatc cgtcaggccg aaacctgcgg cactggagct 1560

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tctatcaact ccttatatag cgcg 1644

<210> 531

<211> 1659

<212> DNA

<213> Artificial Sequence

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<400> 531

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gaattagcat ggggttggtg cgccaacgaa ctgaacgtg catatgctgc ggatggctac 180

gcccgttgca aggggtgctg tgccctgctg actacgttcg gcgtaggaga actgtccgca 240

ctgaatggtg tcgcgggcag ttacgcagag cacctgccag tgatccatat cgttggcgtt 300

cccaactcac acgcgcagca acgcggtgaa ctgttacatc atacactggg tgacggcgac 360

tttcgtcact tctgcgtat cgcggaagag gtaagcgttg ctcaggcgac cctaactcgg 420

gctaacgctt gtaccgaaat cgatcgctg attctggaag cacttaacaa gcaacgaccg 480

ggctatctgc tgcctccgtc ggatgtagcg gaagcacctg cgactcggcc gaccaaactg 540

ctggacgttg ctgctgctgc tgccgaaccg gctactcttg aagcgttcgg tcaactgcgt 600

caggcaaaaa tcgcagagtc tcgttctgca agcctcttgg ccgacttctt ggcgctgcgc 660

tacgggctgc aagaggctct gcaacagtgg atggacggta cccaatgcc tcacgttcc 720

ctgctgatgg gtaaaggcct ttttgatgaa tctaagccgg gattcctcgg tacatattca 780

ggcgcccgca gcgaaccgca ggtgaggcag gggattgaat ctgctggcgt ggttatctgt 840

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caccagcaga taacctgggt cggttgcgct aacgagttaa acgcagctta cgcagcggat	180
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cgcgggtttt atttgctgct accgagcgac gtagcagaag caccgtggc gtctcgtccg	540
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tgtctgcgtg tgagttagcc ggaacaactg tgccaggcac tggacaaaagt gaacgatcgc 1560
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<210> 533

<211> 548

<212> PRT

<213> Lactococcus lactis

<400> 533

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Ile Glu Glu Ile Phe Gly Val Pro Gly Asp Tyr Asn Leu Gln Phe Leu

20 25 30

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

35 40 45

Glu Leu Asn Ala Ser Tyr Met Ala Asp Gly Tyr Ala Arg Thr Lys Lys

50 55 60

Ala Ala Ala Phe Leu Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Val

65 70 75 80

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

85

90

95

Val Gly Ser Pro Thr Ser Lys Val Gln Asn Glu Gly Lys Phe Val His

100

105

110

His Thr Leu Ala Asp Gly Asp Phe Lys His Phe Met Lys Met His Glu

115

120

125

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

130

135

140

Glu Ile Asp Arg Val Leu Ser Ala Leu Leu Lys Glu Arg Lys Pro Val

145

150

155

160

Tyr Ile Asn Leu Pro Val Asp Val Ala Ala Ala Lys Ala Glu Lys Pro

165

170

175

Ser Leu Pro Leu Lys Lys Glu Asn Ser Thr Ser Asn Thr Ser Asp Gln

180

185

190

Glu Ile Leu Asn Lys Ile Gln Glu Ser Leu Lys Asn Ala Lys Lys Pro

195

200

205

Ile Val Ile Thr Gly His Glu Ile Ile Ser Phe Gly Leu Glu Lys Thr

210

215

220

Val Thr Gln Phe Ile Ser Lys Thr Lys Leu Pro Ile Thr Thr Leu Asn

225

230

235

240

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

245

250

255

Tyr Asn Gly Thr Leu Ser Glu Pro Asn Leu Lys Glu Phe Val Glu Ser

260

265

270

Ala Asp Phe Ile Leu Met Leu Gly Val Lys Leu Thr Asp Ser Ser Thr

275

280

285

Gly Ala Phe Thr His His Leu Asn Glu Asn Lys Met Ile Ser Leu Asn

290

295

300

Ile Asp Glu Gly Lys Ile Phe Asn Glu Arg Ile Gln Asn Phe Asp Phe

305

310

315

320

Glu Ser Leu Ile Ser Ser Leu Leu Asp Leu Ser Glu Ile Glu Tyr Lys

325

330

335

Gly Lys Tyr Ile Asp Lys Lys Gln Glu Asp Phe Val Pro Ser Asn Ala
340 345 350

Leu Leu Ser Gln Asp Arg Leu Trp Gln Ala Val Glu Asn Leu Thr Gln
355 360 365

Ser Asn Glu Thr Ile Val Ala Glu Gln Gly Thr Ser Phe Phe Gly Ala
370 375 380

Ser Ser Ile Phe Leu Lys Ser Lys Ser His Phe Ile Gly Gln Pro Leu
385 390 395 400

Trp Gly Ser Ile Gly Tyr Thr Phe Pro Ala Ala Leu Gly Ser Gln Ile
405 410 415

Ala Asp Lys Glu Ser Arg His Leu Leu Phe Ile Gly Asp Gly Ser Leu
420 425 430

Gln Leu Thr Val Gln Glu Leu Gly Leu Ala Ile Arg Glu Lys Ile Asn
435 440 445

Pro Ile Cys Phe Ile Ile Asn Asn Asp Gly Tyr Thr Val Glu Arg Glu
450 455 460

Ile His Gly Pro Asn Gln Ser Tyr Asn Asp Ile Pro Met Trp Asn Tyr
465 470 475 480

Ser Lys Leu Pro Glu Ser Phe Gly Ala Thr Glu Asp Arg Val Val Ser
485 490 495

Lys Ile Val Arg Thr Glu Asn Glu Phe Val Ser Val Met Lys Glu Ala
500 505 510

Gln Ala Asp Pro Asn Arg Met Tyr Trp Ile Glu Leu Ile Leu Ala Lys
515 520 525

Glu Gly Ala Pro Lys Val Leu Lys Lys Met Gly Lys Leu Phe Ala Glu
530 535 540

Gln Asn Lys Ser

545

<210> 534

<211> 546

<212> PRT

<213> *Staphylococcus agnetis*

<400> 534

Met Lys Lys Lys Ile Ser Gln Phe Ile Phe Asp Glu Ile Glu Arg His

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Gly Val Asp Thr Ile Phe Gly Val Pro Gly Asp Phe Asn Leu Ala Phe

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Leu Asp Asp Ile Val Ala His Pro Lys Leu Glu Trp Val Gly Asn Thr

35 40 45

Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Leu Lys

50 55 60

Gly Leu Ser Ala Met Val Thr Thr Phe Gly Val Gly Glu Leu Ser Ala

65 70 75 80

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

85 90 95

Ile Thr Gly Gly Pro Thr Thr Val Val Glu Lys Ala Gly Lys Tyr Val

100 105 110

His His Ser Leu Gly Glu Gly Val Phe Asp Val Tyr Gln Lys Met Tyr

115 120 125

Gln His Ile Thr Val Ala Gln Thr Tyr Val Thr Pro Glu Asn Ala Leu

130 135 140

Thr Glu Ile Pro Arg Val Ile Gln Ala Ala Leu Asp Glu Lys Arg Pro

145 150 155 160

Val His Ile His Leu Pro Ile Asp Thr Ala Met Val Glu Ile Asp Val

165 170 175

Pro Asp Thr Glu Gln Pro Ser Lys Glu Glu Glu Ile Thr Ala Thr Glu

180 185 190

Trp Leu Thr Val Leu Glu His Lys Leu Gln Gln Ala Lys Gln Pro Thr

195 200 205

Leu Ile Val Gly His Glu Ile Asn Ser Phe Arg Leu Gln His Glu Val

210 215 220

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

225				230				235				240			
Gly	Lys	Ser	Ala	Phe	Asp	Glu	Thr	His	Pro	Asn	Tyr	Met	Gly	Ile	Tyr
245				250				255							
Asp	Gly	Ser	Ile	Ala	His	Pro	Ala	Ile	Lys	Asp	Tyr	Val	Asp	His	Ser
260				265				270							
Asp	Leu	Val	Ile	Thr	Leu	Gly	Ala	Lys	Leu	Thr	Asp	Ser	Ala	Thr	Ala
275				280				285							
Gly	Phe	Ser	Tyr	Gln	Phe	Ala	Asp	Glu	Gln	Ile	Val	Thr	Leu	Asn	His
290				295				300							
Lys	Asn	Ile	Gln	Val	Asp	Glu	Val	Thr	Val	Glu	Ser	Met	Ala	Leu	Pro
305				310				315				320			
Glu	Ile	Val	Ser	Gln	Met	Ser	Lys	Leu	Asn	Ser	His	Phe	Asp	Gly	Glu
325				330				335							
Trp	Pro	Gln	Cys	Glu	Arg	Pro	Ser	Asn	Ser	Glu	Val	Val	Val	Asp	Asp
340				345				350							
Ala	Pro	Leu	Thr	Gln	Gln	His	Tyr	Phe	Glu	Leu	Met	Gln	Gln	Phe	Ile
355				360				365							
Lys	Pro	Asn	Asp	Val	Leu	Ile	Ala	Glu	Gln	Gly	Thr	Ser	Phe	Phe	Gly
370				375				380							
Ala	Tyr	Asp	Leu	Val	Leu	Pro	Gln	Gly	Val	Thr	Phe	Ile	Gly	Gln	Pro
385				390				395				400			
Leu	Trp	Gly	Ser	Ile	Gly	Tyr	Thr	Phe	Pro	Ala	Thr	Leu	Gly	Thr	Gln
405				410				415							
Leu	Ala	Asp	Arg	His	Arg	Arg	Asn	Ile	Leu	Leu	Ile	Gly	Asp	Gly	Ser
420				425				430							
Leu	Gln	Leu	Thr	Val	Gln	Asp	Met	Ala	Thr	Met	Leu	Arg	Gln	Asn	Ile
435				440				445							
His	Pro	Ile	Ile	Phe	Ile	Ile	Asn	Asn	Asp	Gly	Tyr	Thr	Val	Glu	Arg
450				455				460							
Lys	Ile	His	Gly	Glu	Asn	Glu	Pro	Tyr	Asn	Asp	Ile	Ser	Lys	Trp	Asp
465				470				475				480			

Tyr His Leu Leu Pro Thr Val Phe Gly His Lys Glu Thr Pro Thr Tyr
485 490 495

Gln Val Ser Thr Ser Lys Ala Leu Lys Glu Val Met Asp Lys Val Asn
500 505 510

Glu Gln Pro Gln Ser Met His Val Ile Glu Val Phe Met Asp Lys His
515 520 525

Asp Ala Pro Glu Lys Leu Thr Asn Ile Ala Lys Ala Phe Ala Thr Gln
530 535 540

Asn Lys

545

<210> 535

<211> 547

<212> PRT

<213> Unknown

<220><223> Mesorhizobium sp. SOD10

<400> 535

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Gly Ile Ser Asp Val Phe Gly Val Pro Gly Asp Tyr Ala Phe Pro Val
20 25 30

Asn Asp Ala Ile Cys Asn Asp Pro Ala Met Arg Trp Ile Gly Cys Ala
35 40 45

Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile Lys
50 55 60

Gly Met Ala Ala Leu Cys Thr Thr Tyr Gly Val Gly Glu Leu Ser Ala
65 70 75 80

Ile Asn Gly Ile Ala Gly Ala Tyr Ala Glu His Leu Pro Ile Phe His
85 90 95

Leu Val Gly Ala Pro Gly Met Ala Val Gln Thr Ser Arg Arg Ala Met
100 105 110

His His Thr Leu Gly Asn Gly Glu Tyr Asp Leu Phe His Arg Met Ser

115	120	125	
Glu Pro Val Val Cys Ala His Ala Val Met Thr Pro Gln Asn Val Ala			
130	135	140	
Tyr Glu Thr Glu Arg Leu Ile Ala Glu Ala Leu Phe His Arg Arg Pro			
145	150	155	160
Val Tyr Met Val Phe Pro Ala Asp Tyr Ala Asn Gln Pro Val Leu Gly			
165	170	175	
Ser Ala Glu Pro Ile Arg Ala Pro Gly Ser Asn Ala Glu Ala Leu Glu			
180	185	190	
Ala Ala Val Ala Ala Ile Val Ala Ala Leu Asp Lys Ala Glu Thr Ala			
195	200	205	
Cys Val Leu Pro Gly Ile Leu Ile Ala Arg Ser Gly Leu Lys Ala Ala			
210	215	220	
Met Gln Ala Val Ile Asp Lys Ser Gly Leu Pro Phe Ala Thr Met Phe			
225	230	235	240
Met Asp Lys Ser Val Leu Asp Glu Gln Gln Ala Gly Phe Val Gly Met			
245	250	255	
Tyr Asp Gly Ala Ile Met Ser Glu Glu Val Arg Gly Phe Val Glu Gly			
260	265	270	
Ser Asp Gln Val Leu Ala Ile Gly Thr Leu Ala Ser Asp Phe Asn Thr			
275	280	285	
Gly Ala Phe Thr Ala Arg Leu Asp Pro Ala Arg Thr Ile Ser Ile Gly			
290	295	300	
His His His Val His Val Gly Gly Lys Thr Tyr Ala Asn Ile Glu Leu			
305	310	315	320
Gly Asp Val Leu Glu Ala Leu Ser Arg Lys Leu Thr Lys Arg Asn Trp			
325	330	335	
Lys Arg Ile Pro Ala Val Ser Leu Gly Val Lys Ser Gly Lys Gly Asn			
340	345	350	
Asp Pro Ile Thr Val Glu Ala Leu Tyr Pro Arg Trp Ala Glu Phe Leu			
355	360	365	

Lys Pro Glu Asp Ile Val Ile Gly Glu Thr Gly Thr Ala Ser Met Gly
370 375 380

Leu Gly Phe Ala Leu Ile Pro Lys Gly Ala Thr Phe His Asn Gln Thr
385 390 395 400

Leu Trp Gly Ser Ile Gly Trp Ala Thr Pro Ala Ala Val Gly Ala Ala
405 410 415

Ala Ala Ala Pro Asp Arg Arg Val Val Leu Val Thr Gly Asp Gly Ser
420 425 430

His Gln Leu Thr Ala Gln Glu Ile Gly Gln Phe Gly Arg Leu Gly Leu
435 440 445

Lys Pro Val Val Phe Val Leu Asn Asn Asp Gly Tyr Leu Ile Glu Arg
450 455 460

Leu Leu Cys Lys Asp Pro Glu Ile Ala Tyr Asn Asp Ile Ala Pro Trp
465 470 475 480

Arg Tyr Thr Glu Leu Pro His Ala Leu Gly Cys Asp Gly Trp Phe Thr
485 490 495

Ala Arg Val Thr Thr Cys Ala Glu Phe Asp Glu Ala Leu Glu Gln Ala
500 505 510

Gly Lys Ala Asp Ser Gly Val Tyr Ile Glu Val Val Thr Asp Ala Tyr
515 520 525

Ala Ala Ser Pro Leu Ala Met Lys Leu His Glu Ser Met Ala Ser Leu
530 535 540

Tyr Lys Ala

545

<210> 536

<211> 550

<212> PRT

<213> Pantoea stewartii

<400> 536

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Cys Gly Ile Arg His Leu Phe Gly Val Pro Gly Asp Phe Asn Leu Gln

20 25 30

Phe Leu Asp Arg Val Ile Ala His Pro Thr Ile Ser Trp Val Gly Cys

35 40 45

Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Gly Arg Cys

50 55 60

Ser Gly Met Ala Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu Ser

65 70 75 80

Ala Ile Asn Gly Leu Ala Gly Ser Phe Ala Glu Tyr Val Pro Val Ile

85 90 95

His Ile Val Gly Ala Pro Ser Ser Gln Ala Met Gln Gln Gly Asp Cys

100 105 110

Val His His Thr Leu Gly Asp Gly Asp Phe Gly His Phe Ile Arg Met

115 120 125

Ala Lys Glu Val Asn Val Ala Thr Ala Gln Leu Thr Ala Glu Asn Ala

130 135 140

Thr Ala Glu Ile Asp Arg Val Leu Ser Ser Val Ile Gln Gln His Arg

145 150 155 160

Pro Gly Tyr Leu Leu Leu Pro Val Asp Val Ala Gln Ala Glu Thr Ala

165 170 175

Ala Pro Val His Pro Leu Val Ser Ser Ala Ser Ser Pro Glu Ser Leu

180 185 190

Arg Ser Ala Phe Arg Gln Ala Ala Glu Arg Leu Leu Ala Pro Ala Gln

195 200 205

Arg Val Ser Leu Leu Ala Asp Phe Leu Ala Gln Arg Trp Gln Gln Gln

210 215 220

Pro Ala Leu Ala Ala Leu Arg Ala Arg Arg Ala Phe Pro Cys Ala Thr

225 230 235 240

Leu Leu Met Gly Lys Gly Val Leu Asp Glu Gln Gln Pro Gly Phe Val

245 250 255

Gly Thr Tyr Ala Gly Glu Gly Ser Glu Gly Arg Val Arg Gln Gln Ile

260 265 270
Glu Glu Ala Asp Val Thr Leu Cys Val Gly Val Arg Phe Thr Asp Thr

275 280 285
Ile Thr Ala Gly Phe Thr Gln Gln Phe Arg Pro Asp Arg Leu Ile Asp

290 295 300

Val Gln Pro His Ser Ala Ser Val Ala Gly Gln Thr Phe Ala Pro Leu

305 310 315 320

Ser Met Ala Asp Ala Leu Gln Thr Leu Leu Pro Leu Phe Glu Arg Tyr

325 330 335

Gly Ala Gly Trp Gln Ser Ala Gly Pro Val Lys Pro Ala Ala Pro Val

340 345 350
Pro Asp Ala Ala Ile Ile Ser Gln Ser Ala Phe Trp Gln Ala Met Gln

355 360 365

Ser Phe Ile Gln Pro Gly Asp Ile Ile Leu Ala Asp Gln Gly Thr Ala

370 375 380

Ala Phe Gly Ala Ala Ala Leu Arg Leu Pro Ala Gly Ala Gln Leu Leu

385 390 395 400

Val Gln Pro Leu Trp Gly Ser Ile Gly Tyr Thr Leu Pro Ala Ala Phe

405 410 415
Gly Ala Gln Thr Ala Arg Pro Ser Gln Arg Val Ile Leu Ile Ile Gly

420 425 430

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

435 440 445

Asp Asp Gln His Pro Ile Ile Phe Leu Leu Asn Asn Glu Gly Tyr Thr

450 455 460

Val Glu Arg Ala Ile His Gly Ala Asp Gln Arg Tyr Asn Asp Ile Ala

465 470 475 480

Gln Trp Asn Trp Thr Ala Leu Pro Gln Ala Phe Ser Leu His Cys Gln

485 490 495

Ala Gln Ser Trp Arg Ile Ser Glu Thr Val Gln Leu Thr Ala Leu Met

500 505 510

Ala Gln Leu Thr Gln Gln His Arg Leu Ser Phe Ile Glu Val Val Met

515 520 525

Gln Lys Asp Asp Leu Pro Pro Leu Leu Arg Lys Val Ser Ala Cys Leu

530 535 540

Ser Gln Arg Asn Gly Gly

545 550

<210> 537

<211> 550

<212> PRT

<213> Unknown

<220><223> Desulfovibrio sp. TomC

<400> 537

Met Gln Gln Thr Val Ile Glu Leu Leu Ile Ala Arg Leu Lys Glu Ile

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Gly Ile Thr Asp Val Phe Gly Val Pro Gly Asp Phe Ala Phe Ala Leu

20 25 30

Asn Asp Ala Ile Asp Asn Asp Pro Asp Met Arg Trp Ile Gly Cys Thr

35 40 45

Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile Lys

50 55 60

Gly Arg Ala Ala Leu Cys Thr Thr Tyr Gly Val Gly Glu Leu Ser Ala

65 70 75 80

Leu Cys Gly Val Ala Gly Ser Tyr Thr Glu His Leu Pro Val Phe His

85 90 95

Leu Val Gly Met Pro Ser Ile Ser Thr Gln Gln Ser Arg Arg Ile Val

100 105 110

His His Thr Leu Gly Asp Gly Leu Phe Asp Ala Phe Ser Thr Met Thr

115 120 125

Lys Pro Val Val Cys Ala Ser Ala Ile Leu Thr Ala Glu Asn Ala Ala

130 135 140

Cys Gln Ile Glu Arg Cys Ile Glu Ala Ala Ile Ala Arg Asn Arg Pro

145 150 155 160

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

165 170 175

Gln Tyr Val Cys Ala Pro Glu Ala Pro Val Ser Asn Pro Pro Val Leu

180 185 190

Ala Ala Ala Ile Glu Ala Ile Val Glu Lys Ile Thr Ala Ala Gly Ser

195 200 205

Thr Val Val Leu Ala Gly Tyr Leu Ile Ala Arg Leu Gly Leu Arg Ser

210 215 220

Ala Ala His Glu Leu Leu Thr Arg Thr Gly Leu Pro Tyr Ala Thr Met

225 230 235 240

Phe Met Asp Lys Thr Ala Leu Asp Glu Thr His Pro Ser Tyr Ile Gly

245 250 255

Leu Tyr Asp Gly Arg Ile Met Asn Pro Glu Val Arg Asp Phe Val Glu

260 265 270

Gly Cys Asp Cys Val Leu Asn Leu Gly Ala Gln Trp Ser Asp Phe Asn

275 280 285

Thr Gly Ala Phe Thr Ala His Ile Asp Pro Ser Arg Met Ile Ala Val

290 295 300

Met Gln His Glu Val Arg Val Gly His Ala Val Phe Ala His Val Glu

305 310 315 320

Met Arg Asp Val Leu Ala Gly Leu Ala Arg Val Leu Pro His Lys Pro

325 330 335

Ala Ser Gly Pro Arg Ala Lys Gly Leu Gly Gln Pro Lys Gly Ala Pro

340 345 350

Gly Asp Pro Ile Thr Pro Asp Tyr Leu Tyr Pro Arg Trp Glu Gln Phe

355 360 365

Leu Arg Pro Gly Asp Val Val Met Ala Glu Thr Gly Thr Val Ser Met

370 375 380

Gly Leu Gly Phe Ala Leu Met Pro Gln Gly Ala Glu Phe Phe Asn Gln

385 390 395 400

Thr Leu Trp Gly Ala Ile Gly Trp Ala Thr Pro Ala Ser Phe Gly Ala

405 410 415
Ala Leu Ala Ala Pro Glu Arg Arg Thr Leu Leu Phe Thr Gly Glu Gly

420 425 430
Ser His Gln Met Thr Ala Gln Glu Leu Gly Gln Phe Gly Met His Gly

435 440 445
Leu Lys Pro Ile Val Phe Cys Leu Asn Asn Asp Gly Tyr Leu Ile Glu

450 455 460
Arg Leu Leu Cys Lys Asn Pro Leu Ser Ser Tyr Asn Asp Leu Ala Pro

465 470 475 480
Trp Asn Tyr Ala Gln Leu Pro Ala Ala Phe Gly Leu Thr Asp Trp Tyr

485 490 495
Cys Ala Lys Val Thr Thr Asn Ala Glu Leu Glu Gln Ala Leu Ala Lys

500 505 510
Ala Glu Thr Cys Gly Thr Gly Ala Tyr Ile Glu Val Val Met Asp Arg

515 520 525
Met Ala Ala Ser Pro Leu Ala Gln Lys Leu Gly Glu Ser Ile Lys Thr

530 535 540
Leu Tyr Ala Ser Ala Lys

545 550

<210> 538

<211> 547

<212> PRT

<213> Staphylococcus petrasii

<400> 538

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Gly Val Asp Lys Val Phe Gly Val Pro Gly Asp Phe Asn Leu Thr Phe

20 25 30

Leu Asp Asp Ile Ile Gly Arg Thr Asp Met Glu Trp Ile Gly Asn Thr

35 40 45

Asn Glu Leu Asn Ala Ser Tyr Ala Ala Asp Gly Tyr Ala Arg Met Lys

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

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

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

 245 250 255
 Asp Gly Ser Ile Ala Glu Glu Arg Ile Lys Tyr Tyr Val Asp His Ser
 260 265 270
 Asp Ala Ile Leu Asn Ile Gly Ala Lys Leu Thr Asp Ser Ala Thr Ala
 275 280 285
 Gly Phe Ser Tyr Gln Phe Asp Ile Asp Asp Val Ile Met Leu Asn His
 290 295 300

Arg Asn Phe Lys Met Asn Glu Thr Arg Asp Asp Asn Val Ala Leu Gln

305 310 315 320

Asp Leu Leu Ile Gly Leu Gln Arg Ile Asp Phe His Phe Asn Gly Asp

325 330 335

Tyr Pro Met Phe Lys Lys Pro Val Pro Asn Asp Asp Val Leu Asp Asp

340 345 350

Thr Pro Leu Thr Gln Gln Thr Tyr Phe Lys Met Met Gln Asp Phe Leu

355 360 365

Asn Arg Asp Asp Val Val Ile Ala Glu Gln Gly Thr Ser Phe Phe Gly

370 375 380

Ala Tyr Asp Leu Ala Leu Thr Lys Thr Asn Lys Phe Ile Gly Gln Pro

385 390 395 400

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

405 410 415

Leu Ala Asp Gly Glu Arg Arg Asn Val Leu Leu Ile Gly Asp Gly Ser

420 425 430

Leu Gln Leu Thr Val Gln Glu Met Ala Thr Met Ile Arg Leu Gln Leu

435 440 445

Lys Pro Val Ile Phe Ile Ile Asn Asn Asp Gly Tyr Thr Val Glu Arg

450 455 460

Lys Ile His Gly Glu Asn Ala Leu Tyr Asn Asp Ile Pro Met Trp Asp

465 470 475 480

Tyr Lys Ala Leu Pro Ser Val Phe Gly Gly Asn Glu Thr Val Ser Val

485 490 495

His Glu Val Asp Ser Ser Val Ser Leu Gln His Ala Phe Asn Glu Ile

500 505 510

Asn Leu Gln Pro Asn Arg Met His Val Ile Glu Val Lys Met Gly Met

515 520 525

His Asp Ala Pro Glu Lys Leu Asn Asp Ile Gly Lys Ala Phe Ala Lys

530 535 540

Gln Asn Gly

545

<210> 539

<211> 587

<212> PRT

<213> Cladophialophora immunda

<400> 539

Met Ala Ala Pro Thr Ile Cys Met Gly Gln Tyr Leu Phe Arg Arg Ile

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20 25 30
Leu Thr Leu Leu Asp Glu Ile Tyr Asn Val Ser Gly Leu Lys Trp Ile
35 40 45
Gly Cys Cys Asn Glu Leu Asn Gly Ala Tyr Ala Ala Asp Gly Tyr Thr
50 55 60
Arg Ile Lys Gly Ser Pro Ala Val Leu Val Thr Thr Tyr Ala Val Gly

65 70 75 80
Glu Leu Ser Ala Met Asn Gly Val Ala Gly Ala Tyr Ala Glu His Ala
85 90 95
Gly Met Ile His Ile Val Gly Met Pro Ala Arg Ser Met Gln Lys Ala
100 105 110
Arg Ala Met Leu His His Thr Met Lys Ala Asn Met Asp His Ala Thr
115 120 125
Tyr Ile His Met Ala Ala Pro Ile Arg Glu Thr His Ala Tyr Leu Met

130 135 140
Asp Asp Lys Ile Met Ala Glu Glu Ile Asp Arg Thr Ile Val Ala Cys
145 150 155 160
Val Arg Ser Arg Leu Pro Val Tyr Ile Tyr Val Pro Val Asp Ala Val
165 170 175
Gln Val Gln Leu Asp Ala Lys Arg Leu Glu Thr Pro Leu Asp Val Gly
180 185 190
Val His Asn Gly Asp Gly Lys Ile Glu Asp Gln Ile Val Ser Ser Ile

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

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

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

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

Val Gly Glu Gly Ser Leu Gln Met Thr Val Gln Glu Ile Gly Ser Tyr

450

455

460

Ile Arg Tyr Gly Phe Lys Pro Ile Ile Phe Val Ile Asn Asn Asn Gly

465

470

475

480

Tyr Ala Ile Glu Arg Ala Ile His Gly Pro Glu Gln Gly Tyr Asn Asp

485

490

495

Val Ser Met Met Trp Asp Tyr Gln Lys Met Leu Gly Phe Phe Gly Ala

500

505

510

Arg Glu Asp Thr Gly Val Lys Ala Lys Ser Arg Ala Thr Lys Thr Val

515

520

525

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

530

535

540

Ser Ile Gln Leu Cys Glu Ile Phe Met Asp Thr Phe Asp Tyr Pro Trp

545

550

555

560

Arg Leu Thr Glu Gln Ile Ala Ile Ser Arg Ala Arg Thr Lys Arg Asp

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575

Ala Asp Lys Leu Thr Ala Ala Ser Gly Glu Ala

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<212> PRT

<213> Fonsecaea pedrosoi

<400> 540

Met Pro Ser Thr Val Lys Leu Ala Glu Tyr Leu Phe Thr Arg Leu His

1

5

10

15

Gln Leu Gly Val Arg Ser Ile His Gly Val Pro Gly Asp Tyr Asn Leu

20

25

30

Thr Leu Leu Asp His Ile Glu Pro Ser Gly Leu His Trp Val Gly Asn

35

40

45

Cys Asn Glu Leu Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Ala Arg Ile

50

55

60

Asn	Gly	Leu	Gly	Ala	Leu	Ile	Thr	Thr	Phe	Gly	Val	Gly	Glu	Leu	Ser
65				70				75				80			
Ala	Val	Asn	Ala	Ile	Ala	Gly	Ala	Tyr	Cys	Glu	Arg	Ser	Ala	Val	Val
85				90				95							
His	Val	Val	Gly	Thr	Pro	Glu	Arg	Ser	Val	Gln	Asp	Ser	Arg	Leu	Lys
100				105				110							
Val	His	His	Thr	Phe	Ala	Asp	Gly	Asn	Phe	Asp	Arg	Phe	Ala	Gln	Met
115				120				125							
His	Ala	Gln	Ile	Thr	Val	Ala	Gln	Ala	Ser	Leu	Trp	Asp	Pro	Leu	Met
130				135				140							
Ala	Pro	Glu	Gln	Ile	Asp	Ala	Val	Leu	Arg	Gln	Cys	Leu	Leu	Gln	Ser
145				150				155				160			
Arg	Pro	Val	Tyr	Ile	Gln	Val	Pro	Val	Asp	Leu	Val	Asp	Ala	Pro	Val
165				170				175							
Glu	Ala	Asp	Arg	Leu	Tyr	Ser	Gln	Cys	Leu	Ser	Ala	Ala	Val	Thr	Ser
180				185				190							
Met	Asn	Ser	Thr	Ile	Thr	Pro	Ala	His	Asp	Thr	Val	Leu	Ser	Leu	Val
195				200				205							
Leu	Lys	Lys	Ile	Lys	Thr	Ala	Lys	His	Pro	Ala	Ile	Leu	Val	Asp	Gly
210				215				220							
Glu	Ser	Arg	Ala	Leu	Gly	Ile	Thr	Glu	Asp	Val	Gln	His	Ile	Val	Arg
225				230				235				240			
Leu	Thr	Lys	Trp	Pro	Thr	Trp	Val	Thr	Val	Phe	Gly	Lys	Gly	Leu	Val
245				250				255							
Asp	Glu	Thr	Ala	Pro	Asn	Val	His	Gly	Val	Tyr	Arg	Gly	Ser	Tyr	Asp
260				265				270							
Pro	Lys	Ala	Lys	Ala	Phe	Val	Asp	Ser	Ser	Asp	Leu	Val	Leu	Cys	Phe
275				280				285							
Gly	Pro	His	Phe	Ser	Thr	Thr	Asn	Thr	Phe	Asp	Ser	Thr	Ser	Ile	Pro
290				295				300							
Pro	Gln	Ala	Val	Thr	Ile	Ser	Tyr	Thr	Asp	Asn	Glu	Val	Arg	Ile	Gln

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

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

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

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

Leu Arg Met Val Glu Ile Val Leu Asp Arg Glu Asp Val Leu Glu Gly

565

570

575

Pro Leu Leu Asp Leu Leu Gln Glu Glu Arg Lys Val Ala Leu Gly Gly

580

585

590

Ala Ser Gln

595

<210> 541

<211> 554

<212> PRT

<213> Bacillus filamentosus

<400> 541

Met Lys Lys Asp Tyr Thr Ile Gly Asp Tyr Leu Leu Asp Arg Leu Ala

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Gln Ile Gly Val Gln His Val Phe Gly Val Pro Gly Asp Tyr Asn Leu

20

25

30

Met Phe Leu Asp Glu Val Leu Lys His Lys Glu Leu Glu Trp Ile Gly

35

40

45

Asn Cys Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg

50

55

60

Leu Asn Gly Ile Gly Ala Val Met Thr Thr Phe Gly Val Gly Glu Leu

65

70

75

80

Ser Ala Val Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Pro Val

85

90

95

Val Lys Val Thr Gly Ala Pro Thr Thr Lys Val Met Lys Glu Gly Ala

100

105

110

Tyr Val His His Thr Leu Gly Asp Gly Asn Phe His Arg Phe Ser Thr

115

120

125

Met Phe Arg Glu Val Thr Cys Ala Gln Thr Ile Leu Thr Val Glu Asn

130

135

140

Ala Ser Gln Glu Ile Asp Arg Val Leu Leu Ala Cys Leu Thr Glu Lys

145

150

155

160

Lys Pro Val His Ile Val Leu Pro Ile Asp Val Tyr Asn Lys Pro Ala
 165 170 175
 Asn Lys Pro Lys Lys Gln Leu Leu Asp Glu Glu Met Lys Ser Asn Glu
 180 185 190
 Lys Ala Met Asp Glu Met Leu Thr Asn Leu Leu Met Lys Ile Asn Lys
 195 200 205
 Ala Lys Lys Pro Val Ile Leu Ala Asp Tyr Glu Val Tyr Arg Tyr Lys
 210 215 220

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

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

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

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Gly	Tyr	Gly	Arg	Leu	Arg	Gly	Met	Ser	Ala	Val	Val	Thr	Thr	Phe	Gly				
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Val	Gly	Glu	Leu	Ser	Ala	Ala	Asn	Ala	Ile	Ala	Gly	Ser	Tyr	Ala	Glu				
85					90					95									
His	Val	Pro	Val	Val	His	Ile	Val	Gly	Gly	Pro	Ser	Lys	Asp	Ala	Gln				
100					105					110									
Gly	Thr	Arg	Arg	Ala	Leu	His	His	Ser	Leu	Gly	Asp	Gly	Asp	Phe	Glu				
115					120					125									
His	Phe	Leu	Arg	Ile	Ser	Arg	Glu	Ile	Thr	Cys	Ala	Gln	Thr	Thr	Leu				
130					135					140									
Met	Pro	Ala	Thr	Ala	Thr	Arg	Glu	Ile	Asp	Arg	Val	Leu	Ser	Glu	Val				
145					150					155					160				
Arg	Glu	Gln	Lys	Gln	Pro	Gly	Tyr	Ile	Leu	Met	Ala	Thr	Asp	Val	Ala				
165					170					175									
Arg	Phe	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Pro	Leu	Pro	Arg	Tyr	Thr	Gly				
180					185					190									
Gly	Thr	Ser	Pro	Arg	Ala	Leu	Ser	Leu	Phe	Ile	Asp	Ala	Ala	Thr	Lys				
195					200					205									
Leu	Ile	Gly	Asp	His	Gln	Val	Thr	Val	Leu	Ala	Asp	Tyr	Leu	Val	His				
210					215					220									
Arg	Leu	Asp	Ala	Ile	Pro	Gln	Leu	Glu	Ala	Leu	Leu	Ser	Ala	Asp	Ala				
225					230					235					240				
Val	Pro	His	Ala	Thr	Leu	Met	Trp	Gly	Lys	Ser	Leu	Val	Asp	Glu	Ser				
245					250					255									
Asn	Pro	Asn	Phe	Leu	Gly	Ile	Tyr	Val	Gly	Ala	Ala	Ser	Ala	Glu	Pro				
260					265					270									
Val	Arg	Arg	Ala	Val	Glu	Glu	Ala	Pro	Val	Leu	Val	Thr	Ala	Gly	Val				
275					280					285									
Val	Phe	Thr	Asp	Met	Val	Ser	Ser	Phe	Phe	Ser	Gln	Arg	Ile	Asp	Pro				
290					295					300									

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

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

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

Arg Ala Leu Gly Val Thr Asn Ala Leu Thr Phe Arg Ala Gln Thr Cys
500 505 510
Gly Glu Leu Asp Asp Ala Phe Thr Ala Ala Ala Arg His Gln Asp Arg
515 520 525
Met Val Phe Ile Glu Ala Val Val Pro Arg Leu Asp Val Pro Asp Leu
530 535 540
Leu Ala Glu Leu Ala Arg Pro Thr Ser Pro Asp Gly Ser Ala Arg Arg

545	550										555										560																																						
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Gly	Val	Gly	His	Ile	Phe	Gly	Val	Pro	Gly	Asp	Tyr	Asn	Leu	Gly	Phe																																												
				20				25				30																																															
Leu	Asp	Met	Ile	Glu	Asp	Asp	Pro	Asn	Leu	Glu	Trp	Ile	Gly	Asn	Cys																																												
35				40				45																																																			
Asn	Glu	Leu	Asn	Ala	Ser	Tyr	Ala	Ala	Asp	Gly	Tyr	Ala	Arg	Ile	Lys																																												
50				55				60																																																			
Pro	Met	Gly	Ala	Leu	Leu	Thr	Thr	Phe	Gly	Val	Gly	Glu	Leu	Ser	Ala																																												
65				70				75				80																																															
Ile	Asn	Gly	Val	Ala	Gly	Ser	Phe	Ala	Glu	Ser	Val	Pro	Val	Val	Lys																																												
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Ile	Val	Gly	Met	Pro	Ser	Arg	Asn	Val	Ser	Glu	Asn	Arg	Arg	Phe	Val																																												
100				105				110																																																			
His	His	Thr	Leu	Gly	Asp	Gly	Glu	Phe	Met	Arg	Phe	Tyr	Ala	Met	Tyr																																												
115				120				125																																																			
Gln	Gly	Ile	Ser	Ala	Ala	Gln	Thr	Ile	Leu	Asn	Lys	Gln	Asn	Ala	Lys																																												
130				135				140																																																			
Ser	Glu	Ile	Asp	Arg	Val	Leu	Ala	Glu	Cys	Ala	Leu	His	Lys	Lys	Pro																																												
145				150				155				160																																															
Val	Tyr	Ile	Gly	Ile	Pro	Ala	Asp	Val	Pro	His	Met	Gln	Ile	Glu	Val																																												
165				170				175																																																			
Ser	Ser	Pro	Met	Leu	Tyr	Lys	Pro	Lys	Ser	Asp	Lys	Lys	Ile	Leu	Asn																																												
180				185				190																																																			
Ala	Phe	Ile	Glu	Ala	Val	Lys	Lys	Thr	Leu	Lys	Thr	Tyr	Lys	Ser	Phe																																												

195 200 205
 Ile Ala Met Ala Asp Tyr Glu Val Asn Arg Tyr His Leu Asn Gln Glu
 210 215 220
 Leu His Asp Phe Ile Glu Ala Thr Asn Leu Pro Ile Ala Ser Leu Ser
 225 230 235 240
 Met Gly Lys Gly Val Phe Ser Glu Gln His Pro Asn Phe Ile Gly Val

 245 250 255
 Tyr Asn Gly Ile Leu Ser Asp Asp Arg Val Thr Asn Ala Ile Lys Glu
 260 265 270
 Ser Asp Cys Thr Ile Leu Val Gly Val Lys Leu Thr Asp Ser Leu Thr
 275 280 285
 Ala Gly Phe His Tyr Ile Cys Glu Glu Pro Thr Pro Lys Ile Glu Val
 290 295 300
 His Pro Leu Tyr Ser Lys Ile Gly Glu Lys Val Tyr Ser Asp Ile Leu

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

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

 435 440 445

Val Leu Val Ile Asn Asn Asp Gly Tyr Thr Val Glu Arg Cys Ile His
450 455 460

Gly Pro Glu Arg Lys Tyr Asn Asp Ile Asn Met Trp His Tyr Thr Lys
465 470 475 480

Leu Leu Glu Ala Phe Asp Val His Leu His Arg Lys Pro Leu Ser Phe
485 490 495

Lys Ala Gly Thr Val Glu Ser Leu Glu Gln Ala Leu Glu Gln Ala Asn

500 505 510

Lys His Pro Asp Lys Leu Ala Phe Ile Glu Val Gln Met Asp Arg Asp
515 520 525

Asp Ala Pro Ala Leu Leu Lys Lys Leu Gly Gly Leu Phe Ser Ala Gln
530 535 540

Asn Ser Tyr
545

<210> 544

<211> 562

<212> PRT

<213> Candida auris

<400> 544

Met Ser Glu Ile Thr Leu Gly Arg Tyr Leu Phe Glu Arg Leu Asn Gln
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Leu Gln Val Gln Thr Ile Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser
20 25 30

Leu Leu Asp Lys Ile Tyr Glu Val Asp Gly Met Arg Trp Ala Gly Asn
35 40 45

Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ser Arg Val
50 55 60

Lys Gly Leu Ala Cys Leu Val Thr Thr Phe Gly Val Gly Glu Leu Ser
65 70 75 80

Ala Leu Asn Gly Val Gly Gly Ala Tyr Ala Glu His Val Gly Leu Leu
85 90 95

His Val Val Gly Val Pro Ser Ile Ser Ser Gln Ala Lys Gln Leu Leu

100	105	110
Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met		
115	120	125
Ser Asn Asn Ile Ser Gln Thr Thr Ala Phe Ile Ser Asp Ile Asn Ser		
130	135	140
Ala Pro Gly Glu Ile Asp Arg Cys Ile Arg Glu Ala Trp Val His Gln		
145	150	155
Arg Pro Val Tyr Val Gly Leu Pro Ala Asn Leu Val Asp Leu Thr Val		
165	170	175
Pro Ala Ser Leu Leu Asp Thr Pro Ile Asp Leu Ser Leu Lys Lys Asn		
180	185	190
Asp Pro Asp Ala Gln Glu Glu Val Ile Glu Thr Val Leu Asp Leu Val		
195	200	205
Asp Lys Ser Lys Asn Pro Ile Ile Leu Val Asp Ala Cys Ala Ser Arg		
210	215	220
His Ser Cys Arg Asp Glu Val Arg Arg Leu Val Asp Ser Thr Ser Phe		
225	230	235
Pro Val Phe Val Thr Pro Met Gly Lys Ser Ala Val Asn Glu Ser His		
245	250	255
Pro Arg Phe Gly Gly Val Tyr Val Gly Ser Leu Ser Glu Pro Asn Val		
260	265	270
Lys Glu Ala Val Glu Asn Ala Asp Leu Val Leu Ser Ile Gly Ala Leu		
275	280	285
Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys		
290	295	300
Asn Ile Val Glu Phe His Ser Asp Tyr Thr Lys Ile Arg Gln Ala Thr		
305	310	315
Phe Pro Gly Val Gln Met Lys Glu Ala Leu Asn Val Leu Leu Glu Lys		
325	330	335
Ile Pro Ser His Val Ala Asn Tyr Lys Pro Leu Pro Val Pro Gln Arg		
340	345	350

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

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

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

Asn Thr Lys Ile Arg Met Val Glu Val Met Leu Pro Arg Met Asp Ala
 530 535 540
 Pro Gln Asn Leu Val Lys Gln Ala Glu Phe Ser Ser Lys Thr Asn Ser
 545 550 555 560
 Glu Asn

<210> 545

<211> 551

<212> PRT

<213> Erwinia iniecta

<400> 545

Met Ser Thr Thr Thr Val Gly Asp Tyr Leu Leu Tyr Arg Leu Asn Glu

1 5 10 15

Ile Gly Ile Glu His Leu Phe Gly Val Pro Gly Asp Tyr Asn Leu Gln

20 25 30

Phe Leu Asp His Val Ile Asp His Pro Gln Leu Thr Trp Val Gly Cys

35 40 45

Thr Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Cys

50 55 60

Arg Pro Ala Ala Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu Ser

65 70 75 80

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

85 90 95

His Ile Val Gly Ala Pro Ser Leu Ser Ala Gln Gln Gln Gly Asp Leu

100 105 110

Ile His His Ser Leu Gly Glu Gly Asp Phe Ser Ser Phe Leu Arg Met

115 120 125

Ser Gln Pro Val Ser Val Ala Gln Ala Ala Leu Thr Pro Asp Asn Ala

130 135 140

Cys Lys Glu Ile Asp Arg Val Leu Ala Glu Val Leu Ile Gln Arg Arg

145 150 155 160

Pro Gly Tyr Leu Leu Leu Ser Thr Asp Val Ala Ala Ala Pro Ala Ala

165 170 175

Leu Pro Gln Ser Thr Leu Ser Leu Pro Thr Ala Pro Asp His Arg Ala

180 185 190

Val Leu Ala Ala Phe Ser Asp Ala Ala Glu Gln Met Leu Ala Gln Ala

195 200 205

Lys Ser Val Ser Leu Leu Ala Asp Phe Leu Ala Asp Arg Phe Gly Val

210 215 220

Thr Arg Ala Leu Ala Ala Trp Leu Gln Gln Val Pro Leu Pro His Ala

225 230 235 240

Thr Leu Leu Met Gly Lys Gly Val Leu Ser Glu Gln Gln Pro Gly Phe
 245 250 255
 Val Gly Thr Tyr Ala Gly Ala Ala Ser Ile Asp Ser Thr Arg Gly Ala
 260 265 270
 Ile Glu Glu Ala Gly Val Ile Ile Gly Val Gly Val Arg Phe Ser Asp
 275 280 285
 Thr Ile Thr Ala Gly Phe Ser Gln Gln Ile Asp Ala Arg Arg Phe Ile
 290 295 300
 Asp Ile Gln Pro Phe Phe Ser Arg Ile Gly Asp Arg Gln Phe Asp His
 305 310 315 320
 Leu Pro Met Gln Ala Ala Val Ala Ala Leu His Gln Leu Cys Leu Arg
 325 330 335
 Tyr Gln Gln Gln Trp Ser Ile Thr Ala Pro Ser Pro Pro Ala Leu Pro
 340 345 350
 Pro Ala Ala Gly Ser Glu Leu Ser Gln Asn Ala Phe Trp Gln Ala Met
 355 360 365
 Gln Asn Phe Ile Arg Pro Gly Asp Leu Leu Val Ala Asp Gln Gly Thr
 370 375 380
 Ala Ala Phe Gly Ala Ala Ala Leu Arg Leu Pro Gln Asn Cys Gln Leu
 385 390 395 400
 Leu Val Gln Pro Leu Trp Gly Ser Ile Gly Tyr Ser Leu Pro Ala Thr
 405 410 415
 Phe Gly Ala Gln Thr Ala Asp Thr Glu Arg Arg Val Ile Leu Ile Ile
 420 425 430
 Gly Asp Gly Ser Ala Gln Leu Thr Ile Gln Glu Leu Ser Ser Met Met
 435 440 445
 Arg Asp Gly Leu Lys Pro Ile Ile Phe Leu Leu Asn Asn Asn Gly Tyr
 450 455 460
 Thr Val Glu Arg Ala Ile His Gly Ala Glu Gln Arg Tyr Asn Asp Ile
 465 470 475 480
 Ala Ala Trp Asn Trp Thr Gln Leu Pro Gln Ala Leu Ser Val His Cys

485 490 495
Pro Ala Gln Ser Trp Arg Val Val Glu Thr Val Gln Leu Thr Asp Val
500 505 510
Met Lys Val Ile Ala Ala Ser Pro Arg Leu Ser Leu Val Glu Val Val
515 520 525
Leu Pro Ala Met Asp Val Pro Pro Leu Leu Gln Ala Val Ser Ala Ala

530 535 540
Leu Asn Gln Arg Asn Ser Ser

545 550

<210> 546

<211> 566

<212> PRT

<213> Bacillus sp. FJAT-18017

<400> 546

Met Thr Ser Met Asp Asn Ser Ser Gln Gln Ile Pro Met Gly Gln Lys

1 5 10 15

Thr Val Gly Glu Tyr Leu Phe Asp Cys Leu Lys Gln Glu Gly Ile Thr

20 25 30

Glu Ile Phe Gly Val Pro Gly Asp Tyr Asn Phe Thr Leu Leu Asp Ala

35 40 45
Leu Gln Glu Tyr Asn Gly Ile Arg Phe Tyr Asn Gly Arg Asn Glu Leu

50 55 60

Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Ala Arg Ile Lys Gly Ile Ser

65 70 75 80

Ala Leu Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Thr Asn Ala

85 90 95

Ile Ala Gly Ala Asn Ser Glu His Val Pro Ile Ile His Ile Val Gly

100 105 110

Ser Pro Pro Glu Lys Ala Gln Lys Glu Arg Lys Leu Met His His Thr

115 120 125

Leu Met Asp Gly Asn Phe Asp Val Phe Arg Lys Val Tyr Glu Pro Leu

130 135 140

Thr Ala Tyr Thr Thr Ile Val Thr Ala Asp Asn Ala Arg Met Glu Ile
145 150 155 160
Pro Ala Ala Ile Arg Ile Ala Lys Glu Arg Arg Lys Pro Val Tyr Leu
165 170 175
Val Val Ala Asp Asp Val Val Ala Lys Pro Ile Thr Gly Arg Glu Val
180 185 190
Pro Ala Ser Pro Leu Pro Ala Ser Asn Gln Asp Lys Leu Leu Ala Ala
195 200 205
Val Glu His Val Arg Arg Leu Leu Glu Pro Ala Arg Gln Pro Val Ile
210 215 220
Leu Val Asp Val Lys Ala Met Arg Phe Gly Leu Gln Thr Ala Val Arg
225 230 235 240
Glu Leu Ala Asn Thr Met Asn Val Pro Val Ala Thr Met Met Tyr Gly
245 250 255
Lys Gly Thr Phe Asp Glu Thr His Pro Asn Tyr Ile Gly Val Tyr Ala
260 265 270
Gly Thr Phe Gly Ser Ser Glu Val Gln Ser Ile Val Glu Asn Ser Asp
275 280 285
Cys Val Ile Ala Val Gly Leu Val Trp Ser Asp Thr Asn Thr Ala Asn
290 295 300
Phe Thr Ala Lys Leu Asn Pro His Asn Thr Ile Glu Val Gln Pro Thr
305 310 315 320
Lys Val Lys Ile Ala Glu Ser Gln Tyr Pro Asp Val Arg Ala Ala Asp
325 330 335
Ile Leu Gln Glu Met Gln Lys Leu Asp Tyr Arg Ser Gln Ser Lys Pro
340 345 350
Glu Lys Ile Ser Phe Pro Tyr Glu Glu Ile Thr Gly Ser Ser Asp Glu
355 360 365
Pro Leu Arg Ala Glu Asn Tyr Phe Pro Arg Phe Gln Arg Met Leu Lys
370 375 380
Glu Asn Asp Ile Val Ile Ala Glu Thr Gly Thr Phe Tyr Tyr Gly Met

385 390 395 400
 Ser Gln Val Lys Leu Pro Ala Asn Thr Thr Tyr Ile Met Gln Gly Gly
 405 410 415
 Trp Gln Ser Ile Gly Tyr Ala Thr Pro Ala Ala Tyr Gly Ala Ser Ile

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

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

 545 550 555 560
 Lys Gln Glu Gln Lys Lys
 565
 <210> 547
 <211> 547
 <212> PRT
 <213> *Staphylococcus schleiferi*
 <400> 547
 Met Lys Lys Arg Val Gly Gln Phe Leu Phe Asp Glu Ile Ala Lys His
 1 5 10 15
 Gly Val Asp Lys Ile Phe Gly Val Pro Gly Asp Phe Asn Leu Ala Phe
 20 25 30

Leu Asp Asp Ile Glu Ser His Glu Thr Leu Gln Trp Val Gly Asn Thr

35

40

45

Asn Glu Leu Asn Ala Ser Tyr Ala Ala Asp Gly Tyr Ala Arg Ile Asn

50

55

60

Gly Leu Ala Ala Met Val Thr Thr Phe Gly Val Gly Glu Leu Ser Ala

65

70

75

80

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

85

90

95

Ile Thr Gly Gly Pro Thr Thr Val Val Glu Lys Ala Lys Lys Tyr Val

100

105

110

His His Ser Leu Gly Thr Gly Ile Phe Asp Ala Tyr Arg Lys Met Phe

115

120

125

Ala His Ile Thr Glu Ala Gln Thr Tyr Leu Thr Thr Asp Asn Ala Leu

130

135

140

Thr Glu Val Pro Arg Ile Ile Gln Val Ala Ile Glu Glu Lys Arg Pro

145

150

155

160

Val His Val His Leu Pro Ile Asp Thr Ala Met Lys Glu Ile Glu Val

165

170

175

Pro Asp Gln Ile Glu Tyr Pro Glu Val Lys Ala Ser Glu Asp Leu Ser

180

185

190

Ser Ile Ile Glu Lys Val Thr Glu Ala Leu Gln Asn Ala Lys Gln Pro

195

200

205

Thr Leu Ile Val Gly His Gln Ile Asn Ser Phe Gly Leu Gln Ala Gln

210

215

220

Val Gln Gln Leu Ala Glu Arg Leu Asn Leu Pro Val Ala Gln Leu Ser

225

230

235

240

Leu Gly Lys Gly Ala Phe Asn Glu Glu Ser Pro Gln Tyr Met Gly Ile

245

250

255

Phe Asp Gly Ser Ile Ala Asp Glu Ala Ile Arg Asp Tyr Val Asn Gly

260

265

270

Ser Asp Val Val Ile Thr Leu Gly Ala Lys Leu Thr Asp Ser Ala Thr

275 280 285
Ala Gly Phe Ser Gln Glu Phe Lys Asp Asp Ile Val Lys Ile Leu Asn

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

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

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

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

Met Asp Ala Pro Glu Lys Leu Asn Ile Ile Ser Lys Ala Phe Ala Asn
530 535 540

Gln Asn Lys
545

<210> 548

<211>
552

<212> PRT

<213> Serratia sp. Leaf51

<400> 548

Met Asp Asn Ile Tyr Thr Val Gly Asp Tyr Leu Leu Asp Arg Leu Ser
1 5 10 15

Phe Ser Gly Ile Ser Glu Leu Phe Gly Val Pro Gly Asp Tyr Asn Leu
20 25 30

Lys Phe Leu Asp Ser Val Ile Ser His Gln Gln Ile Thr Trp Ile Gly
35 40 45

Cys Thr Asn Glu Leu Asn Ala Ala Tyr Gly Ala Asp Gly Tyr Ala Arg
50 55 60

Thr Lys Gly Ile Ala Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu
65 70 75 80

Ser Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu Tyr Val Pro Val
85 90 95

Ile His Ile Val Gly Ala Pro Pro Leu Ser Ala Gln Arg Lys Gly Glu
100 105 110

Leu Leu His His Thr Leu Gly Asp Gly Asp Phe Ser His Phe Met Arg
115 120 125

Met Ser Gln Pro Val Ser Val Ala Gln Ala Ser Leu Thr Pro Glu Asn
130 135 140

Ala Leu Ala Glu Ile Asp Arg Val Ile Glu Asp Val Ile Tyr Ser Ser
145 150 155 160

Arg Pro Gly Tyr Leu Leu Leu Pro Ser Asp Val Ala Ala Leu Pro Val
165 170 175

Ser Thr Arg Ala His Ala Ile Pro Ala Arg Gln Pro Ala Phe Ser Ala

180 185 190

Ser Ser Leu Glu Ala Phe Val Ala Ala Ala Asp Ala Arg Leu Arg Ser

195 200 205

Ala Gly Arg Val Ser Leu Leu Ala Asp Phe Leu Ala Glu Arg Phe Gly

210 215 220

Val Lys Ala Ala Leu Glu Gln Trp Met Glu Glu Val Pro Leu Ala His

225 230 235 240

Ser Thr Leu Leu Met Gly Lys Gly Leu Phe Asn Glu Gln Gln Pro Asn

245 250 255

Phe Ala Gly Thr Tyr Ser Gly Ala Ala Ser Ala Ala Ser Thr Lys Glu

260 265 270

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

275 280 285

Asp Thr Ile Thr Ala Gly Phe Thr Gln Gln Leu Pro Ala Glu Lys Cys

290 295 300

Ile Asp Leu Gln Pro Phe Ser Ala Arg Val Gly Asn Gln Ile Phe His

305 310 315 320

Gln Leu Pro Leu Glu Lys Thr Val Ser Val Leu His Arg Leu Thr Ala

325 330 335

Glu Arg Ala Asp Gln Trp Pro Pro Tyr Ala Val Lys Arg Thr Thr Leu

340 345 350

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

355 360 365

Ile Gln Ala Phe Leu Gln Pro Gly Asp Val Leu Val Ala Glu Gln Gly

370 375 380

Thr Ala Cys Phe Gly Ala Ala Ala Leu Asn Leu Pro Gln Asp Cys Gln

385 390 395 400

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

405 410 415

Ala Phe Gly Val Gln Ile Ala Ala Pro Asp Arg Arg Val Val Leu Leu

420 425 430
Ile Gly Asp Gly Ser Ala Gln Leu Thr Leu Gln Gly Leu Gly Ala Ala

435 440 445
Ile Arg Tyr Gly Leu Pro Pro Val Ile Phe Val Ile Asn Asn Gln Gly

450 455 460
Tyr Thr Val Glu Arg Ala Ile His Gly Glu Thr Gln Arg Tyr Asn Asp

465 470 475 480
Ile Ala Gln Trp Asn Trp Thr Gln Phe Pro Ala Ala Phe Gly Gly Lys

485 490 495
Glu Val Phe Ser Ala Arg Ala Asp Ser Pro Gln Ala Leu Lys Glu Ala

500 505 510
Ile Glu Gln Ala Ser Ala Lys Arg Arg Met Ala Trp Ile Glu Val Ile

515 520 525
Leu Pro Lys Met Asp Ile Pro Ala Leu Leu Asp Ser Val Thr Arg Ser

530 535 540
Leu Ala Lys Arg Asn Ser Gly Glu

545 550

<210> 549

<211> 552

<212> PRT

<213> *Yersinia frederiksenii*

<400> 549

Met Thr Ser His Tyr Thr Val Ala Asp Tyr Leu Leu Asp Arg Leu Ala

1 5 10 15
Glu Ile Gly Ile Arg His Leu Phe Gly Val Pro Gly Asp Phe Asn Leu

20 25 30
His Phe Leu Asp His Val Ile Ser His Pro Val Ile Lys Trp Val Gly

35 40 45
Cys Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg

50 55 60
Val Met Pro Ala Ala Ala Leu Leu Thr Thr Ser Gly Val Gly Glu Leu

65						70						75						80	
Ser	Ala	Ile	Asn	Gly	Ile	Ala	Gly	Ser	Phe	Thr	Glu	Tyr	Leu	Pro	Val				
					85					90					95				
Ile	His	Ile	Val	Gly	Thr	Pro	Thr	Leu	Arg	Ser	Gln	Lys	Asn	Gly	Glu				
					100					105					110				
Leu	Leu	His	His	Ser	Leu	Gly	Asp	Gly	Asn	Phe	Ser	His	Phe	Ser	His				
					115					120					125				
Met	Ala	Lys	Glu	Val	Thr	Cys	Ala	Gln	Ala	Asn	Leu	Thr	Ala	Asp	Asn				
					130					135					140				
Ala	Ala	Tyr	Glu	Ile	Asp	Arg	Val	Leu	Gly	Ala	Ala	Leu	Ser	Gln	Arg				
145					150					155					160				
Arg	Pro	Val	Tyr	Leu	Ser	Leu	Pro	Ser	Asp	Val	Ala	Gln	Thr	Asp	Ile				
					165					170					175				
Ala	Ile	Tyr	Gln	Gly	Thr	Leu	Ala	Leu	Pro	Gln	Pro	Val	Leu	Ser	Pro				
					180					185					190				
Thr	Ala	Leu	Gln	Ala	Phe	Ile	Asn	Ala	Ala	Arg	Glu	Lys	Leu	Gln	Ser				
					195					200					205				
Ala	His	Arg	Val	Ala	Leu	Leu	Ala	Asp	Phe	Leu	Ala	Asp	Arg	Phe	Asp				
210					215					220									
Met	Gln	Leu	Ser	Leu	Asn	Arg	Trp	Leu	Ala	Glu	Val	Asn	Leu	Pro	His				
225					230					235					240				
Ser	Thr	Leu	Leu	Leu	Gly	Lys	Gly	Val	Leu	Asp	Glu	Thr	His	Pro	Leu				
					245					250					255				
Phe	Ile	Gly	Thr	Tyr	Ala	Gly	Ala	Ala	Ser	Glu	Pro	His	Val	Lys	Glu				
					260					265					270				
Cys	Ile	Glu	Asn	Ala	Asp	Val	Leu	Ile	Thr	Val	Gly	Val	Cys	Phe	Ala				
275					280					285									
Asp	Ile	Ile	Thr	Ala	Gly	Phe	Ser	Gln	Asn	Ile	Asn	Gln	Asp	Asn	Cys				
290					295					300									
Ile	Ser	Ile	Gln	Pro	Glu	Gln	Ala	Arg	Ile	Gly	Arg	Thr	Cys	Phe	Ser				
305					310					315					320				

Gln Ile Pro Met Arg Ala Ala Ile Glu Ala Leu His Glu Leu Cys Lys

325 330 335

Thr Leu Gln Asp Glu Trp Gln Gln Pro Val Ile Thr Arg Pro Glu Arg

340 345 350

Ala Glu Pro Lys Ser Asp Val Leu Asp Gln Gln Ala Phe Trp Tyr His

355 360 365

Ile Gln Gln Phe Leu Arg Pro Asn Asp Leu Val Leu Thr Asp Leu Gly

370 375 380

Thr Ser Cys Phe Gly Ala Gly Thr Leu Asn Leu Pro Ser Gly Cys Thr

385 390 395 400

Tyr Met Ser Gln Ala Leu Trp Glu Ser Ile Gly Phe Ser Leu Pro Ala

405 410 415

Ala Tyr Gly Ala Gln Leu Ala Gln Pro Gln Arg Arg Leu Ile Leu Leu

420 425 430

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

435 440 445

Leu Arg Asp Gly Leu Asn Pro Ile Ile Phe Leu Leu Asn Asn Gln Gly

450 455 460

Tyr Thr Val Glu Arg Ala Ile His Gly Pro Gln Gln Arg Tyr Asn Asp

465 470 475 480

Ile Ala Thr Trp Asn Trp Thr Gln Leu Pro Leu Ala Leu Gly Leu Gly

485 490 495

Lys Glu Ser Phe Thr His Arg Val Thr Lys Val Gln Gln Leu Gln Gln

500 505 510

Val Leu Ala Gln Ile Glu Lys Pro Gln Lys Leu Thr Phe Ile Glu Val

515 520 525

Val Leu Pro Pro Met Asp Ile Pro Glu Leu Leu Met His Val Thr Lys

530 535 540

Ser Ile Gln Arg Arg Asn Val Ala

545 550

<210> 550

<211> 548

<212> PRT

<213> Yersinia aldovae

<400> 550

Met Thr Lys Thr Val Val Gln His Val Leu Ser Arg Leu Tyr Asp Leu

1 5 10 15

Gly Ile Ser Asp Ile Phe Gly Val Pro Gly Asp Phe Ala Phe Pro Ile

20 25 30

Gln Asp Ala Val Cys Glu Asp Ser Arg Leu Arg Trp Ile Gly Asn Cys

35 40 45

Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile Arg

50 55 60

Gly Met Ala Ala Leu Asn Thr Thr Phe Ala Val Gly Glu Leu Ser Ala

65 70 75 80

Leu Asn Gly Val Ala Gly Ala Phe Ala Glu Ser Leu Pro Val Phe His

85 90 95

Leu Val Gly Met Pro Ser Ser Thr Val Gln Ala Ser Gly Val Ile Val

100 105 110

His His Thr Leu Gly Asp Gly Asn Phe Thr Ala Phe Tyr Glu Ala Thr

115 120 125

Lys His Phe Val Cys Ala His Ala Ile Met Thr Pro Glu Asn Cys Val

130 135 140

Ala Glu Thr Glu Arg Leu Ile Ala Ala Ala Leu Arg Tyr Arg Lys Pro

145 150 155 160

Val Tyr Met Gly Phe Pro Ser Asp Tyr Ala Glu Met Pro Ile Ile Glu

165 170 175

Ser Asp Val Pro Gln Ala Thr Ala Ala Gln Ser Asn Pro Ala Ala Leu

180 185 190

Ser Leu Ala Val Glu Ala Ile Ala Glu Arg Ile Asn Arg Ser Gln Lys

195 200 205

Thr Cys Ile Leu Pro Gly Ile Ser Ile Ala Arg His Asn Leu Arg Gln

210 215 220
 Glu Ala Leu Glu Leu Val Asn Ser Thr Asn Leu Pro Phe Ala Thr Met
 225 230 235 240
 Phe Met Asp Lys Ser Val Leu Asp Glu Ser His Pro Asn Tyr Val Gly
 245 250 255
 Ile Tyr Asn Gly His Leu Leu Asn Asp Asp Val Ser Glu Phe Val Glu
 260 265 270
 Gly Cys Asp Cys Ile Leu Lys Ile Gly Ala Met Leu Ser Asp Phe Asn

 275 280 285
 Thr Gly Ala Phe Thr Ala Asp Phe Ser Arg Ala Asp Thr Leu Asn Ile
 290 295 300
 Glu Pro Glu Phe Val Gln Ile Gly Glu Thr Arg Tyr Asn Asn Val Met
 305 310 315 320
 Met Arg Asp Val Leu Thr Ser Leu Val Gly Lys Val Val Arg Arg Thr
 325 330 335
 Glu Thr Thr Ser Met Pro His Ala Thr Ala Ile Pro Leu Val Ser Glu

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

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

Arg Leu Leu Cys Lys Asp Ser Asp Ile Tyr Tyr Asn Asp Leu Ala Gln

465 470 475 480

Trp Lys Tyr Ser Lys Leu Pro Glu Ala Met Gly Cys Glu Gly Trp Phe

485 490 495

Ser Ile Arg Val Thr Thr Cys Glu Glu Leu Asn Asp Ala Ile Glu Tyr

500 505 510

Ala Glu Thr Cys Asp Cys Gly Val Tyr Ile Glu Val Val Thr Glu Lys

515 520 525

Tyr Val Thr Ser Ala Leu Ala Ala Lys Leu His Asp Ser Ile Asp Thr

530 535 540

Leu Tyr Ser Met

545

<210> 551

<211> 563

<212> PRT

<213> Mycobacterium europaeum

<400> 551

Met Leu Val Thr Asp Ala Ala Ser Gln Pro Val Tyr Thr Val Gly Asp

1 5 10 15

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

20 25 30

Val Pro Gly Asp Tyr Asn Leu Glu Phe Leu Asp His Ile Val Ala His

35 40 45

Pro Ser Ile Arg Trp Val Gly Ser Ser Asn Glu Leu Asn Ala Gly Tyr

50 55 60

Ala Ala Asp Gly Tyr Gly Arg Leu Arg Gly Met Ser Ala Val Val Thr

65 70 75 80

Thr Phe Gly Val Gly Glu Leu Ser Ala Ala Asn Ala Ile Ala Gly Ser

85 90 95

Tyr Ala Glu Gln Val Pro Val Val His Ile Val Gly Gly Pro Ser Lys

100 105 110

Asp Ala Gln Gly Thr Arg Arg Ala Leu His His Ser Leu Gly Asp Gly
 115 120 125
 Asp Phe Glu His Phe Phe Arg Ile Ser Arg Glu Ile Thr Cys Ala Gln
 130 135 140
 Ala Asn Leu Met Pro Ala Thr Ala Arg Arg Glu Ile Asp Arg Val Leu
 145 150 155 160
 Ser Glu Val Arg Glu Gln Lys Arg Pro Gly Tyr Ile Leu Leu Ser Thr
 165 170 175
 Asp Val Ala Arg Phe Pro Thr Glu Pro Pro Gly Asp Pro Leu Pro Arg
 180 185 190
 Tyr Thr Gly Gly Thr Ser Pro Arg Ala Leu Ser Leu Phe Val Glu Ala
 195 200 205
 Ala Ser Ala Leu Ile Gly Asp His Gln Leu Thr Val Leu Ala Asp Leu
 210 215 220
 Leu Val His Arg Leu Gln Val Val Lys Glu Leu Glu Ala Leu Leu Thr
 225 230 235 240
 Ala Asp Val Val Pro Tyr Ala Thr Leu Met Trp Gly Lys Ser Leu Leu
 245 250 255
 Asp Glu Ser Ser Pro His Tyr Leu Gly Ile Tyr Ala Gly Ser Ala Ser
 260 265 270
 Ala Pro Ala Val Arg Ala Ala Ile Glu Gln Ala Pro Val Leu Val Thr
 275 280 285
 Ala Gly Val Val Phe Thr Asp Met Val Ser Gly Phe Phe Ser Gln Arg
 290 295 300
 Ile Asp Pro Ala Arg Thr Ile Asp Val Gly Gln Tyr Gln Ser Ser Val
 305 310 315 320
 Ala Gly Glu Val Phe Ala Pro Leu Glu Met Gly Ala Ala Leu Glu Ala
 325 330 335
 Leu Ala Thr Ile Leu Thr Arg Arg Pro Val Ser Ser Pro Ala Val Ala
 340 345 350
 Ser Pro Pro Ala Glu Ala Leu Pro Pro Pro Pro Pro Arg Asp Gln Pro

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

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

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

 545 550 555 560
 Val Arg Arg

<210> 552

<211> 548

<212> PRT

<213> Enterococcus rotai

<400> 552

Met Tyr Thr Val Ala Asp Tyr Leu Leu Asp Arg Leu Lys Glu Leu Gly
1 5 10 15
Ile Asp Glu Ile Phe Gly Val Pro Gly Asp Tyr Asn Leu Gln Phe Leu
20 25 30
Asp His Val Thr Ala Arg Glu Asp Leu Glu Trp Ile Gly Asn Ala Asn
35 40 45
Glu Leu Asn Ala Ala Tyr Met Ala Asp Gly Tyr Ala Arg Thr Lys Gly
50 55 60
Ile Ser Ala Phe Val Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Val
65 70 75 80
Asn Gly Leu Ala Gly Ser Phe Ala Glu Asn Val Pro Val Ile Glu Ile
85 90 95
Val Gly Ser Pro Thr Thr Ala Val Gln Ala Ser Lys Lys Leu Val His
100 105 110
His Thr Leu Gly Asp Gly Asp Phe Leu Arg Phe Glu Lys Met His Glu
115 120 125
Glu Val Thr Ala Gly Ile Ala His Leu Thr Ala Asn Asn Ala Leu Thr
130 135 140
Glu Ile Asp Arg Val Leu Leu Ile Ala Ile Thr Glu Lys Arg Pro Val
145 150 155 160
Tyr Ile Asn Leu Pro Ile Asp Ile Ala Thr Ile Thr Val Ser Lys Pro
165 170 175
Gln Ser Lys Leu Asn Ser Gln Ala Glu Gln Leu Thr Ala Val Glu Ala
180 185 190
Ala Ile Leu Thr Lys Val Glu Gln Ala Leu Gln Gln Ala Gln Cys Pro
195 200 205
Val Val Ile Ala Gly His Glu Ile Leu Ser Tyr His Ile Glu Gln Gln
210 215 220
Leu Asp Ala Phe Ile Gln Lys Phe Asn Leu Pro Ile Thr Thr Leu Pro
225 230 235 240
Leu Gly Lys Ser Ala Phe Asn Glu Asp Asp Ala His Tyr Leu Gly Thr

245 250 255
 Tyr Thr Gly Ser Thr Thr Asp Glu Pro Leu Lys Ser Arg Val Asp Thr
 260 265 270
 Ala Asp Leu Val Leu Leu Leu Gly Val Lys Leu Thr Asp Ser Ala Thr
 275 280 285
 Ser Gly Phe Ser Phe Gly Phe Thr Asp Gln Gln Val Ile Ser Ile Gly
 290 295 300

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

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

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

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

Lys Gln Asn Ala

545

<210> 553

<211> 551

<212> PRT

<213> Cosenzaea myxofaciens

<400> 553

Met Ser Asn Thr Val Ile Lys Tyr Leu Leu Asn Ser Leu Tyr Asp Leu
1 5 10 15
Gly Ile His Asp Ile Phe Gly Val Ala Gly Asp Tyr Ala Phe Pro Ile
20 25 30
Glu Asp Thr Val Cys Asn Ser Glu Arg Met Arg Trp Ile Gly Asn Cys
35 40 45
Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys
50 55 60

Gly Val Ala Ala Leu Ser Thr Thr Phe Gly Val Gly Glu Leu Ser Ala
65 70 75 80
Ile Asn Gly Ile Ala Gly Ala Tyr Ala Glu Asn Leu Pro Ile Phe His
85 90 95
Leu Val Gly Met Pro Ala Ser Gly Val Gln Asn Ser Lys Arg Leu Val
100 105 110
His His Thr Leu Gly Asn Gly Asp Phe Asp Val Phe Tyr Glu Leu Gly
115 120 125

Gln Arg Leu Ala Cys Ala His Thr Ile Leu Thr Pro Asp Asn Cys Ile
130 135 140
Glu Glu Thr Ala Arg Leu Ile Asn Thr Ala Leu Lys Glu Arg Arg Pro

145 150 155 160
 Val Tyr Ile Gly Ile Pro Ser Asp Tyr Ala Leu Met Pro Ile Asn Ser
 165 170 175
 Pro Gln Asn Thr Ser Val Val Ser Pro Val Ser Ser Val Ser Asn Lys
 180 185 190

 Glu Asn Leu Glu Lys Ala Ile Ser Thr Ile Ile Lys Lys Ile Thr His
 195 200 205
 Ser Glu Lys Ile Cys Val Leu Pro Gly Ile Leu Ser Ser Arg Phe Gly
 210 215 220
 Val Asp Glu Lys Val Gln Thr Leu Ile Asp Lys Thr Gly Leu Pro Phe
 225 230 235 240
 Ala Thr Met Phe Met Asp Lys Ser Val Leu Ser Glu Ser His Pro Gln
 245 250 255

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

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

 Cys Ser Met Gly Leu Gly Phe Ala Leu Leu Pro Glu Asn Ala Lys Ile
 385 390 395 400

His Asn Gln Thr Leu Trp Gly Ser Ile Gly Trp Ala Thr Pro Ala Ser
405 410 415

Phe Gly Ala Ala Ile Ala Ala Pro Glu Ser Arg Ile Ile Leu Val Thr
420 425 430

Gly Glu Gly Ser His Gln Leu Thr Val Gln Glu Ile Ser Gln Phe Ile
435 440 445

Arg Phe Gly Leu Lys Pro Ile Ile Leu Val Leu Asn Asn Asp Gly Tyr
450 455 460

Leu Ile Glu Arg Leu Leu Cys Asp Tyr Pro Asp Ala Tyr Tyr Asn Asp
465 470 475 480

Leu Ala Gln Trp Asn Tyr His Gln Leu Pro Gln Ala Phe Gly Ala Thr
485 490 495

Asp Trp Tyr Cys Gln Lys Val Thr Ser Thr Asn Glu Leu Asp Glu Ala
500 505 510

Leu Lys Ile Ala Ser Ser Asn Thr Ser Ala Cys Tyr Ile Glu Ile Val
515 520 525

Thr Asp Lys Tyr Glu Ser Ser Glu Leu Ala Gln Lys Leu Asn Glu Phe
530 535 540

Lys Ser Ala Leu Tyr Ser Phe
545 550

<210> 554

<211> 548

<212> PRT

<213> Staphylococcus pseudintermedius

<400> 554

Met Met Lys Lys Arg Ile Gly Gln Phe Leu Ile Asp Glu Ile Ala Lys
1 5 10 15

Gln Gly Val Asp Lys Ile Phe Gly Val Pro Gly Asp Phe Asn Leu Thr
20 25 30

Phe Leu Asp Asp Ile Glu Ala His Glu Thr Leu Glu Trp Val Gly Asn
35 40 45

Thr Asn Glu Leu Asn Ala Ser Tyr Ala Ala Asp Gly Tyr Ala Arg Leu

50 55 60
 Asn Gly Leu Ala Ala Met Val Thr Thr Phe Gly Val Gly Glu Leu Ser
 65 70 75 80

 Ala Val Asn Gly Ile Ala Gly Ser Tyr Ala Glu Asn Val Pro Val Ile
 85 90 95
 Gln Ile Thr Gly Ala Pro Thr Thr Val Val Glu Gln Ala Gly Lys Tyr
 100 105 110
 Val His His Ser Leu Gly Asn Gly Lys Phe Asp Asp Tyr Gln Lys Met
 115 120 125
 Tyr Ala Gln Ile Thr Glu Thr Gln Thr Val Leu Thr Val Asp Asn Ala
 130 135 140

 Leu Thr Glu Ile Pro Arg Ile Ile Lys Val Ala Thr Glu Glu Lys Arg
 145 150 155 160
 Pro Val His Val His Leu Pro Ile Asp Ile Ala Ala Lys Glu Ile Glu
 165 170 175
 Val Pro Asp Asp Val Ala Tyr Pro Ala Thr Gln Lys Ala Glu Asn Val
 180 185 190
 Ser Thr Val Val Glu Lys Leu Thr Glu Arg Leu Lys Ala Ala Gln Gln
 195 200 205

 Val Thr Leu Ile Val Gly His Gln Ile Asn Ser Tyr Gly Leu Gln Lys
 210 215 220
 Asp Val Gln Ala Ile Ala Glu Lys Leu Asn Leu Pro Val Ala Gln Leu
 225 230 235 240
 Ser Leu Gly Lys Gly Ser Phe Asn Glu Glu Ser Ala Gln Tyr Met Gly
 245 250 255
 Val Tyr Asp Gly Tyr Ile Ala Glu Asp Asn Ile Arg Asp Tyr Val Asp
 260 265 270

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

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

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

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

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

Val Leu Asp Ala Pro Ala Asn Leu Asn Glu Ile Ser Lys Ala Phe Ala
 530 535 540
 Ala Gln Asn Lys

545

<210> 555

<211> 552

<212> PRT

<213> *Buttiauxella brennerae*

<400> 555

Met Ser Tyr Cys Val Ala Asp Tyr Leu Leu Asp Arg Leu Thr Glu Ala

1 5 10 15

Gly Ile Arg His Leu Phe Gly Val Pro Gly Asp Tyr Asn Leu Gln Phe

20 25 30

Leu Asp Asn Val Ile Glu Asn Pro Thr Leu Ala Trp Val Gly Cys Ala

35 40 45

Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Cys His

50 55 60

Gly Ala Ala Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu Ser Ala

65 70 75 80

Ile Asn Gly Ile Ala Gly Ser Phe Ala Glu Tyr Val Pro Val Ile His

85 90 95

Ile Val Gly Ala Pro Cys Ile Gly Ala Gln Arg Arg Gly Glu Leu Met

100 105 110

His His Thr Leu Gly Asp Gly Asp Phe Gly His Phe Ala Arg Met Ala

115 120 125

Gln Glu Val Thr Val Val Gln Ala Ser Leu Thr Ala Glu Asn Ala Cys

130 135 140

Tyr Glu Ile Asp Arg Val Leu Ile Gln Val Leu Ser Gln Arg Leu Pro

145 150 155 160

Gly Tyr Leu Leu Leu Pro Ser Asp Val Ser Gln Ala Pro Ala Thr Arg

165 170 175

Pro Thr Lys Ser Leu Leu Ser Pro Pro Val Ser Thr Asp Pro Thr Leu

180 185 190

Leu Thr Glu Phe Arg Ala Cys Ala Gln Ala Arg Leu Ala Glu Ser Arg

195 200 205

Ser Val Ala Leu Leu Ala Asp Phe Leu Ala Met Arg Phe Gly Gln Gln
210 215 220

Lys Thr Leu Gln Gln Trp Met Asp Asp Thr Pro Met Pro His Ala Thr
225 230 235 240

Leu Leu Met Gly Lys Gly Leu Phe Asp Glu Gly Gln Gln Gly Phe Val
245 250 255

Gly Thr Tyr Ser Ala Ala Ala Ser Asp Ala Ser Val Ile Gln Ala Ile
260 265 270

Glu Lys Ala Glu Leu Val Ile Cys Val Gly Val Lys Phe Thr Asp Thr
275 280 285

Leu Thr Ala Gly Phe Thr Gln His Phe Ser Leu Gln Gln Thr Ile Asp
290 295 300

Ile Gln Pro Asn Ala Thr Arg Ile Gly Glu Arg Trp Phe Ser Gly Ile
305 310 315 320

Val Met Glu Glu Ala Val Ser Val Leu His Gln Leu Cys Lys Arg Gln
325 330 335

Val Ser Gly Trp Pro Val Pro Lys Gln Lys Pro Pro Ala Leu Pro Glu
340 345 350

Ala Thr Asn Gly Glu Leu Asp Gln His Ala Phe Trp Gln Leu Met Gln
355 360 365

Lys Phe Leu Gln Ala Gly Asp Ile Ile Leu Ala Asp Gln Gly Thr Ala
370 375 380

Ala Phe Gly Ala Ala Thr Leu Thr Leu Pro Ala Gly Val Thr Phe Ile
385 390 395 400

Thr Gln Pro Leu Trp Gly Ser Ile Gly Phe Thr Leu Pro Ala Ala Phe
405 410 415

Gly Ala Gln Thr Ala Cys Pro Asn Arg Arg Val Val Leu Leu Val Gly
420 425 430

Asp Gly Ser Ala Gln Leu Thr Ile Gln Glu Ile Gly Ser Met Leu Arg
435 440 445

Asp Glu Gln Arg Pro Ile Ile Phe Leu Leu Asn Asn Asp Gly Tyr Thr

450 455 460
Val Glu Arg Ala Ile His Gly Ala Glu Gln Arg Tyr Asn Asp Ile Ala
465 470 475 480

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

Ala Lys Arg Asn Ala Ala Lys Asp

545 550

<210> 556

<211> 565

<212> PRT

<213> Unknown

<220><223> Bacillus sp. FJAT-27225

<400> 556

Met Thr Ser Met Asn Asn Asn Ser Lys Gln Thr Pro Ile Glu Gln Lys
1 5 10 15
Ser Val Gly Glu Tyr Leu Phe Asp Cys Leu Lys Gln Glu Gly Ile Thr
20 25 30
Glu Ile Phe Gly Val Pro Gly Asp Tyr Asn Phe Thr Leu Leu Asp Thr
35 40 45

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

100	105	110	
Ala Pro Pro Glu Lys Ser Gln Lys Asp Gln Lys Leu Met His His Thr			
115	120	125	
Leu Met Asp Gly Asn Phe Asp Val Phe Arg Lys Val Tyr Glu Pro Ile			
130	135	140	
Thr Ala Tyr Thr Ala Val Val Thr Pro Asn Asn Ala Arg Met Glu Ile			
145	150	155	160
Thr Ala Ala Ile Arg Val Ala Lys Glu Lys Lys Lys Pro Val Tyr Leu			
165	170	175	
Val Ile Ala Asp Asp Val Val Ala Lys Pro Val Ser Val Leu Asp Glu			
180	185	190	
Leu Glu Ser Pro Leu Thr Thr Ser Asn Gln Asp Lys Leu Gln Glu Ala			
195	200	205	
Ala Asp His Val Arg Arg Leu Leu Glu Pro Ala Gly Arg Pro Val Ile			
210	215	220	
Leu Val Asp Val Lys Thr Val Arg Phe Gly Leu Glu Thr Ala Val Arg			
225	230	235	240
Glu Leu Ala Asn Ala Met Asn Val Pro Val Ala Thr Met Met Tyr Gly			
245	250	255	
Lys Gly Ala Phe Asp Glu Ser Asn Pro Asn Tyr Ile Gly Met Tyr Ala			
260	265	270	
Gly Thr Phe Gly Ser Ser Glu Val Gln Ser Ile Val Glu Ser Ser Asp			
275	280	285	
Cys Val Ile Ala Ile Gly Pro Val Trp Ala Asp Thr Asn Thr Ala Ser			
290	295	300	
Phe Thr Ala Lys Leu Asn Pro His Asn Thr Ile Glu Ile Gln Pro Asp			
305	310	315	320
Met Val Lys Ile Gly Val Ser Glu Tyr Pro Asp Val Gln Ala Ala Asp			
325	330	335	
Met Leu Gln Glu Val Gln Gln Ile Gly Tyr Arg Ser Lys Ala Lys Pro			
340	345	350	

Glu Lys Val Ser Phe Pro Tyr Glu Glu Ile Thr Gly Ser Thr Asp Asp
355 360 365

Pro Leu Lys Ala Ala Ser Tyr Phe Pro Arg Phe Gln Gln Met Leu Lys
370 375 380

Glu Asp Asp Ile Val Ile Ala Glu Thr Gly Ile Phe Tyr Tyr Gly Met
385 390 395 400

Ser Gln Val Arg Leu Pro Arg Asn Thr Thr Tyr Ile Ser Gln Gly Gly
405 410 415

Trp Gln Ser Ile Gly Tyr Ala Thr Pro Ala Ala Tyr Gly Ala Ser Ile
420 425 430

Ala Ala Pro Glu Arg Arg Val Leu Leu Phe Thr Gly Asp Gly Ser Leu
435 440 445

Gln Leu Thr Ala Gln Glu Ile Ser Ser Met Leu Tyr Tyr Gly Cys Lys
450 455 460

Pro Met Ile Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Tyr
465 470 475 480

Leu Asn Val Lys Thr Glu Pro Asp Glu Gln Gln Tyr Asn Asn Ile Pro
485 490 495

Ala Trp Ser Tyr Thr Lys Leu Ala Glu Ala Phe Gly Gly Asn Leu Phe
500 505 510

Thr Lys Thr Val Arg Thr Asn Gly Glu Leu Glu Gln Ala Ile Thr Glu
515 520 525

Ala Glu Gln Glu Cys Asp Glu Lys Leu Cys Leu Ile Glu Met Ile Ala
530 535 540

Ala Asp Pro Met Asp Ala Pro Glu Tyr Met His Gln Met Arg Lys Phe
545 550 555 560

Lys Gln Gln Gln Met
565

<210> 557

<211> 546

<212> PRT

<213> Staphylococcus aureus

<400> 557

Met Lys Gln Arg Ile Gly Ala Tyr Leu Ile Asp Ala Ile His Arg Ala

1 5 10 15

Gly Val Asp Lys Ile Phe Gly Val Pro Gly Asp Phe Asn Leu Ala Phe

20 25 30

Leu Asp Asp Ile Ile Ser Asn Pro Asn Val Asp Trp Val Gly Asn Thr

35 40 45

Asn Glu Leu Asn Ala Ser Tyr Ala Ala Asp Gly Tyr Ala Arg Leu Asn

50 55 60

Gly Leu Ala Ala Leu Val Thr Thr Phe Gly Val Gly Glu Leu Ser Ala

65 70 75 80

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

85 90 95

Ile Thr Gly Ala Pro Thr Arg Ala Val Glu Gln Ala Gly Lys Tyr Val

100 105 110

His His Ser Leu Gly Glu Gly Thr Phe Asp Asp Tyr Arg Lys Met Phe

115 120 125

Ala His Ile Thr Val Ala Gln Gly Tyr Ile Thr Pro Glu Asn Ala Thr

130 135 140

Thr Glu Ile Pro Arg Leu Ile Asn Thr Ala Ile Ala Glu Arg Arg Pro

145 150 155 160

Val His Leu His Leu Pro Ile Asp Val Ala Ile Ser Glu Ile Glu Ile

165 170 175

Pro Thr Pro Phe Glu Val Thr Ala Ala Lys Asp Thr Asp Ala Ser Thr

180 185 190

Tyr Ile Glu Leu Leu Ala Ser Lys Leu Tyr Gln Ser Lys Gln Pro Ile

195 200 205

Ile Ile Thr Gly His Glu Ile Asn Ser Phe His Leu His Gln Glu Leu

210 215 220

Glu Asp Phe Val Asn Gln Thr Gln Ile Pro Val Ala Gln Leu Ser Leu

225				230				235				240			
Gly	Lys	Gly	Ala	Phe	Asn	Glu	Glu	Asn	Pro	Tyr	Tyr	Met	Gly	Ile	Tyr
245				250				255							
Asp	Gly	Lys	Ile	Ala	Glu	Asp	Lys	Ile	Arg	Asp	Tyr	Val	Asp	Asn	Ser
260				265				270							
Asp	Leu	Ile	Leu	Asn	Ile	Gly	Ala	Lys	Leu	Thr	Asp	Ser	Ala	Thr	Ala
275				280				285							
Gly	Phe	Ser	Tyr	Gln	Phe	Asn	Ile	Asp	Asp	Val	Val	Met	Leu	Asn	His
290				295				300							
His	Asn	Ile	Lys	Ile	Asp	Asp	Val	Thr	Asn	Asp	Glu	Ile	Ser	Leu	Pro
305				310				315				320			
Ser	Leu	Leu	Gln	Gln	Leu	Thr	Asp	Ile	Ser	Tyr	Thr	Asn	Asn	Ala	Ser
325				330				335							
Phe	Pro	Ala	Tyr	His	Arg	Pro	Thr	Ser	Pro	Asp	Tyr	Thr	Val	Gly	Thr
340				345				350							
Glu	Leu	Leu	Thr	Gln	Gln	Thr	Tyr	Phe	Lys	Met	Met	Gln	Asn	Phe	Leu
355				360				365							
Lys	Pro	Asn	Asp	Val	Ile	Ile	Ala	Asp	Gln	Gly	Thr	Ser	Phe	Phe	Gly
370				375				380							
Ala	Tyr	Asp	Leu	Ala	Leu	Tyr	Lys	Asn	Asn	Thr	Phe	Ile	Gly	Gln	Pro
385				390				395				400			
Leu	Trp	Gly	Ser	Ile	Gly	Tyr	Thr	Leu	Pro	Ala	Thr	Leu	Gly	Ser	Gln
405				410				415							
Leu	Ala	Asp	Lys	Asp	Arg	Arg	Asn	Leu	Leu	Leu	Ile	Gly	Asp	Gly	Ser
420				425				430							
Leu	Gln	Leu	Thr	Val	Gln	Ala	Ile	Ser	Thr	Met	Ile	Arg	Gln	His	Ile
435				440				445							
Lys	Pro	Val	Leu	Phe	Val	Ile	Asn	Asn	Asp	Gly	Tyr	Thr	Val	Glu	Arg
450				455				460							
Leu	Ile	His	Gly	Met	Tyr	Glu	Pro	Tyr	Asn	Asp	Ile	His	Met	Trp	Asp
465				470				475				480			

Tyr Lys Ala Leu Pro Ala Val Phe Gly Gly Lys Asn Val Glu Ile His
485 490 495

Asp Val Glu Ser Ser Lys Asp Leu Gln Asp Thr Phe Asn Ala Ile Asn
500 505 510

Ser His Pro Asp Val Met His Phe Val Glu Val Lys Met Ser Val Glu
515 520 525

Asp Ala Pro Lys Lys Leu Ile Asp Ile Ala Lys Ala Phe Ser Gln Gln
530 535 540

Asn Lys

545

<210> 558

<211> 549

<212> PRT

<213> Unknown

<220><223> Proteus

<400> 558

Met Thr Asn Thr Val Ile Lys Tyr Val Leu Asp Arg Leu Tyr Asp Leu

1 5 10 15

Gly Ile Lys Asp Ile Phe Gly Val Ala Gly Asp Tyr Ala Phe Pro Ile

20 25 30

Glu Asp Thr Val Cys Asn Asn Gln Gln Gln Arg Trp Ile Gly Asn Cys

35 40 45

Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile Lys

50 55 60

Gly Met Ala Ala Leu Ser Thr Thr Phe Gly Val Gly Glu Leu Ser Ala

65 70 75 80

Ile Asn Ala Ile Ala Gly Ala Tyr Ala Glu Asn Leu Pro Ile Phe His

85 90 95

Leu Val Gly Met Pro Ala Ser Gly Val Gln Lys Ser Lys Arg Leu Val

100 105 110

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

115 120 125

Gln Arg Leu Ala Cys Ala His Thr Ile Leu Thr Pro Glu Asn Cys Val

130

135

140

Glu Glu Met Glu Arg Val Ile Asp Val Ala Leu Lys Glu Arg Arg Pro

145

150

155

160

Val Tyr Ile Gly Ile Pro Ser Asp Tyr Ala Asn Ser Gln Val Val Glu

165

170

175

Pro Leu Ser Val Thr Ala Pro Gln Lys Pro Thr Ser Asp Lys Ala Thr

180

185

190

Leu Glu Lys Ala Val Ser Ala Ile Val Glu Lys Leu Thr His Ser Asn

195

200

205

Asn Val Cys Val Leu Pro Gly Phe Leu Ser Ala Arg Leu Gly Leu Thr

210

215

220

Asp Lys Ile Gln His Phe Ile Asp Lys Thr Gly Leu Pro Tyr Ala Thr

225

230

235

240

Met Phe Met Asp Lys Ser Ile Leu Ser Glu Ser Asn Thr Gln Tyr Val

245

250

255

Gly Met Tyr Asp Gly Gln Leu Met Thr Pro Glu Val Arg Glu Phe Val

260

265

270

Glu Ser Ser Glu Tyr Ile Leu Gly Ile Gly Thr Leu Leu Thr Asp Phe

275

280

285

Asn Thr Gly Ser Phe Thr Ala Asn Ile Lys Ser Glu Gln Phe Ile Ser

290

295

300

Ile Met Pro Asp Tyr Val Glu Ile Asp Ser Val Ile Tyr Ser Cys Val

305

310

315

320

Tyr Met Thr Asp Ile Leu Ser Glu Leu Thr Gln Arg Leu Pro Asn Lys

325

330

335

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

340

345

350

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

355

360

365

Phe Phe Lys Pro Asn Asp Ile Ile Ile Ala Glu Thr Gly Thr Ser Ser

370 375 380
Met Gly Leu Gly Phe Ala Leu Leu Pro Glu Gly Ala Gln Phe His Asn

385 390 395 400
Gln Thr Leu Trp Gly Ser Ile Gly Trp Ala Thr Pro Ala Ala Leu Gly

405 410 415
Ala Ala Leu Ala Ala Pro Glu Lys Arg Ile Ile Leu Ile Thr Gly Glu

420 425 430
Gly Ser His Gln Leu Thr Val Gln Glu Ile Ser Gln Phe Val Arg Phe

435 440 445
Gly Leu Lys Pro Ile Ile Leu Val Leu Asn Asn Asp Gly Tyr Leu Ile

450 455 460
Glu Arg Leu Leu Cys Asp Tyr Pro Glu Ala Tyr Tyr Asn Asp Leu Ala

465 470 475 480
Gln Trp Asn Tyr His Gln Leu Pro Gln Ala Phe Gly Ala Thr Asp Trp

485 490 495
Tyr Ser Glu Lys Val Thr Thr Ala Ser Glu Leu Asp Asn Ala Leu Asn

500 505 510
Lys Ala Ala Leu Thr Asp Ser Ala Ser Tyr Ile Glu Ile Val Thr Glu

515 520 525
Arg Tyr Glu Ala Ser Glu Leu Ala Gln Lys Leu Lys Glu Ser Lys Ser

530 535 540
Ser Leu Tyr Ser Phe

545

<210> 559

<211> 565

<212> PRT

<213> Microbacterium pygmaeum

<400> 559

Met Thr Asp Glu Arg Leu Glu Ile Pro Tyr Thr Val Ala Asp Tyr Leu
1 5 10 15

Leu Asp Arg Leu Ala Glu Ala Gly Val Arg His Leu Phe Gly Val Pro

20 25 30
 Gly Asp Phe Thr Leu Ala Phe Leu Asp His Val Gln Arg His Pro Leu
 35 40 45
 Ile Glu Trp Val Gly Cys Ala Asn Glu Leu Gly Ala Ala Tyr Ala Ala
 50 55 60
 Asp Gly Tyr Gly Arg Met His Gly Leu Gly Ala Leu Ser Thr Thr Phe
 65 70 75 80
 Gly Val Gly Glu Leu Ser Ala Ile Gly Ala Ile Ala Gly Ser Tyr Ala

 85 90 95
 Glu His Val Pro Val Leu His Val Val Gly Ala Pro Thr Thr Ala Thr
 100 105 110
 Gln Ala Ala Gly Arg Ala Thr His His Thr Leu Gly Asp Gly Asp Phe
 115 120 125
 Gly His Phe Ala Arg Met Thr Ala Glu Val Thr Val Asp Gln Ala Arg
 130 135 140
 Leu Thr Ala Ala Gly Tyr Ser Ala Glu Ile Asp Arg Val Ile Val Ala

 145 150 155 160
 Ala Arg Asp Arg Arg Leu Pro Gly Tyr Leu Ile Val Pro Ala Asp Val
 165 170 175
 Ser Glu Ala Pro Ala Glu Pro Pro Arg Gln Ala Leu Pro Gln His Pro
 180 185 190
 Ala Ile Thr Asp Pro Asp Val Val Asp Arg Phe Arg Gln Ala Val Ala
 195 200 205
 Ala Arg Leu Ala Ala Ala Arg Ser Val Ala Val Leu Ala Asp Ile Leu

 210 215 220
 Val Ser Arg Met Ser Ala Glu Asp Ser Leu Arg Gly Leu Leu Arg Leu
 225 230 235 240
 Gly Val Pro His Ala Thr Leu Leu Trp Gly Arg Arg Val Val Asp Glu
 245 250 255
 Ser Ala Glu Ala Tyr Leu Gly Ser Tyr Leu Gly Ala Ala Ser Asp Gly
 260 265 270

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

275 280 285
Val Gln Phe Thr Asp Leu Thr Ser Gly Phe Phe Ser Gln Arg Ile Asp
290 295 300
Ser Ala Arg Thr Ile Glu Ile Arg Gly Glu Tyr Ala Thr Val Gly Gly
305 310 315 320
Glu Arg Phe Glu Pro Leu Ala Met Ser Ala Ala Leu His Ala Val Thr
325 330 335
Ser Ala Val Arg Glu Glu Ala Glu His Leu Gln Leu Ile Pro Thr Gly

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

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

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

515 520 525
Gly Ser Glu Ser Leu Thr Leu Ile Gln Ala Val Val Pro Pro Leu Asp

530 535 540
Val Pro Pro Val Leu Arg Ala Leu Gly Ala Ala Ala Ala Asn Ala Asn
545 550 555 560
Arg Pro Leu Asp Arg

565
<210> 560
<211> 549
<212> PRT
<213> *Morganella morganii*
<400> 560

Met Thr Lys Thr Val Val Glu His Val Leu Ser Arg Leu Gln Asp Leu
1 5 10 15
Gly Ile Arg His Val Phe Gly Val Ala Gly Asp Phe Ala Phe Pro Ile

20 25 30
Glu Asp Ala Val Cys Glu Ser Arg Thr Met Gln Trp Met Gly Asn Cys
35 40 45
Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile Lys
50 55 60
Gly Ala Ala Ala Leu Ser Thr Thr Phe Gly Val Gly Glu Leu Ser Ala
65 70 75 80
Ile Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Leu Pro Val Phe His

85 90 95
Leu Val Gly Met Pro Ala Ser Gly Val Gln Lys Ser Gly Arg Leu Val
100 105 110
His His Thr Leu Gly Asp Gly Asn Phe Ser Leu Phe Cys Glu Leu Gly
115 120 125
Gln Arg Leu Ser Cys Ala His Ala Val Met Thr Pro Glu Asn Cys Val
130 135 140
Ala Glu Thr Glu Arg Leu Ile Ala Ala Ala Leu Arg Glu Arg Arg Pro

145 150 155 160
 Val Tyr Ile Gly Leu Pro Phe Asp Tyr Ala Thr Gln Pro Val Gln Ile
 165 170 175
 Pro Glu His Leu Thr Ala Pro Ala Gln Pro Val Ser Asp Lys Thr Ala
 180 185 190
 Leu Thr Glu Ala Val Ala Ala Ile Arg Ala Lys Leu Ala Asp Ser Pro
 195 200 205
 Ser Ala Cys Ile Leu Pro Gly Met Leu Ala Ala Arg Ser Gly Leu Ile

 210 215 220
 Asp Asp Val Gln Ala Leu Ile Arg Gln Thr Gly Leu Pro Tyr Ala Thr
 225 230 235 240
 Met Phe Met Asp Lys Ala Ile Ile Ser Glu Ser Asp Pro His Tyr Ala
 245 250 255
 Gly Met Tyr Asn Gly Gln Leu Met Asn Pro Gln Ile Arg Glu Phe Val
 260 265 270
 Glu Asn Ser Asp Cys Val Leu Gly Ile Gly Ala Val Met Thr Asp Phe

 275 280 285
 Asn Thr Gly Ser Phe Thr Ala Asp Ile Ala Pro Glu Lys Leu Ile Ser
 290 295 300
 Ile Met Ala Asp His Val Arg Val Gly Ala Ala Thr Trp Gln Asn Val
 305 310 315 320
 Tyr Met Arg Asp Leu Leu Pro Ala Leu Thr Ala Val Leu Pro His Arg
 325 330 335
 Glu Cys His Ile Pro Ala Ala Thr Gly Leu Gly Lys Pro Val Ala Asp

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

Gln Thr Leu Trp Gly Ser Ile Gly Trp Ala Thr Pro Ala Ala Val Gly

405 410 415

Ala Ala Ile Ala Ala Pro Asp Arg Arg Leu Ile Leu Ile Thr Gly Glu

420 425 430

Gly Ser His Gln Leu Thr Ala Gln Glu Ile Ser Gln Phe Gly Arg Phe

435 440 445

Gly Leu Lys Pro Leu Ile Phe Val Leu Asn Asn Asp Gly Tyr Leu Ile

450 455 460

Glu Arg Leu Leu Cys Lys Asp Pro Glu Ala Val Tyr Asn Asp Leu Pro

465 470 475 480

Gln Trp Arg Tyr Ala Gln Leu Pro Gln Ala Leu Gly Cys Asp Asn Trp

485 490 495

Tyr Cys Arg Arg Val Thr Thr Ser Thr Glu Leu Asp Glu Ala Ile Arg

500 505 510

Glu Ala Glu Thr Gly Asp Arg Ala Ala Tyr Ile Glu Ile Ile Thr Glu

515 520 525

Arg Tyr Ala Ala Ser Asp Leu Ala Lys Lys Leu Gly Glu Ser Val Ala

530 535 540

Thr Leu Tyr Ser Phe

545

<210> 561

<211> 557

<212> PRT

<213> Unknown

<220><223> Mycobacterium sp. SWH-M5

<400> 561

Met Thr Asp Asp Gly Tyr Thr Val Gly Asp Tyr Leu Leu Asp Arg Leu

1 5 10 15

Ala Glu Leu Gly Val Thr Glu Ile Phe Gly Val Pro Gly Asp Tyr Gln

20 25 30

Leu Glu Phe Leu Asp His Ile Val Ala His Pro Arg Ile Thr Trp Ile

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

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

 165 170 175
 Thr Glu Pro Pro His Met Pro Leu Pro Arg Tyr Thr Asp Gly Thr Ser
 180 185 190
 Pro Arg Ala Arg Ser Leu Phe Thr Glu Ala Ala Ala Gln Leu Ile Gly
 195 200 205
 Glu His Arg Leu Thr Val Leu Ala Asp Val Leu Val His Arg Met Gly
 210 215 220
 Cys Val Glu Glu Leu Gly Lys Leu Leu Ala Ala Asp Thr Val Pro His

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

Asp Met Val Ser Gly Phe Phe Ser Gln Arg Ile Asp Pro Ala Arg Thr

290

295

300

Ile Asp Ile Gly Val Asn Gln Ser Met Val Ala Gly Gln Val Phe Ala

305

310

315

320

Pro Leu Asp Met Ala Ala Ala Leu Asp Val Leu Thr Ala Ile Leu Thr

325

330

335

Glu Arg Gly Ile Glu Ser Pro Ala Leu Pro Pro Pro Ala Ala Pro Glu

340

345

350

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

355

360

365

Trp Asp Arg Leu Ser Glu Ala Leu Thr Pro Gly Asn Val Val Leu Ala

370

375

380

Asp Gln Gly Thr Ser Phe Tyr Gly Leu Ala Gly His Arg Leu Ala Ser

385

390

395

400

Gly Val Thr Phe Ile Gly Gln Pro Leu Trp Ala Ser Ile Gly Tyr Thr

405

410

415

Leu Pro Ala Ala Val Gly Ala Gly Leu Ala Asp Arg Asp Arg Arg Thr

420

425

430

Val Leu Leu Ile Gly Asp Gly Ala Ala Gln Leu Thr Ile Gln Glu Leu

435

440

445

Gly Ala Phe Gly Arg Glu Gly Leu Thr Pro Val Val Val Val Val Asn

450

455

460

Asn Asp Gly Tyr Thr Val Glu Arg Ala Ile His Gly Val Thr Ala Glu

465

470

475

480

Tyr Asn Asp Ile Thr Gly Trp Arg Trp Thr Glu Leu Pro Ala Ala Leu

485

490

495

Gly Val Pro Asp Ala Leu Thr Phe Arg Cys Arg Thr Tyr Gly Glu Leu

500

505

510

Asp Asp Ala Leu Thr Val Ala Ala Glu Thr Gln Asp Arg Met Val Phe

515

520

525

Val Glu Val Met Leu Glu Arg Met Asp Ile Pro Pro Leu Leu Ser Glu

530 535 540
 Leu Ala Gln Ser Ala Ser Ala Ala Asn Ala Ala Ser Gly

 545 550 555
 <210> 562
 <211> 547
 <212> PRT
 <213> *Staphylococcus fleurettii*
 <400> 562
 Met Lys Lys Arg Val Gly Glu Tyr Leu Met Asp Ala Leu Ser Thr Val
 1 5 10 15
 Gly Val Glu Lys Val Phe Gly Val Pro Gly Asp Phe Asn Leu Ala Phe
 20 25 30
 Leu Asp Asp Ile Val Ser Arg Asp Asp Met Glu Trp Val Gly Asn Thr
 35 40 45

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

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

 Val Glu Ala Phe Lys Pro Ala Glu Ala Val Lys Gln Asp Val Ser Lys

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

 Gly Lys Gly Ala Phe Asn Glu Glu Ser Pro Tyr Tyr Met Gly Ile Tyr
 245 250 255
 Asp Gly Ser Ile Ala Glu Glu Asn Ile Arg Asn Tyr Val Asp Asn Ser
 260 265 270
 Asp Ala Ile Leu Asn Ile Gly Ala Lys Leu Thr Asp Ser Ala Thr Ala
 275 280 285
 Gly Tyr Ser Tyr Gly Phe Asp Ile Asp Asp Val Val Met Ile Asn His
 290 295 300

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

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

Leu Gln Leu Thr Ala Gln Asp Ile Ser Thr Met Ile Arg Glu Asp Leu

435 440 445

Lys Pro Val Ile Phe Val Ile Asn Asn Asp Gly Tyr Thr Val Glu Arg

450 455 460

Lys Ile His Gly Glu His Gln Pro Tyr Asn Asp Ile Gln Met Trp Asp

465 470 475 480

Tyr Lys Leu Leu Pro Val Val Phe Gly Gly Lys Asp Lys Val Ala Ile

485 490 495

His Asp Val Glu Thr Ser Ala Asp Leu Glu Asn Val Phe Leu Gln Ile

500 505 510

Asn Asn Glu Pro Asn Gln Met His Phe Ile Glu Val Lys Met Thr Ala

515 520 525

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

530 535 540

Gln Asn Ser

545

<210> 563

<211> 551

<212> PRT

<213> Mycobacteroides abscessus

<400> 563

Met Thr Tyr Thr Val Ser Asp Tyr Leu Leu Asp Arg Leu Asn Glu Leu

1 5 10 15

Gly Leu Arg Asp Leu Phe Gly Val Pro Gly Asp Phe Asn Leu Gln Phe

20 25 30

Leu Asp His Val Ile Glu His Glu Gly Ile Val Trp Val Gly Asn Ala

35 40 45

Asn Glu Leu Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Ala Arg Val Asn

50 55 60

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

65 70 75 80

Ile Asn Ala Thr Ala Gly Ser Tyr Ala Glu Gln Val Pro Val Leu His

85	90	95	
Ile Val Gly Ala Pro Ser Lys Asp Ala Gln Ala Ala His Leu Thr Met			
100	105	110	
His His Thr Leu Gly Asp Gly Asp Phe Thr His Phe Ile Arg Met Ala			
115	120	125	
Ser Glu Val Ser Cys Thr Val Ala Asp Leu Glu His Ala Thr Ala Val			
130	135	140	
Ser Glu Ile Asp Arg Val Leu Arg Glu Met Met Ile His Lys Arg Pro			
145	150	155	160
Gly Tyr Ile Leu Leu Ala Thr Asp Val Ala Arg Val Glu Val Asp Pro			
165	170	175	
Pro Ala Ala Pro Leu Asn Val Pro Ala Lys Leu Ser Ser Pro Gly Ala			
180	185	190	
Arg Glu Ser Phe Arg Lys Asp Leu Thr Thr Leu Leu Ala Gly Lys Lys			
195	200	205	
Thr Thr Val Leu Ala Asp Leu Leu Val His Arg Met Gly Ala Gln Ser			
210	215	220	
Asn Leu Thr Glu Met Leu Asp Ala Thr Gly Leu Pro Tyr Ala Thr Leu			
225	230	235	240
Met Trp Gly Lys Thr Leu Val Asp Glu Ser Lys Pro Glu Phe Ala Gly			
245	250	255	
Ile Tyr Ala Gly Val Val Ser Asn Glu Arg Thr Lys Lys Ala Val Glu			
260	265	270	
Asp Ala Glu Ile Leu Ile Cys Ala Gly Val Thr Phe Thr Asp Thr Thr			
275	280	285	
Thr Ala Gly Phe Ser Gln Asn Leu Pro Glu His Thr Val Phe Leu Asp			
290	295	300	
Ala Gln Thr Ala Arg Leu Gly Arg Lys Thr Tyr Ala Pro Leu Thr Leu			
305	310	315	320
Asp Thr Ser Leu Asp Ile Val Arg Glu Val Ala Leu Glu Val Gly Ala			
325	330	335	

Leu Pro Gln Asp Leu Leu Pro Trp Glu Glu Glu Asp His Ala Asp Ile
 340 345 350
 Asp Met Asp Ala Pro Leu Thr Gln Asp Val Leu Trp Ser Leu Leu Ser
 355 360 365
 Arg Glu Leu Thr Pro Gly Asn Ile Val Val Ala Asp Gln Gly Thr Ser
 370 375 380

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

 Gln Lys Ile Asn Pro Val Val Val Leu Ile Asn Asn Asp Gly Tyr Thr
 450 455 460
 Val Glu Arg Ala Ile His Gly Ala Thr Gln Pro Tyr Asn Asp Ile Arg
 465 470 475 480
 Thr Tyr Asn Trp Gln Leu Leu Pro Ala Ala Leu Gly Ala Arg Glu Asp
 485 490 495
 Glu Val Leu Met Leu Arg Val Asn Thr Ala Thr Glu Leu Val Asp Ala
 500 505 510

 Ala Arg Leu Thr Gln Gln Thr Arg Asp Arg Leu Val Phe Met Glu Ile
 515 520 525
 Met Met Asp Lys Asp Asp Val Pro Ala Leu Leu Ala Asp Val Ala Ser
 530 535 540
 Ala Leu Thr Arg Ala Asn Ser
 545 550
 <210> 564
 <211> 564
 <212> PRT
 <213> *Cyberlindnera fabianii*

<400> 564

Met Ser Asp Ile Thr Leu Gly Arg Tyr Leu Phe Glu Arg Leu Arg Gln
1 5 10 15

Val Glu Val Gln Thr Ile Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser
20 25 30

Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Leu Arg Trp Ala Gly Asn
35 40 45

Ala Asn Glu Leu Asn Ser Ala Tyr Ala Ala Asp Gly Tyr Ser Arg Val
50 55 60

Lys Gly Ile Ser Ala Leu Val Thr Thr Phe Gly Val Gly Glu Leu Ser
65 70 75 80

Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ser Glu His Val Gly Val Ile
85 90 95

His Ile Val Gly Val Pro Ser Ile Ser Ser Gln Ala Lys Gln Leu Leu
100 105 110

Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
115 120 125

Ser Ser Asn Ile Ser Gln Thr Thr Ala Phe Ile Lys Asp Ile Asn Ser
130 135 140

Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Ala Tyr Val Tyr Gln
145 150 155 160

Lys Pro Val Tyr Leu Ala Val Pro Ala Asn Leu Val Asp Asp Val Val
165 170 175

Ser Ser Asn Leu Leu Asn Thr Pro Ile Asp Leu Ser Leu Lys Ala Asn
180 185 190

Glu Glu Glu Ala Glu Ser Glu Val Ile Glu Thr Val Cys Gln Met Val
195 200 205

Glu Asn Ala Lys Asn Pro Val Ile Leu Val Asp Ala Cys Ala Ala Arg
210 215 220

His Asn Val Lys Ala Glu Thr Lys Glu Leu Val Asp Ala Thr Gln Phe
225 230 235 240

Pro Val Phe Val Thr Pro Met Gly Lys Gly Val Val Asp Glu Gln His
245 250 255

Pro Arg Phe Gly Gly Val Tyr Val Gly Thr Leu Ser Lys Pro Asp Val
260 265 270

Lys Glu Ala Val Glu Ser Ala Asp Leu Val Leu Ser Val Gly Ala Leu
275 280 285

Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
290 295 300

Asn Ile Val Glu Phe His Ser Asp His Ile Lys Ile Arg Asn Ala Thr
305 310 315 320

Phe Pro Gly Val Gln Phe Lys Pro Val Leu Gln Lys Leu Asn Lys Val
325 330 335

Ile Ala Ala Ser Val Lys Asn Tyr Ile Pro Val Pro Val Pro Ser Leu
340 345 350

Lys Leu Thr Asn Ser Pro Ala Gly Ala Asn Thr Pro Leu Thr Gln Glu
355 360 365

Trp Ile Trp Thr Lys Met Ser Ser Trp Leu Arg Glu Gly Asp Ile Val
370 375 380

Leu Thr Glu Thr Gly Thr Ser Ala Phe Gly Ile Ile Gln Thr Arg Phe
385 390 395 400

Pro Ser Asn Thr Thr Gly Ile Ser Gln Val Leu Trp Gly Ser Ile Gly
405 410 415

Tyr Ser Val Gly Ala Thr Leu Gly Ala Val Ala Ala Ala Glu Glu Leu
420 425 430

Asp Lys Ser Arg Arg Val Ile Leu Phe Val Gly Asp Gly Ser Leu Gln
435 440 445

Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Asn Pro
450 455 460

Tyr Ile Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Arg Leu Ile
465 470 475 480

His Gly Glu Arg Ala Gln Tyr Asn Asp Ile Gln Ser Trp Asp His Leu

485 490 495
 Ala Leu Leu Pro Thr Phe Gly Ala Lys Asn Tyr Asp Ala Val Arg Val
 500 505 510
 Ser Asn Thr Gly Glu Phe Asn Lys Ile Cys Asp Asp Lys Glu Phe Ala
 515 520 525

 Glu Pro Ser Lys Ile Arg Leu Ile Glu Val Met Leu Pro Thr Met Asp
 530 535 540
 Ala Pro Gln Asn Leu Val Lys Gln Ala Gln Leu Thr Ala Ser Thr Asn
 545 550 555 560
 Ser Gln Gln Glu

 <210> 565
 <211> 551
 <212> PRT
 <213> Leclercia adecarboxylata
 <400> 565
 Met Gln Thr Pro Tyr Thr Val Ala Asp Tyr Leu Leu Asp Arg Leu Thr
 1 5 10 15

 Asp Cys Gly Ala Asp His Leu Phe Gly Val Pro Gly Asp Tyr Asn Leu
 20 25 30
 Gln Phe Leu Asp His Val Ile Ala Ser Pro Asp Ile Gly Trp Val Gly
 35 40 45
 Cys Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg
 50 55 60
 Cys Lys Gly Phe Ala Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu
 65 70 75 80

 Ser Ala Met Asn Gly Ile Ala Gly Ser Phe Ala Glu His Val Pro Val
 85 90 95
 Leu His Ile Val Gly Ala Pro Gly Ser Ala Ser Gln Lys Lys Gly Glu
 100 105 110
 Leu Leu His His Thr Leu Gly Asp Gly Glu Phe Arg His Phe Tyr Lys
 115 120 125

Met Ser Glu Pro Val Thr Val Ala Gln Ala His Leu Thr Glu Gln Asn
130 135 140

Ala Cys Tyr Glu Ile Asp Arg Val Leu Thr Glu Met Leu Arg Glu Arg
145 150 155 160

Arg Pro Gly Tyr Ile Met Leu Pro Ala Asp Val Ala Lys Lys Pro Ala
165 170 175

Thr Pro Pro Val Ser Ala Leu Ile Asp Arg Leu Tyr Glu Ser Asp Ser
180 185 190

Phe Arg Leu Asp Ala Phe Arg Gln Ala Ala Glu Lys Arg Leu Ala Ala
195 200 205

Ser Glu Arg Thr Ala Leu Leu Ala Asp Phe Leu Val Leu Arg Tyr Gly
210 215 220

Leu Gln Ser Gln Leu Gln Arg Trp Val Glu Gln Thr Pro Met Ala His
225 230 235 240

Ala Thr Leu Leu Met Gly Lys Gly Ile Phe Asp Glu Arg Lys Pro Gly
245 250 255

Phe Ala Gly Thr Tyr Ser Gly Ser Ala Ser Ala Ala Gly Val Asn Glu
260 265 270

Ala Ile Glu Gly Ala Asp Thr Val Ile Cys Val Gly Thr Arg Phe Thr
275 280 285

Asp Thr Leu Thr Ala Gly Phe Thr His Lys Leu Thr Gln Gln Gln Thr
290 295 300

Ile Asp Val Gln Pro His Ala Ser Arg Ile Gly Asp Val Trp Tyr Thr
305 310 315 320

Gly Ile Pro Met Thr Gln Ala Ile Glu Val Leu Ser Ser Leu Cys His
325 330 335

Gln Tyr Ala Ser Ala Thr Thr Ala Thr Arg Pro Ala Arg Gln Leu His
340 345 350

Ala Val His Pro Gly Thr Leu Ser Gln Asp Ser Phe Trp Gln Thr Leu
355 360 365

Gln Thr Phe Ile Arg Pro Gly Asp Ile Ile Leu Ala Asp Gln Gly Thr

370 375 380
 Ser Ala Phe Gly Ala Gly Ala Leu Arg Leu Pro Glu Asp Val Asn Phe
 385 390 395 400

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

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

 Leu Pro Lys Ala Asp Val Pro Pro Leu Leu Ser Gly Ile Ile Gln Ala
 530 535 540
 Leu Glu Ala Arg Lys Ser Ala
 545 550
 <210> 566
 <211> 549
 <212> PRT
 <213> Clostridium thermobutyricum
 <400> 566
 Met Lys Thr Thr Val Gly Asn Tyr Leu Ile Asp Ser Leu Lys Glu Tyr
 1 5 10 15
 Gly Val Lys His Ile Phe Gly Val Pro Gly Asp Tyr Asn Leu Ser Phe

20				25				30							
Leu	Asp	Gln	Ile	Asp	Asp	Ser	Glu	Asp	Ile	Glu	Trp	Ile	Gly	Asn	Cys
35				40				45							
Asn	Glu	Leu	Asn	Ala	Ser	Tyr	Ala	Ala	Asp	Gly	Tyr	Gly	Arg	Ile	Lys
50				55				60							
Gly	Met	Ala	Ala	Ile	Ala	Thr	Thr	Phe	Gly	Val	Gly	Glu	Leu	Ser	Ala
65				70				75				80			
Val	Asn	Gly	Ile	Ala	Gly	Ser	Tyr	Ala	Glu	Asn	Val	Pro	Val	Val	Lys
85				90				95							
Ile	Val	Gly	Ile	Pro	Ser	Ser	Lys	Val	Val	Glu	Asn	Arg	Lys	Leu	Val
100				105				110							
His	His	Thr	Leu	Gly	Asp	Gly	Glu	Phe	Tyr	Arg	Phe	Asn	Glu	Met	Phe
115				120				125							
Lys	Glu	Val	Ser	Val	Ala	Gln	Thr	Ile	Leu	Asn	Glu	Ile	Asn	Ala	Lys
130				135				140							
Glu	Glu	Ile	Asp	Arg	Val	Leu	Arg	Glu	Cys	Tyr	Leu	Tyr	Lys	Lys	Pro
145				150				155				160			
Val	Tyr	Ile	Gly	Met	Pro	Val	Asp	Leu	Ala	Thr	Lys	Val	Ile	Asn	Val
165				170				175							
Ser	Glu	Lys	Thr	Ser	Tyr	Asn	Leu	Glu	Ser	Asp	Lys	Asn	Ser	Leu	Asn
180				185				190							
Ser	Phe	Ile	Ser	Asn	Val	Lys	Ser	Leu	Met	Ser	Asn	Ser	Lys	Lys	Gln
195				200				205							
Met	Ile	Leu	Ala	Asp	Phe	Glu	Val	Asn	Arg	Tyr	Asn	Leu	Asn	Lys	Glu
210				215				220							
Leu	Gln	Glu	Phe	Val	Glu	Ala	Ser	Asn	Leu	Pro	Val	Ser	Ser	Leu	Ala
225				230				235				240			
Met	Gly	Lys	Gly	Val	Ile	Asp	Glu	Thr	His	Pro	Asn	Phe	Val	Gly	Val
245				250				255							
Tyr	Ser	Gly	Ser	Leu	Ser	Asn	Glu	Asn	Ile	Thr	Lys	Leu	Val	Lys	Ser
260				265				270							

Cys Asp Leu Ala Phe Leu Ile Gly Val Lys Leu Thr Asp Ser Ile Thr
275 280 285

Ala Gly Phe Ser Tyr Ile Asn Lys Asn Ile Thr Leu Val Glu Val His
290 295 300

Pro Leu Tyr Cys Arg Ile Gly Glu Asn Leu Phe Ser Asn Ile Leu Met
305 310 315 320

Lys Asp Ala Leu Glu Ser Leu Lys Asn Leu Asn Val Glu Phe Ser Lys
325 330 335

Asn Asp Thr Pro His Val Ser Leu Ile Asn Asn Phe Glu Ala Thr Asn
340 345 350

Thr Pro Leu Thr Gln Lys Arg Phe Phe Gln Gly Ile Glu Ser Phe Leu
355 360 365

Asn Glu Asn Asp Ile Leu Ile Ala Glu Gln Gly Thr Ser Phe Phe Gly
370 375 380

Ser Cys Leu Val Asn Met Lys Lys Gly Cys Thr Phe Ile Gly Gln Pro
385 390 395 400

Leu Trp Gly Ser Ile Gly Tyr Thr Val Gly Ala Leu Leu Gly Thr Gln
405 410 415

Ile Ala Asp Arg Asn Arg Arg Asn Ile Leu Leu Val Gly Asp Gly Ser
420 425 430

Phe Gln Leu Thr Ala Gln Glu Val Ser Thr Met Ile Arg Glu Asn Leu
435 440 445

Ser Pro Ile Ile Met Val Ile Asn Asn Asp Gly Tyr Thr Val Glu Arg
450 455 460

Leu Ile His Gly Pro Asn Arg Lys Tyr Asn Asp Ile Asn Met Trp Asp
465 470 475 480

Tyr Ser Lys Leu Val Ser Val Phe Asp Leu Glu Gly Asn Arg Ser Ile
485 490 495

Ser Phe Lys Ala Lys Thr Glu Ile Glu Leu Met Asn Ala Leu Lys Glu
500 505 510

Ala Asp Asn Asn Lys Asp Lys Leu Thr Phe Ile Glu Val Cys Met Asp

515 520 525
 Lys Met Asp Ser Pro Gln Leu Leu Lys Asp Leu Gly Glu Leu Phe Ser
 530 535 540

Lys Gln Asn Ser Tyr

545

<210> 567

<211> 573

<212> PRT

<213> *Penicillium steckii*

<400> 567

Met Ser Ser Asp Thr Val Lys Leu Gly Asp Tyr Leu Phe Thr Arg Leu
 1 5 10 15
 Leu Gln Leu Gly Val Ala Asp Ile Phe Gly Val Pro Gly Asp Tyr Asn
 20 25 30
 Leu Arg Leu Leu Asp Tyr Val Val Pro Ala Gly Leu His Trp Val Gly
 35 40 45

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

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

165 170 175
 Val Ser Ser Ala Asn Leu Lys Thr Pro Ile Arg Val Pro Leu Val Pro
 180 185 190
 Ser Pro Pro His Glu Pro Lys Val Val Ser Arg Ile Leu Asp Arg Leu
 195 200 205
 Tyr Ser Ala Gln Arg Pro Phe Ile Leu Val Asp Gly Glu Ser Arg Ser
 210 215 220
 Leu Gly Ile Leu Asp Glu Leu Asp Ala Leu Ile Gln Lys Thr Asn Trp
 225 230 235 240

 Pro Thr Trp Thr Thr Val Phe Gly Lys Gly Leu Val Asn Glu Ser Leu
 245 250 255
 Pro Asn Val Tyr Gly Leu Tyr Ala Ala Ser Phe Gly Asp Lys Pro Ala
 260 265 270
 Gln Glu Tyr Phe Glu Thr Ala Asp Leu Ile Leu Thr Phe Gly Pro His
 275 280 285
 Tyr Ser Asp Thr Asn Ser Tyr Phe Trp Thr Thr Val Pro Lys Asp Ala
 290 295 300

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

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

Met Leu Pro Ala Thr Leu Gly Ala Ala Leu Ala Lys Arg Gly Gln Asn

420 425 430

Lys Val Thr Gly Ala Ser Ser Gln Ala Val Leu Val Ile Gly Asp Gly

435 440 445

Ser Leu Gln Met Thr Ala Gln Glu Ile Ser Val Met Ile Lys Glu Asn

450 455 460

Leu Asn Ile Leu Ile Ile Ile Ile Asn Asn Glu Gly Tyr Thr Ile Glu

465 470 475 480

Arg Val Ile His Gly Arg Lys Gln Pro Tyr Asn Asp Val Pro Phe Trp

485 490 495

Arg His Thr Gln Ala Leu Ser Tyr Phe Gly Ala Asn Glu Glu Gln Ile

500 505 510

Ala Asn Ser Val Phe Thr Ala Arg Thr Cys Gly Glu Leu Arg Glu Val

515 520 525

Leu Lys Asn Glu Arg Val His Ser Gly Thr Gly Leu Arg Ile Val Glu

530 535 540

Val Ala Met Glu Arg Glu Asp Val Gln Gly Pro Leu Leu Tyr Leu Leu

545 550 555 560

Asn Lys Gln Ile Ala Glu Glu Gln Ala Ala Thr Ser Asn

565 570

<210> 568

<211> 551

<212> PRT

<213> Pantoea alhagi

<400> 568

Met Ser Gly Leu Thr Val Ser Asp Tyr Leu Leu Gln Arg Leu Asn Glu

1 5 10 15

Ile Gly Ile Asp His Leu Phe Gly Val Pro Gly Asp Phe Asn Leu Ala

20 25 30

Phe Leu Asp Arg Val Ile Ala His Pro Arg Leu Ala Trp Val Gly Cys

35 40 45

Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ser
50 55 60
Arg Arg Ala Gly Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu Ser
65 70 75 80
Ala Ile Asn Gly Ile Ala Gly Ser Tyr Ala Glu Tyr Val Pro Val Ile
85 90 95
His Ile Val Gly Ala Pro Ser Leu Ser Ala Gln Gln Arg Gly Asp Leu
100 105 110
Ile His His Ser Leu Gly Asp Gly Asp Phe Ser His Phe Leu Arg Met
115 120 125
Gln Arg Glu Val Thr Val Ala Gln Ala Thr Leu Thr Ala Asp Asn Ala
130 135 140
Cys Val Glu Ile Asp Arg Val Met Arg Glu Ala Leu Thr Gln Arg Arg
145 150 155 160
Pro Gly Tyr Leu Leu Leu Pro Val Asp Val Ala Gly Ala Pro Ala Cys
165 170 175
Ser Pro Gly Gln Pro Leu Thr Leu Gln Thr Gln Pro Asp Asp Gln Ala
180 185 190
Leu Gln Ala Phe Arg Cys Ala Ala Glu Ala Leu Leu Ser Gly Ala Arg
195 200 205
Ser Val Ser Leu Leu Ala Asp Phe Leu Ala Asp Arg Phe Gly Val Gln
210 215 220
Gln Gln Leu Ala His Trp Leu Glu Thr Val Pro Leu Pro His Ala Thr
225 230 235 240
Leu Leu Met Gly Lys Gly Val Leu Asp Glu Gln Arg Thr Gly Phe Ala
245 250 255
Gly Thr Tyr Ala Gly Glu Gly Cys Ala Asp Gly Thr Arg Arg Val Ile
260 265 270
Glu Gln Ala Asp Val Ile Ile Thr Val Gly Val Arg Phe Thr Asp Thr
275 280 285
Ile Thr Val Gly Phe Thr Gln Gln Ile Gly Thr Ala Lys Asn Ile Asp

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

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

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

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

545

550

<210> 569

<211> 558

<212> PRT

<213> *Mycobacterium aquaticum*

<400> 569

Met Ser Glu Asn Ala Tyr Thr Val Gly Asp Tyr Leu Leu Asp Arg Leu

1 5 10 15

Ala Glu Leu Gly Val Thr Glu Ile Phe Gly Val Pro Gly Asp Tyr Gln

20 25 30

Leu Glu Phe Leu Asp His Ile Leu Ala His Pro Arg Val Arg Trp Val

35 40 45

Gly Gly Ala Asn Glu Leu Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Gly

50 55 60

Arg Leu Arg Gly Met Ala Ala Leu Val Thr Thr Phe Gly Val Gly Glu

65 70 75 80

Leu Ser Ala Ala Asn Ala Val Ala Gly Ser Tyr Ala Glu His Val Pro

85 90 95

Val Val His Ile Val Gly Ala Pro Ser Lys Asp Ala Gln Gly Ala Arg

100 105 110

Arg Ile Val His His Thr Leu Gly Asp Gly Asp Phe Asp His Phe Leu

115 120 125

Arg Ile Ser Arg Glu Ile Thr Cys Ala Gln Ala Asn Leu Val Pro Ala

130 135 140

Thr Ala Thr Arg Glu Ile Asp Arg Val Leu Ser Glu Val Arg Glu Gln

145 150 155 160

Lys Arg Pro Gly Tyr Leu Leu Ile Ala Thr Asp Val Ala Arg Phe Pro

165 170 175

Thr Glu Pro Pro Ala Ala Pro Leu Pro Arg Tyr Thr Ala Gly Thr Ser

180 185 190

Pro Arg Ala Leu Thr Leu Phe Thr Ala Ala Ala Ala Glu Leu Ile Asp

195 200 205
 Asn His Arg Ile Ala Val Leu Ala Asp Phe Leu Val His Arg Leu Gly
 210 215 220
 Cys Val Lys Glu Leu Asn Ala Leu Leu Ala Ala Asp Thr Val Pro His
 225 230 235 240
 Ala Thr Leu Met Trp Gly Lys Ser Leu Val Asp Glu Ser Ser Pro Asn

 245 250 255
 Tyr Val Gly Ile Tyr Ala Gly Ala Ala Ser Glu Asp Ser Val Arg Glu
 260 265 270
 Val Ile Glu Asp Ala Pro Val Leu Val Thr Ala Gly Val Leu Phe Thr
 275 280 285
 Asp Met Val Ser Gly Phe Phe Ser Gln Arg Leu Asp Pro Ala Arg Thr
 290 295 300
 Ile Asp Ile Gly Val Asn Gln Ser Val Ile Ala Gly Gln Val Tyr Ala

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

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

 435 440 445

Gly Thr Phe Gly Arg Glu Gly Leu Ala Pro Val Val Val Val Val Asn
450 455 460
Asn Asp Gly Tyr Thr Val Glu Arg Ala Ile His Gly Val Thr Ala Glu
465 470 475 480
Tyr Asn Asp Ile Ala Ala Trp Arg Trp Ser Asp Leu Pro Ala Ala Leu
485 490 495
Gly Val Thr Asp Ala Leu Thr Phe Arg Val Thr Thr Cys Gly Glu Leu
500 505 510
Ala Asp Ala Leu Ala Ala Ala Ala Thr Ala Asp Arg Met Val Phe
515 520 525
Ile Glu Ala Val Leu Ala Arg Met Asp Ile Pro Pro Leu Leu Thr Glu
530 535 540
Leu Ala Gln Ser Ala Ser Glu Ala Asn Ser Arg Gly Ala Ser
545 550 555
<210> 570
<211> 551
<212> PRT
<213> Mycobacterium kubicae
<400> 570
Met Ser Thr Thr Pro Thr Val Ile Asp Tyr Val Leu Arg Arg Leu His
1 5 10 15
Glu Ile Gly Ile Ser Asp Val Phe Gly Val Pro Gly Asp Phe Ala Phe
20 25 30
Pro Met His Asp Ala Ile Val Ala His Pro Glu Ile Asn Trp Ile Gly
35 40 45
Cys Cys Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg
50 55 60
Val Arg Gly Val Gly Ala Val Ser Thr Thr Tyr Gly Val Gly Glu Leu
65 70 75 80
Ser Ala Ile Ser Ala Val Ala Gly Ala Tyr Ala Glu His Leu Pro Val
85 90 95
Phe His Leu Val Gly Met Pro Asn Leu Ala Thr Gln Ala Asn Arg Ala

100	105	110	
Leu Val His His Thr Leu Gly Asn Gly Glu Phe Glu Leu Phe Arg Lys			
115	120	125	
Met Ala Asp Ile Val Val Gly Ala Ser Ala Ile Ile Thr Pro Ala Asn			
130	135	140	
Val Val Ser Glu Thr Glu Arg Leu Ile His Glu Ala Leu Tyr Asn Arg			
145	150	155	160
Arg Pro Val Tyr Leu Ala Phe Pro Thr Asp Val Val Asp Lys Pro Ile			
165	170	175	
Leu Ala Thr Ser Ala Pro Leu Pro Leu Pro Val Ser Glu Pro Glu Ala			
180	185	190	
Leu Thr Ala Ala Val Asp Ala Val Ala Gln Ala Leu Ser Ala Ala Ser			
195	200	205	
Thr Ala Cys Val Leu Pro Gly Leu Leu Leu His Arg Leu His Ile Thr			
210	215	220	
Asp Ile Ala Thr Gln Phe Val Asp Ala Ala Gly Leu Pro Phe Ala Thr			
225	230	235	240
Met Phe Ala Asp Lys Ser Ala Ile Asp Glu Asp His Pro Arg Tyr Ile			
245	250	255	
Gly Met Tyr Asp Gly Gln Leu Met Glu Glu Asp Val Arg Val Phe Val			
260	265	270	
Glu Ser Ala Asp Val Val Ile Thr Val Gly Thr Met Gln Thr Asp Phe			
275	280	285	
Asn Thr Gly Ala Phe Thr Ala Arg Leu Asp Pro Ala Arg Thr Ile Asp			
290	295	300	
Ile Gly Leu His Arg Thr Thr Val Gly Ser Ala Val Tyr Gln Asn Val			
305	310	315	320
Glu Met Ala Asp Val Leu Arg Glu Leu Ala Ser Arg Ala Trp Thr Lys			
325	330	335	
Arg Phe Pro Pro Gly Pro Arg Pro Thr Ser Leu Gly Pro Val Val Gly			
340	345	350	

Ser Ala Ala Glu Pro Ile Thr Ala Ala Ala Leu Tyr Pro Arg Trp Ala

355 360 365

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

370 375 380

Ser Met Gly Leu Ala Phe Ala Gln Leu Pro His Gly Ala Arg Phe Tyr

385 390 395 400

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

405 410 415

Gly Ala Ala Val Ala Ala Pro Asp Arg Arg Val Val Leu Ile Thr Gly

420 425 430

Glu Gly Ser His Gln Leu Thr Val Gln Glu Ile Ser Gln Phe His Arg

435 440 445

Leu Gly Leu Arg Pro Ile Ile Phe Val Leu Asn Asn Ser Gly Tyr Leu

450 455 460

Ile Glu Arg Leu Leu Cys Lys Asp Pro Gly Ile Val Tyr Asn Asp Val

465 470 475 480

Ala Thr Trp Asn Tyr Ala Glu Leu Pro His Ala Leu Gly Cys Asp Asp

485 490 495

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

500 505 510

Ala Lys Ala Ala Gln Gly Asp Gln Ala Thr Tyr Ile Glu Val Val Thr

515 520 525

Asp Thr Tyr Glu Ala Pro Pro Leu Pro Asn Lys Leu His Glu Asn Val

530 535 540

Lys Thr Leu Tyr Asn Ile Gly

545 550

<210> 571

<211> 558

<212> PRT

<213> Mycobacterium szulgai

<400> 571

Met Val Val Thr Glu Pro Val Tyr Thr Val Gly Asp Tyr Leu Leu Asp

1 5 10 15

 Arg Leu Ala Glu Leu Gly Val Thr Glu Ile Phe Gly Val Pro Gly Asp
 20 25 30
 Tyr Asn Leu Lys Phe Leu Asp His Ile Val Ala His Pro Ala Ile Arg
 35 40 45
 Trp Val Gly Asn Ala Asn Glu Leu Asn Ala Gly Tyr Ala Ala Asp Gly
 50 55 60
 Tyr Gly Arg Leu Arg Gly Met Ala Ala Val Val Thr Thr Phe Gly Val
 65 70 75 80

 Gly Glu Leu Ser Ala Thr Asn Ala Ile Ala Gly Ser Tyr Ala Glu His
 85 90 95
 Val Pro Val Val His Ile Val Gly Gly Pro Thr Lys Asp Ala Gln Val
 100 105 110
 Ala Arg Arg Ala Leu His His Ser Leu Gly Asp Gly Asp Phe Glu His
 115 120 125
 Phe Phe Arg Ile Ser Arg Glu Ile Thr Cys Ala Gln Ala Asn Leu Met
 130 135 140

 Pro Ala Thr Ala Cys Arg Glu Ile Asp Arg Val Leu Cys Glu Val Arg
 145 150 155 160
 Glu Gln Lys Arg Pro Gly Tyr Ile Leu Leu Ser Ser Asp Val Ala Arg
 165 170 175
 Phe Pro Thr Glu Pro Pro Ala Asp Pro Leu Pro Arg Tyr Thr Gly Gly
 180 185 190
 Thr Ser Pro Arg Ala Leu Ala Leu Phe Thr Glu Ala Ala Thr Lys Leu
 195 200 205

 Ile Asp Asp His Gln Leu Thr Val Leu Ala Asp Leu Leu Val His Arg
 210 215 220
 Leu His Ala Val Ser Glu Leu Glu Ala Leu Leu Ala Ala Asp Val Val
 225 230 235 240
 Pro His Ala Thr Leu Met Trp Gly Lys Ser Leu Leu Asp Glu Ser Ser
 245 250 255

Pro Asn Phe Leu Gly Ile Tyr Ala Gly Ala Ala Ser Thr Glu Arg Val
260 265 270

Arg Val Ala Ile Glu Asp Ala Pro Val Leu Val Thr Ala Gly Val Val
275 280 285

Phe Thr Asp Met Val Ser Gly Phe Phe Ser Gln Arg Ile Asn Pro Ala
290 295 300

Arg Thr Ile Asp Ile Gly Gln Tyr Gln Ser Ser Val Gly Asp Glu Val
305 310 315 320

Phe Ala Pro Leu Glu Met Gly Ala Ala Leu Ala Ala Leu Thr Glu Ile
325 330 335

Leu Thr Arg Arg Gly Val Ser Ser Pro Ala Val Ala Ala Pro Pro Glu
340 345 350

Ala Pro Pro Pro Ile Thr Pro Ala Arg Asp Glu Pro Leu Thr Gln Gln
355 360 365

Met Val Trp Asp Arg Leu Cys Ala Ala Leu Thr Pro Gly Asn Val Val
370 375 380

Leu Ala Asp Gln Gly Thr Ser Phe Tyr Gly Met Ala Asp His Arg Leu
385 390 395 400

Pro His Gly Val Thr Phe Ile Gly Gln Pro Leu Trp Gly Ser Ile Gly
405 410 415

Tyr Thr Leu Pro Ala Ala Leu Gly Ala Gly Leu Ala His Pro Glu Arg
420 425 430

Arg Thr Val Leu Leu Ile Gly Asp Gly Ala Ala Gln Leu Thr Val Gln
435 440 445

Glu Leu Gly Thr Phe Ser Arg Glu Gly Leu Ser Pro Val Ile Val Val
450 455 460

Val Asn Asn Asp Gly Tyr Thr Val Glu Arg Ala Ile His Gly Glu Thr
465 470 475 480

Ala Pro Tyr Asn Asp Ile Val Gly Trp Ser Trp Thr Glu Val Pro Asn
485 490 495

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

500 505 510
 Glu Leu Asp Asp Ala Phe Thr Ala Ala Ala Val His Gln Asp Arg Met
 515 520 525

Val Phe Val Glu Val Ala Leu Pro Arg Leu Glu Ile Pro Arg Leu Leu
 530 535 540

Gly Gln Leu Val Gly Ser Met Ser Pro Pro Asp Asp Arg Arg
 545 550 555

<210> 572

<211> 559

<212> PRT

<213> Unknown

<220><223> Agreia sp. VKM Ac-1783

<400> 572

Met Thr Ile Thr Asp Gly Phe Val Ser Val Gly Gln Tyr Leu Ala Thr
 1 5 10 15

Arg Leu Leu Gln Leu Gly Val Arg His Val Phe Gly Leu Pro Gly Asp

20 25 30
 Phe Asn Leu Asn Leu Leu Asp Glu Met Ala Thr Val Glu Gly Ile Glu

35 40 45
 Trp Val Gly Ser Ser Asn Glu Leu Asn Ala Ala Tyr Ser Ala Asp Gly

50 55 60
 Tyr Ala Arg Val Gly Arg Cys Ala Gly Ala Leu Val Thr Thr Phe Gly

65 70 75 80
 Val Gly Glu Leu Ser Ala Leu Asn Gly Ile Ala Gly Ser Phe Ala Glu

85 90 95
 His Val Pro Val Ile His Ile Gly Gly Leu Pro Ala Arg Ala Ser Met

100 105 110
 Asp Ser Ser Ala Pro Leu His His Thr Leu Leu Asp Gly Asp Tyr Gly

115 120 125
 His Phe Val Arg Met Phe Arg Glu Val Thr Val Ala Asp Ala Ile Ile

130 135 140

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

145 150 155 160

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

165 170 175

Lys Ala Pro Val Ser Ala Arg Ser Leu Asp Val Pro Leu Ala Pro Leu

180 185 190

Ala Ser Asp Pro His Ala Leu Ser Ala Phe Ala Val Ala Leu Ser Arg

195 200 205

Glu Phe Ala Asp Ala Arg Ser Leu Val Val Leu Ala Gly Pro Asp Ile

210 215 220

His Arg Arg Gly Ile Glu Arg Asp Val Ala Glu Leu Ala Glu Leu Pro

225 230 235 240

Gly Ile Ser Ile Ala Ser Gln Ser Gly Ser Lys Ala Ile Leu Asp Glu

245 250 255

Ser His Pro Ser Ser Leu Gly Thr Tyr Leu Gly Ala Thr Thr Arg Asn

260 265 270

Ala Glu Ser Arg Ala Arg Val Asp Asp Ala Glu His Leu Val Met Ile

275 280 285

Gly Thr Ala Phe Ser Asp Phe Thr Thr Gly Phe Phe Thr His Gly Tyr

290 295 300

Asp Pro Ala Ser Ala Val Glu Leu Ala Leu Asp His Ala Arg Ile Gly

305 310 315 320

His Ala Val Tyr Pro Gly Val Arg Leu Asp Asp Ala Val Arg Ala Leu

325 330 335

Arg His Ala Ala Glu Leu Ala Pro Leu Gln Val Gly Pro Val Ile Glu

340 345 350

Pro Val Ala Ala Ala Ser Arg Val Thr Val Glu Gly Asp Ser Ala Leu

355 360 365

Ala His Asp Ser Phe Trp Pro Glu Ile Gln Asp Trp Leu Glu Pro Asp

370 375 380

Thr Thr Ile Ala Ala Glu Ala Gly Thr Ala Phe Tyr Gly Val Leu Asp

385 390 395 400
 Leu Asp Leu Pro Glu Arg Ser Asp Leu Met Gly Gln Pro Ile Trp Ser

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

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

 530 535 540
 Leu Leu Glu Val Leu Ala Arg Gly Ile Ser Glu Val Asn Lys His
 545 550 555
 <210> 573
 <211> 549
 <212> PRT
 <213> Proteus mirabilis
 <400> 573
 Met Asn Lys Thr Val Val Glu Tyr Met Leu Asn Arg Leu Tyr Asp Leu
 1 5 10 15
 Gly Ile Ser Asp Val Phe Gly Val Ala Gly Asp Tyr Ala Phe Pro Ile
 20 25 30
 Glu Asp Thr Ile Cys Asn Ser Asn His Ile Arg Trp Ile Gly Asn Cys

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

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

 Val Tyr Ile Gly Leu Pro Ser Asp Tyr Ala Val Met Pro Val Ile Glu
 165 170 175
 Asn Thr Ser Val Thr Thr Gln Lys Lys Pro Ile Ser Asp Lys Glu Ile
 180 185 190
 Leu Glu Lys Val Val Ser Leu Ile Ile Asp Lys Leu Thr Gln Ser Asn
 195 200 205
 Asn Ile Cys Val Leu Pro Gly Ile Leu Ser Thr Arg Leu Gly Leu Ser
 210 215 220

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

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

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

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

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

530

535

540

Ser Leu Tyr Ser Phe

545

<210> 574

<211> 561

<212> PRT

<213> Bacillus cereus

<400> 574

Met Ile His Leu Lys Thr Gln Tyr Thr Val Ser Thr Tyr Leu Leu Asp

1 5 10 15

Arg Leu Ser Glu Leu Gly Ile Glu His Ile Phe Gly Val Pro Gly Asp

20 25 30

Tyr Asn Leu Ala Phe Leu Asp Asp Val Ile Ala His Glu Asn Val Glu

35 40 45

Trp Ile Gly Asn Cys Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly

50 55 60

Tyr Ala Arg Ile Lys Gly Ile Gly Ala Leu Ile Thr Thr Phe Gly Val

65 70 75 80

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

85 90 95

Val Pro Val Ile Lys Ile Thr Gly Thr Pro Thr Thr Lys Val Met Glu

100 105 110

Asn Gly Ala Leu Val His His Thr Leu Gly Asp Gly Lys Phe Asp His

115 120 125

Phe Ser Lys Met Tyr Arg Glu Ile Thr Val Ala Gln Thr Asn Leu Thr

130 135 140

Pro Glu His Ala Ala Glu Glu Ile Asp Arg Val Leu Arg Ala Cys Trp

145 150 155 160

Asn Glu Lys Arg Pro Val His Ile Asn Leu Pro Ile Asp Val Tyr Asn

165 170 175

Lys Pro Ile Asn Lys Pro Thr Glu Pro Ile Leu His Lys Pro Ile Leu

180	185	190	
Ser Asn Lys Glu Thr Leu Asp Lys Met Leu Leu His Ala Ile Ser Lys			
195	200	205	
Ile Asn Ser Ala Lys Lys Pro Val Ile Leu Ala Asp Phe Glu Val Asp			
210	215	220	
Arg Phe His Ala Lys Glu Tyr Leu Tyr Gln Phe Val Glu Lys Thr Gly			
225	230	235	240
Phe Pro Ile Ala Thr Leu Ser Met Gly Lys Gly Ile Phe Pro Glu Lys			
245	250	255	
His Pro Gln Phe Ile Gly Ile Tyr Thr Gly Asp Val Ser Ser Pro Tyr			
260	265	270	
Leu Arg Lys Arg Ile Asp Glu Ser Asp Cys Ile Ile Ser Ile Gly Val			
275	280	285	
Lys Leu Thr Asp Thr Ile Thr Gly Gly Phe Thr Gln Gly Phe Thr Lys			
290	295	300	
Glu Gln Val Ile Glu Ile His Pro Tyr Thr Val Lys Ile Thr Asp Lys			
305	310	315	320
Lys Tyr Gly Pro Val Val Met Lys Asp Val Leu Gln Gln Leu Ser Asn			
325	330	335	
Val Ile Glu His Arg Asn Glu Glu Thr Phe Asp Ile Lys Pro Phe Ile			
340	345	350	
Ser Glu Ser Leu Ser Ile Thr Glu Lys Phe Asn Pro Lys Pro Gln Met			
355	360	365	
Val Thr Gln Lys Arg Phe Trp Gln Gln Ile Tyr His Phe Leu Gln Glu			
370	375	380	
Asn Asp Val Leu Leu Ala Glu Gln Gly Thr Pro Phe Phe Gly Ser Ala			
385	390	395	400
Ala Ile Pro Leu Pro Asn Asp Thr Thr Tyr Val Ala Gln Pro Leu Trp			
405	410	415	
Gly Ser Ile Gly Tyr Thr Leu Pro Ala Leu Leu Gly Thr Gln Leu Ala			
420	425	430	

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

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

Ser

<210> 575

<211> 548

<212> PRT

<213> Staphylococcus carnosus

<400> 575

Met Met Lys Lys Arg Val Gly Glu Tyr Leu Met Asp Cys Leu Ser Asn
 1 5 10 15
 Thr Gly Val Glu Lys Val Phe Gly Val Pro Gly Asp Phe Asn Leu Ala
 20 25 30
 Phe Leu Asp Asp Ile Ile Ser Arg Asp Asp Ile Glu Trp Val Gly Asn
 35 40 45
 Thr Asn Glu Leu Asn Ala Ser Tyr Ala Ala Asp Gly Tyr Ala Arg Met
 50 55 60

Lys Gly Ile Ser Ala Met Val Thr Thr Phe Gly Val Gly Glu Leu Ser

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

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

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

 245 250 255
 Tyr Asp Gly Ser Ile Ala Glu Glu Asn Ile Arg Asp Tyr Val Asp Asn
 260 265 270
 Ser Asp Ala Ile Leu Asn Ile Gly Ala Lys Leu Thr Asp Ser Ala Thr
 275 280 285
 Ala Gly Phe Ser Phe Glu Phe Asp Ile Asp Asp Val Val Met Leu Asn
 290 295 300
 Gln His Asn Phe Lys Met Asn Glu Thr Val Ala Glu Asp Val Thr Leu

 305 310 315 320

Pro Asp Leu Met Asp Gly Leu Met Glu Met Asp Tyr Val Asn Glu Ala
325 330 335

Asp Tyr Pro Lys Phe Lys Arg Pro Glu Thr Gly Gln Tyr Glu Leu Asn
340 345 350

Gly Asp Ala Leu Thr Gln Glu Thr Tyr Phe Lys Met Met Gln Asp Phe
355 360 365

Leu Ala Pro Ser Asp Val Ile Leu Ala Glu Gln Gly Thr Ser Phe Phe
370 375 380

Gly Ala Tyr Asp Leu Ala Leu Tyr Lys Gly Asn Lys Phe Val Gly Gln
385 390 395 400

Pro Leu Trp Gly Ser Ile Gly Tyr Thr Leu Pro Ala Thr Ile Gly Thr
405 410 415

Gln Ile Ala Asp Pro Lys Arg Arg Asn Leu Leu Leu Ile Gly Asp Gly
420 425 430

Ser Leu Gln Leu Thr Val Gln Gly Ile Ser Thr Met Ile Arg Gln Gly
435 440 445

Leu Lys Pro Val Leu Phe Val Ile Asn Asn Asp Gly Tyr Thr Val Glu
450 455 460

Arg Lys Ile His Gly Glu Asn Glu Pro Tyr Asn Asp Ile Phe Met Trp
465 470 475 480

Asp Tyr Lys Ala Leu Pro Ala Val Phe Gly Gly Glu Asp Val Val Lys
485 490 495

Val Arg Asp Val Ser Thr Ser Glu Glu Leu Asp Gln Ala Phe Glu Ala
500 505 510

Ile Lys Ala Tyr Pro Asp Met Met His Phe Val Glu Val Lys Met Ala
515 520 525

Met His Asp Ala Pro His Lys Leu Asp Ala Ile Gly Lys Ala Phe Ala
530 535 540

Lys Gln Asn Ser
545

<210> 576

<211> 550

<212> PRT

<213> *Citrobacter youngae*

<400> 576

Met Gln Thr Pro Tyr Ser Val Ala Asp Tyr Leu Leu Asp Arg Leu Ala

1 5 10 15
Asp Cys Gly Val Asp His Leu Phe Gly Val Pro Gly Asp Tyr Asn Leu

20 25 30
Gln Phe Leu Asp His Val Ile Glu His Pro Ser Val Arg Trp Val Gly

35 40 45
Cys Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg

50 55 60
Val Ala Gly Ala Gly Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu

65 70 75 80
Ser Ala Ile Asn Gly Ile Ala Gly Ser Tyr Ala Glu Tyr Val Pro Val

85 90 95
Leu His Ile Val Gly Ala Pro Cys Cys Gly Ala Gln Arg Arg Gly Glu

100 105 110
Leu Met His His Thr Leu Gly Asp Gly Asp Phe Gln His Phe Tyr Arg

115 120 125
Met Gln Gln Ala Val Thr Thr Ala Ser Ala Val Leu Asp Glu Gln Asn

130 135 140
Ala Cys Tyr Glu Ile Asp Arg Val Leu Arg Ala Met Leu Thr Glu Arg

145 150 155 160
Arg Pro Gly Tyr Leu Met Leu Pro Ala Asp Val Ala Lys Gln Pro Ala

165 170 175
Thr Pro Pro Asn Asp Pro Leu Ile Val Ser Gln Ser Glu Pro Ala Ser

180 185 190
Ser Val Ala Ala Ala Phe Arg Tyr His Ala Arg Glu Arg Leu Leu Asp

195 200 205
Ser Pro Arg Val Ala Leu Leu Ala Asp Phe Leu Ala Leu Arg Phe Gly

210 215 220

Leu Gln Pro Val Leu Gln Arg Trp Met Ala Glu Thr Pro Met Ala His
 225 230 235 240
 Ala Thr Leu Leu Met Gly Lys Gly Leu Phe Asp Glu Arg His Pro Ala
 245 250 255
 Phe Val Gly Thr Tyr Ser Ala Gly Ala Ser Ser Asp Tyr Val Arg Gln
 260 265 270
 Ala Ile Glu Glu Ala Asp Thr Ile Met Cys Val Gly Thr Gln Phe Val
 275 280 285
 Asp Thr Leu Thr Ala Gly Phe Thr Gln Arg Leu Pro Pro Glu Arg Thr
 290 295 300
 Ile Glu Val Gln Pro His Ala Ser Arg Val Gly Ser Gln Trp Phe Asn
 305 310 315 320
 Val Pro Met Glu Gln Ala Val Thr Thr Leu Arg Glu Leu Cys Leu Glu
 325 330 335
 Met Ser Phe Ser Leu Pro Pro Glu Arg Pro Pro Val Glu Arg Ile Gln
 340 345 350
 Ile Glu Lys Gly Leu Leu Thr Gln Glu Asn Phe Trp His Thr Val Gln
 355 360 365
 His Tyr Leu Ala Pro Asp Asp Ile Ile Leu Val Asp Gln Gly Thr Ala
 370 375 380
 Ala Phe Gly Ala Ala Ala Leu Ser Leu Pro Ser Gly Ala Glu Val Leu
 385 390 395 400
 Val Gln Pro Leu Trp Gly Ser Ile Gly Tyr Thr Leu Pro Ala Ala Phe
 405 410 415
 Gly Ala Gln Thr Ala Cys Pro Asp Arg Arg Val Ile Leu Ile Ile Gly
 420 425 430
 Asp Gly Ala Ala Gln Leu Thr Ile Gln Glu Leu Gly Ser Met Leu Arg
 435 440 445
 Asp Gly Gln Ser Pro Val Ile Leu Leu Leu Asn Asn Asp Gly Tyr Thr
 450 455 460
 Val Glu Arg Ala Ile His Gly Ala Asn Gln Arg Tyr Asn Asp Ile Ala

465 470 475 480
 Gly Trp Asn Trp Thr Gln Val Pro Gln Ala Leu Ser Arg Glu Cys Gln
 485 490 495
 Ala Glu Cys Trp Arg Val Lys Gln Ala Val Gln Leu Glu Glu Val Leu
 500 505 510
 Ala Arg Leu Ser His Pro Gln Arg Leu Ser Leu Ile Glu Val Val Leu

 515 520 525
 Pro Lys Ala Asp Leu Pro Glu Leu Leu Arg Thr Val Thr Arg Ala Leu
 530 535 540
 Glu Ser Arg Asn Gly Gly
 545 550
 <210> 577
 <211> 554
 <212> PRT
 <213> Providencia rettgeri
 <400> 577
 Met Glu Ile Ser Met Met Asn Lys Thr Val Ile Glu Tyr Val Leu Asp
 1 5 10 15
 Arg Leu Tyr Gln Ile Gly Ile His Asp Ile Phe Gly Val Ala Gly Asp

 20 25 30
 Tyr Ala Phe Pro Ile Glu Asp Ala Val Cys Glu Ser Glu Lys Met Arg
 35 40 45
 Trp Ile Gly Asn Cys Asn Glu Leu Asn Ala Ser Tyr Ala Ala Asp Gly
 50 55 60
 Tyr Ala Arg Val Lys Gly Val Ala Ala Leu Ser Thr Thr Phe Gly Val
 65 70 75 80
 Gly Glu Leu Ser Ala Leu Asn Gly Ile Ala Gly Ala Tyr Ala Glu His

 85 90 95
 Leu Pro Ile Phe His Leu Val Gly Met Pro Ala Ser Gly Val Gln Lys
 100 105 110
 Asn His Arg Leu Val His His Thr Leu Gly Asn Gly Asp Phe Asp Val
 115 120 125

Phe Tyr Gln Met Ser Gln His Leu Ser Cys Ala His Ala Ile Leu Thr
 130 135 140
 Pro Glu Asn Cys Ile Ala Glu Thr Glu Arg Leu Ile Thr Thr Ala Leu

 145 150 155 160
 Gln Glu Ser Arg Pro Val Tyr Leu Gly Phe Pro Ser Asp Tyr Ala Val
 165 170 175
 Met Pro Ile Lys Ala Asp Lys Thr Ser Glu Thr Ile Thr Ile Asn Lys
 180 185 190
 Ser His Ser Glu Ser Leu Ser Ala Ala Val Thr Ala Ile Val Glu Lys
 195 200 205
 Leu Thr Ser Ser Thr Lys Ala Cys Ile Ile Pro Gly Ile Leu Thr Ala

 210 215 220
 Arg Phe Gly Leu Thr Thr Asp Val Glu Ala Ile Ile Gln Lys Thr Gly
 225 230 235 240
 Leu Pro Tyr Ala Thr Met Phe Met Asp Lys Gly Val Leu Ser Glu Ser
 245 250 255
 Asn Ser Arg Tyr Met Gly Ile Tyr Asn Gly Lys Leu Met Asn Pro Glu
 260 265 270
 Val Arg Glu Phe Val Glu Ser Cys Asp Cys Val Met Gly Ile Gly Ala

 275 280 285
 Val Leu Thr Asp Phe Asn Ser Gly Ser Phe Thr Ala Ala Ile Ala Pro
 290 295 300
 Glu Ser Cys Ile Asn Ile Leu Ser Asp His Val Lys Val Gly Ser Ala
 305 310 315 320
 Ile Tyr Pro Asn Val Leu Met Lys Asp Val Leu His Lys Leu Lys Glu
 325 330 335
 Leu Val Pro Ser Leu Asn His Val Gly Ile Lys Ala Gln Asp Leu Gly

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

370 375 380
 Thr Gly Thr Ala Ser Met Gly Leu Gly Phe Ala Leu Leu Pro Glu Asn
 385 390 395 400
 Ala Gln Phe His Asn Gln Thr Leu Trp Gly Ser Ile Gly Trp Ala Thr

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

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

 530 535 540
 Gly Lys Ser Val Ala Ser Leu Tyr Ser Phe
 545 550
 <210> 578
 <211> 547
 <212> PRT
 <213> Edwardsiella tarda
 <400> 578
 Met Thr Ser Val Ile Glu Tyr Val Leu Ser Arg Leu Tyr Asp Leu Gly
 1 5 10 15
 Ile Arg Asp Ile Phe Gly Val Pro Gly Asp Tyr Ala Phe Pro Ile Glu
 20 25 30

Asp Ala Val Cys Ala Asp Pro Arg Leu Arg Trp Ile Gly Asn Cys Asn

35

40

45

Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Leu His Gly

50

55

60

Leu Ala Ala Leu Ser Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Leu

65

70

75

80

Asn Gly Ile Ala Gly Ala Tyr Ala Glu Ser Leu Pro Leu Phe His Leu

85

90

95

Val Gly Met Pro Ala Ser Gly Val Gln Ala Ala Gly Lys Leu Val His

100

105

110

His Thr Leu Gly Asp Gly Asn Phe Thr His Phe Ala Gln Ala Ser Ala

115

120

125

Ala Val Val Cys Ala His Thr Ile Leu Thr Pro Glu Asn Cys Val Ala

130

135

140

Glu Met Glu Arg Leu Ile Asp Ala Ala Leu Arg Tyr Arg Lys Pro Val

145

150

155

160

Tyr Ile Gly Ile Pro Ser Asp Tyr Ala Val Met Pro Phe Ser Ala Thr

165

170

175

Thr Thr Pro Ser Thr Pro Leu Arg Ser Asp Pro Gln Thr Leu Ala Glu

180

185

190

Val Ser Ala Gln Ile Val Glu Arg Leu Gln Gln Ser Gln Gln Ala Cys

195

200

205

Ala Leu Pro Gly Ile Tyr Leu Thr Arg His Gln Val Arg Gln Glu Ala

210

215

220

Gln Ala Leu Ile Glu Ala Ala Asp Leu Cys Phe Ala Thr Met Val Met

225

230

235

240

Asp Lys Ser Val Leu Asp Glu Ser His Pro Asn Tyr Ile Gly Met Tyr

245

250

255

Asn Gly His Leu Leu Asn Pro Glu Val Arg Asp Phe Val Glu Arg Cys

260

265

270

Asp Cys Val Leu Leu Met Gly Thr Leu Leu Ser Asp Phe Asn Thr Gly

275 280 285
Gly Phe Thr Ala Arg Leu Asp Pro Ser His Cys Ile Thr Leu Leu Pro

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

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

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

485 490 495
Arg Val Ser Thr Cys Glu Ala Leu Asp Glu Ala Ile Arg His Ala Glu
500 505 510
His Cys Asp Ser Ala Ala Tyr Ile Glu Val Ile Thr Gly Glu Tyr Val
515 520 525

Ala Ser Pro Leu Ala Glu Lys Met His Gln Ala Met Ala Ser Leu Tyr
530 535 540

His Ala Asp
545

<210> 579

<211>
548

<212> PRT

<213> *Listeria grayi*

<400> 579

Met Tyr Thr Val Gly Gln Tyr Leu Val Asp Arg Leu Glu Glu Ile Gly
1 5 10 15

Ile Asp Lys Val Phe Gly Val Pro Gly Asp Tyr Asn Leu Thr Phe Leu
20 25 30

Asp Tyr Ile Gln Asn His Glu Gly Leu Ser Trp Gln Gly Asn Thr Asn
35 40 45

Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Glu Arg Gly
50 55 60

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

Asn Gly Thr Ala Gly Ser Phe Ala Glu Gln Val Pro Val Ile His Ile
85 90 95

Val Gly Ser Pro Thr Met Asn Val Gln Ser Asn Lys Lys Leu Val His
100 105 110

His Ser Leu Gly Met Gly Asn Phe His Asn Phe Ser Glu Met Ala Lys
115 120 125

Glu Val Thr Ala Ala Thr Thr Met Leu Thr Glu Glu Asn Ala Ala Ser
130 135 140

Glu Ile Asp Arg Val Leu Glu Thr Ala Leu Leu Glu Lys Arg Pro Val
145 150 155 160

Tyr Ile Asn Leu Pro Ile Asp Ile Ala His Lys Ala Ile Val Lys Pro
165 170 175

Ala Lys Ala Leu Gln Thr Glu Lys Ser Ser Gly Glu Arg Glu Ala Gln

180 185 190

Leu Ala Glu Ile Ile Leu Ser His Leu Glu Lys Ala Ala Gln Pro Ile

195 200 205

Val Ile Ala Gly His Glu Ile Ala Arg Phe Gln Ile Arg Glu Arg Phe

210 215 220

Glu Asn Trp Ile Asn Gln Thr Lys Leu Pro Val Thr Asn Leu Ala Tyr

225 230 235 240

Gly Lys Gly Ser Phe Asn Glu Glu Asn Glu His Phe Ile Gly Thr Tyr

245 250 255

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

260 265 270

Asp Phe Val Leu His Phe Gly Gly Lys Ile Ile Asp Asn Ser Thr Ser

275 280 285

Ser Phe Ser Gln Gly Phe Lys Thr Glu Asn Thr Leu Thr Ala Ala Asn

290 295 300

Asp Ile Ile Met Leu Pro Asp Gly Ser Thr Tyr Ser Gly Ile Ser Leu

305 310 315 320

Asn Gly Leu Leu Ala Glu Leu Glu Lys Leu Asn Phe Thr Phe Ala Asp

325 330 335

Thr Ala Ala Lys Gln Ala Glu Leu Ala Val Phe Glu Pro Gln Ala Glu

340 345 350

Thr Pro Leu Lys Gln Asp Arg Phe His Gln Ala Val Met Asn Phe Leu

355 360 365

Gln Ala Asp Asp Val Leu Val Thr Glu Gln Gly Thr Ser Ser Phe Gly

370 375 380

Leu Met Leu Ala Pro Leu Lys Lys Gly Met Asn Leu Ile Ser Gln Thr

385 390 395 400

Leu Trp Gly Ser Ile Gly Tyr Thr Leu Pro Ala Met Ile Gly Ser Gln

405 410 415

Ile Ala Ala Pro Glu Arg Arg His Ile Leu Ser Ile Gly Asp Gly Ser

420 425 430
Phe Gln Leu Thr Ala Gln Glu Met Ser Thr Ile Phe Arg Glu Lys Leu

435 440 445
Thr Pro Val Ile Phe Ile Ile Asn Asn Asp Gly Tyr Thr Val Glu Arg

450 455 460

Ala Ile His Gly Glu Asp Glu Ser Tyr Asn Asp Ile Pro Thr Trp Asn

465 470 475 480

Leu Gln Leu Val Ala Glu Thr Phe Gly Gly Asp Ala Glu Thr Val Asp

485 490 495

Thr His Asn Val Phe Thr Glu Thr Asp Phe Ala Asn Thr Leu Ala Ala

500 505 510

Ile Asp Ala Thr Pro Gln Lys Ala His Val Val Glu Val His Met Glu

515 520 525

Gln Met Asp Met Pro Glu Ser Leu Arg Gln Ile Gly Leu Ala Leu Ser

530 535 540

Lys Gln Asn Ser

545

<210> 580

<211> 553

<212> PRT

<213> Unknown

<220><223> Psychrobacter sp. 1501(2011)

<400> 580

Met Ser Glu His Ala Tyr Thr Ile Ala Asp Tyr Leu Phe Asp Arg Val

1 5 10 15

Ala Glu Ala Gly Ala Thr Glu Val Phe Gly Val Pro Gly Asp Tyr Asn

20 25 30

Leu Ser Phe Leu Asp Asn Ile Ile Ala Ser Asp Lys Leu Arg Trp Val

35 40 45

Gly Asn Thr Asn Glu Leu Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Ala

50 55 60

Arg Glu Arg Arg Phe Ala Ala Met Val Thr Thr Phe Gly Val Gly Glu

65 70 75 80

Leu Ser Ala Ile Asn Ala Thr Ala Gly Ser Phe Ala Glu Tyr Ala Pro

85 90 95

Val Leu His Ile Val Gly Ala Pro Asp Thr Glu Leu Arg Lys Gly Lys

100 105 110

Arg Arg Leu His His Ser Leu Gly Asp Gly Glu Phe Asn His Phe Ile

115 120 125

Lys Met Ala Glu Pro Val Ser Val Ala Arg Ala Glu Ile Thr Ala Lys

130 135 140

Asn Ala Ala Ser Glu Ile Asp Arg Val Ile Arg Met Val Leu Lys Lys

145 150 155 160

Gln Arg Pro Gly Tyr Leu Leu Leu Ser Pro Asp Ile Ala Lys Leu Pro

165 170 175

Ile Tyr Pro Pro Thr Thr Lys Leu Lys Asp Ser Glu Glu Asp Ile Thr

180 185 190

Ser Gln Met Ala Leu Ala Asp Phe Lys Glu Glu Leu Ala Ala Phe Ile

195 200 205

Gln Gly Lys Ala Thr Thr Leu Ile Ala Asp Leu Met Val His Arg Leu

210 215 220

Gly Leu Gln Ser Gln Leu Lys Ala Leu Ile Ser Asp Thr Lys Ile Pro

225 230 235 240

Tyr Ala Thr Leu Ser Trp Gly Lys Ser Leu Ile Asp Glu Asn Gly Glu

245 250 255

Arg Trp Ala Gly Val Tyr Val Gly Glu Ala Ser Gln Pro Val Val Lys

260 265 270

Asp Ala Val Glu Asn Ala Glu Cys Leu Ile Lys Leu Gly Val Asn Tyr

275 280 285

Thr Asp Thr Thr Thr Ala Gly Phe Thr Gln Asn Ile Glu Arg Ser Arg

290 295 300

Val Val Asp Ile His Gln Glu Arg Ala Thr Val Gly Asp Lys Phe Phe

305 310 315 320
 Ala Pro Ile Ala Met Lys Asp Ala Leu Gln Ala Leu His Glu Val Leu

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

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

 450 455 460
 Asn Asn Ser Gly Tyr Thr Val Glu Arg Ala Ile His Gly Glu Lys Gln
 465 470 475 480
 Pro Tyr Asn Asp Ile Pro Met Cys Asp Trp Gln Leu Met Pro Lys Ala
 485 490 495
 Phe Gly Ala Asn Glu Gly Asn Cys Val Thr Leu Lys Val Asn Thr Pro
 500 505 510
 Val Glu Leu Lys Ser Ala Leu Glu Gln Ala Lys Asn Thr Pro Asp Lys

 515 520 525
 Met Val Phe Ile Glu Val Val Thr Glu Val Met Asp Ile Pro Ser Leu
 530 535 540
 Leu Lys Gln Val Ala Ala Ala Leu Gln
 545 550

<210> 581

<211> 557

<212> PRT

<213> *Hafnia alvei*

<400> 581

Met Ser Lys Thr Leu Asn Ser Asn Ile Tyr Ser Val Ser Asp Tyr Leu

1 5 10 15

Leu Asp Arg Leu Ser Gln Ala Gly Ile Gln His Val Phe Gly Val Pro

20 25 30

Gly Asp Tyr Asn Leu Arg Phe Leu Asp Phe Val Thr Ala His Pro Gln

35 40 45

Leu Glu Trp Val Gly Cys Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala

50 55 60

Asp Gly Tyr Ala Arg Cys Ala Pro Ala Ala Ala Leu Val Thr Thr Phe

65 70 75 80

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

85 90 95

Glu Tyr Leu Pro Val Ile His Ile Val Gly Ala Pro Asn Arg Arg Ser

100 105 110

Gln Gln Lys Gly Glu Leu Leu His His Thr Leu Gly Asp Gly Asp Tyr

115 120 125

Gly His Phe Tyr Arg Met Ala Ala Glu Val Thr Cys Ser Gln Ala Val

130 135 140

Leu Thr Pro Glu Asn Ala Ala Leu Glu Ile Asp Arg Val Leu Ser Asp

145 150 155 160

Val Leu Tyr His Arg Arg Pro Gly Tyr Ile Leu Leu Pro Ser Asp Val

165 170 175

Cys Asp Glu Pro Ile Arg Thr Glu Leu Tyr Pro Phe Ala Ala Arg Gln

180 185 190

Asp Glu Val Thr Gly Leu Ser Glu Phe Ile Gln Ala Ala Arg Glu Leu

195 200 205

Leu Lys Pro Ala Arg Lys Val Ala Leu Leu Ala Asp Phe Leu Ala Asp

210 215 220

Arg Phe Gly Gln Lys Gln Gln Val Gln Gln Leu Ser Asp Leu Gln Gly

225 230 235 240

Val Ala Ser Ala Thr Leu Leu Met Gly Lys Gly Val Leu Asp Glu Ser

245 250 255

Arg Pro Asn Phe Ile Gly Thr Tyr Ala Gly Gly Ala Ser Gln Pro Lys

260 265 270

Val Lys Ala Ala Met Glu Asn Ala Asp Val Leu Ile Ser Val Gly Val

275 280 285

Arg Leu Thr Asp Ser Val Thr Ala Gly Phe Thr His Gln Ile Ala Ala

290 295 300

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

305 310 315 320

Val Phe Ser Gln Leu Pro Met Gly Asp Ala Leu Ala Ala Leu Thr Glu

325 330 335

Leu Ala Lys Glu Leu Ser Val Glu Trp Gln Ala Pro Glu Ser Leu Arg

340 345 350

Asp Cys Leu Pro Glu Ser His Gly Asn Lys Leu Asp Gln Pro Ala Phe

355 360 365

Trp Gln Gln Met Gln Arg Phe Leu Arg Pro Asp Asp Ile Val Val Ala

370 375 380

Glu Gln Gly Thr Ala Ser Phe Gly Ser Ala Thr Leu Arg Leu Pro Lys

385 390 395 400

Gly Val Thr Phe Ile Val Gln Pro Leu Trp Gly Ser Ile Gly Tyr Thr

405 410 415

Leu Pro Ala Ile Leu Gly Ala Gln Leu Ala Gln Pro His Arg Arg Val

420 425 430

Val Leu Ile Ile Gly Asp Gly Ser Ala Gln Leu Thr Ile Gln Glu Leu

435 440 445

Gly Thr Leu Leu Arg His Gly Leu Lys Pro Val Ile Ile Leu Leu Asn

450 455 460
Asn Asp Gly Tyr Thr Val Glu Arg Ala Ile His Gly Pro Glu Glu Ser

465 470 475 480
Tyr Asn Asp Ile Ala Ala Trp Asn Trp Thr Lys Ile Pro Ser Ala Leu

485 490 495
Ser Val Asn Gly Asp Phe Ser Thr Tyr Lys Ala Asp Ser Val Pro Ala

500 505 510
Leu Glu Lys Val Leu Ser Glu Val Asn Val Pro Lys Ala Leu Thr Leu

515 520 525
Ile Glu Val Met Leu Pro Lys Met Asp Val Pro Glu Tyr Leu Ala Lys

530 535 540
Leu Ser Lys Ala Ile Ala Glu Arg Asn Ala Ala His Glu

545 550 555

<210> 582

<211> 560

<212> PRT

<213> Rhizopus delemar

<400> 582

Met Pro Ser Ile Gln Ile Gly Gln His Leu Leu Asn Arg Leu Lys Glu

1 5 10 15

Ile Asn Ile Asp Val Val Phe Gly Val Pro Gly Asp Phe Asn Met Pro

20 25 30

Leu Leu Asp Ile Ile Glu Asp Asp Pro Lys Leu Thr Trp Gly Asn Asn

35 40 45

Ala Asn Glu Leu Asn Ala Ser Tyr Ala Ala Asp Gly Tyr Ala Arg Ile

50 55 60

Arg Gly Ala Gly Ala Val Val Thr Thr Phe Gly Val Gly Glu Leu Ser

65 70 75 80

Ala Val Asn Gly Val Ala Gly Ser Tyr Ala Glu Met Leu Pro Val Ile

85 90 95

His Ile Val Gly Thr Pro Ser Thr Lys Ser Gln Ala Ala Gly Ala Met

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

Thr Gly Tyr Ile Gly Ile Pro Ile Asp Leu Ile Lys Thr Glu Val Glu
 165 170 175
 Ile Pro Glu Glu Leu Ser Pro Leu Gln Thr Thr Leu Pro Lys Asn Asn
 180 185 190
 Pro Glu Val Gln Ala Ile Ala Leu Lys Val Val Thr Glu Ala Ile Gln
 195 200 205
 Ser Ala Lys His Pro Val Ile Ile Val Asp Gly Cys Val Leu Arg His
 210 215 220

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

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

Pro Ile Gln Pro Gly Thr Glu Ile Thr His Asn Tyr Phe Trp His Lys
355 360 365

Val Pro Glu Tyr Met Glu Glu Asn Ala Ile Val Cys Ala Glu Thr Gly
370 375 380

Thr Ala Glu Phe Ala Ser Leu Asn Met Asp Gly Pro Lys Gly Thr Thr
385 390 395 400

Tyr Ile Thr Gln Ile Leu Trp Gly Ser Ile Gly Phe Thr Val Gly Ala
405 410 415

Ser Val Gly Ala Ala Ile Ala Ala Arg Asp Arg Arg Val Tyr Leu Phe
420 425 430

Val Gly Asp Gly Ser Phe Gln Leu Thr Cys Gln Glu Ile Ala Val Phe
435 440 445

Leu Arg His Gly Leu Thr Pro Val Ile Phe Leu Leu Asn Asn Asp Gly
450 455 460

Tyr Leu Ile Glu Lys Leu Ile His Gly Pro Asp Arg Ala Tyr Asn Asn
465 470 475 480

Tyr Gln Met Trp Asn Tyr His Lys Thr Leu Asp Tyr Phe Gly Ala His
485 490 495

Leu Glu His Asn Lys Ser Met Gly Val Pro Pro Val Gly Phe Glu Gly
500 505 510

Lys Val Ala Thr Arg Asp Glu Phe Glu Ser Ala Met Lys Gln Val Gln
515 520 525

Ala Asn Pro Asn Lys Ile His Phe Leu Glu Val Ile Met Pro Gln Phe
530 535 540

Asp Ala Pro Arg Glu Leu Glu Leu Leu Val Ala Asn Ser Glu Asn Arg
545 550 555 560

<210> 583

<211> 550

<212> PRT

<213> Unknown

<220><223> Pantoea sp. GM01

<400> 583

Met Lys Thr Leu Asn Val Gly Glu Tyr Leu Leu His Arg Leu His Gln
1 5 10 15
Ser Gly Ile Arg His Leu Phe Gly Val Pro Gly Asp Tyr Asn Leu Gln
20 25 30
Phe Leu Asp Ser Val Ile Ala His Pro Glu Ile Ala Trp Val Gly Cys
35 40 45
Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Gly Arg Cys
50 55 60
Asn Gly Ala Ala Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu Ser
65 70 75 80
Ala Ile Asn Gly Ile Ala Gly Ser Tyr Ala Glu Tyr Val Pro Val Ile
85 90 95
His Ile Val Gly Ala Pro Ala Ser Lys Val Gln Gln Gln Gly Asp Cys
100 105 110
Val His His Ser Leu Gly Asp Gly Asp Phe Gly His Phe Leu Arg Met
115 120 125
Ala Gln Glu Val Ser Ala Ala Ser Ala Val Leu Thr Ala Asp Asn Ala
130 135 140
Val Ala Glu Ile Asp Arg Val Ile Asp Glu Ala Leu Gln Gln His Arg
145 150 155 160
Pro Gly Tyr Leu Leu Leu Ala Val Asp Val Ala Ala Ala Glu Val Thr
165 170 175
Met Pro Ala Val Lys Ser Asp Ala Gln Pro Ser His His Gln Ile Ala
180 185 190
Ala Ala Phe Ala Asp Ala Ala Glu Arg Leu Leu Ala Pro Ala Gln Arg
195 200 205
Val Ala Leu Leu Ala Asp Phe Leu Ala Ser Arg Trp Gln Leu Gln Pro
210 215 220
Gln Leu Glu Thr Leu Arg Gln Leu Arg Ala Ile Pro Ala Ala Thr Leu
225 230 235 240
Leu Met Gly Lys Gly Val Leu Asn Glu Gln Gln Pro Gly Tyr Val Gly

245 250 255
 Thr Tyr Ala Ala Glu Gly Ser Ser Asp Ala Val Arg Gln Ala Ile Glu
 260 265 270
 Asp Thr Asp Val Thr Leu Cys Val Gly Val Arg Phe Thr Asp Thr Leu
 275 280 285
 Thr Ala Gly Phe Thr Gln Asn Leu Pro Glu Ala Arg Val Ile Asp Leu

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

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

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

 485 490 495

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

<210> 584

<211> 571

<212> PRT

<213> *Yarrowia lipolytica*

<400> 584

Met Ser Asp Ser Glu Pro Gln Met Val Asp Leu Gly Asp Tyr Leu Phe
1 5 10 15
Ala Arg Phe Lys Gln Leu Gly Val Asp Ser Val Phe Gly Val Pro Gly
20 25 30
Asp Phe Asn Leu Thr Leu Leu Asp His Val Tyr Asn Val Asp Met Arg
35 40 45
Trp Val Gly Asn Thr Asn Glu Leu Asn Ala Gly Tyr Ser Ala Asp Gly

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

115 120 125
Phe Ala Gln Met Ser Lys Leu Ile Ser Glu Tyr Thr His His Ile Glu
130 135 140
Asp Pro Ser Glu Ala Ala Asp Val Ile Asp Thr Ala Ile Arg Ile Ala

145 150 155 160
 Tyr Thr His Gln Arg Pro Val Tyr Ile Ala Val Pro Ser Asn Phe Ser
 165 170 175
 Glu Val Asp Ile Ala Asp Gln Ala Arg Leu Asp Thr Pro Leu Asp Leu

 180 185 190
 Ser Leu Gln Pro Asn Asp Pro Glu Ser Gln Tyr Glu Val Ile Glu Glu
 195 200 205
 Ile Cys Ser Arg Ile Lys Ala Ala Lys Lys Pro Val Ile Leu Val Asp
 210 215 220
 Ala Cys Ala Ser Arg Tyr Arg Cys Val Asp Glu Thr Lys Glu Leu Ala
 225 230 235 240
 Lys Ile Thr Asn Phe Ala Tyr Phe Val Thr Pro Met Gly Lys Gly Ser

 245 250 255
 Val Asp Glu Asp Thr Asp Arg Tyr Gly Gly Thr Tyr Val Gly Ser Leu
 260 265 270
 Thr Ala Pro Ala Thr Ala Glu Val Val Glu Thr Ala Asp Leu Ile Ile
 275 280 285
 Ser Val Gly Ala Leu Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr
 290 295 300
 Ser Tyr Ser Thr Lys Asn Val Val Glu Leu His Ser Asp His Val Lys

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

 370 375 380
 Ser Tyr Phe Leu Arg Pro Thr Asp Ile Val Val Thr Glu Thr Gly Thr
 385 390 395 400

Ser Ser Phe Gly Ile Ile Gln Thr Lys Phe Pro His Asn Val Arg Gly
405 410 415
Ile Ser Gln Val Leu Trp Gly Ser Ile Gly Tyr Ser Val Gly Ala Ala
420 425 430
Cys Gly Ala Ser Ile Ala Ala Gln Glu Ile Asp Pro Gln Gln Arg Val
435 440 445
Ile Leu Phe Val Gly Asp Gly Ser Leu Gln Leu Thr Val Thr Glu Ile
450 455 460
Ser Cys Met Ile Arg Asn Asn Val Lys Pro Tyr Ile Phe Val Leu Asn
465 470 475 480
Asn Asp Gly Tyr Thr Ile Glu Arg Leu Ile His Gly Glu Asn Ala Ser
485 490 495
Tyr Asn Asp Val His Met Trp Lys Tyr Ser Lys Ile Leu Asp Thr Phe
500 505 510
Asn Ala Lys Ala His Glu Ser Ile Val Val Asn Thr Lys Gly Glu Met
515 520 525
Asp Ala Leu Phe Asp Asn Glu Glu Phe Ala Lys Pro Asp Lys Ile Arg
530 535 540
Leu Ile Glu Val Met Cys Asp Lys Met Asp Ala Pro Ala Ser Leu Ile
545 550 555 560
Lys Gln Ala Glu Leu Ser Ala Lys Thr Asn Val
565 570

<210> 585

<211> 574

<212> PRT

<213> Unknown

<220><223> Acinetobacter sp. CAG:196

<400> 585

Met Asn Thr Ala Glu Tyr Leu Val Lys Lys Leu Glu Glu Leu Gly Val
1 5 10 15
Asn Glu Phe Phe Gly Leu Pro Gly Asp Tyr Asn Phe Asn Leu Leu Tyr
20 25 30

Ala Val Glu Asn Asn Pro Asn Thr Cys Trp Ile Gly Cys Thr Asn Glu
35 40 45
Leu Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Ala Arg Met Arg Gly Tyr
50 55 60
Gly Ala Leu Ile Thr Thr Tyr Gly Val Gly Glu Leu Ser Ala Met Asn
65 70 75 80
Ala Ile Ala Gly Ser Leu Ala Glu Asn Val Pro Val Ile Ser Ile Val
85 90 95
Gly Val Pro Ala Thr Lys Thr Ile Glu Asn Lys Thr Cys Val His His
100 105 110
Asn Phe Gln Asp Val Asp Tyr His Ala Cys Tyr Glu Ala His Lys His
115 120 125
Val Thr Ala Ala Ala Ala Phe Leu Thr Arg Asp Asn Ala Lys Met Glu
130 135 140
Ile Asp Arg Val Leu Lys Thr Phe Val Lys Glu Arg Lys Pro Val Tyr
145 150 155 160
Ile Ala Val Pro Leu Asp Ile Ala Lys Met Glu Ile Ser Asp Lys Glu
165 170 175
Val Ser Tyr Asp Trp Ile Ser Asp Glu Glu Thr Leu Arg Leu Val Ser
180 185 190
Asn Lys Ile Ala Ala Lys Ile Asn Asn Ala Gln Lys Pro Val Ile Leu
195 200 205
Gly Asp Leu Leu Val Lys Arg Phe Asp Ser Arg Ile Glu Tyr Lys Glu
210 215 220
Phe Val Glu Lys Thr Arg Ile Pro Thr Thr Asn Phe Leu Met Gly Thr
225 230 235 240
Asn Leu Ile Asp Met Asp Tyr Asp Leu Tyr Leu Gly Gly Tyr Tyr Ala
245 250 255
Gly Phe Glu Asn Pro Thr Ala Glu Lys Tyr Val Asn Glu Thr Asp Cys
260 265 270
Leu Ile Ala Val Gly Pro Val Tyr Thr Asp Leu Asn Ala Phe Gly Phe

275 280 285
 Asn Leu Pro Tyr Lys Ile Asn Asn Gln Ile Ala Ile Tyr Gly Thr His
 290 295 300
 Thr Tyr Val Glu Gly Glu Lys Tyr Asp Asn Val Lys Met Ser Asp Val

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

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

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

 500 505 510
 Lys Met Cys Tyr Ile Glu Ile Cys Thr Glu Ala Met Asp Met Pro Lys
 515 520 525

Leu Thr Gln Asp Leu Ile Ala Asn Leu Lys Ser Lys Ala Pro Lys Ile
530 535 540

Glu Ala Val Lys Lys Glu Glu Pro Val Lys Leu Glu Asn Ser Gly Ser
545 550 555 560

Met Ala Phe Glu Thr Thr Val His Lys Gly Phe Thr Glu Glu

565 570

<210> 586

<211> 548

<212> PRT

<213> Plesiomonas shigelloides

<400> 586

Met Ala Lys Thr Val Ile Gln His Val Leu Ser Arg Leu Tyr Asp Leu
1 5 10 15

Gly Ile Ser Asp Ile Phe Gly Val Pro Gly Asp Tyr Ala Phe Pro Ile
20 25 30

Glu Asp Ala Val Cys Asp Asp Asn Arg Leu Arg Trp Ile Gly Asn Cys
35 40 45

Asn Glu Leu Asn Ala Ala Tyr Ser Ala Asp Gly Tyr Ala Arg Ile His
50 55 60

Gly Met Ala Ala Leu Ser Thr Thr Phe Gly Val Gly Glu Leu Ser Ala
65 70 75 80

Ile Ser Gly Ile Ala Gly Ala Phe Ala Glu Ser Leu Pro Ile Phe His
85 90 95

Leu Val Gly Met Pro Ala Ser Ser Val Gln Ala Gln Gly Gly Leu Val
100 105 110

His His Thr Leu Gly Asp Gly His Phe Thr Thr Phe Tyr Glu Ala Thr
115 120 125

Ala Pro Phe Val Cys Ala Arg Ala Ile Met Thr Pro Glu Asn Cys Val
130 135 140

Ala Glu Thr Glu Arg Leu Ile Ala Ala Ala Leu Arg Tyr Arg Lys Pro
145 150 155 160

Val Tyr Met Val Phe Pro Ser Asp Tyr Ala Thr Met Pro Ile Val Glu

165	170	175
Met Ala Val Pro Ala Thr Val Thr Glu Ser Ser Asp Pro Val Val Leu		
180	185	190
Thr Glu Val Val Asp Ile Leu Ala Asp Arg Leu Asn Asn Ser Gln Gln		
195	200	205
Ala Cys Val Leu Pro Gly Ile Tyr Leu Ala Arg His Gly Val Arg Gln		
210	215	220
Glu Thr Leu Ser Leu Ile Glu Ala Ala Asn Leu Pro Phe Ala Thr Met		
225	230	235
		240
Met Met Asp Lys Ser Val Leu Asp Glu Ser His Ser Asn Tyr Ile Gly		
245	250	255
Met Tyr Asn Gly Asn Leu Met Asp Ala Asn Val Arg Asp Phe Val Glu		
260	265	270
Ser Ser Asp Cys Val Leu Arg Ile Gly Ala Ile Met Ser Asp Phe Asn		
275	280	285
Thr Gly Ala Phe Thr Ala Arg Leu Asp Ser Arg Lys Cys Ile Ala Ile		
290	295	300
Met Pro Glu Ser Val Gln Ile Gly Gly Ala Val Tyr Asn Arg Val Leu		
305	310	315
		320
Met Lys Asp Val Leu Glu Ala Val Ala Lys Lys Val Ser Lys Lys Ala		
325	330	335
Phe Pro Ala His Ala Pro Lys Val Thr Ala Leu Pro Val Val Thr Ala		
340	345	350
Ser Gly Lys Ile Thr Ala Glu Tyr Leu Tyr Ser Arg Trp Gln Gln Met		
355	360	365
Leu Lys Pro Asn Asp Ile Leu Met Ala Glu Thr Gly Thr Ser Ser Met		
370	375	380
Gly Leu Gly Phe Ala Arg Met Pro Gln Gly Ser Thr Phe His Asn Gln		
385	390	395
		400
Thr Leu Trp Gly Ala Ile Gly Trp Ala Thr Pro Ala Ala Phe Gly Ala		
405	410	415

Ala Met Ala Ala Pro Glu Gln Arg Thr Val Leu Ile Thr Gly Glu Gly
420 425 430

Ser His Gln Leu Thr Ala Gln Glu Ile Ser Gln Phe Tyr Arg Phe Gly
435 440 445

Leu Lys Pro Leu Ile Phe Val Leu Asn Asn Asp Gly Tyr Leu Ile Glu
450 455 460

Arg Leu Leu Cys Lys Asp Gly Asp Ile Tyr Tyr Asn Asp Leu Ala Gln
465 470 475 480

Trp Lys Tyr Glu Lys Leu Pro Glu Ala Met Gly Cys Glu Asn Trp Phe
485 490 495

Thr Ala Arg Val Thr Thr Cys Glu Glu Leu Asp Ala Ala Ile Arg Gln
500 505 510

Ala Glu Thr Cys Gly Thr Gly Ala Tyr Ile Glu Val Ile Thr Glu Lys
515 520 525

Tyr Ala Ser Ser Glu Leu Ala Glu Lys Leu His Gln Ser Ile Asn Ser
530 535 540

Leu Tyr Ser Ala
545

<210> 587

<211> 553

<212> PRT

<213> *Cedecea davisae*

<400> 587

Met Arg Tyr Cys Val Ala Asp Tyr Leu Val Asp Arg Leu Asn Glu Cys
1 5 10 15

Gly Ile Arg His Leu Phe Gly Val Pro Gly Asp Tyr Asn Leu Val Phe
20 25 30

Leu Asp His Val Ile Ala His Pro Glu Leu Ala Trp Val Gly Cys Ala
35 40 45

Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Cys Lys
50 55 60

Gly Ala Ala Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu Ser Ala
 65 70 75 80
 Leu Asn Gly Val Ala Gly Ser Tyr Ala Glu His Leu Pro Val Ile His
 85 90 95
 Ile Val Gly Ala Pro Asn Ser His Ala Gln Gln Arg Gly Glu Leu Leu
 100 105 110
 His His Thr Leu Gly Asp Gly Asp Phe Arg His Phe Leu Arg Ile Ala
 115 120 125

 Glu Glu Val Ser Val Ala Gln Ala Thr Leu Thr Pro Ala Asn Ala Cys
 130 135 140
 Thr Glu Ile Asp Arg Val Ile Leu Glu Ala Leu Lys Gln Gln Arg Pro
 145 150 155 160
 Gly Tyr Leu Leu Leu Pro Ser Asp Val Ala Glu Ala Pro Ala Thr Arg
 165 170 175
 Pro Thr Lys Arg Leu Asp Val Ala Ala Ala Ala Ala Glu Pro Ala Thr
 180 185 190

 Leu Glu Ala Phe Arg His Cys Ala Gln Ala Lys Ile Ala Glu Ser Arg
 195 200 205
 Ser Ala Ser Leu Leu Ala Asp Phe Leu Ala Leu Arg Tyr Gly Leu Gln
 210 215 220
 Glu Ala Leu Gln Gln Trp Met Asp Gly Thr Pro Met Pro His Ala Ser
 225 230 235 240
 Leu Leu Met Gly Lys Gly Leu Phe Asp Glu Ser Lys Pro Gly Phe Leu
 245 250 255

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

305						310						315						320	
Ser	Met	Ala	Gln	Ala	Val	Asp	Val	Leu	His	Gln	Leu	Cys	Lys	Arg	Gln				
					325							330							335
Ala	Ser	Ala	Trp	Pro	Ala	Ala	Thr	Gln	Arg	Pro	Ser	Glu	Leu	Gln	Pro				
					340							345							350
Gly	Asn	Gly	Asp	Lys	Leu	Asp	Gln	His	Ala	Leu	Trp	His	Thr	Leu	Gln				
					355							360							365
Asn	Ala	Leu	Gln	Pro	Gly	Asp	Ile	Val	Leu	Ala	Asp	Gln	Gly	Thr	Ala				
					370							375							380
Ala	Phe	Gly	Ala	Ala	Ala	Leu	Thr	Leu	Pro	Glu	Gly	Val	Thr	Phe	Ile				
					385							390							395
Ala	Gln	Pro	Leu	Trp	Gly	Ser	Ile	Gly	Tyr	Thr	Leu	Pro	Ala	Ala	Phe				
					405							410							415
Gly	Ala	Gln	Thr	Ala	His	Pro	Asn	Arg	Arg	Val	Leu	Leu	Leu	Ile	Gly				
					420							425							430
Asp	Gly	Ser	Ala	Gln	Leu	Thr	Ile	Gln	Glu	Leu	Gly	Ser	Met	Leu	Arg				
					435							440							445
Asp	Gly	Gln	Lys	Pro	Val	Val	Leu	Leu	Leu	Asn	Asn	Asp	Gly	Tyr	Thr				
					450							455							460
Val	Glu	Arg	Ala	Ile	His	Gly	Pro	Glu	Gln	Arg	Tyr	Asn	Asp	Ile	Ala				
					465							470							475
Ala	Trp	Asp	Trp	Thr	Arg	Leu	Pro	Gln	Ala	Leu	Ser	Val	Asp	Gly	Gln				
					485							490							495
Ala	Glu	Cys	Trp	Arg	Val	Thr	Glu	Thr	Ala	Gln	Leu	Ala	Ala	Val	Met				
					500							505							510
Glu	Lys	Leu	Ala	Ser	Pro	Glu	Arg	Leu	Ala	Leu	Ile	Glu	Ile	Met	Leu				
					515							520							525
Pro	Lys	Gln	Asp	Ile	Pro	Glu	Leu	Leu	Arg	Ala	Val	Thr	Ser	Ser	Leu				
					530							535							540
Gly	Lys	Arg	Asn	Ser	Glu	Met	Glu	His											
					545							550							

<210> 588

<211> 553

<212> PRT

<213> *Chania multitudinisentens*

<400> 588

Met Ser Lys Asn Tyr Thr Val Ala Asp Tyr Leu Leu Asp Arg Leu Ala

1 5 10 15

Gln Ile Gly Ile Arg His Phe Phe Gly Val Pro Gly Asp Tyr Asn Leu

20 25 30

Gln Phe Leu Asp His Val Ile Ala His Gln Gln Ile Thr Trp Val Gly

35 40 45

Cys Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg

50 55 60

Cys Lys Pro Ala Ala Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu

65 70 75 80

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

85 90 95

Ile His Val Val Gly Thr Pro Thr Leu Arg Ala Gln Arg Ala Gly Asp

100 105 110

Leu Leu His His Ser Leu Gly Asp Gly Asp Phe Gly His Phe Ser Arg

115 120 125

Met Ala Lys Glu Val Thr Val Ala Gln Ala Ser Leu Thr Ala Ser Asn

130 135 140

Ala Glu Ala Glu Ile Asp Arg Leu Leu Thr Thr Ala Leu Phe Glu His

145 150 155 160

Arg Pro Val Tyr Leu Leu Leu Pro Ser Asp Val Ala Glu Ala Pro Leu

165 170 175

Ala Ser Arg Pro Ala Pro Leu Met Leu Arg Gln Pro Asn Leu Ser Glu

180 185 190

Ala Ser Leu Gln Gly Phe Ile Ala Ala Ala Arg Glu Lys Leu Gln Ala

195 200 205

Ala Gln Arg Val Ser Leu Leu Ala Asp Phe Leu Ala Glu Arg Phe Gly
210 215 220

Ala Glu Lys Ala Leu Glu Gln Trp Met Asn Glu Val Asn Ile Pro His
225 230 235 240

Ser Thr Leu Leu Leu Gly Lys Ser Val Leu Asp Glu Thr His Ala Cys
245 250 255

Phe Thr Gly Thr Tyr Ala Gly Ala Ala Ser Asp Pro Gln Val Lys Gln
260 265 270

Leu Ile Glu Gly Ala Asp Val Val Ile Asn Val Gly Val Arg Phe Thr
275 280 285

Asp Thr Ile Thr Ala Gly Phe Ser His Gln Leu Pro Tyr Glu Lys Cys
290 295 300

Ile Asp Leu Gln Pro Phe Glu Ala Arg Val Gly Gln Gln Val Phe Ser
305 310 315 320

Gln Ile Pro Met His Asp Ala Ile Lys Ala Leu His Gln Leu Thr Leu
325 330 335

Ser Leu Ala Pro Leu Trp Gln Leu Pro Ala Ile Thr Arg Pro Ser Leu
340 345 350

Pro Glu Pro Asn Gly Ser Gly Leu Asp Gln His Ala Phe Trp Gln Gln
355 360 365

Met Gln Asn Phe Leu Gln Pro Gly Asp Ile Leu Ile Ala Glu Gln Gly
370 375 380

Thr Ser Cys Phe Gly Ala Ala Ala Leu Asn Leu Pro Arg Gly Cys Arg
385 390 395 400

Phe Ile Val Gln Ser Leu Trp Gly Ser Ile Gly Tyr Thr Leu Pro Ala
405 410 415

Ala Phe Gly Val Gln Thr Ala Glu Pro Glu Arg Arg Val Leu Leu Leu
420 425 430

Ile Gly Asp Gly Ala Ala Gln Leu Thr Val Gln Glu Leu Gly Ser Met
435 440 445

Leu Arg Asp Gly Gln Lys Pro Val Val Phe Leu Leu Asn Asn Asn Gly

450	455	460	
Tyr Thr Val Glu Arg Ala Ile His Gly Pro Glu Gln Arg Tyr Asn Asp			
465	470	475	480
Ile Ala Gln Trp Asn Trp Thr Gln Leu Pro Gln Ala Leu Ala Leu Glu			
	485	490	495
Pro Gln Val Lys Cys Leu Arg Val Ser Glu Pro Glu Gln Leu Cys Gln			
	500	505	510
Ala Leu Asp Lys Val Asn Asp Arg Glu Tyr Leu Leu Phe Ile Glu Val			
	515	520	525
Met Leu Pro Gln Met Asp Ile Pro Glu Leu Leu Asp Thr Ile Ser Arg			
	530	535	540
Ala Ile Gln Ala Arg Asn Met Ala Ala			
545	550		
<210>	589		
<211>	1047		
<212>	DNA		
<213>	Artificial Sequence		
<220><223>	Synthetic polynucleotide		
<400>	589		
atgtcgtacc cagaaactca gaaggctatt atattttatg agtcaaacgg caaactcgaa		60	
cataaagaca ttcccggtgcc taaaccgaaa ccgaatgaac ttctgattaa cgtaaagtac		120	
agcggagtct gccacacgga ttgcatgcc tggcacgggg attggccgtt accgacaaaa		180	
ctgcctctgg tgggtgggtca tgaggcgcg ggctgtgttg tgggtatggg agaaaatgtc		240	
aaaggctgga aaatcggcga ctatgcaggg atcaagtggc tgaacgggtc ttgtatggcg		300	
tgcgagtact gtgaattagg taatgaatcc aactgccac acgcagatct gagtggttat		360	
acctatgacg gcagcttcca agaatacgcc acagcggatg ccgtgcaggc agctcacatt		420	
ccgaaggaa ctgatcttgc ggaagtagcc ccaattctgt gcgcgggcat cacggtatat		480	
aaagctctca aaagtgcaaa cttgcgcgcc ggtcattggg ctgcgatttc gggtagcgcg		540	
ggcgggctgg gatcattagc tggtcagtac gcgaaggcaa tgggttatcg agttctgggc		600	
atcgacggcg ggccccggtaa agaagagcta ttaccagcc tcggcggtga ggtcttcac		660	
gattttacca aagaaaaaga tatcgtgtcc gcagtcgtga aagcaacaa tggcggcgct		720	

cacggaatta taaatgtgtc tgtatcagaa gcggcgattg aagccagcac gcgttatgtg 780
 cgcggaacg gcacagtggg tctggtaggc ctgcccgcg gtgcgaaatg tagctcggac 840
 gtgttcaatc atgtggtgaa gagtatttcc attgttggat cttacgtagg gaaccgtgcg 900
 gatacgcggg aggcactgga tttttttgca aggggcttgg ttaaaagccc gatcaaagtc 960
 gtgggtctgt cgtctctacc tgaaatata gagaaaatgg aaaagggaca gatcgccgga 1020

cgctacgtcg tcgacacctc aaagtga 1047

<210> 590

<211> 1017

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 590

atgcgcgtga tgcagattca agacgattgg ggccttggga atctgcgtct agccgagcgg 60
 gcgcagccgc agccagggtc tggccagggt ctgctgcgta tgcgcgtgc aagtctcaac 120
 tategtgacc tggctgtacc ggaaaggggt tacggatcct tcaactgtac gtgccccta 180
 atccccgttt cggatggcgt aggtgaagtt gtggaagttg gcgctggtgt acgccgtgtt 240
 gcgccgggcg accgtgtgtg tccatgcttt ttccaaggat ggataagcgg tgatccggag 300

ctgggccgta tgaccgggtc actgggcggg ccgctggacg gcgcaatggc tgaatttatg 360
 tgctctctg aacagggcgt tgtcaaaatc cctctctgcc tgagcgatct ggaagccgct 420
 aactgcctt gtgcagcttt gactgcgtgg tctgcgtgg tcaccacagg tcgagtgggt 480
 ccgggtgaac gcgttctggt ccaggaagc gggggcgtag cactgttcgc tttagcgttc 540
 gcacgtatcg ctggcgccca tgtaactgtt atttcttct ctgatgaaaa gatcgagaga 600
 ctgcgtgctc tgggtgctga cgcgaccatc aactacacgc gactccgga atggtcgaaa 660
 accgcacgtg agattactgg tggccgcggt ttgaccaca tcgttgagct gggcggtgag 720

aaaacctac cgcaatcgct ccgttgcatc cgtgcaggcg gtaccctgtc tatgattggg 780
 gtgctgagcg gtctctctg tctgtgcca ctgggggtga tcgtaactcg ccaggttcgt 840
 ctgcaaggca ttacggtggg acaccgtgac ggcttcgaag ctatgctgcg cgcattagaa 900
 cagcatcgtc cggccatcac cgttgataga gtttttgaat ttactgctct tcgcaagcg 960
 ctagcttata tgcgtagtgg tgttcagttc ggcaaaattt gcatccgtca ccctgat 1017

<210> 591

<211> 1098

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 591

atgaaggcgg cagtagtta tagcgtgggt gggggcttca ctatagaaga cattgagatc	60
gccgaaccga tcggccgcga agtcctcttt gatgttaaag cttccggtct gtgccgttct	120
gatttaacac tgtcaaccac gaacttcggt ttcccatctt cccaagttct gggccatgaa	180
gctgcgggtg tagtgactgc tgttggccct gacgtaaaag agattaaagt cggtgaccac	240
gtggttgcac ctctgatcca gtactgtggg cactgccgtg cctgccggga atcgcgcatg	300
tatgagtgtg aatttcgga agaaacctt cgtggccctg atgaggctcc gcgcctgagt	360
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<210> 592

<211> 1047

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 592

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gatgtacact tacatgacgg ttattttgat ctgggtggcg gtaataaact cgatgttcgt	180

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tgcggcgagt gcccgcgtg taaacgagat gaagaacagc tgtgcaacaa acctagacag 360
ctgggtatcc aggtcgccgg tggctatgca actcacgtaa tggttccgga tgcgaaatac 420
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<210> 593
<211> 1089
<212> DNA
<213> Artificial Sequence
<220><223> Synthetic polynucleotide
<400> 593

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ccagaccatc tgaaacctga caaacattc ttaatcgaca gcaaagagc acagaataag 720

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caactcgtgg acgttgggct gccgcggat gggccgtttg agttggactc gttcgccatg 900

aacttcaaag aacagaccat acgtggctgc ctgatttgca ctctgagca gtgtcaggat 960

atgatcaatc tgcacgcgga caacggctgc actacctta tcgaaaagac ctatagtgtt 1020

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atggtattc 1089

<210> 594

<211> 930

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 594

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cctgttccga cccccgtga aggcgaagtt ctggtcaaac tggaatatag cggggtttgt 180

cattctgacg tgcactctgt acgtggtgaa actccgatgt taactgatgt cgcaggccat 240

gaggggtgtt gccgcgtggt tcaggaatac ctggttaagtc cggcggctca cgtaacaaaa 300

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tactctcca tcatgaaaac taaaaccctg ccaggcgact ggatcgttct gcctggagct 420

gggggcggtt tgggtcatat ggggtgtccag attgcggtga aaaagggcct gaaagtcac 480

gccattgata gcggcgaaaa aaagaaacag ctgtgcctca aactgggtgc aactatcttt 540

ctggattata aaaccgacaa cgttgaatct gaggtcaagg ccctcactag cggcttgggg 600

gtcacgcg tttatctgtac tgcgcaaagc gaagctgcgt acgaacagtc ttacgtctg 660

ctgcgatccc tgggtgttct ggtgtgcgtt ggtatcccga acgttccgtt ccgtctaccg 720

gcttccccct tcgatatgat tgtaaaaggc cttacgatcg ttggcaactc tgctggtacc 780

gcacgcgaaa tggaagaact gatggagatg gccgtggcag gtgacgtcaa agcgcacatt 840

gagtgtctcg aatttgacca gatcgatgat gtgatacagc gccttggcgg ctcggaaatc 900

gatggacgtg ctgtaatgcg tattccagaa 930

<210> 595

<211> 1092

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 595

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cattcagatc tacacgcgat caacggccaa tatacgcaca acttaccact cgttctgggt 180
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gaccactggg ttctgtcctg gctgccgagt tgcggcaaat gcaggccctg ccttcgaggc 300
cgtccggcaa actgtgagga cgcattcttg ccgtctgctg gtacactgcg tgatggaacc 360
tcgcgttttg gcaagaatgg taaaaccgtg ttccactacg gcgtaccag cactttctcc 420
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cgtttagttg atttttacaa aagtggctct ctgaaactcg atgaaatgat cgaagttcgt 1020
ccgctggaag atataaactt agcattctcc aaccttgcta agagcacagg gggccggact 1080
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<210> 596

<211> 939

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 596

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gatgttggcg ttatcgaagg cgtaacgact ccgagcttgg ggaaaattcc aatgatctta 180

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cctctgctac atcagatcaa attcgacgag atttccgaag gtctgcaaca gttggcggac 900
aacaaagtaa ccgggcgttt ggtggcgggt atcgacaac 939

<210> 597
<211> 1011
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide
<400> 597

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gatattcatg ctgctcacgg cgactggcct gtgaaaccgc gccctccatt cgttccgggt 180
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ctgccagcag ataacgcagc tattaacgta cctatcttcg aaaccgttct gagcgttatt 840
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<210> 598
 <211> 1044
 <212> DNA
 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 598

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 gcggaactgc gtgaatttgt tgcgtggct cgtgaaaaag gggtacctgc tgcaccctg 960

gataaacgcc cgctgtccgc cgctccagcc gccctggcag acttaaaagc gggtcgtgtt 1020
 atcgggcggg tagtcttaca gccg 1044

<210> 599

<211> 1080

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 599

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ttaaaggatga actactgcgg tgtctgtcac agtcatgttc atcttcacga cggctacttc	180
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aaggaaaaaa atctgccgcc aattcatatt gaacaccgcc cgctggaatc ggccgctcag	1020
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<210> 600

<211> 1029

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 600

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 aactttgcc ctacggccgc ggtatggcag accattgaac aagcgcaaaa cccgatgtct 780

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 <210> 601
 <211> 1044
 <212> DNA
 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 601

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<210> 602

<211> 1053

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 602

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<210> 603

<211> 1050

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 603

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gataattcgc ttcacgaggg ctacttcgac atgggcggtg gcaataaagc tgatgttact 180

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ggaccaggtg tcaccggcgc taaaccgggc gacaaacgta ttgtgtaccg gtggatcggg 300

tgcggcgact gcccgaaatg caacagtggg gaggatcagt cctgtgcgcg tccacgtaac 360

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gctaaaactg tagtctttga tatcgacgac gcaaaactgg aagctgcgac ccgtgccggg 660

gcggattacg tgttcaactc cggtgcaaaa gaaacacgca aggaagtat gaaactaacg 720

aatgggtggcc tgtctgggtc tgttgatttc gttggcagcg ataaaagcgc tctgtttgga 780

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tccttgcaag agatgagtga tatgatggag ttagttcgcg ctgggaaagt tcctccgatg 960

ccggtaaaaa ctcggccact ggacgtgcc tgggaaacce ttgaggatct acgcatggt 1020

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<210> 604

<211> 1029

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 604

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tgggctgatt acctgctggg tccagcggca cgtcacctgg tgagcctggg ggatctggac	420
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<210> 605

<211> 993

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 605

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tccgatctgc acgttctcga cgggtggaatc cccctgccgg gtcaatttgt aatgggccat	180
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ctgaatgccc ttaaacctgc taagaccttc ggcagttacg ttacgcac tgacctgaaa 600

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tggggcacga gcaatgagct ggctgaatgt ctgcgcctgt gccagctggg cctgatcaac 900

ccgaaatata ctgtggtgcc tcttgaagaa gcgccgaaat atatggaagc aatggctcat 960

gggaaagtag aaggtcgtat cgttttccac ccg 993

<210> 606

<211> 1155

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 606

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cgcaccgata tcgatgtacg tgacggctat ctccaactc ccaccctgt ggttttaggt 180

catgagggtc caggtgttgt cgttcgtgtg ggccgcctcg tacgtcaatt cgcgccgggt 240

gaccacgtcg ttaatgtcat gggctcttgc ggcgatgcc cgagttgcca ggtaggtatg 300

ccggcgtagt gcgttcagca cgtgccgtg aactttatgg gctcccgcc tgatggtagc 360

gtgtgtatgc atgaacacgg tgaacgcgtt cactctcact tcttctcca gtctagccat 420

gcaagtttta cagtcgtca tcaatctagc ctggtgaaag ttgccgacga tgtggacctg 480

cgttggttag gaccgtggc ttgcggagtc atgaccggcg cagggggcgt tattaatact 540

ctgaaaccag aagctggtag ctccatcgtt atattcgtg ccggcactgt aggtctaagc 600

gcattgatgg cgtctaaaa ttagcttgc tccgtagga tcgttgtgga taacaaaccg 660

gagcgcttgg cgcttgctcg tgaactgggt gctacagaca cgatcctggc aactgccgac 720

gctgatgtcg cgctcaggt tcgtgctctg accgacggcc taggcgcga caacgcttc 780

gagtcacgg gtgttaagtc tgtcatggc gccgcgtca ccgaattcg cgaacgtgg 840

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<210> 607

<211> 1023

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 607

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<210> 608

<211> 1353

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 608

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tatgtccgtg atgacaccga aagttcttac accaaaaacg aatccaacaa gcgtgctaaa	180
cttaccatta aagagaactt gcacactaaa acccatggtc tatttggcga agtacctgag	240
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<210> 609

<211> 1086

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 609

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gatttacatt tcgtagacgg cgcttaccct caccgcctcc cagctattcc gggccatgaa	180
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tacatgcgtg gccttcttga cctggacacc atcatcgctg agcgtctgcc tctgagccag	1020
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<210> 610

<211> 1044

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 610

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gactggcacg gctggaaagg tcatgacct gatattaaac tcccacacgt gccgggccat	180
gaacttgctg gcactatcgt tgaagtaggt aaagatatta aaaattggaa gcgtggcgac	240
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ccacaagtct gcgaccatca gtttcagccg ggattcactg cgtggggttc cticgctgaa 360
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<210> 611

<211> 999

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 611

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ctggatccgc ttgatatcaa cgtgttcagc ctgataatgg cgcagcgttc tatctctggt 840

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gtaaagccag ttattgaaa gttttcttc gcagatatta acaaagcat tgaacgtctg 960

cgtagcggta atgctcacta ccgcatcgtt cttcatcgt 999

<210> 612

<211> 1020

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 612

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gaaaaaaaaag aaattgaggt acccaaacct gacgccgta aggttttact gaaagtggct 120

gcggcagggg tatgtcacag cgatctccat gttctgcacg gtggccttc gtaccggac 180

ggtctgatcc tgggcatga aattgctggc cacatcgtgg cctatggaga tgggtgtgat 240

aaagctgcat ttccgtccga cgcgtatac gctgtcgttg gtccgaatcc gtgcggcatg 300

tgcaaggcat gccgtacggg ggccgacaac gtatgtgaag atccgagtcg cactcacatg 360

ggtttgggct ctccaggtag ctacagcaa tatacacagg tgtctgcgcg gaacatcact 420

aaagtctctg aaggcattcc ggctgctgta gcagccgca gcaccgacgc tgttctgact 480

ccgtaccatg cactgaaacg tgctgggtata aacggaatga cgcgtctgct tatcgttgg 540

ctgggcggtc tgggtatcaa tgccgtccag attgccaagg ctttcggctc ttatgtgac 600

gctgttgacc caaaagaatc cagcccgat ctggcaaac aatacggagc gaacgaggtt 660

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aaaggcctag ttacaccgca ggttgaaact acgtcttggg tgaacgtcaa caaagtactg 960

aaggatctgg atgaaggtaa aatcaaaagc agaatgggcc tggttcataa tgaagacaac 1020

<210> 613

<211> 1023

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 613

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<210> 614

<211> 1047

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 614

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ctgcgtattg atggtaccct cgttagcgta ggcgcgccag caaagccgga cacttattca 840

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gaaacgcaag aaatgctgga tttcgccgt gagcatggta ttgaacaaa aatcgaagtt 960

atcggcgcag atcaggttga tgaagcctac gagcgtattc tgcgttctga cgtccggtac 1020

cgttttgta tcgacatttc tacgtg 1047

<210> 615

<211> 852

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 615

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gtttgccatt ccgatgtgca caatgtgct aacgactggg ggtctgtca atateccatg 180

gttcggggc atgaaatcgt aggttgcgtt ttggaagttg gtagtgaagt aacacgcttt 240

aaggcaggcg atcacgtggg tgctggctgt atggtagagt cctgccgtca ctgcaacgcg 300

tgtggaaaag gctgggaaca gtactgcgaa aacggcgcaa cctacacgta taacgtacc 360

gacccgattg atggtactcg tacttacagc ggctacagcg agaaaatcgt ggttgctgaa 420

catttctgt taaaagtcc tgatggtctg gacctggcag gtgctgcgcc gctgctgtgt 480

gccggcatta ccacctatc tccgtgcga cattggaag tagggccagg atctaaggtt 540

gcaatcgtag gtcttggcgg tctgggtcat atggcctga aacttgctaa agcgatgggg 600

actgaagta cactgttttc tcgtccccg ggcaaagagg ctgatgcgcg tcgtctaggc 660

gcagaccaca tagttatgag taccgacact gctcagatgg cggctgctgt ggatgggatc 720

gatgctatcg ttctgactca cggttccgac ggcggtggtc atggcgctg cggcgtgct 780
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cgccgcttgc ac 852

<210> 616

<211> 1071

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 616

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gtttgtcata gtgatctgca cctgtgggat gggtactatg acttaggcag cgctggtcgc 180
tacgaaatcg tacaacgtgg cattactctg ccgctggctc tgggccatga aatcgtaggt 240
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<210> 617

<211> 1119

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 617

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attgctggcg ttgggtgttg ccatacagat ctctgtgtgc gggatggttt ccctgttccg	180
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ccattcgacc gctgatcac tcgtaccgt tttgaccaga ttaacgaagc cctgcatgct	1080
accgagaaag gggaagcaat taaaccggtt ctggtcttt	1119

<210> 618

<211> 1023

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 618

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gatttacaca tcattgacga aggtacggtt gtaggcactg ttttcacctt gggatcatgaa	180
aacgttggtt ggatcgaaga ggttggcgaa aacgtcgaag gttataaaaa gggagatgct	240
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<210> 619
<211> 1089
<212> DNA
<213> Artificial Sequence
<220><223> Synthetic polynucleotide
<400> 619

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tactcgggtg tatgttcacg cgacgttggc gtgctctcgg gtgcttacgg tccagtccat 180
gaagaagtat gcggccacga aatcattggc accgttacac gtgtcgggcc ggagggaag 240

cacctgcgcg ttagtgatca tgttggagtg ggtggccagt gcgactgttg cacgcactgc 300
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gaggaagacg cccgtaaaact gggcgcaaaa cactacatcg ctactggctc tgatctgaaa 720

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aaaaccggtg ttaaaccatg ggtacagctg tgggaatfff ctgatatcaa caaggccatc 1020
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ggtgaactg 1089

<210> 620

<211> 1116

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 620

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gcagttatcg gtcacgaaat ttcaggcatc gtagaggctg ttggcccgga agtgtcgggt 240
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tgctgaagg gccagccgca gtctgcacc cagcaacagg agtgtgtacg tggcgtgga 360
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gggttcgagg aaaaagcttt gattcacgag aatcagctgg ccgtagttaa caaccaggtt 480
aatgggatg aagctgcatg cattggctgc gcgacaatca ccggggcagg cgctgcgatt 540
aacactgccc atgtccggcc tggatgatac gtggctgtca tcggtaccgg cggcatcgga 600
ctgaatatta tctcgggtgc tcgcatctgc ggtgctaagc gtattatagc aattgacctg 660
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atagtgagcc aacatatcaa attgtctcag attgatgaag catataaaca attagtaaac 1080

ggcgaggtta tccgtagcgt tattactgaa ttgac 1116

<210> 621

<211> 1062

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 621

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gatattcatt ttgggaagg gtattacgat atcggcgaag aaaaaaact ggagttaaaa 180
gaccgtgcta tcaagctgcc tatgactctg ggtcacgaaa ttgtcggcac catcgtgcta 240
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ctgactactt actctgctat caagaaaatc gaccagtcca tctatacaca gaaaccgatt 540
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gtagggaacc tgaacgaatt ttacagctg atggacctgg ttataaaaaa taaaatcact 960
ccgactccgg tccaggccta ccatttcgat cgtattaacg aagcgatgga cgacttacgt 1020
accggcaacg tgatcggctg tgcgtactt gttcacgact ct 1062

<210> 622

<211> 927

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 622

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gctcatgtgc gtcgtaaacac gtgtggcgaa tgcagtgaat gcttaggtcc ggatgtttgg 180

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gagtacntag tcgtgactc tcgttggagc gttaaagtgc cgaaggttt tcccttcacc 300

gtagcggccc cgttggcttg cgcaggcgcc accagcttcc gggcagtga aatggctggg 360

ctggaacgtg gccagtgtt ggcatcgtt ggttccggcg gcgttctggg acacctgtct 420

atacactttg ctaaaccatg tggctgaac gttatcggtt ttgacgcgcg cgatgcaggc 480

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gtgtggcagg tggctcaacc gcgtgatgtt gctgtaccgt accaggaact ggttctgagg 720

gatatccgtc tgcgtgggtc cgttatttgc tctccaatgg atgccagga aatgatcgca 780

accgtcgccg gtatgggcgg tgacatcgta gctgtgcgta catacgttgg actggaatcg 840

cttcctaagc tacttcagga cgtgagagcc cagcacgtg tcggtaaagc gatcatcgtt 900

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<210> 623

<211> 1062

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<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 623

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acggttatag agaccgtgcc cgcgcagaaa caaccatctg aactcttacc gggggaatgt 120

cttgttaaac tggaatatc cggtgtatgc cacagcgatc tgcattttat gctgggcgag 180

ttcgtccgc cgtctctgcc tactgtcggg gccacgaag gtgttgcca tatcattgct 240

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aaggtaaccc cccattttga agttcgccg cacgtgaaa tcaatgatgt tctggagcga 1020
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<210> 624

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 624

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tatgaaatcc tagttaaagt gaaagcagct tccctgtgtc actctgatct gatgttattt 180
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<210> 625

<211> 1065

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 625

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 aaagtctgtg actctggcgt gtgtcacact gatctgcatg ctcaattagg ggattggccg 180
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<210> 626

<211> 975

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 626

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<210> 627

<211> 1050

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 627

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<211> 1065

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 628

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<220><223> Synthetic polynucleotide
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<211> 1137
<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 630

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atcttataca cctctctctg ccatacagat gtgtatTTTT gggaggctaa gggtcagact 180

cctgttttcc cgcgtatTTT cggtcacgaa gcaggcggta tcatcgaatc ggtcggcgaa 240

ggagtactg acgttgacc cggatgacac gtgctgccg tattcaccgg cgagtcaaaa 300

gaatgccgc actgtaaaag cgccgagtc aacatgtgc acctgctgc tatcaatacc 360

gtgcgcgggt ttatgattgg tgatggcaaa tctcgattta gcataaacgg gaaaccaatt 420

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acgggtctgg gtgctagcat caacgttgct aagcctccga aaggtctac cgtggccatc 600

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agaatcatcg gattgatct gaatccgtcc cgtttcgagg aggctaaaaa atttgctgc 720

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aaagagctgg aagttgaaaa gttcatcact cactctgttc catTTTcgga aattaacaag 1080

gcgttcgacc taatggctaa aggcaaggc atccgctgca tcatccgtat ggaaaac 1137

<210> 631

<211> 1140

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 631

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aaaattctct acatttcctt gtgtcacact gatgtatatt tctgggaagc aaaaggccag 180

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gagggcggtta ccgaactggg tccgggacac cacgtgctgc cgggtttcac cggcgaatgc 300
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aataaagagc tggaactaga aaagttcatt actcacacct tgccattcgc agaaattaac 1080
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<210> 632

<211> 1140

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 632

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atataccact ttgttggtac ttctaccttc tctgaatata ctgtagtcca cgtaggctgt 480
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tcgcgcata taggtgttga tctgaacgcc tctcgcttcg aacaagcaaa aaaatttggg 720

gtcacccaat ttgtgaatcc taaagactat tccaagccgg tacaggaagt aattgcggag 780

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aataaagagc tggaactcga aaagttcatt actcacacct taccattcgc tgaaattaac 1080

aaagcggttcg acctgatgtt aaaaggagaa ggctgcgtt gcatcatcac tatggaagac 1140

<210> 633

<211> 1011

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 633

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cttcactgta aaaaaggga ctttggcgat gagacaggtc gtatcactgg acatgaaggt 180

attggcatcg tcaacaagt aggtgaaggc gttacttctt taaaagtcgg tgaccgtgct 240

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cctggccagt ggctggcaat ctatggcctg ggtgggcttg ggaatctgac tctgcaatac 540

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aaagtgaac ctaaggtaac taaacgtaaa gtggaagaaa ttaacaaat ctttgatgaa 960

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<210> 634

<211> 1146

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 634

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tgccagcagt gccggcattg caagagtga gagagcaata tgtgtgattt actgcgtata 360

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gcaatTTTcg gactgggtgc tgttggcctg gcggtgcgg aaggtgcgcg tatcgctggg 660

gcaagccgca tcattggtgt cgatctgaat cttccccgt tcaacgacgc caaaaaattc 720

ggcgttaccg agtttgtaa ccgaaaagac cacggcgata aaccggtaca gcaggttatc 780

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atcaacaagg cgttcgacta catgctgaaa ggtgaatcga tccgatgtat gattaccatg 1140

gagcac 1146

<210> 635

<211> 1140

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 635

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aataaagaac tggaactcga aaagttcatc actcacacct tgccattcgc tgaaattaac 1080

aaagcgttcg acctgatgtt aaaaggagaa ggcttgcgtt gcatcatcac catggctgac 1140

<210> 636

<211> 1008

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 636

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<210> 637
 <211> 1098
 <212> DNA
 <213> Artificial Sequence
 <220><223> Synthetic polynucleotide
 <400> 637

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<210> 638

<211> 1158

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 638

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cccatcagcg aagtctgtc tgagatgact ggaacaacg tgggttacac ctttgaagtt 840
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agcgttggtg tcggtgtccc gccttccgt aagatgctga cctacgatcc aatgctgctg 960
ttcactggtc gaacttggaagg gctgcgtg ttggtgggtc tgaaatctcg tgacgatgtt 1020
ccgaaattgg taaccgaatt tctggcgaaa aaatttgacc tggatcaact cattacccat 1080
gtacttccgt tcaagaaaat ctccgagggc ttcgaactgt taaacagtgg acagagcatc 1140

cgcacctgac taaccttc 1158

<210> 639

<211> 1017

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 639

atgaaggcgg cagtagttga acagttcaaa gagccctga aaataaaaga agtcgaaaag 60
ccgaccatct cctacggcga ggtgcttgtt aggatcaaag cctgtggtgt gtgccacact 120
gatttacatg ctgctcacgg ggactggcct gtaaaaccaa aattgccgct gattccgggt 180
catgaaggcg ttggtattgt cgaagaagt ggcccggtg ttacgcacct gaaagtgggc 240
gaccgtgtag gtatcccggt gctctatagt gcatgcggac actgcgatta ctgtctgagc 300
ggccaagaga cactgtgcga acatcagaaa aacgcgggat attcagtaga tgggtgttac 360

gtgaataact gccgcgcgcg tgcggactac gtctgaaga tccctgacaa tctgtcgttt 420
gaaggaggctg ctctatattt ctgtgcgggc gttaccactt ataaggcact aaaagttact 480
ggcgccaaac caggtgaatg ggtggcaatc tacgggatcg gcggtctggg tcacgttgca 540
gttcagtatg ctaaagctat gggcctgaac gtctgtctg tagatattgg ggatgaaaaa 600
ctggagcttg ctaaggaact gggcgccgac ctggttgtga accactcaa agaggacgcg 660
gcgaaattta tgaagaaaa agttgggtggc gtgcatgcag cagtcgtcac ggctgtatct 720
aagccggcct tccaatctgc gtacaacagc atccgtcgcg gtggcgcttg cgtgctggta 780

ggtttaccgc cggaagagat gccgatcccc atcttcgata ccgttctcaa tggatttaag 840
attatcggtc ccatcggtggg tacccgtaaa gacttgcagg aagcactgca attcgccgcc 900
gaaggtaaag ttaaaacat aattgaagtc cagccgcttg aaaaaatcaa cgaggttttt 960
gatagaatgc tgaaggcca gatcaacggc cgtgtagtgc tgactttgga agataaa 1017

<210> 640

<211> 1008

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 640

atgcgcgcgg cagtagttac taaggacat aaagtcagca ttgaggataa aaaactgcga 60

gccttgaagc ctggcgaagc tctcgtgcaa acggaatatt gcggtgtttg tcacaccgat 120

cttcacgtaa aaaatgctga ctttggggat gtgacagggtg ttacttttagg ccatgaaggt 180

atcggcaaag tcatcgaagt tgctgaggac gtagaatctc tgaaaattgg cgaccgtgtt 240

agtatcgcat ggatgttcga atcctgcggt cgttgcgagt actgcaccac tggccgcgaa 300

accctgtgtc ggtcagtga gaacgcgggt tacacggtgg atggagccat ggctgaacag 360

gtcatcgtaa ccgcggacta tgctgtaaaa gttccagaga aactggatcc ggcagcagct 420

agctccatta ctgctgtgg tgttaccacc tacaaggcgg tcaaagtgtc taacgtaaaa 480

ccgggccagt ggctgggcgt tttcggatc gggggtctgg gcaacctggc gcttcagtac 540

gcgaaaaacg ttatgggcgc taaaattgtt gcatttgaca tcaatgatga caagctagcg 600

ttcgctaaag aactgggtgc tgacgccata atcaacagca aagatgtgga tcccgtcgcg 660

gaggtgatga agctcactga caacaaaggt ttggatgcaa cggttgtaac ttctgtcgcg 720

aaaaccccg tcaatcaagc tgttgatgtg gtttaaggccg gtgcccgcgt ttagctgtg 780

ggactgccgg ttgataaaat gaacctggac atcccgcgtc tggtagtaga cggcattgaa 840

gttgtcgggt cgcttgtggg cacaaggcag gacctgcgtg aagctttcga gtttcagct 900

gaaaacaaag tactcctaa ggttcagctg cgaaaactgg aagaataaa cgatatcttc 960

gaagagatgg aaaatggaac catcactggt cgtatggtta tcaaattc 1008

<210> 641

<211> 1095

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 641

atggcaaaga gtcagaaat ttagcaccct gtaaaagcgt ttgggtgggc cgctcgcgac 60

acgactggct tgctgtcccc attcaaattc agccgtcgtg caaccggtga aaaagatgtt 120

cgattaaaag tgcttttttg cgggtgtctgt catagtgate accatatgat acacaataac 180

tggggcttca ccacttatcc gatcgttccc ggtcatgaaa tcgtaggcgt ggttacagaa 240

gtgggctcta aggttgagaa agttaaagta ggtgacaacg tcggaatcgg ttgcctggtg 300

ggctcgtgcc gcctttgtga atcctgctgt gacaaccgtg aatcgactg cgagaatacc 360

attgatactt acggatctat ctacttcgac ggtacatga cccacggcgg gtatagcgat 420

acgatggttg ctgacgaaca ttttatcttg cgttggccga aaaacctgcc gctggactct 480

ggtgctcctc tgctctgcgc gggatatcact acatactccc cgctgaagta ctatggcctc 540

gataaacccg gtactaaaat cggcgttggt ggccctgggtg gtcctgggcca cgtggctgta 600
 aaaatggcaa aggccttcgg tgcgcaagta accgttatag atattagcga atctaaaagg 660
 aaggaggctc tggaaaaact aggcgcagat tctttcctgc tgaacagcga ccaggaacag 720

atgaaaggcg cgcgttcctc ccttgatgga atcatcgaca ctgtcccgtg taaccatcca 780
 ctggctccgt tgtttgacct cctgaagccg aatgggaaac tggatgatgt aggtgctccc 840
 gaaaaaccgt tcgaactgcc ggtgttctcc ctgctgaaag gccgtaagct gctgggtggt 900
 accatcaacg gcggcattaa agaaactcag gagatgcttg attttgcggc taaacacaac 960
 atcacggccg atgttgaggt catccctatg gattacgtta acaccgcaat ggaacggtta 1020
 gtcaaatcag acgtgcgcta tcgtttcgta attgatatag ccaataccat gcgcactgaa 1080
 gaaagcctgg gcgcg 1095

<210> 642

<211> 1008

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 642

atgcgcgcgg cagtagttac taaggacat aaagtcagca ttgaggataa aaaactgcga 60
 gccttgaagc ctggcgaagc tctcgtgcaa acggaatatt gcggtgtttg tcacaccgat 120
 cttcacgtaa aaaatgctga ctttggggat gtgacagggt ttactttagg ccatgaaggt 180
 atcggaagc tcatgaagt tgctgaggac gtagaatctc tgaaaattgg cgaccgtgtt 240
 agtatcgcat ggatgttcga atcctgcggt cgttgcgagt actgcaccac tggccgcgaa 300
 accctgtgtc ggtcagtga gaacgcgggt tacacggtgg atggagccat ggctgaacag 360

gtcatcgta ccgcggacta tgctgtaaaa gtccagaga aactggatcc ggcagcagct 420
 agtccatta cttgcgctgg tgttaccacc tacaaggcgg tcaaagtgc taacgtaaaa 480
 ccgggccagt ggctgggcgt tttcgggtatc gggggtctgg gcaacctggc gtttcagtac 540
 gcgaaaaacg ttatgggcgc taaaattgtt gcatttgaca tcaatgatga caagctagcg 600
 ttcgctaag aactgggtgc tgacgccata atcaacagca aagatgtgga tcccgtcgcg 660
 gaggtgatga agctcactga caacaaaggt ttggatgcaa cggttgtaac ttctgtcgcg 720
 aaaaccccg tcaatcaagc tgttgatgtg gtttaaggccg gtgcccgcgt ttagctgtg 780

ggactgccgg ttgataaaat gaacctggac atcccgcgtc tggctactaga cggcattgaa 840
 gttgtcgggt cgcttgtggg cacaaggcag gacctgcgtg aagctttcga gtttcagct 900

gaaaacaaag tcactcctaa gggttcagctg cgaaaactgg aagaaataaa cgatatcttc 960

gaagagatgg aaaaaggaac catcactggt cgtatgggta tcaaattc 1008

<210> 643

<211> 1038

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 643

atgcaggcgc tggtaggtgc tgagaccggc gggtatcgct tagcagataa cgtcgaaaag 60

ccggttctgc aaccaggctc catcctctgt cacgtgaaag ccgttgctct gaatcccat 120

gacgctaaaa ttgttgacta ctcaaactgt ccgggtgcac tgggtggctg cgattttgca 180

ggcgtagtgg tagaaatcgg taacggcgtt aaacgtttca aagaaggtga ccgagtgttc 240

gcggtcactt ttggtatgaa tgcttctgat aagacggcgg gcgcgttcac ccagtacgcc 300

gtagcaactg aggacttgag ctgcctgatt ccggaagcta tgtcgttcac tgaagcttgc 360

agtatgggtc tggcaatcgc taccgccgga cttgcactgt tccagacacc gggcctgcaa 420

ctgagcatgc agggcggtaa cggatgaagc gtctctggtgt ctggaggggc taccgcgact 480

ggcaccatgg caatccagtt tctccgtata gcagggtata caccggctct tacttgctct 540

ccttccaaca acgctctgtg tgagtccttt ggcgccgaaa tttgtttcga ttaccacagc 600

cctacttgcg gcgctgatat tcgctccag accggtaaca aattgaggca tgttctggac 660

tgcgttgttg acatctccac gatgaaaatg agctacgacg ccatcggtag ctctggcggc 720

gcgtatgtgg ctcttgaagc gatcccgacc aatatcaagt acaccgtcg cgatatattgc 780

gctaactggc tcatggcacc atctatcctt ggcaccccag taaacaaaa aggtgcttac 840

ggtcgtccga gtatgccga acaccgtcaa ttcggtacgt accgttcgc tctggcggag 900

aaatggctgc aagatggaag cattaacac catccgatcg aaatccgca agggggtctg 960

cgtagcatcc gtgaaggat tgatgatctg cgccggggca atgtgcacgc taaaaagctg 1020

gtatatcctt taccagca 1038

<210> 644

<211> 1053

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 644

atgacagcga cgaaggctta tgcagcccaa agttccacct ctgggatggc tccccacgac 60
 atagatcgcc gtagcctccg taacgacgat atcgcgattg agatcgatta ctgcggcggtt 120
 tgtcatactg acattcactt cgctcagaat gactgggggtg taactcagta ccctgtcgtt 180
 ccaggtcacg aaatcgtagg ccgcgtaacc gcagttgggtc cgggcgtcaa agcctatcag 240

gaaggcgatg tggttgggtg tggttgcatg gtggactcgt gcaggacctg ttcagcttgc 300
 gaagcgggcc tggagcaata ctgctctgaa gggatgactg gcacctataa cggatgaagac 360
 cgtcaggatc atagcatcac ttttggcggg tactccgagc ggatcgtggt aagcgaaaga 420
 ttcgttggtc gtattccgga taaactggat atcacgaaag cagctccgct gctttgtgca 480
 ggtattacca cttactctcc gctgcgccac tacggcgtaa agccgggaca taaagtggg 540
 gttatcggta tgggcgggtt gggtcacatg ggcgtaaaat ttgctaaagc gttaggagct 600
 gaagtcacca tcttcactcg ctccgagtct aaagtgggcg aagcgaagaa acagggcgca 660

gactatgtgg ttgttagtac agacgaagat cagatggcgg ctgctgccga aacgttcgat 720
 tttatgctag acactgtacc agttcagcac gatatcaacc cgtacctgaa ctgcttgagc 780
 tatgatggca cccatatcat ggtgggtctg ctggaacctc tggaaccagc gctgcaaacc 840
 ggcgcactgg tcttcaaagc tcgtgttctg gcgggttcat taattggcgg tatgccgaa 900
 acgcaggaag tgctggactt ttgcgtgag catgatattt cctgtgacgt tgaaatgctg 960
 gacatccaca atattaacga tgcctacgag cgtatgaaga aagtgatgt caaataccgc 1020
 ttcgttatcg acatggctac gctgaaagac agc 1053

<210> 645

<211> 348

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 645

Met Ser Ile Pro Glu Thr Gln Lys Ala Ile Ile Phe Tyr Glu Ser Asn

1 5 10 15

Gly Lys Leu Glu His Lys Asp Ile Pro Val Pro Lys Pro Lys Pro Asn

20 25 30

Glu Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu

35 40 45

His Ala Trp His Gly Asp Trp Pro Leu Pro Thr Lys Leu Pro Leu Val

50

55

60

Gly	Gly	His	Glu	Gly	Ala	Gly	Val	Val	Val	Gly	Met	Gly	Glu	Asn	Val
65				70				75				80			
Lys	Gly	Trp	Lys	Ile	Gly	Asp	Tyr	Ala	Gly	Ile	Lys	Trp	Leu	Asn	Gly
85				90				95							
Ser	Cys	Met	Ala	Cys	Glu	Tyr	Cys	Glu	Leu	Gly	Asn	Glu	Ser	Asn	Cys
100				105				110							
Pro	His	Ala	Asp	Leu	Ser	Gly	Tyr	Thr	His	Asp	Gly	Ser	Phe	Gln	Glu
115				120				125							
Tyr	Ala	Thr	Ala	Asp	Ala	Val	Gln	Ala	Ala	His	Ile	Pro	Gln	Gly	Thr
130				135				140							
Asp	Leu	Ala	Glu	Val	Ala	Pro	Ile	Leu	Cys	Ala	Gly	Ile	Thr	Val	Tyr
145				150				155				160			
Lys	Ala	Leu	Lys	Ser	Ala	Asn	Leu	Arg	Ala	Gly	His	Trp	Ala	Ala	Ile
165				170				175							
Ser	Gly	Ala	Ala	Gly	Gly	Leu	Gly	Ser	Leu	Ala	Val	Gln	Tyr	Ala	Lys
180				185				190							
Ala	Met	Gly	Tyr	Arg	Val	Leu	Gly	Ile	Asp	Gly	Gly	Pro	Gly	Lys	Glu
195				200				205							
Glu	Leu	Phe	Thr	Ser	Leu	Gly	Gly	Glu	Val	Phe	Ile	Asp	Phe	Thr	Lys
210				215				220							
Glu	Lys	Asp	Ile	Val	Ser	Ala	Val	Val	Lys	Ala	Thr	Asn	Gly	Gly	Ala
225				230				235				240			
His	Gly	Ile	Ile	Asn	Val	Ser	Val	Ser	Glu	Ala	Ala	Ile	Glu	Ala	Ser
245				250				255							
Thr	Arg	Tyr	Cys	Arg	Ala	Asn	Gly	Thr	Val	Val	Leu	Val	Gly	Leu	Pro
260				265				270							
Ala	Gly	Ala	Lys	Cys	Ser	Ser	Asp	Val	Phe	Asn	His	Val	Val	Lys	Ser
275				280				285							
Ile	Ser	Ile	Val	Gly	Ser	Tyr	Val	Gly	Asn	Arg	Ala	Asp	Thr	Arg	Glu
290				295				300							
Ala	Leu	Asp	Phe	Phe	Ala	Arg	Gly	Leu	Val	Lys	Ser	Pro	Ile	Lys	Val

305 310 315 320
Val Gly Leu Ser Ser Leu Pro Glu Ile Tyr Glu Lys Met Glu Lys Gly

 325 330 335

Gln Ile Ala Gly Arg Tyr Val Val Asp Thr Ser Lys

 340 345

<210> 646

<211> 339

<212> PRT

<213> Candidatus Accumulibacter

<400> 646

Met Arg Val Met Gln Ile Gln Asp Asp Trp Gly Leu Gly Asn Leu Arg

1 5 10 15

Leu Ala Glu Arg Ala Gln Pro Gln Pro Gly Pro Gly Gln Val Leu Leu

 20 25 30

Arg Met Arg Ala Ala Ser Leu Asn Tyr Arg Asp Leu Val Val Pro Glu

 35 40 45

Arg Gly Tyr Gly Ser Phe Thr Gly Thr Leu Pro Leu Ile Pro Val Ser

 50 55 60

Asp Gly Val Gly Glu Val Val Glu Val Gly Ala Gly Val Arg Arg Val

65 70 75 80

Ala Pro Gly Asp Arg Val Cys Pro Cys Phe Phe Gln Gly Trp Ile Ser

 85 90 95

Gly Asp Pro Glu Leu Gly Arg Met Thr Gly Ser Leu Gly Gly Pro Leu

 100 105 110

Asp Gly Ala Met Ala Glu Phe Met Cys Leu Ser Glu Gln Gly Val Val

 115 120 125

Lys Ile Pro Ser Cys Leu Ser Asp Leu Glu Ala Ala Thr Leu Pro Cys

 130 135 140

Ala Ala Leu Thr Ala Trp Ser Ala Leu Val Thr His Gly Arg Val Gly

145 150 155 160

Pro Gly Glu Arg Val Leu Val Gln Gly Ser Gly Gly Val Ala Leu Phe

 165 170 175

Ala Leu Ala Phe Ala Arg Ile Ala Gly Ala His Val Thr Val Ile Ser
180 185 190
Ser Ser Asp Glu Lys Ile Glu Arg Leu Arg Ala Leu Gly Ala Asp Ala
195 200 205

Thr Ile Asn Tyr Thr Arg Thr Pro Glu Trp Ser Lys Thr Ala Arg Glu
210 215 220
Ile Thr Gly Gly Arg Gly Phe Asp His Ile Val Glu Leu Gly Gly Glu
225 230 235 240
Lys Thr Leu Pro Gln Ser Leu Arg Cys Ile Arg Ala Gly Gly Thr Leu
245 250 255
Ser Met Ile Gly Val Leu Ser Gly Ser Leu Leu Ala Val Pro Leu Gly
260 265 270

Leu Ile Val Thr Arg Gln Val Arg Leu Gln Gly Ile Thr Val Gly His
275 280 285
Arg Asp Gly Phe Glu Ala Met Leu Arg Ala Leu Glu Gln His Arg Pro
290 295 300
Ala Ile Thr Val Asp Arg Val Phe Glu Phe Thr Ala Leu Arg Glu Ala
305 310 315 320
Leu Ala Tyr Leu Arg Ser Gly Val Gln Phe Gly Lys Ile Cys Ile Arg
325 330 335

His Pro Asp

<210> 647

<211> 366

<212> PRT

<213> Actinotignum schaalii

<400> 647

Met Lys Ala Ala Val Val Asn Ser Val Gly Gly Gly Phe Thr Ile Glu
1 5 10 15
Asp Ile Glu Ile Ala Glu Pro Ile Gly Arg Glu Val Leu Phe Asp Val
20 25 30
Lys Ala Ser Gly Leu Cys Arg Ser Asp Leu Thr Leu Ser Thr Thr Asn

35 40 45
 Phe Gly Phe Pro Phe Pro Gln Val Leu Gly His Glu Ala Ala Gly Val

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

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

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

 245 250 255
 Leu Gly Ile Val Pro Thr Met Glu Thr Ala Ile Ala Ala Thr Arg Gln
 260 265 270
 Gly Gly Asp Val Tyr Val Ala Gly Val Phe Lys Pro Glu Met Glu Trp
 275 280 285

Thr Ile Asn Pro Leu Asn Glu Phe Phe Val His Arg Arg His Ile His
290 295 300

Ala Val Tyr Met Gly Asn Thr Asp Ile Lys Thr Asp Ile Pro Gln Tyr

305 310 315 320

Val Glu Phe Tyr Gln Gln Gly Arg Leu His Leu Asp Asp Leu Val Ala
325 330 335

Thr Glu Ile Ala Leu Asp Asp Ile Asp Ala Thr Tyr Lys Ala Met Val
340 345 350

Asp His His Ala Gly Ile Gly Arg Val Val Ile Thr Ser Phe
355 360 365

<210> 648

<211> 349

<212> PRT

<213> Tepidicaulis marinus

<400> 648

Met Lys Ser Gln Ala Ile Val Glu Tyr Gly Gln Pro Leu Gln Glu Val
1 5 10 15

Thr Ala Asp Met Pro Glu Pro Lys Gly Gly Glu Val Leu Val Lys Val
20 25 30

Ser His Cys Gly Val Cys His Ser Asp Val His Leu His Asp Gly Tyr
35 40 45

Phe Asp Leu Gly Gly Gly Asn Lys Leu Asp Val Arg Gly Gly Arg Gln
50 55 60

Leu Pro Phe Thr Leu Gly His Glu Ile Glu Gly Glu Val Val Ala Val
65 70 75 80

Gly Pro Asp Ala Lys Gly Val Gln Val Gly Asp Gln Arg Val Val Tyr
85 90 95

Pro Trp Ile Gly Cys Gly Glu Cys Pro Thr Cys Lys Arg Asp Glu Glu
100 105 110

Gln Leu Cys Asn Lys Pro Arg Gln Leu Gly Ile Gln Val Ala Gly Gly
115 120 125

Tyr Ala Thr His Val Met Val Pro Asp Ala Lys Tyr Leu Leu Asp Tyr
 130 135 140
 Ser Gly Val Lys Glu Gly Leu Ala Ala Thr Tyr Met Cys Ser Gly Leu
 145 150 155 160
 Thr Ala Tyr Ser Ala Met Lys Lys Leu Gly Asp Ile Ser Pro Glu Glu
 165 170 175
 Arg Val Met Val Val Gly Leu Gly Gly Val Gly Met Met Gly Leu Gln
 180 185 190

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

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

 Val Glu Glu Arg Pro Leu Asp Gln Ala Ser Lys Ser Leu Asp Asp Leu
 325 330 335
 Arg Glu Gly Lys Ile Met Gly Arg Val Val Leu Lys Pro
 340 345
 <210> 649
 <211> 363
 <212> PRT
 <213> Sporisorium scitamineum

<400> 649

Met Ser Ser Glu Ser Ile Pro Gln Lys Met Arg Ala Ala Thr Ile Lys

1 5 10 15

Asp Phe Lys Lys Gly Tyr Glu Val Lys Asp Ile Asp Val Pro Thr Asp

20 25 30

Leu Gly Pro Asn Asp Ile Leu Val Lys Ile Ala Ala Ala Gly Tyr Cys

35 40 45

His Thr Asp Leu Gln Val Met Glu Gly Val Tyr Glu Ser Gln Gly Ala

50 55 60

Lys Pro Gly Leu Val Gly Ser His Glu Pro Val Gly Ile Val Val Lys

65 70 75 80

Ala Gly Ser Asp Ala Gly Lys Ser Gly Ile Lys Val Gly Asp Arg Val

85 90 95

Gly Ser Ile Asn Thr Tyr Gly Phe Cys Gly Lys Cys Asp Ser Cys Lys

100 105 110

Gln Gly Lys Gln Leu Cys Asp Lys Leu Pro Gly Met Leu Gly Leu Thr

115 120 125

Leu Ser Gly Gly Phe Ser Gln Tyr Met Lys Ala Asp Ala Arg Val Val

130 135 140

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

145 150 155 160

Cys Ala Gly Ala Thr Val Tyr Gly Ala Leu Leu Ala Val Lys Pro Glu

165 170 175

Lys Gly Gln Trp Leu Ala Met Val Gly Ile Gly Gly Leu Gly His Leu

180 185 190

Gly Val Gln Tyr Ala Lys Ala Met Gly Cys Lys Val Ile Ala Ile Asp

195 200 205

Asn Arg Arg Glu Gly Leu Asp Leu Ala Asn Lys Ser Pro Asp His Leu

210 215 220

Lys Pro Asp Lys Thr Phe Leu Ile Asp Ser Lys Glu Ala Gln Asn Lys

225 230 235 240

Val Ala Glu Glu Leu Ser Gly Ser Phe Tyr Glu Thr Asn Pro Gly Val
245 250 255
Asp Arg Val Val Ile Asn Cys Glu Asp Arg Ser Leu Ile Lys Phe Ser
260 265 270
Gln Gln Phe Leu Arg Lys Gly Gly Gln Leu Val Asp Val Gly Leu Pro
275 280 285
Ala Asp Gly Pro Phe Glu Leu Asp Ser Phe Ala Met Asn Phe Lys Glu
290 295 300
Gln Thr Ile Arg Gly Arg Leu Ile Cys Thr Pro Glu Gln Cys Gln Asp
305 310 315 320
Met Ile Asn Leu His Ala Asp Asn Gly Cys Thr Thr Phe Ile Glu Lys
325 330 335
Thr Tyr Ser Val Asp Glu Ala Asn Asp Met Ala Glu His Tyr Asn Ser
340 345 350
Lys Lys Leu Gln Gly Arg Leu Cys Met Val Phe
355 360
<210> 650
<211> 310
<212> PRT
<213> Aspergillus rambellii
<400> 650
Ile Ser His Thr Arg Asn Leu Gln Ile Met Thr Ala Val Ala Ile Pro
1 5 10 15
Lys Thr Gln Ile Ala Ala Val Leu Pro Ser Gly Ala Thr Leu Glu Ala
20 25 30
Arg Leu Asp Ile Arg Asn Asp Arg Pro Val Pro Thr Pro Ala Glu Gly
35 40 45
Glu Val Leu Val Lys Leu Glu Tyr Ser Gly Val Cys His Ser Asp Val
50 55 60
His Ser Val Arg Gly Glu Thr Pro Met Leu Thr Asp Val Ala Gly His
65 70 75 80
Glu Gly Val Gly Arg Val Val Gln Glu Tyr Leu Val Ser Pro Ala Ala

85 90 95
His Val Thr Lys Ile Pro Ala Glu Leu Asp Pro Asp Thr Ala Ala Pro

100 105 110
Leu Leu Cys Ala Gly Ile Ala Met Tyr Ser Ser Ile Met Lys Thr Lys

115 120 125
Thr Leu Pro Gly Asp Trp Ile Val Leu Pro Gly Ala Gly Gly Gly Leu

130 135 140
Gly His Met Gly Val Gln Ile Ala Val Lys Lys Gly Leu Lys Val Ile

145 150 155 160
Ala Ile Asp Ser Gly Glu Lys Lys Lys Gln Leu Cys Leu Lys Leu Gly

165 170 175
Ala Thr Ile Phe Leu Asp Tyr Lys Thr Asp Asn Val Glu Ser Glu Val

180 185 190
Lys Ala Leu Thr Ser Gly Leu Gly Ala His Ala Val Ile Cys Thr Ala

195 200 205
Gln Ser Glu Ala Ala Tyr Glu Gln Ser Leu Arg Leu Leu Arg Ser Leu

210 215 220
Gly Val Leu Val Cys Val Gly Ile Pro Asn Val Pro Phe Arg Leu Pro

225 230 235 240
Ala Ser Pro Phe Asp Met Ile Val Lys Gly Leu Thr Ile Val Gly Asn

245 250 255
Ser Ala Gly Thr Ala Arg Glu Met Glu Glu Leu Met Glu Met Ala Val

260 265 270
Ala Gly Asp Val Lys Ala His Ile Glu Cys Phe Glu Phe Asp Gln Ile

275 280 285
Asp Asp Val Ile Gln Arg Leu Gly Arg Ser Glu Ile Asp Gly Arg Ala

290 295 300
Val Met Arg Ile Pro Glu

305 310
<210> 651
<211> 364

<212> PRT

<213> Ensifer adhaerens

<400> 651

Met Lys Ser Lys Ala Ala Leu Leu Val Asp Tyr Asn Ala Pro Leu Val

1 5 10 15

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

20 25 30

Arg Ile Lys Ala Ala Gly Val Cys His Ser Asp Leu His Ala Ile Asn

35 40 45

Gly Gln Tyr Thr His Asn Leu Pro Leu Val Leu Gly His Glu Gly Ala

50 55 60

Gly Ile Val Glu Asp Val Gly Gln Gly Val Thr Asn Val Arg Pro Gly

65 70 75 80

Asp His Val Val Leu Ser Trp Leu Pro Ser Cys Gly Lys Cys Arg Pro

85 90 95

Cys Leu Arg Gly Arg Pro Ala Asn Cys Glu Asp Ala Ser Trp Pro Ser

100 105 110

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

115 120 125

Thr Val Phe His Tyr Gly Ala Thr Ser Thr Phe Ser Glu Leu Thr Val

130 135 140

Val Pro Ser Gln Ser Ala Val Pro Val Ala Arg Asp Ala Pro Leu Thr

145 150 155 160

Ala Leu Ser Leu Ile Gly Cys Ala Val Ser Thr Gly Val Gly Ala Ala

165 170 175

Leu Asn Thr Ala Lys Leu Ser Pro Gln Asp Arg Val Ala Val Val Gly

180 185 190

Cys Gly Gly Val Gly Leu Asn Ile Val Gln Gly Ala Arg Ile Ala Gly

195 200 205

Ala Gln Thr Ile Val Ala Val Asp Arg Ser Ser Glu Asn Leu Glu Leu

210 215 220

Ala Arg Arg Leu Gly Ala Thr His Leu Val Asn Ser Glu Glu Gly Asp

225 230 235 240

Val Ile Ala Asn Val Gln Ala Ile Thr Asp Gly Gly Val Asp Phe Ala

245 250 255

Phe Glu Ala Val Gly Arg Arg Val Thr Ile Ala Leu Ala Met Ala Leu

260 265 270

Leu Ala Arg Gly Gly Arg Leu Val Leu Val Gly Met Ala Ser Arg Glu

275 280 285

Glu Val Leu Gly Leu Asp Val Leu Asp Thr Val Val Arg Glu Val Gly

290 295 300

Val Val Gly Cys Trp Tyr Gly Ser Cys Asp Pro Gln Arg Asp Phe Pro

305 310 315 320

Arg Leu Val Asp Phe Tyr Lys Ser Gly Ser Leu Lys Leu Asp Glu Met

325 330 335

Ile Glu Val Arg Pro Leu Glu Asp Ile Asn Leu Ala Phe Ser Asn Leu

340 345 350

Ala Lys Ser Thr Gly Gly Arg Thr Val Ile Ala Phe

355 360

<210> 652

<211> 313

<212> PRT

<213> Bacillus campisalis

<400> 652

Met Lys Ala Trp Gln Phe Thr Glu Val Asn Lys Pro Leu Glu Leu Ile

1 5 10 15

Glu Ala Pro Glu Pro Thr Pro Gly Lys Asp Glu Val Lys Ile Lys Val

20 25 30

Lys Ala Ser Gly Leu Cys His Ser Asp Val Gly Val Ile Glu Gly Val

35 40 45

Thr Thr Pro Ser Leu Gly Lys Ile Pro Met Ile Leu Gly His Glu Ile

50 55 60

Ala Gly Val Ile Thr Glu Leu Gly Glu Gly Val Thr Asp Phe Glu Val
65 70 75 80
Gly Asp Arg Val Ala Val Arg Ala Gly Ala Asp Ala Pro Gly Ser Ala
85 90 95
Thr Asp Gly Gly Tyr Ala Glu Phe Thr Val Ser Pro Ser Lys Phe Val
100 105 110
Val Lys Ile Pro Asp Asn Val Asp Phe Ile Ser Ala Ala Ser Ala Thr
115 120 125
Asp Gly Gly Met Thr Ser Tyr His Ala Leu Ser Val Thr Gly Gln Val
130 135 140
Lys Glu Gly Asp Lys Val Ala Ile Val Gly Leu Gly Gly Leu Gly Leu
145 150 155 160
Tyr Gly Ala Gln Ile Ala Leu Gly Leu Gly Ala Thr Val Tyr Gly Val
165 170 175
Asp Ile Lys Glu Glu Ser Arg Lys Ala Ala Glu Gln Met Gly Val Lys
180 185 190
Asn Cys Val Lys Asp Val Arg Glu Leu Ala Asp Glu Glu Ile Asp Val
195 200 205
Val Val Asp Phe Val Gly Tyr Glu Thr Thr Leu Ser Gly Ser Ile Glu
210 215 220
Ala Val Arg Pro Asn Gly Arg Val Val Leu Ile Gly Leu Gly Gly Ser
225 230 235 240
Glu Gly Lys Ile Asn Ile Phe Lys Phe Val Thr Lys Ser Leu Thr Met
245 250 255
Ala Ser Ser Ile Gly Gly Thr Thr Asp Asp Leu Lys Ala Val Leu Glu
260 265 270
Leu Ile Gly Asn Gly Asp Val Lys Pro Leu Leu His Gln Ile Lys Phe
275 280 285
Asp Glu Ile Ser Glu Gly Leu Gln Gln Leu Ala Asp Asn Lys Val Thr
290 295 300
Gly Arg Leu Val Ala Val Ile Asp Asn

305 310

<210> 653

<211> 337

<212> PRT

<213> Unknown

<220><223> Streptomyces sp. MMG1533

<400> 653

Met Lys Ala Ala Val Val Thr Asp Leu Gly Lys Pro Leu Glu Ile Gln
1 5 10 15
Glu Leu Pro Val Pro Glu Pro Gly Pro Gly Gln Val Leu Val Lys Met
20 25 30
Glu Ala Ser Gly Leu Cys His Thr Asp Ile His Ala Ala His Gly Asp
35 40 45
Trp Pro Val Lys Pro Arg Pro Pro Phe Val Pro Gly His Glu Gly Val
50 55 60
Gly Pro Val Gln Ala Val Gly Glu Gly Val Ser Ala Asp Leu Val Gly
65 70 75 80
Lys Arg Val Ala Ile Pro Trp Leu Gly Ser Ser Cys Gly Thr Cys Arg
85 90 95
Tyr Cys Val Ser Gly Trp Glu Thr Leu Cys Glu Ser Gln Val Asn Ser
100 105 110
Gly Tyr Ser Val Asp Gly Cys Tyr Ala Glu Tyr Ala Val Ala Asp Ala
115 120 125
Gly Ala Val Val Pro Val Pro Gln Gly Val Ser Ser Phe Asp Ala Ala
130 135 140
Pro Leu Thr Cys Ala Gly Val Thr Thr Tyr Lys Ala Ile Lys Val Ala
145 150 155 160
Arg Val Val Pro Ala Glu Arg Val Ala Val Phe Gly Val Gly Gly Leu
165 170 175
Gly His Leu Ala Val Gln Tyr Ala Arg Leu Val Gly Gly Phe Val Thr
180 185 190
Ala Val Asp Leu Glu Pro Asp Lys Leu Gly Leu Ala His Arg Leu Glu

195 200 205
Ala Asp Gln Leu Val Asn Ala Arg Thr His Asp Pro Val Glu Glu Ile
210 215 220
Lys Lys Ala Gly Gly Ala Asp Val Ala Val Val Leu Ala Ala Ser Pro

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

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

<210> 654

<211> 348

<212> PRT

<213> Bosea vaviloviae

<400> 654

Met Arg Cys Tyr Gln Ile Asn Glu Phe Gly Gly Ser Val Glu Pro Ala
1 5 10 15

Asp Ile Glu Leu Leu Pro Val Thr Gly Ser Ser Val Arg Leu Lys Val
20 25 30
Ile Ala Ala Gly Val Cys His Ser Asp Val His Ile Cys Glu Gly His
35 40 45
Tyr Asp Leu Gly Gly Gly Arg Lys Ile Ser Phe Ala Glu Arg Ile Lys
50 55 60

Phe Pro Arg Thr Leu Gly His Glu Val Ser Gly Glu Val Val Glu Val
65 70 75 80

Gly Pro Asp Val Glu Gly Val Ala Val Gly Asp Val Cys Leu Val Cys
85 90 95

Ser Trp Ile Gly Cys Gly Glu Cys Glu Gln Cys Ala Gln Gly Leu Glu
100 105 110

Asn Leu Cys Val Asn Pro Arg Phe Val Gly Val Asn Arg Asp Gly Gly
115 120 125

Phe Ala Glu Phe Val Asp Val Pro Asp Pro Arg Tyr Leu Ile Asp Leu
130 135 140

Gly Gln Leu Asp Pro Ile Ala Ala Ala Pro Met Val Cys Ser Gly Leu
145 150 155 160

Thr Thr Phe Ser Ala Leu Lys Lys Phe Gly Pro Leu Glu Gly Arg Arg
165 170 175

Pro Ile Val Val Val Gly Ala Gly Gly Leu Gly Leu Ile Ala Ile Ala
180 185 190

Val Ala Arg Met Leu Gly Ser Val Gly Val Val Val Val Glu Leu Asp
195 200 205

Ala Ala Lys Arg Glu Ala Ala Leu Ala Ala Gly Ala Leu Ala Ala Ile
210 215 220

Ala Pro Gly Glu Ser Ala Leu Glu Asp Ile Arg Gln Ala Val Gly Gly
225 230 235 240

Pro Val Trp Ala Val Leu Asp Leu Val Gly Ser Gly Ser Thr Ala Lys
245 250 255

Leu Ala Val Asp Ala Leu Asp Lys Thr Gly Lys Leu Val Val Val Gly
260 265 270

Leu Phe Gly Gly Ala Ile Asp Leu Pro Val Pro Thr Phe Pro Leu Lys
275 280 285

Val Leu Thr Ile Gln Gly Ser Tyr Thr Gly Ser Pro Ala Glu Leu Arg
290 295 300

Glu Phe Val Ala Leu Ala Arg Glu Lys Gly Leu Pro Ala Ala Pro Leu

305	310										315					320				
Asp	Lys	Arg	Pro	Leu	Ser	Ala	Ala	Pro	Ala	Ala	Leu	Ala	Asp	Leu	Lys					
325					330					335										
Ala	Gly	Arg	Val	Ile	Gly	Arg	Val	Val	Leu	Gln	Pro									
340					345															
<210>	655																			
<211>	360																			
<212>	PRT																			
<213>	Alcanivorax dieselolei																			
<400>	655																			
Met	Thr	Ala	Glu	Gln	Gln	Asn	Gly	Val	Ser	Asp	Ser	Arg	Arg	Phe	Glu					
1	5				10				15											
Phe	Gln	Glu	Phe	Gly	Gly	Pro	Ile	Ala	Pro	Gln	Thr	Tyr	Gln	Leu	Pro					
20				25				30												
Ala	Pro	Ala	Ser	Asp	Glu	Val	Leu	Leu	Lys	Val	Asn	Tyr	Cys	Gly	Val					
35				40				45												
Cys	His	Ser	Asp	Val	His	Leu	His	Asp	Gly	Tyr	Phe	Glu	Leu	Gly	Gly					
50		55				60														
Asp	Lys	Arg	Leu	Asn	Phe	Ala	Met	Pro	Leu	Pro	Leu	Thr	Leu	Gly	His					
65	70				75				80											
Glu	Val	Ile	Gly	Thr	Val	Val	Ala	Val	Gly	Asp	Gln	Val	Thr	Gly	Val					
85				90				95												
Lys	Pro	Gly	Asp	Gln	Arg	Leu	Ile	Tyr	Pro	Trp	Ile	Gly	Cys	Gly	Lys					
100				105				110												
Cys	Gly	Ala	Cys	Gln	Lys	Gly	Glu	Glu	Asn	Leu	Cys	Val	Thr	Pro	Ala					
115				120				125												
His	Leu	Gly	Val	Asn	Lys	Pro	Gly	Gly	Tyr	Ala	Asp	His	Ile	Val	Val					
130		135				140														
Pro	His	Ser	Arg	Tyr	Leu	Leu	Asp	Ile	Ser	Gly	Leu	Asn	Pro	Gly	Asp					
145	150				155				160											
Ala	Ala	Thr	Leu	Ala	Cys	Ser	Gly	Leu	Thr	Thr	Phe	Ser	Ala	Ile	Asn					

165 170 175
 Lys Val Leu Pro Leu Ala Asp Asp Gln Trp Ile Val Val Ile Gly Cys
 180 185 190
 Gly Gly Leu Gly Gln Met Ala Leu Arg Ile Leu Gln Ala Met Gly Ile
 195 200 205
 Gly Asn Val Ile Gly Ile Asp Leu Ser Glu Glu Lys Arg Lys Leu Ala
 210 215 220
 His Glu Ser Gly Ala Arg His Ser Phe Asp Pro Asn Thr Pro Lys Leu

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

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

355 360

<210> 656

<211> 343

<212> PRT

<213> Unknown

<220><223> Rhizobium sp. Leaf453

<400> 656

Met Ile Pro Lys Met Met Lys Ala Ala Leu Cys Thr Gly Ala Ala Thr

1 5 10 15
 Pro Leu Val Cys Gln Glu Ile Glu Thr Pro Val Pro Gln Ala Gly Gln
 20 25 30
 Leu Leu Val Cys Leu Glu Ser Cys Gly Val Cys His Ser Asp Leu His
 35 40 45
 Leu Arg Asn Gly Asp Glu Asn Leu Pro Asp Glu Phe Tyr Pro Leu Val

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

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

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

 245 250 255

Asn Pro Met Ser Asp Ile Val Ala Ile Ala Leu Val His Asp Pro Val
260 265 270

Pro Leu Ser Met Met Trp Leu Ile Asp Gly Gly His Arg Val Phe Gly
275 280 285

Ser Ser Val Gly Thr Arg Gln Asp Leu Arg Asp Phe Leu Asp Phe Ala
290 295 300

Val Lys Asn Arg Leu Asp Ala Asp Val Glu Val Ile Pro Leu Ser Gln

305 310 315 320

Val Asp Thr Ala Leu Asp Arg Leu Gln Ala Gly Ser Val Thr Gly Arg
325 330 335

Leu Cys Ile Asp Phe Ser Leu
340

<210> 657

<211> 348

<212> PRT

<213> Unknown

<220><223> Mycobacterium sp. Root265

<400> 657

Met Ser Thr Gln Thr Met Arg Ala Gln Arg Phe Tyr Ala Asp Thr Lys
1 5 10 15

Ile Ile Ala Val Glu Asp Val Pro Ile Pro Glu Pro Gly Pro Gly Glu

20 25 30

Val Leu Val Lys Val Ala Phe Cys Gly Ile Cys His Ser Asp Leu Ser
35 40 45

Leu Ile Asn Gly Thr Phe Pro Ser Gln Leu Pro Val Val Thr Gln Gly
50 55 60

His Glu Ala Ser Gly Thr Val Ala Ala Leu Gly Pro Gly Val Thr Gly
65 70 75 80

Trp Ala Glu Gly Asp Arg Val Val Val Ala Ala Gly Arg Pro Cys Gln

85 90 95

Gly Cys Pro Asn Cys Ala Arg Gly Asp Phe Gly Asn Cys Leu Arg Ile
100 105 110

Arg Leu Met Ala Phe Ala Tyr Asp Gly Ala Trp Ala Gln Tyr Thr Val
115 120 125
Ala Gln Ala Phe Gly Leu Thr Arg Val Pro Asp Asn Val Pro Leu Glu
130 135 140
Gln Ala Ala Ile Leu Ala Asp Ala Val Ser Thr Pro Tyr Gly Ala Val
145 150 155 160
Val Arg Thr Gly Lys Val Gly Ile Gly Glu Ser Val Gly Val Trp Gly
165 170 175
Val Gly Gly Val Gly Thr His Ile Val Gln Leu Ala Arg Leu Val Gly
180 185 190
Ala Ala Pro Ile Ile Ala Val Asp Ile Lys Pro Ala Val Leu Asp Arg
195 200 205
Ala Leu Ala Leu Gly Ala Asp Tyr Ala Phe Asp Ala Arg Asp Gly Ala
210 215 220
Leu Gly Glu Lys Ile Ala Glu Leu Thr Gly Gly Arg Gly Leu Asp Ile
225 230 235 240
Ala Phe Asp Ala Val Gly Leu Gly Ser Thr Phe Asp Gln Ala Leu Ala
245 250 255
Ser Leu Thr Met Gly Gly Arg Leu Val Gly Val Gly Met Ser Ala Asp
260 265 270
Ala Pro Ser Ile Gly Pro Thr Ser Phe Phe Asn Leu Thr Arg Lys Gln
275 280 285
Val Leu Gly His Leu Gly Tyr Gln Asn Ala Asp Ile Ala Thr Leu Ala
290 295 300
Asn Leu Val Ser Leu Gly Arg Leu Asp Leu Ser Arg Ser Ile Ser Glu
305 310 315 320
Ile Val Ser Leu Glu Glu Val Ala Ala Gly Ile Glu Lys Leu Glu Arg
325 330 335
Ala Asp Gly Asp Pro Ile Arg Ile Leu Val Gln Pro

340

345

<210> 658

<211> 351

<212> PRT

<213> Didymella rabiei

<400> 658

Met Ser Ser Thr Pro Asp Phe Asn Gly Trp Val Ala His Asp Pro Ser

1 5 10 15

Ala Ala Glu Gly Asn Met Lys Trp Gly Asn Phe Glu Pro Lys Ala Phe

20 25 30

Glu Glu Thr Asp Ile Glu Met Glu Ile Ser His Cys Gly Val Cys Gly

35 40 45

Ser Asp Ile His Thr Leu Arg Ser Gly Trp Gly Pro Ser Asp Tyr Pro

50 55 60

Leu Val Val Gly His Glu Ile Ile Gly His Val Thr Lys Val Gly Lys

65 70 75 80

Asp Val Lys Asp Leu Lys Val Gly Asp Arg Val Gly Val Gly Ala Gln

85 90 95

Ser Glu Cys Cys Glu Ser Cys Arg Pro Cys Lys Met Lys Gln Glu Ser

100 105 110

Asn Cys Asn Ser Leu Thr Met Thr Tyr Asn Ala Lys His Ser Asn Gly

115 120 125

Asp Lys Ser Tyr Gly Gly Tyr Ala Lys Ala Trp Arg Gly Pro Ala Ser

130 135 140

Phe Ala Ile Pro Ile Pro Glu Gly Leu Pro Ser Glu Phe Ala Ala Pro

145 150 155 160

Leu Met Cys Gly Gly Val Thr Val Tyr Asn Pro Leu Val Ser Asn Gly

165 170 175

Ala Gly Pro Gly Lys Arg Val Gly Val Val Gly Val Gly Gly Leu Gly

180 185 190

His Phe Ala Leu Leu Phe Ala Lys Ala Leu Gly Ala Asp Glu Val Val

195 200 205

Ala Ile Ser Arg Ser Ser Ser Lys Lys Glu Asp Ala Ile Lys Leu Gly

210 215 220

Ala Asp Arg Phe Ile Ala Thr Gly Glu Asp Pro Asp Trp Ala Thr Lys
225 230 235 240

Asn Ala Asn Gly Leu Asp Leu Ile Ile Ser Thr Ile Ser Gly Ser Phe
245 250 255

Pro Leu Asp Gln Tyr Leu Asn Leu Leu Asp Val Asn Gly Thr Phe Val
260 265 270

Gln Leu Gly Ala Pro Asp Asp Pro Leu Pro Ser Phe Ser Pro Met Gly
275 280 285

Leu Ile Phe Lys Asn Leu Lys Ile Ala Gly Ser Leu Ile Gly Thr Arg
290 295 300

Gln Gln Ile Arg Asp Met Leu Glu Leu Ala Lys Lys Thr Asn Leu Gln
305 310 315 320

Ala Trp Val Gln Val Arg Pro Met Ser Glu Ala Asn Gln Val Ile Val
325 330 335

Asp Phe Glu Lys Gly Leu Pro Arg Tyr Arg Tyr Val Leu Lys Asn
340 345 350

<210> 659

<211> 350

<212> PRT

<213> Rhizobiales bacterium

<400> 659

Met Arg Ser Met Gln Phe Asp Glu Tyr Gly Ala Pro Leu Lys Ala Phe

1 5 10 15
Ser Tyr Glu Asp Pro Thr Pro Gln Gly Lys Glu Val Val Val Arg Ile

20 25 30

Glu Ala Cys Gly Val Cys His Ser Asp Ile His Leu His Glu Gly Tyr

35 40 45

Phe Asp Met Gly Gly Gly Asn Lys Ala Asp Val Thr Arg Ala Arg Glu

50 55 60

Leu Pro Phe Thr Leu Gly His Glu Ile Val Gly Glu Val Val Ala Thr

65 70 75 80

Gly Pro Gly Val Thr Gly Ala Lys Pro Gly Asp Lys Arg Ile Val Tyr
85 90 95
Pro Trp Ile Gly Cys Gly Asp Cys Pro Lys Cys Asn Ser Gly Glu Asp
100 105 110
Gln Ser Cys Ala Arg Pro Arg Asn Leu Gly Val His Val Asp Gly Gly
115 120 125
Tyr Ser Thr His Val Lys Ile Pro Asp Glu Lys Phe Leu Phe Ala Tyr
130 135 140
Asp Gly Ile Pro Thr Glu Leu Ala Gly Thr Tyr Ala Cys Ser Gly Ile
145 150 155 160
Thr Ala Tyr Gly Ala Leu Met Lys Ala Lys Glu Ala Ala Glu Arg Ser
165 170 175
Gly Tyr Ile Gly Leu Ile Gly Ala Gly Gly Val Gly Met Ala Gly Leu
180 185 190
Met Leu Ala Lys Ala Ala Ile Gly Ala Lys Thr Val Val Phe Asp Ile
195 200 205
Asp Asp Ala Lys Leu Glu Ala Ala Thr Arg Ala Gly Ala Asp Tyr Val
210 215 220
Phe Asn Ser Gly Ala Lys Glu Thr Arg Lys Glu Val Met Lys Leu Thr
225 230 235 240
Asn Gly Gly Leu Ser Gly Ala Val Asp Phe Val Gly Ser Asp Lys Ser
245 250 255
Ala Leu Phe Gly Ile Asn Ala Leu Gly Gln Asn Gly Val Leu Val Ile
260 265 270
Ile Gly Leu Phe Gly Gly Ala Met Thr Val Pro Val Pro Leu Phe Pro
275 280 285
Leu Lys Gly Ile Thr Val Arg Gly Ser Tyr Val Gly Ser Leu Gln Glu
290 295 300
Met Ser Asp Met Met Glu Leu Val Arg Ala Gly Lys Val Pro Pro Met
305 310 315 320
Pro Val Lys Thr Arg Pro Leu Asp Ala Ala Trp Glu Thr Leu Glu Asp

325 330 335
 Leu Arg His Gly Lys Ile Val Gly Arg Val Val Leu Thr Pro
 340 345 350
 <210> 660
 <211> 343
 <212> PRT
 <213> Unknown
 <220><223> Nocardia sp. 852002-20019_SCH5090214
 <400> 660
 Met Arg Ala Ala Gln Leu Pro Ser Leu Gly Ser Asp Leu Glu Ile Val
 1 5 10 15
 Glu Val Pro Asp Pro Thr Pro Gly Pro Gly Glu Val Val Val Arg Ile
 20 25 30

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

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

 Val Leu Glu Arg Leu Ser Gly Ser Asp Arg Ser Val Gly Ile Ile Gly
 165 170 175
 Ala Gly Gly Leu Gly Gln Phe Ala Ile Lys Tyr Leu Ala Ala Leu Thr

180 185 190
 Ser Ala Thr Ile Val Ala Ile Asp Thr Asp Glu Ala Lys Arg Ala His
 195 200 205
 Ala Leu Asp Ile Gly Ala Ala Leu Ser Val Asp Pro Thr Thr Asp Asp
 210 215 220

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

 Ser Thr Ser Ser Leu Gly Ser Arg Ala Asp Leu Ala Thr Val Ile Glu
 290 295 300
 Leu Trp Lys Glu His Gly Ile Asn Ala Glu Thr Thr Arg Tyr Arg Leu
 305 310 315 320
 Asp Glu Val Asn Asp Ala Leu Arg Asp Leu Ala Ala His Lys Ile Gly
 325 330 335
 Glu Arg Ala Val Leu Val Leu
 340
 <210> 661
 <211> 331
 <212> PRT
 <213> Tortispora caseinolytica

 <400> 661
 Met Gln Thr Ala Phe Leu Tyr Lys Pro Gly His Glu Asn Leu Val Arg
 1 5 10 15
 Ser Glu Ile Pro Ile Pro Lys Ala Gly Arg Gly Glu Val Val Leu Glu
 20 25 30
 Ile Lys Ala Ala Gly Met Cys His Ser Asp Leu His Val Leu Asp Gly
 35 40 45

Gly Ile Pro Leu Pro Gly Gln Phe Val Met Gly His Glu Ile Val Gly
50 55 60

Thr Ile His Glu Ile Gly Gln Asp Val Thr Gly Phe Lys Gln Gly Asp
65 70 75 80

Leu Tyr Ala Val His Gly Pro Asn Pro Cys Gly Ile Cys Thr Leu Cys
85 90 95

Arg Glu Gly Phe Asp Asn Asp Cys Thr Thr Val Ala Lys Thr Gly Gln
100 105 110

Trp Phe Gly Leu Gly Leu Asp Gly Gly Tyr Gln Lys Tyr Ile Arg Ile
115 120 125

Pro Asn Val Arg Ser Ile Val Lys Val Pro Glu Gly Val Ser Ala Glu
130 135 140

Ala Ala Ala Ser Cys Thr Asp Ala Val Leu Thr Pro Tyr Arg Ala Leu
145 150 155 160

Lys Gln Ala Gly Ala Ser Asn Ser Thr Arg Val Leu Ile Leu Gly Leu
165 170 175

Gly Gly Leu Gly Leu Asn Ala Leu Lys Leu Ala Lys Thr Phe Gly Ser
180 185 190

Tyr Val Tyr Ala Ser Asp Leu Lys Pro Ser Ala Arg Glu Ala Ala Lys
195 200 205

Ala Ala Gly Ala Asp Glu Val Leu Glu Ser Leu Pro Glu Asp Pro Leu
210 215 220

Gly Val Asp Ile Val Leu Asp Val Val Gly Val Gln Ser Thr Phe Asn
225 230 235 240

Leu Ala Gln Lys His Val Gly Pro Arg Gly Ile Ile Val Pro Val Gly
245 250 255

Leu Ala Ser Pro Gln Leu Ser Phe Asn Leu Thr Asp Leu Ala Leu Arg
260 265 270

Glu Ile Arg Val Gln Gly Thr Phe Trp Gly Thr Ser Asn Glu Leu Ala
275 280 285

Glu Cys Leu Arg Leu Cys Gln Leu Gly Leu Ile Asn Pro Lys Tyr Thr

290 295 300
Val Val Pro Leu Glu Glu Ala Pro Lys Tyr Met Glu Ala Met Ala His
305 310 315 320

Gly Lys Val Glu Gly Arg Ile Val Phe His Pro
325 330

<210> 662

<211> 385

<212> PRT

<213> Unknown

<220><223> Duganella sp. HH101

<400> 662

Met Lys Ile Thr Ala Ala Leu Ala Arg Gly Ala Arg Gln Ala Leu Ala
1 5 10 15

Val Thr Glu Leu Glu Leu Asp Glu Pro Arg Asp Asp Glu Val Leu Val
20 25 30

Arg Val Val Ala Ser Gly Ile Cys Arg Thr Asp Ile Asp Val Arg Asp

35 40 45
Gly Tyr Leu Pro Thr Pro Thr Pro Val Val Leu Gly His Glu Gly Ser
50 55 60

Gly Val Val Val Arg Val Gly Arg Leu Val Arg Gln Phe Ala Pro Gly
65 70 75 80

Asp His Val Val Met Ser Met Gly Ser Cys Gly Val Cys Pro Ser Cys
85 90 95

Gln Val Gly Met Pro Ala Tyr Cys Val Gln His Val Pro Leu Asn Phe

100 105 110
Met Gly Ser Arg Pro Asp Gly Ser Val Cys Met His Glu His Gly Glu
115 120 125

Arg Val His Ser His Phe Phe Ser Gln Ser Ser His Ala Ser Phe Thr
130 135 140

Val Ala His Gln Ser Ser Leu Val Lys Val Ala Asp Asp Val Asp Leu
145 150 155 160

Arg Trp Leu Gly Pro Leu Ala Cys Gly Val Met Thr Gly Ala Gly Gly

165 170 175

Val Ile Asn Thr Leu Lys Pro Glu Ala Gly Thr Ser Ile Val Ile Phe

180 185 190

Gly Ala Gly Thr Val Gly Leu Ser Ala Leu Met Ala Ser Lys Ile Val

195 200 205

Ala Cys Ser Arg Arg Ile Val Val Asp Asn Lys Pro Glu Arg Leu Ala

210 215 220

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

225 230 235 240

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

245 250 255

His Asn Ala Phe Glu Ser Ser Gly Val Lys Ser Val Ile Gly Ala Ala

260 265 270

Leu Thr Ala Ile Arg Glu Arg Gly Thr Cys Val Ile Thr Gly Val Leu

275 280 285

Pro Gln Gly Ser Val Val Glu Phe Asp Ala Trp Gln Leu Leu Arg Gly

290 295 300

Arg Thr Val Arg Gly Ser Val Met Gly Asp Cys Leu Pro Ser Gln Phe

305 310 315 320

Ile Pro Arg Leu Val Glu Phe Tyr Arg Gln Gly Gln Leu Pro Leu Glu

325 330 335

Lys Ile Ser Arg Leu Tyr Pro Leu Ala Asp Ile Asn Gln Ala Ile Glu

340 345 350

Asp Gly Ile Ser Gly Ala Val Val Lys Ala Ile Val Val Met Pro His

355 360 365

Pro Asp Ala Ser Thr Thr Gln Asp Tyr His Asp Arg Thr Gln Gln Ser

370 375 380

Phe

385

<210> 663

<211> 341

<212> PRT

<213> Chloroflexi bacterium

<400> 663

Met Arg Ala Leu Glu Leu Val Gly Phe Asp Gly Pro Gly Ser Leu Arg

1 5 10 15

Leu Gly Asp Arg Pro Glu Pro Ala Pro Gly Pro Arg Gln Val Arg Val

20 25 30

Arg Leu Arg Ala Ser Ala Leu Asn His Leu Asp Val Phe Val Thr Arg

35 40 45

Gly Leu Pro Lys Arg Pro Leu Pro Ala Ile Leu Gly Ala Asp Gly Ala

50 55 60

Gly Val Ile Asp Ala Val Gly Val Gly Val Glu Arg Arg Arg Val Gly

65 70 75 80

Asp Glu Val Val Ile Tyr Pro Val Val Ser Cys Gly Ala Cys Glu Trp

85 90 95

Cys Thr Arg Arg Glu Glu Val His Cys Pro Thr Phe Gly Ile Leu Gly

100 105 110

Glu His Ile Asp Gly Thr Phe Gln Glu Ser Leu Val Val Ala Glu Arg

115 120 125

Ser Ala Phe Thr Arg Pro Gln Arg Leu Ser Trp Pro Glu Val Ala Ala

130 135 140

Leu Pro Leu Ser Phe Leu Thr Ala Trp Arg Leu Leu Phe Thr Arg Gly

145 150 155 160

Arg Leu Glu Arg Gly Asp Ser Leu Val Ile Val Gly Ile Gly Gly Gly

165 170 175

Val Ala Leu Ala Ala Leu Leu Leu Gly Lys Ala Arg Gly Leu Arg Val

180 185 190

Phe Val Thr Ser Arg Asp Pro Ala Lys Leu Glu Arg Ala Lys Met Leu

195 200 205

Gly Ala Asp Ala Ala Tyr Pro Ser Asn Ala Phe Ala Lys Pro Val Arg

210 215 220

Glu Ala Thr Gly Gly Ala Gly Ala Arg Ala Val Val Asp Thr Val Gly

225 230 235 240

Pro Ala Thr Phe Glu Glu Ser Phe Arg Ala Leu Ala Arg Glu Gly Glu

245 250 255

Leu Leu Thr Val Gly Ser Thr Ser Gly Pro Lys Val Glu Leu Met Leu

260 265 270

Pro Arg Leu Phe Phe Arg His Leu Ser Leu Val Thr Ser Thr Met Gly

275 280 285

Thr Ser Arg Glu Phe Glu Ala Met Leu Ala Asp Val Ala Arg Phe His

290 295 300

Ile Arg Pro Val Val Asp Glu Thr Tyr Pro Leu Ala Lys Gly Ala Asp

305 310 315 320

Ala Phe Ala Arg Leu Glu Ala Gly Glu Gln Phe Gly Lys Ile Val Leu

325 330 335

Glu Pro Gly Ser Gly

340

<210> 664

<211> 451

<212> PRT

<213> Unknown

<220><223> Fungal sp. no.14919

<400> 664

Met Glu Val Leu Ser Thr His Pro Asp Met Pro Glu Pro Leu Gly Ala

1 5 10 15

Met Asn His Gly Ser Ser Gly Gln Pro Arg Pro Pro Thr Ser Arg Ile

20 25 30

Glu Thr Pro Asn Leu Gln Thr Pro Tyr Val Arg Asp Asp Thr Glu Ser

35 40 45

Ser Tyr Thr Lys Asn Glu Ser Asn Lys Arg Ala Lys Leu Thr Ile Lys

50 55 60

Glu	Asn	Leu	His	Thr	Lys	Thr	His	Gly	Leu	Phe	Gly	Glu	Val	Pro	Glu
65				70				75				80			
Glu	Gln	Val	Ala	Ile	Leu	Thr	Pro	Phe	Val	Ser	Lys	Pro	Leu	Thr	Leu
85				90				95							
Glu	Leu	Arg	Thr	Val	Pro	Val	Ile	Arg	Pro	Ser	Leu	Gly	Glu	Val	Val
100				105				110							
Val	Arg	Ile	Ala	Trp	Thr	Gly	Ile	Cys	Ala	Ser	Asp	Ile	Tyr	Phe	Ala
115				120				125							
Thr	Gly	Thr	Asp	Ala	Thr	Tyr	Cys	Ser	His	Ser	His	Ile	Gly	Gly	His
130				135				140							
Glu	Gly	Ile	Gly	His	Ile	Val	Gln	Ser	His	Asp	Pro	Ala	His	Ile	Gly
145				150				155				160			
Gln	Ala	Val	Gly	Met	Arg	Phe	Met	Ala	Tyr	Thr	Cys	Gly	Val	Cys	Cys
165				170				175							
Tyr	Cys	Leu	Lys	Gly	Val	Pro	Glu	Ser	Cys	Pro	Arg	Gln	Val	Cys	Phe
180				185				190							
Thr	Arg	His	Leu	Arg	Gly	Ser	Tyr	Gln	Gln	Tyr	Ala	Thr	Val	Pro	Tyr
195				200				205							
Thr	Ser	Leu	Ala	Ile	Leu	Pro	Asp	Tyr	Val	Phe	Gln	His	Glu	Asn	Pro
210				215				220							
Ala	Ile	Tyr	Thr	Thr	Ala	Leu	Cys	Ser	Gly	Ala	Ala	Ala	Leu	Lys	Ala
225				230				235				240			
Leu	Arg	Lys	Ala	Gly	Ile	Arg	Pro	Asn	Asp	Val	Val	Val	Val	Ile	Gly
245				250				255							
Ile	Gly	Gly	Gln	Ile	Gly	Tyr	Leu	Ala	Gly	Val	Met	Ala	Arg	Arg	Val
260				265				270							
Tyr	Ser	Ala	Arg	Val	Val	Gly	Ile	Asp	Ile	Ala	Ser	Lys	Ala	Asn	Ser
275				280				285							
Pro	Thr	Ile	Ser	Glu	Ala	Cys	Asp	Val	Tyr	Leu	Pro	Ser	Pro	Thr	Glu
290				295				300							
Gly	Gly	Thr	His	Met	Ser	Asp	Glu	Phe	Gln	Ser	Leu	Leu	Gln	Ser	Thr

305											310											315											320															
Cys	Thr	Lys	Leu	Arg	Ala	Asp	Pro	Asn	Leu	Pro	Arg	Gly	Ala	Asp	Ala																																	
															325											330											335											
Val	Ile	Ala	Ala	Gly	Ser	Ser	Val	Asp	Ser	Tyr	Arg	Asp	Leu	Pro	Ser																																	
															340											345											350											
Tyr	Val	Cys	Asp	Gly	Gly	Ser	Ile	Gly	Phe	Val	Gly	Ser	Pro	Thr	Tyr																																	
															355											360											365											
Ser	Ile	Thr	Phe	Asp	Val	Lys	Arg	Ile	Leu	Glu	Arg	Gln	Leu	Ser	Ile																																	
															370											375											380											
Lys	Gly	Thr	Leu	Met	Gly	Asp	Arg	Lys	Asp	Ser	Tyr	Gln	Val	Met	Asp																																	
															385											390											395											400
Tyr	Ile	Arg	Ser	Gly	Ile	Leu	Lys	Pro	Lys	Ile	Asn	Glu	Ile	Glu	Leu																																	
															405											410											415											
Gln	Asp	Leu	Pro	Glu	Tyr	Met	Gln	Gly	Phe	Leu	Ala	Gln	Lys	Asn	Trp																																	
															420											425											430											
Gly	Lys	Gly	Val	Ala	Arg	Ile	Asn	Gly	Pro	Leu	Pro	Ser	Ala	Ala	Pro																																	
															435											440											445											
Leu	Thr	Arg																																														
																	450																															
<210>	665																																															
<211>	362																																															
<212>	PRT																																															
<213>	Sphingomonas jeddahensis																																															
<400>	665																																															
Met	Lys	Ala	Ala	Val	Ile	Phe	Glu	Thr	Lys	Ala	Pro	Leu	Gln	Ile	Glu																																	
1					5					10					15																																	
Asp	Val	Val	Val	Ser	Asn	Pro	Gly	Pro	His	Glu	Val	Leu	Ile	Arg	Thr																																	
															20											25											30											
Val	Ala	Cys	Gly	Val	Cys	Arg	Ser	Asp	Leu	His	Phe	Val	Asp	Gly	Ala																																	
															35											40											45											
Tyr	Pro	His	Pro	Leu	Pro	Ala	Ile	Pro	Gly	His	Glu	Ala	Ala	Gly	Ile																																	

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

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

 Asp Val Thr Pro Gly Glu Thr Val Cys Val Val Gly Cys Gly Gly Ile
 180 185 190
 Gly Leu Ala Ala Val Asn Ala Ala Lys Ile Ala Gly Ala Gly Lys Ile
 195 200 205
 Ile Ala Leu Asp Pro Val Pro Glu Lys Arg Ala Val Ala Glu Lys Leu
 210 215 220
 Gly Ala Thr His Thr Tyr Asp Pro Leu Lys Glu Gly Val Val Gly Glu
 225 230 235 240

 Val Val Glu Leu Thr Lys Gly Gly Val His His Ala Ile Glu Ala Val
 245 250 255
 Gly Arg Thr Gln Ser Ala Gln Thr Thr Val Asp Val Leu Arg Arg Gly
 260 265 270
 Gly Thr Ala Thr Ile Leu Gly Met Met Pro Leu Asp Ala Lys Val Gly
 275 280 285
 Leu Ser Ala Met Glu Leu Leu Ser Gly Lys Lys Leu Gln Gly Gly Ile
 290 295 300

Met Gly Ser Asn Arg Phe Pro Val Asp Ile Pro Arg Leu Val Asp Phe
305 310 315 320
Tyr Met Arg Gly Leu Leu Asp Leu Asp Thr Ile Ile Ala Glu Arg Leu
325 330 335
Pro Leu Ser Gln Ile Asn His Ala Phe Asp Glu Leu Arg Lys Gly Asp
340 345 350
Ala Thr Arg Ser Val Ile Val Phe Asp Gln
355 360
<210> 666
<211> 348
<212>
> PRT
<213> Spirochaetes bacterium
<400> 666
Met Lys Ala Ala Ile Phe Thr Gln Phe Gly Gly Pro Ile Thr Ile Thr
1 5 10 15
Glu Val Pro Asp Pro Val Val Ala Ala Asp Gly Val Val Leu Lys Ile
20 25 30
Asp Ala Thr Gly Ile Cys Arg Ser Asp Trp His Gly Trp Lys Gly His
35 40 45
Asp Pro Asp Ile Lys Leu Pro His Val Pro Gly His Glu Leu Ala Gly
50 55 60
Thr Ile Val Glu Val Gly Lys Asp Ile Lys Asn Trp Lys Arg Gly Asp
65 70 75 80
Arg Val Thr Met Pro Phe Val Ala Gly Cys Gly His Cys Leu Pro Cys
85 90 95
Leu Thr Gly Asn Pro Gln Val Cys Asp His Gln Phe Gln Pro Gly Phe
100 105 110
Thr Ala Trp Gly Ser Phe Ala Glu Phe Val Ala Ile Arg Tyr Ala Asp
115 120 125
Met Asn Leu Val Arg Leu Pro Thr Thr Leu Asp Ser Ala Thr Ala Ala
130 135 140
Ser Leu Gly Cys Arg Phe Ala Thr Ala Phe Arg Ala Leu Asp Ala Gln

145 150 155 160
 Ala Lys Leu Arg Pro Gly Glu Trp Val Ala Ile Tyr Gly Cys Gly Gly
 165 170 175
 Val Gly Leu Ser Ala Ile Met Ile Ala Ala Ala Met Gly Ala Arg Ile

 180 185 190
 Ile Ala Ile Asp Ile Gln Lys Glu Lys Leu Glu Lys Ala Lys Glu Leu
 195 200 205
 Gly Ala Asn Val Val Phe Asn Ser Arg Glu Val Pro Asp Ile Val Ala
 210 215 220
 Ala Ile His Glu Val Thr His Gly Gly Ala His Val Ser Met Asp Ala
 225 230 235 240
 Leu Gly Ser Pro Glu Thr Cys Phe Asn Ala Ile Ala Ser Leu Ala Lys

 245 250 255
 Arg Gly Arg His Val Gln Val Gly Leu Met Leu Ala Asp Gln Lys His
 260 265 270
 Pro Ala Ile Pro Met Asp Leu Val Ile Ala Arg Glu Leu Glu Ile Tyr
 275 280 285
 Gly Ser His Gly Ile Gln Ala His Arg Tyr Gly Ala Leu Leu Gly Met
 290 295 300
 Ile Glu Ala Gly Arg Leu Tyr Pro Glu Arg Leu Ile Gln Ala Arg Leu

 305 310 315 320
 Thr Leu Arg Gln Gly Val Asp Phe Leu Gln Lys Met Asp Gln Phe Pro
 325 330 335
 Gly Val Gly Ile Ser Val Ile Thr Ser Ile Ser Pro
 340 345

 <210> 667
 <211> 333
 <212> PRT
 <213> Unknown
 <220><223> Sulfuriferula sp. AH1
 <400> 667
 Met Ile Lys Ala Phe Ala Ala Phe Glu Pro His Gly Glu Leu Lys Pro

1 5 10 15

 Phe Glu Tyr Asp Pro Gly Gln Leu Lys Pro Asp Glu Val Glu Ile Asp
 20 25 30
 Val Gln Tyr Cys Gly Ile Cys His Ser Asp Leu Ser Val Ile Asp Asn
 35 40 45
 Glu Trp Gly Ile Thr Glu Tyr Pro Val Val Pro Gly His Glu Val Val
 50 55 60
 Gly Thr Ile Gly Lys Ile Gly Ala Asp Val Lys His Leu Lys Ile Gly
 65 70 75 80

 Gln Val Val Gly Leu Gly Trp His Ala Gly Tyr Cys Asn Glu Cys Glu
 85 90 95
 Pro Cys Lys Thr Gly Asp Asn Asn Leu Cys Ala Thr Ala Gln Ala Thr
 100 105 110
 Ile Val Gly His His Gly Gly Phe Ala Asp Lys Val Arg Ala Ser Ala
 115 120 125
 Asn Ser Val Val Pro Ile Pro Glu Gly Ile Asp Leu Glu Ser Ala Gly
 130 135 140

 Pro Leu Phe Cys Gly Gly Ile Thr Val Phe Asn Pro Leu Val Gln Phe
 145 150 155 160
 Asp Ile Lys Pro Thr Asp Lys Val Ala Val Ile Gly Ile Gly Gly Leu
 165 170 175
 Gly His Met Ala Leu Gln Phe Leu Asn Gly Trp Gly Cys Asp Val Thr
 180 185 190
 Ala Phe Thr Ser Ser Glu Asn Lys Lys Lys Glu Ala Leu Glu Leu Gly
 195 200 205

 Ala His His Thr Leu Asn Ser Arg Asp Pro Lys Gln Ile Glu Ala Ala
 210 215 220
 Ala Gly Arg Phe Asp Met Ile Ile Ser Thr Val Asn Val Lys Leu Asp
 225 230 235 240
 Trp Asn Leu Tyr Leu Gly Thr Leu Lys Pro Arg Gly Arg Leu His Phe
 245 250 255

Val Gly Ala Thr Leu Asp Pro Leu Asp Ile Asn Val Phe Ser Leu Ile
260 265 270

Met Ala Gln Arg Ser Ile Ser Gly Ser Pro Val Gly Ser Pro Leu Thr
275 280 285

Ile Ala Arg Met Leu Glu Phe Ala Lys Arg His His Val Lys Pro Val
290 295 300

Ile Glu Lys Phe Ser Phe Ala Asp Ile Asn Lys Ala Ile Glu Arg Leu
305 310 315 320

Arg Ser Gly Asn Ala His Tyr Arg Ile Val Leu His Arg
325 330

<210> 668

<211> 340

<212> PRT

<213> Magnusiomyces capitatus

<400> 668

Met Ala Glu Ile Pro Glu Lys Gln Thr Ala Phe Val Phe Lys Asn Gly
1 5 10 15

Ser Phe Ala Leu Glu Lys Lys Glu Ile Glu Val Pro Lys Pro Asp Ala
20 25 30

Gly Lys Val Leu Leu Lys Val Ala Ala Ala Gly Val Cys His Ser Asp
35 40 45

Leu His Val Leu His Gly Gly Leu Pro Tyr Pro Asp Gly Leu Ile Leu

50 55 60

Gly His Glu Ile Ala Gly His Ile Val Ala Tyr Gly Asp Gly Val Asp
65 70 75 80

Lys Ala Ala Phe Pro Ser Asp Ala Leu Tyr Ala Val Val Gly Pro Asn
85 90 95

Pro Cys Gly Met Cys Lys Ala Cys Arg Thr Gly Ala Asp Asn Val Cys
100 105 110

Glu Asp Pro Ser Arg Thr His Met Gly Leu Gly Ser Pro Gly Gly Tyr

115 120 125

Glu Gln Tyr Thr Gln Val Ser Ala Arg Asn Ile Thr Lys Val Pro Glu
 130 135 140
 Gly Ile Pro Ala Ala Val Ala Ala Ala Ser Thr Asp Ala Val Leu Thr
 145 150 155 160
 Pro Tyr His Ala Leu Lys Arg Ala Gly Ile Asn Gly Met Thr Arg Leu
 165 170 175
 Leu Ile Val Gly Leu Gly Gly Leu Gly Ile Asn Ala Val Gln Ile Ala
 180 185 190
 Lys Ala Phe Gly Ser Tyr Val Ile Ala Val Asp Pro Lys Glu Ser Ser
 195 200 205
 Arg Asp Leu Ala Lys Gln Tyr Gly Ala Asn Glu Val Tyr Ala Lys Leu
 210 215 220
 Pro Glu Glu Ser Leu Asp Val Asp Val Ala Ala Asp Phe Tyr Gly Ser
 225 230 235 240
 Gln Gly Thr Phe Asp Leu Cys Gln Lys His Val Lys Ala Gln Gly Ile
 245 250 255
 Leu Leu Pro Val Gly Leu Gln Asp Pro Lys Ile Thr Phe Asp Leu Asn
 260 265 270
 His Leu Ala Phe Arg Glu Tyr Thr Ile Ile Gly Asn Phe Trp Gly Thr
 275 280 285
 Ser Gln Asp Gln Thr Glu Val Phe Glu Leu Val Lys Lys Gly Leu Val
 290 295 300
 Thr Pro Gln Val Glu Thr Thr Ser Trp Leu Asn Val Asn Lys Val Leu
 305 310 315 320
 Lys Asp Leu Asp Glu Gly Lys Ile Lys Ser Arg Met Val Leu Val His
 325 330 335
 Asn Glu Asp Asn
 340
 <210> 669
 <211> 341
 <212> PRT
 <213> Salmonella arizonae

<400> 669

Met Lys Ala Leu Ser Lys Leu Lys Ala Glu Glu Gly Ile Trp Met Thr

1 5 10 15

Asp Val Pro Glu Pro Glu Val Gly His Asn Asp Leu Leu Ile Lys Ile

20 25 30

Arg Lys Thr Ala Ile Cys Gly Thr Asp Val His Ile Tyr Asn Trp Asp

35 40 45

Glu Trp Ser Gln Lys Thr Ile Pro Val Pro Met Val Val Gly His Glu

50 55 60

Tyr Val Gly Glu Val Val Gly Ile Gly Gln Glu Val Lys Gly Phe Asn

65 70 75 80

Ile Gly Asp Arg Val Ser Gly Glu Gly His Ile Thr Cys Gly His Cys

85 90 95

Arg Asn Cys Arg Gly Gly Arg Thr His Leu Cys Arg Asn Thr Thr Gly

100 105 110

Val Gly Val Asn Arg Pro Gly Cys Phe Ala Glu Tyr Leu Val Ile Pro

115 120 125

Ala Phe Asn Ala Phe Lys Ile Pro Asp Asn Ile Ser Asp Asp Leu Ala

130 135 140

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

145 150 155 160

Asp Leu Val Gly Glu Asp Val Leu Val Ser Gly Ala Gly Pro Ile Gly

165 170 175

Val Met Ala Ala Ala Val Ala Lys His Val Gly Ala Arg His Val Val

180 185 190

Ile Thr Asp Val Asn Glu Tyr Arg Leu Glu Leu Ala Arg Lys Met Gly

195 200 205

Val Thr Arg Ala Val Asn Val Ala Lys Glu Ser Leu Thr Asp Val Met

210 215 220

Ala Glu Leu Gly Met Thr Glu Gly Phe Asp Val Gly Leu Glu Met Ser

225 230 235 240

Gly Ala Pro Pro Ala Phe Arg Thr Met Leu Asp Thr Met Asn His Gly
245 250 255

Gly Arg Ile Ala Met Leu Gly Ile Pro Pro Ala Asp Met Ser Ile Asp
260 265 270

Trp Thr Lys Val Ile Phe Lys Gly Leu Phe Ile Lys Gly Ile Tyr Gly
275 280 285

Arg Glu Met Phe Glu Thr Trp Tyr Lys Met Ala Ala Leu Ile Gln Ser
290 295 300

Gly Leu Asp Leu Ser Pro Ile Ile Thr His Arg Phe Ser Ile Asp Asp
305 310 315 320

Phe Gln Lys Gly Phe Asp Ala Met Arg Ser Gly Gln Ser Gly Lys Val
325 330 335

Ile Leu Ser Trp Asp
340

<210

> 670

<211> 349

<212> PRT

<213> Bacillus subtilis

<400> 670

Met Cys Asn Gln His Gln Thr Arg Val Leu Ser Val Ser His Ala Lys
1 5 10 15

Ala Lys Phe Glu Gln Thr Thr Ile Glu Arg Arg Gly Leu Arg Pro His
20 25 30

Asp Val Leu Ile Asp Ile Lys Phe Ser Gly Ile Cys His Ser Asp Ile
35 40 45

His Ser Ala Phe Asp Glu Trp Gly Gly Gly Ile Phe Pro Met Val Pro
50 55 60

Gly His Glu Ile Ala Gly Val Val Thr Ala Val Gly Thr Lys Val Thr
65 70 75 80

Lys Leu Ala Val Gly Asp Arg Val Gly Val Gly Cys Phe Val Asp Ser
85 90 95

Cys Gly Glu Cys Glu Tyr Cys Leu Asn Ala Glu Glu Gln Phe Cys Thr

100 105 110
Lys Gly Val Val Gln Thr Tyr Asn Ser Val Asp Tyr Asp Gly Asn Pro

115 120 125
Thr Tyr Gly Gly Tyr Ser Gln Lys Ile Val Val Thr Asp Arg Phe Val

130 135 140
Val Arg Ile Pro Asp Arg Leu Glu Met Asp Val Ala Ser Pro Leu Leu

145 150 155 160
Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Lys His Trp Asn Val Gly

165 170 175
Pro Gly Lys Lys Val Ala Ile Val Gly Val Gly Gly Leu Gly His Leu

180 185 190
Ala Ile Gln Phe Ala His Ala Met Gly Ala Glu Val Thr Val Leu Ser

195 200 205
Arg Ser Met Asn Lys Lys Glu Glu Ala Leu Glu Leu Gly Ala Asn His

210 215 220
Tyr Phe Ala Thr Ser Asp Pro Ala Thr Phe Thr Ala Leu Ala Gly Arg

225 230 235 240
Phe Asp Val Ile Leu Asn Thr Val Ser Ala Asn Leu Asp Val Asp Ala

245 250 255
Tyr Leu Ser Met Leu Arg Ile Asp Gly Thr Leu Val Ser Val Gly Ala

260 265 270
Pro Ala Lys Pro Asp Thr Tyr Ser Val Phe Ser Leu Ile Met Gly Arg

275 280 285
Arg Ser Ile Ala Gly Ser Leu Val Gly Gly Ile Gln Glu Thr Gln Glu

290 295 300
Met Leu Asp Phe Ala Ala Glu His Gly Ile Glu Pro Lys Ile Glu Val

305 310 315 320
Ile Gly Ala Asp Gln Val Asp Glu Ala Tyr Glu Arg Ile Leu Arg Ser

325 330 335
Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Ser Thr Leu

340 345

<210> 671

<211> 284

<212> PRT

<213> *Ralstonia solanacearum*

<400> 671

Met Pro Tyr Ala Val Lys Ser Tyr Ala Ala His Ser Pro Thr Ser Arg

1 5 10 15

Leu Gly Leu Phe Glu Cys Asp Arg Arg Ser Pro Gln Pro Asp Asp Val

20 25 30

Val Ile Glu Ile Leu Tyr Cys Gly Val Cys His Ser Asp Val His Asn

35 40 45

Val Arg Asn Asp Trp Gly Ser Ala Gln Tyr Pro Met Val Pro Gly His

50 55 60

Glu Ile Val Gly Cys Val Leu Glu Val Gly Ser Glu Val Thr Arg Phe

65 70 75 80

Lys Ala Gly Asp His Val Gly Val Gly Cys Met Val Glu Ser Cys Arg

85 90 95

His Cys Asn Ala Cys Gly Lys Gly Trp Glu Gln Tyr Cys Glu Asn Gly

100 105 110

Ala Thr Tyr Thr Tyr Asn Gly Thr Asp Pro Ile Asp Gly Thr Arg Thr

115 120 125

Tyr Ser Gly Tyr Ser Glu Lys Ile Val Val Ala Glu His Phe Val Leu

130 135 140

Lys Val Pro Asp Gly Leu Asp Leu Ala Gly Ala Ala Pro Leu Leu Cys

145 150 155 160

Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg His Trp Lys Val Gly Pro

165 170 175

Gly Ser Lys Val Ala Ile Val Gly Leu Gly Gly Leu Gly His Met Gly

180 185 190

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

195 200 205

Ser Pro Gly Lys Glu Ala Asp Ala Arg Arg Leu Gly Ala Asp His Ile
 210 215 220
 Val Met Ser Thr Asp Thr Ala Gln Met Ala Ala Ala Val Asp Gly Ile
 225 230 235 240
 Asp Ala Ile Val Leu Thr His Gly Ser Asp Gly Gly Gly His Gly Ala
 245 250 255
 Cys Ala Arg Ala Arg Arg Pro Gly Ala Ala Leu Gly Arg Arg Thr Phe
 260 265 270

Phe Ser Pro Pro Asp Pro Ser Leu Arg Arg Leu His
 275 280

<210> 672

<211> 357

<212> PRT

<213> Acidiphilium multivorum

<400> 672

Met Ser Ala Thr Met Lys Ala Trp Ala Val Val Glu Asn Gly Ala Pro
 1 5 10 15
 Leu Lys Glu Ile Asp Leu Pro Met Pro Glu Pro Thr Gly Arg Glu Ile
 20 25 30
 Leu Leu Glu Val Thr His Cys Gly Val Cys His Ser Asp Leu His Leu

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

100 105 110
 Lys Ala Gly Glu Asp Asn Leu Cys Ala Lys Gln Arg Ser Leu Gly Ile
 115 120 125
 Tyr Gln His Gly Gly Tyr Ala Thr His Val Ile Ala Ala His Ala Gly

130 135 140
 His Leu Val Asp Pro Gly Asp Leu Asp Pro Ala Leu Ala Ala Thr Tyr
 145 150 155 160
 Ala Cys Ser Gly Ile Thr Val Tyr Ala Ala Ile Arg Lys Val Met Pro

 165 170 175
 Leu Pro Ala Asp Thr Pro Val Val Leu Ile Gly Ala Gly Gly Leu Gly
 180 185 190
 Leu Ser Ala Ile Ala Val Leu Arg Ala Leu Gly His Lys Ala Ile Val
 195 200 205
 Ser Val Asp Thr Ser Ala Arg Lys Arg Glu Ala Ala Leu Ala Ala Gly
 210 215 220
 Ala Thr Ala Val Val Asp Gly Asn Asp Pro Ala Leu His Lys Ala Ile

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

 290 295 300
 Thr Pro Gly Asp Leu Arg Glu Leu Val Asp Leu Ala Gln Gly Gly Ala
 305 310 315 320
 Leu Pro Lys Leu Gln Ile Glu Thr Val Pro Gln Arg Glu Ala Asp Ala
 325 330 335
 Ala Ile His Arg Leu Lys Ala Gly Asp Val Thr Gly Arg Leu Val Leu
 340 345 350
 Val Ala Asp Gly Ala
 355

 <210
 > 673
 <211> 373

<212> PRT

<213> Castellaniella defragrans

<400> 673

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

1 5 10 15

Gln Val Gly Gly Pro Leu Ala Val Glu Pro Val Arg Ile Ser Met Pro

20 25 30

Lys Gly Asp Glu Val Leu Ile Arg Ile Ala Gly Val Gly Val Cys His

35 40 45

Thr Asp Leu Val Cys Arg Asp Gly Phe Pro Val Pro Leu Pro Ile Val

50 55 60

Leu Gly His Glu Gly Ser Gly Thr Val Glu Ala Val Gly Glu Gln Val

65 70 75 80

Arg Thr Leu Lys Pro Gly Asp Arg Val Val Leu Ser Phe Asn Ser Cys

85 90 95

Gly His Cys Gly Asn Cys His Asp Gly His Pro Ser Asn Cys Leu Gln

100 105 110

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

115 120 125

Val Leu Asp Gly Ala Gly His Pro Val Gln Ser Met Phe Phe Gly Gln

130 135 140

Ser Ser Phe Gly Thr His Ala Val Ala Arg Glu Ile Asn Ala Val Lys

145 150 155 160

Val Gly Asp Asp Leu Pro Leu Glu Leu Leu Gly Pro Leu Gly Cys Gly

165 170 175

Ile Gln Thr Gly Ala Gly Ala Ala Ile Asn Ser Leu Gly Ile Gly Pro

180 185 190

Gly Gln Ser Leu Ala Ile Phe Gly Gly Gly Gly Val Gly Leu Ser Ala

195 200 205

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

210 215 220

Pro Asn Ala Ala Arg Arg Ala Leu Ala Leu Glu Leu Gly Ala Ser His

225 230 235 240
 Ala Leu Asp Pro His Ala Glu Gly Asp Leu Val Ala Ala Ile Lys Ala

 245 250 255
 Ala Thr Gly Gly Gly Ala Thr His Ser Leu Asp Thr Thr Gly Leu Pro
 260 265 270
 Pro Val Ile Gly Ser Ala Ile Ala Cys Thr Leu Pro Gly Gly Thr Val
 275 280 285
 Gly Met Val Gly Leu Pro Ala Pro Asp Ala Pro Val Pro Ala Thr Leu
 290 295 300
 Leu Asp Leu Leu Ser Lys Ser Val Thr Leu Arg Pro Ile Thr Glu Gly

 305 310 315 320
 Asp Ala Asp Pro Gln Arg Phe Ile Pro Arg Met Leu Asp Phe His Arg
 325 330 335
 Ala Gly Lys Phe Pro Phe Asp Arg Leu Ile Thr Arg Tyr Arg Phe Asp
 340 345 350
 Gln Ile Asn Glu Ala Leu His Ala Thr Glu Lys Gly Glu Ala Ile Lys
 355 360 365
 Pro Val Leu Val Phe
 370

 <210
 > 674
 <211> 341
 <212> PRT
 <213> Unknown
 <220><223> Flavobacterium sp. F52
 <400> 674

 Met Lys Ala Val Arg Phe Phe Gly His Lys Asp Val Arg Val Val Asn
 1 5 10 15
 Asp Ile Glu Arg Pro Val Pro Lys Gly Asp Glu Val Leu Leu Lys Ile
 20 25 30
 Gly Gly Ala Gly Val Cys His Ser Asp Leu His Ile Ile Asp Glu Gly
 35 40 45

Thr Val Val Gly Thr Val Phe Thr Leu Gly His Glu Asn Ala Gly Trp

50 55 60

Ile Glu Glu Val Gly Glu Asn Val Glu Gly Tyr Lys Lys Gly Asp Ala

65 70 75 80

Val Leu Val Tyr Gly Pro Trp Gly Cys Gly His Cys Lys Pro Cys Gln

85 90 95

Gln Ser Lys Glu Asn Tyr Cys Asp His Gln Ser Glu Gln Ala Tyr Gly

100 105 110

Gly Gly Leu Gly Leu Asp Gly Gly Met Ala Asp Tyr Met Leu Val Pro

115 120 125

Ser Ser Arg Leu Leu Val Pro Ile Phe Asp Leu Asp Pro Val Ile Ala

130 135 140

Ala Pro Leu Thr Asp Ala Ala Leu Thr Pro Tyr Ser Ala Ile Lys Arg

145 150 155 160

Ser Leu Pro Lys Leu Met Ala Asp Glu Tyr Val Val Val Ile Gly Val

165 170 175

Gly Gly Leu Gly His Val Ala Leu Gln Ile Leu Arg Glu Ile Ser Gly

180 185 190

Ala Glu Ile Ile Ala Cys Asp Val Thr Glu Asp Lys Leu Ala Phe Ala

195 200 205

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

210 215 220

Thr Glu Gln Ile Gln Lys Ile Thr Gly Ile Lys Lys Ala Lys Val Val

225 230 235 240

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

245 250 255

Val Ser Leu Asp Gly Asp Leu Thr Ile Val Gly Leu Gly Gly Gly His

260 265 270

Tyr Gln Tyr Ser Met Asn Gly Leu Pro Phe Gly Val Ser Met Thr Asn

275 280 285

Pro Tyr Trp Gly Ser Arg Thr Glu Leu Met Glu Val Val Gly Leu Ala

290 295 300
 Arg Gln Lys Lys Ile His Ile Glu Ile Glu Lys His Lys Leu Asp Asp

305 310 315 320
 Ala Asn Glu Val Tyr Glu Arg Met Arg Gln Gly Lys Ile Lys Gly Arg

325 330 335
 Ala Val Leu Ile Pro

340
 <210> 675
 <211> 363
 <212> PRT
 <213> Trichosporon asahii
 <400> 675

Met Gly Glu Pro Phe Thr Gln Ile Asp Ala Trp Tyr Ser Asn Asp Pro
 1 5 10 15
 Gln Lys Pro Leu Gln Phe Gly Lys Leu Asp Ala Lys Pro Ile Glu Asp

20 25 30
 Tyr Asp Ile Asp Val Lys Val Leu Tyr Cys Gly Leu Cys Ser Ser Asp

35 40 45
 Val Gly Val Leu Ser Gly Ala Tyr Gly Pro Val His Glu Glu Val Cys

50 55 60
 Gly His Glu Ile Ile Gly Thr Val Thr Arg Val Gly Pro Glu Val Lys

65 70 75 80
 His Leu Arg Val Ser Asp His Val Gly Val Gly Gly Gln Cys Asp Cys

85 90 95
 Cys Thr His Cys Pro Ala Cys Glu Arg Gly Asp Glu His Met Cys Pro

100 105 110
 Gly Leu Thr Phe Thr Ile Gly Met Ile Gln Gly Pro Tyr Lys Arg Gly

115 120 125
 Lys Ala Lys Gly Arg Leu Gly Gln Gly Gly Phe Ala Lys Gln Trp Arg

130 135 140
 Gly Asn Ala Arg Phe Ala Phe Lys Ile Pro Asp Gly Val Glu Leu Ala

145 150 155 160
 Ser Ala Gly Pro Leu Phe Cys Ala Gly Thr Thr Val Phe Thr Pro Leu
 165 170 175
 Arg Arg Phe Gly Ala Gly Lys Glu Arg Asn Arg Val Gly Val Ile Gly
 180 185 190
 Leu Gly Gly Leu Gly His Leu Gly Ile Gln Leu Ala Ala Ala Leu Gly
 195 200 205
 Ala Asp Val Thr Ala Ile Ser Arg Gly Asn Ser Lys Glu Glu Asp Ala

 210 215 220
 Arg Lys Leu Gly Ala Lys His Tyr Ile Ala Thr Gly Ser Asp Leu Lys
 225 230 235 240
 Lys Asp Phe Glu Lys His Gln Gly Ser Leu Asp Leu Ile Ile Cys Thr
 245 250 255
 Ile Asn Pro Pro Asp Leu Asp Val Asp Ala Tyr Phe Thr Leu Leu Ser
 260 265 270
 Ala Gly Gly Leu Phe Val Pro Leu Gly Ile Pro His Lys Pro Leu Val

 275 280 285
 Ile Asp Pro Ile Gly Leu Ile Leu Gly Gln Lys Gly Val Val Gly Ser
 290 295 300
 Ala Leu Gly Ala Pro Gln Asp Ile Lys Ala Leu Leu Glu Leu Cys Ala
 305 310 315 320
 Lys Thr Gly Val Lys Pro Trp Val Gln Leu Trp Glu Phe Ser Asp Ile
 325 330 335
 Asn Lys Ala Ile Glu Ala Phe Asn Arg Gly Glu Pro Arg Tyr Arg Phe

 340 345 350
 Val Leu Val Asn Thr Asp Asn Gly Gly Glu Leu
 355 360
 <210> 676
 <211> 372
 <212> PRT
 <213> Bifidobacterium asteroides
 <400> 676

Met Pro Gln Lys Ile Lys Ala Ser Ile Ala Tyr Gly Ile Gly Lys Gly
1 5 10 15
Phe Ala Gln Pro Glu Glu Ile Ile Ile Asp Asp Pro Ile Gly Ala Glu
20 25 30
Val Leu Val Asp Val Gln Ala Ser Gly Leu Cys His Ser Asp Leu His
35 40 45
Leu Val Glu Asp Asp Asp Lys Phe Phe Pro Phe Pro Ala Val Ile Gly
50 55 60
His Glu Ile Ser Gly Ile Val Glu Ala Val Gly Pro Glu Val Ser Gly
65 70 75 80
Ile Lys Val Gly Asp His Val Val Ala Ser Leu Glu Gln Val Cys Gly
85 90 95
His Cys Ala Asn Cys Leu Lys Gly Gln Pro Gln Ser Cys Thr Gln Gln
100 105 110
Gln Glu Cys Val Arg Gly Ala Gly Glu Lys Pro Arg Leu Ser Phe Pro
115 120 125
Asp Gly Arg Pro Ile Thr Gln Ala Phe Gly Thr Gly Gly Phe Ala Glu
130 135 140
Lys Ala Leu Ile His Glu Asn Gln Leu Ala Val Val Asn Asn Gln Val
145 150 155 160
Lys Trp Asp Glu Ala Ala Cys Ile Gly Cys Ala Thr Ile Thr Gly Ala
165 170 175
Gly Ala Ala Ile Asn Thr Ala His Val Arg Pro Gly Asp Thr Val Ala
180 185 190
Val Ile Gly Thr Gly Gly Ile Gly Leu Asn Ile Ile Ser Gly Ala Arg
195 200 205
Ile Cys Gly Ala Lys Arg Ile Ile Ala Ile Asp Leu Leu Asp Asn Lys
210 215 220
Leu Glu Phe Ala Arg Lys Phe Gly Ala Thr Asp Val Val Asn Ser Lys
225 230 235 240
Asn Glu Asp Pro Val Ala Lys Val Arg Glu Leu Thr Asp Gly Gly Val

245 250 255
 Asp Lys Ala Phe Glu Ala Ile Gly Leu Pro Val Thr Met Lys Gln Ala
 260 265 270
 Trp Asp Met Leu Gly Val Gly Gly Thr Ala Tyr Pro Ile Gly Leu Thr
 275 280 285

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

 Glu Ala Tyr Lys Gln Leu Val Asn Gly Glu Val Ile Arg Ser Val Ile
 355 360 365
 Thr Glu Phe Asp
 370
 <210> 677
 <211> 354
 <212> PRT
 <213> Candidatus Kinetoplastibacterium
 <400> 677
 Met Lys Cys Tyr Cys Leu Asn Lys Phe Leu Thr Pro Leu Lys Lys Gln
 1 5 10 15
 Glu Ile Asp Thr Pro Thr Pro Ser Gly Glu Glu Val Leu Leu Lys Ile
 20 25 30

 Lys Ala Ser Gly Ile Cys His Ser Asp Ile His Phe Trp Glu Gly Tyr
 35 40 45
 Tyr Asp Ile Gly Glu Asp Lys Lys Leu Glu Leu Lys Asp Arg Gly Ile
 50 55 60
 Lys Leu Pro Met Ile Leu Gly His Glu Ile Val Gly Thr Ile Val Leu
 65 70 75 80

Lys Gly Ser Asp Val Ile Asp Leu Glu Ile Gly Asp Asn Cys Ile Val
85 90 95

Tyr Pro Trp Ile Gly Cys Gly Asn Cys Glu Ser Cys Asn Ile Ser Gln
100 105 110

Glu Asn Tyr Cys Val Asn Pro Arg Tyr Leu Gly Ile Gln Arg Ser Gly
115 120 125

Gly Phe Ala Glu Tyr Val Leu Val Pro Ser Tyr Lys Tyr Leu Ile Asp
130 135 140

Ile Lys Asn Asn Asn Pro Val Thr Thr Ala Gln Tyr Ala Cys Ser Gly
145 150 155 160

Leu Thr Thr Tyr Ser Ala Ile Lys Lys Ile Asp Gln Ser Ile Tyr Thr
165 170 175

Lys Lys Pro Ile Val Ile Phe Gly Ala Gly Gly Leu Gly Leu Thr Ala
180 185 190

Ile Ser Ile Leu Lys Ala Leu Asn Ser Phe Gly Val Leu Val Val Glu
195 200 205

Lys Asp Glu Ser Lys Arg Lys Ala Ala Leu Lys Ala Gly Ala Leu Asp
210 215 220

Val Phe Asp Leu Phe Asp Glu Asn Leu Glu Ser Lys Leu Leu Glu Tyr
225 230 235 240

Asn Asn Gly Asn Lys Tyr Lys Ala Val Ile Asp Leu Ile Gly Asn Asn
245 250 255

Leu Thr Ser Arg Ile Ser Phe Asn Val Leu Asp Lys Phe Ser Thr Leu
260 265 270

Val Ile Val Gly Met Phe Gly Gly Leu Ser Ser Trp Pro Ile Ala Leu
275 280 285

Ile Pro Met Lys Ala Ile Lys Ile Ile Gly Ser Tyr Val Gly Asn Leu
290 295 300

Asn Glu Phe Tyr Glu Leu Met Asp Leu Val Ile Lys Asn Lys Ile Thr
305 310 315 320

Pro Thr Pro Val Gln Ala Tyr His Phe Asp Arg Ile Asn Glu Ala Met

325 330 335
 Asp Asp Leu Arg Thr Gly Asn Val Ile Gly Arg Ala Val Leu Val His
 340 345 350

Asp Ser

<210> 678

<211> 309

<212> PRT

<213> Baudoinia panamericana

<400> 678

Met Val Met Asp Gly Val Phe Asn Ala Pro Leu Pro Leu Ile Gly Ser

1 5 10 15

His Glu Gly Ala Gly Thr Val Thr Ala Val Gly Ser Ala Val Glu Asn

20 25 30

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

35 40 45

Gly Glu Cys Ser Glu Cys Leu Gly Pro Asp Val Trp Lys Tyr Cys Cys

50 55 60

Thr Ala Pro Arg Asp Ser Leu Gly Ile Thr Thr Asp Gly Ala Phe Ala

65 70 75 80

Glu Tyr Leu Val Ala Asp Ser Arg Trp Ser Val Lys Leu Pro Lys Gly

85 90 95

Phe Pro Phe Thr Val Ala Ala Pro Leu Ala Cys Ala Gly Ala Thr Ser

100 105 110

Phe Arg Ala Val Lys Met Ala Gly Leu Glu Arg Gly Gln Trp Leu Ala

115 120 125

Ile Val Gly Ser Gly Gly Gly Leu Gly His Leu Ser Ile His Phe Ala

130 135 140

Lys His Arg Gly Leu Asn Val Ile Gly Ile Asp Ala Arg Asp Ala Gly

145 150 155 160

Leu Ala Leu Ser Leu Arg Ser Gly Ala Asp His Val Leu Asp Ala Arg

165 170 175

Lys Gly Lys Asp Arg Ile Val Asn Gln Val Gln Ser Leu Thr Lys Gly

180 185 190

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

195 200 205

Ser Met Ser Cys Ala Ile Thr Arg Ile His Gly Thr Val Trp Gln Val

210 215 220

Ala Gln Pro Arg Asp Val Ala Val Pro Tyr Gln Glu Leu Val Leu Arg

225 230 235 240

Asp Ile Arg Leu Arg Gly Ser Val Ile Cys Ser Pro Met Asp Ala Gln

245 250 255

Glu Met Ile Ala Thr Val Ala Gly Met Gly Gly Asp Ile Val Ala Val

260 265 270

Arg Thr Tyr Val Gly Leu Glu Ser Leu Pro Lys Leu Leu Gln Asp Val

275 280 285

Arg Ala His Asp Ala Val Gly Lys Ala Ile Ile Val Val Asp Arg Ala

290 295 300

Gln Val Thr Gln Ala

305

<210

> 679

<211> 354

<212> PRT

<213> Ceriporiopsis subvermispora

<400> 679

Met Ser Ser Ser Ser Ile Leu Ser Gly Arg Ala Ala Ile Ile Arg Glu

1 5 10 15

Val Gly Leu Lys Thr Val Ile Glu Thr Val Pro Ala Gln Lys Gln Pro

20 25 30

Ser Glu Leu Leu Pro Gly Glu Cys Leu Val Lys Leu Glu Tyr Ser Gly

35 40 45

Val Cys His Ser Asp Leu His Phe Met Leu Gly Glu Phe Ala Pro Pro

50 55 60

Ser Leu Pro Thr Val Gly Gly His Glu Gly Val Gly His Ile Ile Ala
 65 70 75 80
 Ile Gly Glu Gln Ser Asp Arg Cys Arg Phe Arg Val Gly Asp Lys Val
 85 90 95
 Gly Ile Thr Leu Leu Gly Ser Thr Cys Met Gln Cys Glu Leu Cys Leu
 100 105 110
 Ser Gly Lys Glu Gln Tyr Cys Ala Lys Phe Lys Thr Leu Gly Phe Glu
 115 120 125
 Ala Trp Gly Thr Phe Ser Glu Tyr Val Val Ala His Thr Asp Tyr Val
 130 135 140
 Val Pro Ile Pro Ala Asn Leu Pro Ser Pro Val Ala Thr Pro Val Leu
 145 150 155 160
 Cys Ala Gly Ala Thr Val Tyr Ser Ala Leu Lys Asn Ser Met Ser Ser
 165 170 175
 Val Gly Asp Trp Leu Ala Val Ser Gly Ala Gly Gly Gly Leu Gly His
 180 185 190
 Leu Ala Ile Gln Tyr Gly Val Ala Met Gly Leu Arg Val Ile Ala Ile
 195 200 205
 Asp Thr Gly Glu Glu Lys Lys Asn Leu Cys Leu Ser Leu Gly Ala Glu
 210 215 220
 Gln Trp Ile Asp Tyr Lys Glu Ser Ser Asp Val Ile Ala Asp Val Arg
 225 230 235 240
 Ala Ala Ala Gly Gly Val Gly Pro His Val Ala Leu Ile Ala Ile Gly
 245 250 255
 Ser His Ala Pro Tyr Leu Gln Ala Ser Leu Tyr Leu Arg Pro Met Gly
 260 265 270
 Arg Leu Leu Cys Val Gly Leu Pro Ser Gly Pro Leu Asn Gly Leu Leu
 275 280 285
 Leu Thr Pro Phe Ala Val Arg Gly Ile Lys Leu Ile Gly Ser Val Leu
 290 295 300
 Gly Ser Arg Lys Glu Ile Val Glu Ala Leu Asp Leu Ala Ala Arg Gly

305 310 315 320
 Lys Val Thr Pro His Phe Glu Val Arg Pro His Ala Glu Ile Asn Asp
 325 330 335
 Val Leu Glu Arg Met His Lys Gly Leu Leu Val Gly Arg Val Leu Leu
 340 345 350
 Lys Tyr

 <210> 680
 <211> 365
 <212> PRT
 <213> Pseudocercospora fijiensis
 <400> 680
 Met Ala Ser Ser Thr Thr Asn Gly Ser Asn Ser Val Pro Ala Thr Gln
 1 5 10 15

 Lys Ala Ala Gln Phe Asn Pro Ser Asp Gln Ser Val Ser Ile Asn Glu
 20 25 30
 Ile Pro Val Pro Ser Ile Lys Pro Tyr Glu Ile Leu Val Lys Val Lys
 35 40 45
 Ala Ala Ser Leu Cys His Ser Asp Leu Met Leu Phe Glu Glu Asn Glu
 50 55 60
 Gln Gly Leu Lys Leu Gly Ser Gly Glu Pro Phe Thr Met Gly His Glu
 65 70 75 80

 Gly Cys Gly Thr Ile Ile Glu Val Gly Ser Glu Val Gly Asp Asn Phe
 85 90 95
 Lys Pro Gly Asp Arg Ile Gly Trp Leu Pro Ile Val Asp Cys Cys Tyr
 100 105 110
 Asp Cys Glu Glu Cys Gln Ile His Asn Leu Tyr Cys Glu Lys Gly Thr
 115 120 125
 Ser Lys Val Gln Gly Met Thr Val Asp Gly Tyr Phe Gln Glu Tyr Ala
 130 135 140

 Ala Ile Asn Trp Arg Asn Ala Ala His Ile Pro Asp Gly Met Asp Leu
 145 150 155 160

Ala Asn Leu Ala Pro Leu Phe Cys Ala Gly Cys Thr Ala Phe Asn Ser
165 170 175

Val Thr Asp Thr Ile Ala Glu Leu Lys Gly Ile Pro Glu Glu Asn Trp
180 185 190

Val Ala Val Val Gly Cys Gly Gly Leu Gly His Leu Gly Ile Gln Tyr
195 200 205

Leu Lys Ala Phe Gly Tyr Lys Val Ile Gly Ile Asp Leu Ser Ala Asp
210 215 220

Ala Val Glu Glu Ala Leu Ala Gln Gly Ala Asp His Val Phe Asn Pro
225 230 235 240

Met Lys Cys Ala Asp Tyr Ile Asp Gln Val Arg Gln Ile Thr Gly Gly
245 250 255

Lys Gly Cys His Ala Val Ile Asn Tyr Thr Asn Ser Val Pro Ala Tyr
260 265 270

Ser Asn Ala Val Gly Leu Leu Arg Met Asn Gly Val Leu Met Val Thr
275 280 285

Gly Ile Pro Gln Lys Pro Leu Gln Phe Ser Ala Met Asp Val Ser Met
290 295 300

Lys Arg Ile Arg Val Arg Gly Ser Asn Asn Gly Thr Thr Pro Arg Leu
305 310 315 320

Lys Lys Cys Val Glu Phe Ser Tyr Lys His Gly Ile Glu Pro His Val
325 330 335

Thr Gln Phe Lys Leu Glu Glu Phe Pro Lys Met Val Glu Leu Met Arg
340 345 350

Ser Asn Arg His Lys Gly Arg Leu Gly Val Leu Phe Gln
355 360 365

<210> 681

<211> 355

<212> PRT

<213> Dacryopinax primogenitus

<400> 681

Met Thr Pro Glu Gln Ile Pro Gln Thr Gln Lys Ala Ala Val Val Arg

1 5 10 15
 Asn Lys Gln Val Ala Ile Glu Thr Val Pro Val Val Gln Pro Ala Asp

 20 25 30
 Leu Lys Pro Asn Glu Ala Leu Val Lys Val Leu Tyr Ser Gly Val Cys
 35 40 45
 His Thr Asp Leu His Ala Gln Leu Gly Asp Trp Pro Leu Ile His Lys
 50 55 60
 Glu Pro Leu Ile Gly Gly His Glu Gly Ala Gly Ile Ile Val Ala Ile
 65 70 75 80
 Gly Glu His Ser Asp Thr Asp Leu Lys Leu Gly Asp Arg Val Gly Ile

 85 90 95
 Lys Trp Leu Ala Asp Ser Cys Leu Lys Cys Ser Tyr Cys Arg Gln Gly
 100 105 110
 Tyr Glu Pro Leu Cys His His Ala Leu Cys Ser Gly Phe Ser Val Asp
 115 120 125
 Gly Ser Phe Gln Gln Tyr Ala Val Ser Phe Thr Arg His Leu Thr Lys
 130 135 140
 Ile Pro Lys Glu Leu Pro Met Asp Lys Ala Ala Pro Ile Leu Cys Ala

 145 150 155 160
 Gly Val Thr Val Tyr Lys Ala Leu Lys Gln Ser Asn Ala Arg Pro Gly
 165 170 175
 Glu Trp Val Val Leu Pro Gly Ala Gly Gly Gly Leu Gly His Leu Ala
 180 185 190
 Val Gln Tyr Ala His Tyr Met Gly Leu Arg Cys Ile Ala Val Asp Thr
 195 200 205
 Gly Ala Glu Lys Lys Ala Leu Cys Glu Arg Leu Gly Ala Glu Arg Trp

 210 215 220
 Ile Asp Phe Lys Glu Thr Lys Asp Ile Val Ala Ala Val Lys Ala Ala
 225 230 235 240
 Thr Pro Asp Gly Asp Gly Pro His Ala Ala Ile Val Thr Ser Ser Val
 245 250 255

Gly Ala Ala Tyr Glu Glu Ala Leu Gln Tyr Val Arg Pro His Gly Thr
260 265 270
Val Val Ala Val Gly Leu Pro Pro Asp Ala Lys Val Ser Ala Asp Val
275 280 285
Phe Trp Thr Val Phe Leu Glu Lys Gln Leu Lys Gly Ser Tyr Val Gly
290 295 300
Asn Arg Gln Asp Ala Ile Glu Ala Leu Glu Ile Ala Ala Ser Gly Ala
305 310 315 320
Leu Glu Thr Ser Phe Arg Thr Leu Pro Leu Lys Asp Leu Pro Ser Val
325 330 335
Tyr Asp Gln Leu His Ala Gly Ser Leu Val Gly Arg Val Val Leu Asp
340 345 350
Leu Trp Ala
355
<210> 682
<211> 325
<212> PRT
<213> Schizosaccharomyces pombe
<400> 682
Met Gln Tyr Tyr Gln Met Met Lys Ala Leu Arg Met Leu Lys Lys Pro
1 5 10 15
Lys Pro Gly Cys Leu Gly Ile Glu Ile Gln Ser Val Pro Ile Pro Gln
20 25 30
Pro Lys Asn Gly Glu Leu Leu Val Lys Ile Glu Ala Ala Ala Ile Asn
35 40 45
Pro Ser Asp Leu Met Asn Ala Thr Gly Gly Phe Pro Tyr Thr Val Tyr
50 55 60
Pro Arg Ile Val Gly Arg Asp Tyr Ala Gly Thr Val Ile Ser Gly Ala
65 70 75 80
Ser His Leu Val Gly Thr Arg Val Phe Gly Thr Ser Gly Ser Glu Leu
85 90 95

Ser Phe Thr Lys Asp Gly Thr His Ala Glu Tyr Cys Ile Ile Pro Glu

100 105 110

Lys Ala Ala Val Arg Met Pro Ser Asn Leu Ser Phe Thr Glu Ala Ala

115 120 125

Ser Val Gly Val Pro Phe Thr Thr Ala Tyr Leu Ala Leu Ser Arg Gly

130 135 140

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

145 150 155 160

Val Gly Ser Ala Val Cys Gln Ile Ala Glu Asp Trp Gly Cys Lys Val

165 170 175

Ile Thr Val Ser Arg Ser Gly Ser Thr Asp Ile Asn Thr Val Val Asp

180 185 190

Pro Glu Leu Lys Arg Val His Glu Leu Val Glu Lys Val Asp Val Val

195 200 205

Ile Asp Thr Val Gly Asp Pro Leu Leu Met Lys Ser Ala Leu Asn Gln

210 215 220

Leu Gly Ile Gly Gly Arg Leu Ser Tyr Ile Ser Ala Pro Lys Gln Gly

225 230 235 240

Ser Ile Glu Phe Ser Tyr Asp Met Lys Gln Ile Tyr Arg Lys Asn Leu

245 250 255

Lys Ile Ile Gly Cys Asn Ser Leu Leu Leu Ser Leu Val Glu Ser Asn

260 265 270

Ser Leu Leu Lys Asn Met Val Ala Lys Phe Glu Ala Gly Lys Tyr Lys

275 280 285

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

290 295 300

Asn Ser Tyr Arg Lys Leu Met Asn Glu Cys Ser Thr Lys Phe Val Ile

305 310 315 320

Thr Met Ser Thr Asn

325

<210> 683

<211> 350

<212> PRT

<213> Emericella nidulans

<400> 683

Met Ser Ile Pro Thr Met Gln Trp Ala Gln Val Ala Glu Lys Val Gly

1 5 10 15

Gly Pro Leu Val Tyr Lys Gln Ile Pro Val Pro Lys Pro Gly Pro Asp

20 25 30

Gln Ile Leu Val Lys Ile Arg Tyr Ser Gly Val Cys His Thr Asp Leu

35 40 45

His Ala Met Met Gly His Trp Pro Ile Pro Val Lys Met Pro Leu Val

50 55 60

Gly Gly His Glu Gly Ala Gly Ile Val Val Ala Lys Gly Glu Leu Val

65 70 75 80

His Glu Phe Glu Ile Gly Asp Gln Ala Gly Ile Lys Trp Leu Asn Gly

85 90 95

Ser Cys Gly Glu Cys Glu Phe Cys Arg Gln Ser Asp Asp Pro Leu Cys

100 105 110

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

115 120 125

Tyr Ala Leu Gly Lys Ala Ser His Ala Ser Lys Ile Pro Ala Gly Val

130 135 140

Pro Leu Asp Ala Ala Ala Pro Val Leu Cys Ala Gly Ile Thr Val Tyr

145 150 155 160

Lys Gly Leu Lys Glu Ala Gly Val Arg Pro Gly Gln Thr Val Ala Ile

165 170 175

Val Gly Ala Gly Gly Gly Leu Gly Ser Leu Ala Gln Gln Tyr Ala Lys

180 185 190

Ala Met Gly Ile Arg Val Val Ala Val Asp Gly Gly Asp Glu Lys Arg

195 200 205

Ala Met Cys Glu Ser Leu Gly Thr Glu Thr Tyr Val Asp Phe Thr Lys

210 215 220
 Ser Lys Asp Leu Val Ala Asp Val Lys Ala Ala Thr Pro Asp Gly Leu
 225 230 235 240
 Gly Ala His Ala Val Ile Leu Leu Ala Val Ser Glu Lys Pro Phe Gln
 245 250 255
 Gln Ala Thr Glu Tyr Val Arg Ser Arg Gly Thr Ile Val Ala Ile Gly
 260 265 270
 Leu Pro Pro Asp Ala Tyr Leu Lys Ala Pro Val Ile Asn Thr Val Val

275 280 285
 Arg Met Ile Thr Ile Lys Gly Ser Tyr Val Gly Asn Arg Gln Asp Gly
 290 295 300
 Val Glu Ala Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Ala Pro Phe
 305 310 315 320
 Lys Thr Ala Pro Leu Lys Asp Leu Pro Lys Ile Tyr Glu Leu Met Glu
 325 330 335
 Gln Gly Arg Ile Ala Gly Arg Tyr Val Leu Glu Met Pro Glu

340 345 350

<210> 684

<211> 355

<212> PRT

<213> Gallus gallus

<400> 684

Met Ala Ala Thr Gly Gln Asn Leu Ala Val Val Val His Arg Ala Gly
 1 5 10 15
 Asp Leu Arg Leu Glu Asn Arg Pro Ile Pro Glu Pro Gly Pro Asn Glu
 20 25 30
 Val Leu Leu Arg Met His Ser Val Gly Ile Cys Gly Ser Asp Val His
 35 40 45
 Tyr Trp Gln His Gly Arg Ile Gly Asp Phe Val Val Lys Asp Pro Met
 50 55 60
 Val Leu Gly His Glu Ala Ser Gly Thr Val Ile Lys Val Gly Ala Gly
 65 70 75 80

Val Thr His Leu Lys Pro Gly Asp Arg Val Ala Ile Glu Pro Gly Val
85 90 95

Pro Arg Glu Thr Asp Glu Phe Cys Lys Thr Gly Arg Tyr Asn Leu Ser
100 105 110

Pro Thr Ile Phe Phe Cys Ala Thr Pro Pro Asp Asp Gly Asn Leu Cys
115 120 125

Arg Tyr Tyr Lys His Ser Ala Ser Tyr Cys Tyr Lys Leu Pro Asp Ser
130 135 140

Val Thr Phe Glu Glu Gly Ala Leu Ile Glu Pro Leu Ser Val Gly Ile
145 150 155 160

His Ala Cys Lys Arg Ala Gly Val Thr Leu Gly Ser Arg Val Phe Val
165 170 175

Ser Gly Ser Gly Pro Ile Gly Leu Val Asn Val Ile Ile Ala Lys Met
180 185 190

Met Gly Ala Ala Ala Val Val Val Thr Asp Leu Ser Ala Ser Arg Leu
195 200 205

Gln Thr Ala Lys Glu Leu Gly Ala Asp Phe Thr Ile Gln Ile Lys Asn
210 215 220

Glu Thr Pro Gln Glu Val Ala Ala Lys Val Glu Ser Leu Leu Gly Cys
225 230 235 240

Met Pro Glu Ile Thr Val Glu Cys Thr Gly Val Gln Ala Cys Ile Gln
245 250 255

Ala Ser Ile Tyr Ala Thr Arg Ser Gly Gly Thr Leu Val Leu Val Gly
260 265 270

Leu Gly Pro Glu Met Val Thr Val Pro Ile Val Asn Ala Ala Val Arg
275 280 285

Glu Val Asp Ile Arg Gly Ile Phe Arg Tyr Cys Asn Thr Trp Pro Val
290 295 300

Ala Ile Ser Leu Leu Ala Ser Lys Arg Ile Asn Ile Lys Pro Leu Val
305 310 315 320

Thr His Arg Phe Pro Leu Glu Lys Ala Leu Glu Ala Phe Glu Thr Thr

325 330 335
 Lys Arg Gly Glu Gly Val Lys Ile Met Leu Lys Cys Asp Pro Thr Asp
 340 345 350
 Gln Asn Pro
 355
 <210> 685
 <211> 380
 <212> PRT
 <213> Trifolium repens
 <400> 685
 Met Ser Asn Thr Ala Gly Gln Val Ile Lys Cys Arg Ala Ala Val Ala

 1 5 10 15
 Trp Glu Ala Gly Lys Pro Leu Val Ile Glu Glu Val Glu Val Ala Pro
 20 25 30
 Pro Gln Ala Gly Glu Val Arg Leu Lys Ile Leu Phe Thr Ser Leu Cys
 35 40 45
 His Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly Gln Thr Pro Leu Phe
 50 55 60
 Pro Arg Ile Phe Gly His Glu Ala Gly Gly Ile Val Glu Ser Val Gly

 65 70 75 80
 Glu Gly Val Thr His Leu Lys Pro Gly Asp His Ala Leu Pro Val Phe
 85 90 95
 Thr Gly Glu Cys Gly Glu Cys Pro His Cys Lys Ser Glu Glu Ser Asn
 100 105 110
 Met Cys Asn Leu Leu Arg Ile Asn Thr Asp Arg Gly Val Met Ile Asn
 115 120 125
 Asp Asn Lys Ser Arg Phe Ser Ile Lys Gly Gln Pro Val His His Phe

 130 135 140
 Val Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Val His Ala Gly Cys
 145 150 155 160
 Val Ala Lys Ile Asn Pro Asp Ala Pro Leu Asp Lys Val Cys Ile Leu
 165 170 175

Ser Cys Gly Ile Cys Thr Gly Leu Gly Ala Thr Val Asn Val Ala Lys
180 185 190

Pro Lys Pro Gly Ser Ser Val Ala Ile Phe Gly Leu Gly Ala Val Gly
195 200 205

Leu Ala Ala Ala Glu Gly Ala Arg Met Ser Gly Ala Ser Arg Ile Ile
210 215 220

Gly Val Asp Leu Val Ser Ser Arg Phe Glu Leu Ala Lys Lys Phe Gly
225 230 235 240

Val Asn Glu Phe Val Asn Pro Lys Asp His Asp Lys Pro Val Gln Gln
245 250 255

Val Ile Ala Glu Met Thr Asp Gly Gly Val Asp Arg Ala Val Glu Cys
260 265 270

Thr Gly Ser Ile Gln Ala Met Ile Ser Ala Phe Glu Cys Val His Asp
275 280 285

Gly Trp Gly Val Ala Val Leu Val Gly Val Pro Lys Lys Asp Asp Ala
290 295 300

Phe Lys Thr His Pro Met Asn Phe Leu Asn Glu Arg Thr Leu Lys Gly
305 310 315 320

Thr Phe Tyr Gly Asn Tyr Lys Pro Arg Thr Asp Leu Pro Asn Val Val
325 330 335

Glu Gln Tyr Met Lys Gly Glu Leu Glu Leu Glu Lys Phe Ile Thr His
340 345 350

Ser Ile Pro Phe Ser Glu Ile Asn Lys Ala Phe Asp Tyr Met Leu Lys
355 360 365

Gly Glu Ser Ile Arg Cys Ile Ile Arg Met Glu Glu
370 375 380

<210> 686
<211> 379
<212> PRT
<213> Cenchrus americanus
<400> 686

Met Ala Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Ala Trp
1 5 10 15
Glu Ala Gly Lys Pro Leu Ser Ile Glu Glu Val Glu Val Ala Pro Pro
20 25 30
Gln Ala Met Glu Val Arg Val Lys Ile Leu Tyr Thr Ser Leu Cys His
35 40 45
Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly Gln Thr Pro Val Phe Pro
50 55 60
Arg Ile Phe Gly His Glu Ala Gly Gly Ile Ile Glu Ser Val Gly Glu
65 70 75 80
Gly Val Thr Asp Val Ala Pro Gly Asp His Val Leu Pro Val Phe Thr
85 90 95
Gly Glu Cys Lys Glu Cys Pro His Cys Lys Ser Ala Glu Ser Asn Met
100 105 110
Cys Asp Leu Leu Arg Ile Asn Thr Val Arg Gly Val Met Ile Gly Asp
115 120 125
Gly Lys Ser Arg Phe Ser Ile Asn Gly Lys Pro Ile Tyr His Phe Val
130 135 140
Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Met His Val Gly Cys Val
145 150 155 160
Ala Lys Ile Asn Pro Glu Ala Pro Leu Asp Lys Val Cys Val Leu Ser
165 170 175
Cys Gly Ile Ser Thr Gly Leu Gly Ala Ser Ile Asn Val Ala Lys Pro
180 185 190
Pro Lys Gly Ser Thr Val Ala Ile Phe Gly Leu Gly Ala Val Gly Leu
195 200 205
Ala Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile Ile Gly
210 215 220
Val Asp Leu Asn Pro Ser Arg Phe Glu Glu Ala Lys Lys Phe Gly Cys
225 230 235 240
Thr Glu Phe Val Asn Pro Lys Asp His Asn Lys Pro Val Gln Glu Val

[illegible]

65				70				75				80			
Glu	Gly	Val	Thr	Glu	Leu	Gly	Pro	Gly	Asp	His	Val	Leu	Pro	Val	Phe
85				90				95							
Thr	Gly	Glu	Cys	Lys	Asp	Cys	Ala	His	Cys	Lys	Ser	Glu	Glu	Ser	Asn
100				105				110							
Met	Cys	Ser	Leu	Leu	Arg	Ile	Asn	Thr	Asp	Arg	Gly	Val	Met	Ile	Asn
115				120				125							
Asp	Gly	Gln	Ser	Arg	Phe	Ser	Ile	Asn	Gly	Lys	Pro	Ile	Tyr	His	Phe
130				135				140							
Val	Gly	Thr	Ser	Thr	Phe	Ser	Glu	Tyr	Thr	Val	Val	His	Val	Gly	Cys
145				150				155				160			
Val	Ala	Lys	Ile	Asn	Pro	Leu	Ala	Pro	Leu	Asp	Lys	Val	Cys	Val	Leu
165				170				175							
Ser	Cys	Gly	Ile	Ser	Thr	Gly	Leu	Gly	Ala	Thr	Leu	Asn	Val	Ala	Lys
180				185				190							
Pro	Thr	Lys	Gly	Ser	Ser	Val	Ala	Ile	Phe	Gly	Leu	Gly	Ala	Val	Gly
195				200				205							
Leu	Ala	Ala	Ala	Glu	Gly	Ala	Arg	Ile	Ala	Gly	Ala	Ser	Arg	Ile	Ile
210				215				220							
Gly	Val	Asp	Leu	Asn	Ala	Ser	Arg	Phe	Glu	Gln	Ala	Lys	Lys	Phe	Gly
225				230				235				240			
Val	Thr	Glu	Phe	Val	Asn	Pro	Lys	Asp	Tyr	Ser	Lys	Pro	Val	Gln	Glu
245				250				255							
Val	Ile	Ala	Glu	Met	Thr	Asp	Gly	Gly	Val	Asp	Arg	Ser	Val	Glu	Cys
260				265				270							
Thr	Gly	His	Ile	Asp	Ala	Met	Ile	Ser	Ala	Phe	Glu	Cys	Val	His	Asp
275				280				285							
Gly	Trp	Gly	Val	Ala	Val	Leu	Val	Gly	Val	Pro	His	Lys	Glu	Ala	Val
290				295				300							
Phe	Lys	Thr	His	Pro	Met	Asn	Leu	Leu	Asn	Glu	Arg	Thr	Leu	Lys	Gly
305				310				315				320			

Thr Phe Phe Gly Asn Tyr Lys Pro Arg Ser Asp Ile Pro Ser Val Val
325 330 335
Glu Lys Tyr Met Asn Lys Glu Leu Glu Leu Glu Lys Phe Ile Thr His
340 345 350
Thr Leu Pro Phe Ala Glu Ile Asn Lys Ala Phe Asp Leu Met Leu Lys
355 360 365
Gly Glu Gly Leu Arg Cys Ile Ile Thr Met Glu Asp

370 375 380

<210> 688

<211> 380

<212> PRT

<213> Solanum tuberosum

<400> 688

Met Ser Thr Thr Val Gly Gln Val Ile Arg Cys Lys Ala Ala Val Ala
1 5 10 15
Trp Glu Ala Gly Lys Pro Leu Val Met Glu Glu Val Asp Val Ala Pro
20 25 30
Pro Gln Lys Met Glu Val Arg Leu Lys Ile Leu Tyr Thr Ser Leu Cys
35 40 45

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

Met Cys Ser Leu Leu Arg Ile Asn Thr Asp Arg Gly Val Met Ile Asn
115 120 125
Asp Gly Gln Ser Arg Phe Ser Ile Asn Gly Lys Pro Ile Tyr His Phe
130 135 140
Val Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Val His Val Gly Cys

145 150 155 160
Val Ala Lys Ile Asn Pro Leu Ala Pro Leu Asp Lys Val Cys Val Leu
165 170 175

Ser Cys Gly Ile Ser Thr Gly Leu Gly Ala Thr Leu Asn Val Ala Lys
180 185 190
Pro Thr Lys Gly Ser Ser Val Ala Ile Phe Gly Leu Gly Ala Val Gly
195 200 205
Leu Ala Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile Ile
210 215 220
Gly Val Asp Leu Asn Ala Ser Arg Phe Glu Gln Ala Lys Lys Phe Gly
225 230 235 240

Val Thr Glu Phe Val Asn Pro Lys Asp Tyr Ser Lys Pro Val Gln Glu
245 250 255
Val Ile Ala Glu Met Thr Asp Gly Gly Val Asp Arg Ser Val Glu Cys
260 265 270
Thr Gly His Ile Asp Ala Met Ile Ser Ala Phe Glu Cys Val His Asp
275 280 285
Gly Trp Gly Val Ala Val Leu Val Gly Val Pro His Lys Glu Ala Val
290 295 300

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

Gly Glu Gly Leu Arg Cys Ile Ile Thr Met Glu Asp
370 375 380

<210> 689

<211> 337

<212> PRT

<213> *Zymomonas mobilis*

<400> 689

Met Lys Ala Ala Val Ile Thr Lys Asp His Thr Ile Glu Val Lys Asp

1 5 10 15

Thr Lys Leu Arg Pro Leu Lys Tyr Gly Glu Ala Leu Leu Glu Met Glu

20 25 30

Tyr Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe

35 40 45

Gly Asp Glu Thr Gly Arg Ile Thr Gly His Glu Gly Ile Gly Ile Val

50 55 60

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

65 70 75 80

Ser Val Ala Trp Phe Phe Lys Gly Cys Gly His Cys Glu Tyr Cys Val

85 90 95

Ser Gly Asn Glu Thr Leu Cys Arg Asn Val Glu Asn Ala Gly Tyr Thr

100 105 110

Val Asp Gly Ala Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ser

115 120 125

Val Lys Val Pro Asp Gly Leu Asp Pro Ala Val Ala Ser Ser Ile Thr

130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Val Ser Gln Ile Gln

145 150 155 160

Pro Gly Gln Trp Leu Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu

165 170 175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile

180 185 190

Asp Val Asn Asp Glu Gln Leu Ala Phe Ala Lys Glu Leu Gly Ala Asp

195 200 205

Met Val Ile Asn Pro Lys Asn Glu Asp Ala Ala Lys Ile Ile Gln Glu

210 215 220

Lys Val Gly Gly Ala His Ala Thr Val Val Thr Ala Val Ala Lys Ser

225					230					235					240		
Ala	Phe	Asn	Ser	Ala	Val	Glu	Ala	Ile	Arg	Ala	Gly	Gly	Arg	Val	Val		
				245					250					255			
Ala	Val	Gly	Leu	Pro	Pro	Glu	Lys	Met	Asp	Leu	Ser	Ile	Pro	Arg	Leu		
				260					265					270			
Val	Leu	Asp	Gly	Ile	Glu	Val	Leu	Gly	Ser	Leu	Val	Gly	Thr	Arg	Glu		
				275					280					285			
Asp	Leu	Lys	Glu	Ala	Phe	Gln	Phe	Ala	Ala	Glu	Gly	Lys	Val	Lys	Pro		
				290					295					300			
Lys	Val	Thr	Lys	Arg	Lys	Val	Glu	Glu	Ile	Asn	Gln	Ile	Phe	Asp	Glu		
				310					315					320			
Met	Glu	His	Gly	Lys	Phe	Thr	Gly	Arg	Met	Val	Val	Asp	Phe	Thr	His		
				325					330					335			
His																	
<210>	690																
<211>	382																
<212>	PRT																
<213>	Petunia hybrida																
<400>	690																
Met	Ser	Ser	Asn	Thr	Ala	Gly	Gln	Val	Ile	Arg	Cys	Lys	Ala	Ala	Val		
1					5					10					15		
Ala	Trp	Glu	Ala	Gly	Lys	Pro	Leu	Val	Ile	Glu	Glu	Val	Glu	Val	Ala		
				20					25					30			
Pro	Pro	Gln	Lys	Met	Glu	Val	Arg	Leu	Lys	Ile	Leu	Phe	Thr	Ser	Leu		
				35					40					45			
Cys	His	Thr	Asp	Val	Tyr	Phe	Trp	Glu	Ala	Lys	Gly	Gln	Thr	Pro	Leu		
				50					55					60			
Phe	Pro	Arg	Ile	Phe	Gly	His	Glu	Ala	Gly	Gly	Ile	Val	Glu	Ser	Val		
				65					70					75			80
Gly	Glu	Gly	Val	Thr	Asp	Leu	Lys	Pro	Gly	Asp	His	Val	Leu	Pro	Val		

85 90 95
 Phe Thr Gly Glu Cys Gln Gln Cys Arg His Cys Lys Ser Glu Glu Ser
 100 105 110
 Asn Met Cys Asp Leu Leu Arg Ile Asn Thr Asp Arg Gly Val Met Ile
 115 120 125
 His Asp Gly Gln Thr Arg Phe Ser Lys Asp Gly Lys Pro Ile Tyr His
 130 135 140
 Phe Val Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Cys His Ser Gly

 145 150 155 160
 Cys Val Thr Lys Ile Asp Pro Gln Ala Pro Leu Asp Lys Val Cys Val
 165 170 175
 Leu Ser Cys Gly Ile Ser Thr Gly Leu Gly Ala Thr Leu Asn Val Ala
 180 185 190
 Lys Pro Thr Lys Gly Ser Thr Val Ala Ile Phe Gly Leu Gly Ala Val
 195 200 205
 Gly Leu Ala Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile

 210 215 220
 Ile Gly Val Asp Leu Asn Pro Ser Arg Phe Asn Asp Ala Lys Lys Phe
 225 230 235 240
 Gly Val Thr Glu Phe Val Asn Pro Lys Asp His Gly Asp Lys Pro Val
 245 250 255
 Gln Gln Val Ile Ala Glu Met Thr Asp Gly Gly Val Asp Arg Ser Val
 260 265 270
 Glu Cys Thr Gly Asn Val Asn Ala Met Ile Ser Ala Phe Glu Cys Val

 275 280 285
 His Asp Gly Trp Gly Val Ala Val Leu Val Gly Val Pro Asn Lys Asp
 290 295 300
 Asp Ala Phe Lys Thr His Pro Met Asn Leu Leu Asn Glu Arg Thr Leu
 305 310 315 320
 Lys Gly Thr Phe Phe Gly Asn Tyr Lys Pro Lys Ser Asp Ile Pro Ser
 325 330 335

Val Val Asp Lys Tyr Met Lys Lys Glu Leu Glu Leu Glu Lys Phe Ile

340 345 350

Thr His Gln Val Pro Phe Ser Glu Ile Asn Lys Ala Phe Asp Tyr Met

355 360 365

Leu Lys Gly Glu Ser Ile Arg Cys Met Ile Thr Met Glu His

370 375 380

<210> 691

<211> 380

<212> PRT

<213> Solanum lycopersicum

<400> 691

Met Ser Thr Thr Val Gly Gln Val Ile Arg Cys Lys Ala Ala Val Ala

1 5 10 15

Trp Glu Ala Gly Lys Pro Leu Val Met Glu Glu Val Asp Val Ala Pro

20 25 30

Pro Gln Lys Met Glu Val Arg Leu Lys Ile Leu Tyr Thr Ser Leu Cys

35 40 45

His Thr Asp Val Tyr Phe Trp Glu Ala Lys Gly Gln Asn Pro Val Phe

50 55 60

Pro Arg Ile Leu Gly His Glu Ala Ala Gly Ile Val Glu Ser Val Gly

65 70 75 80

Glu Gly Val Thr Asp Leu Ala Pro Gly Asp His Val Leu Pro Val Phe

85 90 95

Thr Gly Glu Cys Lys Asp Cys Ala His Cys Lys Ser Glu Glu Ser Asn

100 105 110

Met Cys Ser Leu Leu Arg Ile Asn Thr Asp Arg Gly Val Met Leu Asn

115 120 125

Asp Gly Lys Ser Arg Phe Ser Ile Asn Gly Asn Pro Ile Tyr His Phe

130 135 140

Val Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val Val His Val Gly Cys

145 150 155 160

Val Ala Lys Ile Asn Pro Leu Ala Pro Leu Asp Lys Val Cys Val Leu
165 170 175

Ser Cys Gly Ile Ser Thr Gly Leu Gly Ala Ser Leu Asn Val Ala Lys
180 185 190

Pro Thr Lys Gly Ser Ser Val Ala Ile Phe Gly Leu Gly Ala Val Gly
195 200 205

Leu Ala Ala Ala Glu Gly Ala Arg Ile Ala Gly Ala Ser Arg Ile Ile
210 215 220

Gly Val Asp Leu Asn Ala Ser Arg Phe Glu Gln Ala Lys Lys Phe Gly
225 230 235 240

Val Thr Glu Phe Val Asn Pro Lys Asp Tyr Ser Lys Pro Val Gln Glu
245 250 255

Val Ile Ala Glu Met Thr Asp Gly Gly Val Asp Arg Ser Val Glu Cys
260 265 270

Thr Gly His Ile Asp Ala Met Ile Ser Ala Phe Glu Cys Val His Asp
275 280 285

Gly Trp Gly Val Ala Val Leu Val Gly Val Pro His Lys Glu Ala Val
290 295 300

Phe Lys Thr His Pro Leu Asn Phe Leu Asn Glu Arg Thr Leu Lys Gly
305 310 315 320

Thr Phe Phe Gly Asn Tyr Lys Pro Arg Ser Asp Ile Pro Cys Val Val
325 330 335

Glu Lys Tyr Met Asn Lys Glu Leu Glu Leu Glu Lys Phe Ile Thr His
340 345 350

Thr Leu Pro Phe Ala Glu Ile Asn Lys Ala Phe Asp Leu Met Leu Lys
355 360 365

Gly Glu Gly Leu Arg Cys Ile Ile Thr Met Ala Asp
370 375 380

<210> 692

<211> 336

<212> PRT

<213> Escherichia coli

<400> 692

Met Lys Ala Ala Val Val Thr Lys Asp His His Val Asp Val Thr Tyr
1 5 10 15

Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu
20 25 30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
35 40 45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
50 55 60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
65 70 75 80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
85 90 95

Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser
100 105 110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
115 120 125

Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Ala Ser Ser Ile Thr
130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg
145 150 155 160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
165 170 175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
180 185 190

Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Glu Met Gly Ala Asp
195 200 205

Leu Ala Ile Asn Ser His Thr Glu Asp Ala Ala Lys Ile Val Gln Glu
210 215 220

Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
225 230 235 240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
245 250 255

Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu
260 265 270

Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln
275 280 285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
290 295 300

Lys Val Ala Leu Arg Pro Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu
305 310 315 320

Met Glu Glu Gly Lys Ile Arg Gly Arg Met Val Ile Asp Phe Arg His
325 330 335

<210> 693

<211> 366

<212> PRT

<213> Pseudomonas putida

<400> 693

Met Glu Ile Lys Ala Ala Ile Val Arg Gln Lys Asn Gly Pro Phe Leu
1 5 10 15

Leu Glu His Val Ala Leu Asn Glu Pro Ala Glu Asp Gln Val Leu Val
20 25 30

Arg Leu Val Ala Thr Gly Leu Cys His Thr Asp Leu Val Cys Arg Asp
35 40 45

Gln His Tyr Pro Val Pro Leu Pro Met Val Phe Gly His Glu Gly Ala

50 55 60

Gly Val Val Glu Arg Val Gly Ser Ala Val Lys Lys Val Gln Pro Gly
65 70 75 80

Asp His Val Val Leu Thr Phe Tyr Thr Cys Gly Ser Cys Asp Ala Cys
85 90 95

Leu Ser Gly Asp Pro Thr Ser Cys Ala Asn Ser Phe Gly Pro Asn Phe
100 105 110

Met Gly Arg Ser Val Thr Gly Glu Cys Thr Ile His Asp His Gln Gly

115 120 125

Ala Glu Val Gly Ala Ser Phe Phe Gly Gln Ser Ser Phe Ala Thr Tyr

130 135 140

Ala Leu Ser Tyr Glu Arg Asn Thr Val Lys Val Thr Lys Asp Val Pro

145 150 155 160

Leu Glu Leu Leu Gly Pro Leu Gly Cys Gly Ile Gln Thr Gly Ala Gly

165 170 175

Ser Val Leu Asn Ala Leu Asn Pro Pro Ala Gly Ser Ala Ile Ala Ile

180 185 190

Phe Gly Ala Gly Ala Val Gly Leu Ser Ala Val Met Ala Ala Val Val

195 200 205

Ala Gly Cys Thr Thr Ile Ile Ala Val Asp Val Lys Glu Asn Arg Leu

210 215 220

Glu Leu Ala Ser Glu Leu Gly Ala Thr His Ile Ile Asn Pro Ala Ala

225 230 235 240

Asn Asp Pro Ile Glu Ala Ile Lys Glu Ile Phe Ala Asp Gly Val Pro

245 250 255

Tyr Val Leu Glu Thr Ser Gly Leu Pro Ala Val Leu Thr Gln Ala Ile

260 265 270

Leu Ser Ser Ala Ile Gly Gly Glu Ile Gly Ile Val Gly Ala Pro Pro

275 280 285

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

290 295 300

Lys Leu Arg Gly Ile Val Glu Gly Gln Ser Ile Ser Asp Ile Phe Ile

305 310 315 320

Pro Arg Leu Val Glu Leu Tyr Arg Gln Gly Lys Phe Pro Phe Asp Lys

325 330 335

Leu Ile Lys Phe Tyr Pro Phe Asp Glu Ile Asn Arg Ala Ala Glu Asp

340 345 350

Ser Glu Lys Gly Val Thr Leu Lys Pro Val Leu Arg Ile Gly

355 360 365

<210> 694

<211> 386

<212> PRT

<213> Homo sapiens

<400

> 694

Met Phe Ala Glu Ile Gln Ile Gln Asp Lys Asp Arg Met Gly Thr Ala

1 5 10 15

Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp Glu Gln Lys Gln

20 25 30

Pro Phe Ser Ile Glu Glu Ile Glu Val Ala Pro Pro Lys Thr Lys Glu

35 40 45

Val Arg Ile Lys Ile Leu Ala Thr Gly Ile Cys Arg Thr Asp Asp His

50 55 60

Val Ile Lys Gly Thr Met Val Ser Lys Phe Pro Val Ile Val Gly His

65 70 75 80

Glu Ala Thr Gly Ile Val Glu Ser Ile Gly Glu Gly Val Thr Thr Val

85 90 95

Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Leu Pro Gln Cys Arg Glu

100 105 110

Cys Asn Ala Cys Arg Asn Pro Asp Gly Asn Leu Cys Ile Arg Ser Asp

115 120 125

Ile Thr Gly Arg Gly Val Leu Ala Asp Gly Thr Thr Arg Phe Thr Cys

130 135 140

Lys Gly Lys Pro Val His His Phe Met Asn Thr Ser Thr Phe Thr Glu

145 150 155 160

Tyr Thr Val Val Asp Glu Ser Ser Val Ala Lys Ile Asp Asp Ala Ala

165 170 175

Pro Pro Glu Lys Val Cys Leu Ile Gly Cys Gly Phe Ser Thr Gly Tyr

180 185 190

Gly Ala Ala Val Lys Thr Gly Lys Val Lys Pro Gly Ser Thr Cys Val

195 200 205
 Val Phe Gly Leu Gly Gly Val Gly Leu Ser Val Ile Met Gly Cys Lys
 210 215 220
 Ser Ala Gly Ala Ser Arg Ile Ile Gly Ile Asp Leu Asn Lys Asp Lys
 225 230 235 240
 Phe Glu Lys Ala Met Ala Val Gly Ala Thr Glu Cys Ile Ser Pro Lys
 245 250 255

 Asp Ser Thr Lys Pro Ile Ser Glu Val Leu Ser Glu Met Thr Gly Asn
 260 265 270
 Asn Val Gly Tyr Thr Phe Glu Val Ile Gly His Leu Glu Thr Met Ile
 275 280 285
 Asp Ala Leu Ala Ser Cys His Met Asn Tyr Gly Thr Ser Val Val Val
 290 295 300
 Gly Val Pro Pro Ser Ala Lys Met Leu Thr Tyr Asp Pro Met Leu Leu
 305 310 315 320

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

Thr Phe

385

<210> 695

<211> 339

<212> PRT

<213> Geobacillus stearothermophilus

<400> 695

Met Lys Ala Ala Val Val Glu Gln Phe Lys Glu Pro Leu Lys Ile Lys

1

5

10

15

Glu Val Glu Lys Pro Thr Ile Ser Tyr Gly Glu Val Leu Val Arg Ile
 20 25 30
 Lys Ala Cys Gly Val Cys His Thr Asp Leu His Ala Ala His Gly Asp
 35 40 45
 Trp Pro Val Lys Pro Lys Leu Pro Leu Ile Pro Gly His Glu Gly Val
 50 55 60
 Gly Ile Val Glu Glu Val Gly Pro Gly Val Thr His Leu Lys Val Gly
 65 70 75 80
 Asp Arg Val Gly Ile Pro Trp Leu Tyr Ser Ala Cys Gly His Cys Asp
 85 90 95
 Tyr Cys Leu Ser Gly Gln Glu Thr Leu Cys Glu His Gln Lys Asn Ala
 100 105 110
 Gly Tyr Ser Val Asp Gly Gly Tyr Ala Glu Tyr Cys Arg Ala Ala Ala
 115 120 125
 Asp Tyr Val Val Lys Ile Pro Asp Asn Leu Ser Phe Glu Glu Ala Ala
 130 135 140
 Pro Ile Phe Cys Ala Gly Val Thr Thr Tyr Lys Ala Leu Lys Val Thr
 145 150 155 160
 Gly Ala Lys Pro Gly Glu Trp Val Ala Ile Tyr Gly Ile Gly Gly Leu
 165 170 175
 Gly His Val Ala Val Gln Tyr Ala Lys Ala Met Gly Leu Asn Val Val
 180 185 190
 Ala Val Asp Ile Gly Asp Glu Lys Leu Glu Leu Ala Lys Glu Leu Gly
 195 200 205
 Ala Asp Leu Val Val Asn Pro Leu Lys Glu Asp Ala Ala Lys Phe Met
 210 215 220
 Lys Glu Lys Val Gly Gly Val His Ala Ala Val Val Thr Ala Val Ser
 225 230 235 240
 Lys Pro Ala Phe Gln Ser Ala Tyr Asn Ser Ile Arg Arg Gly Gly Ala
 245 250 255
 Cys Val Leu Val Gly Leu Pro Pro Glu Glu Met Pro Ile Pro Ile Phe

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

305 310 315 320
 Asp Arg Met Leu Lys Gly Gln Ile Asn Gly Arg Val Val Leu Thr Leu
 325 330 335
 Glu Asp Lys

<210> 696

<211> 336

<212> PRT

<213> Staphylococcus aureus

<400> 696

Met Arg Ala Ala Val Val Thr Lys Asp His Lys Val Ser Ile Glu Asp
 1 5 10 15
 Lys Lys Leu Arg Ala Leu Lys Pro Gly Glu Ala Leu Val Gln Thr Glu
 20 25 30

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

Thr Gly Arg Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Thr
 100 105 110
 Val Asp Gly Ala Met Ala Glu Gln Val Ile Val Thr Ala Asp Tyr Ala
 115 120 125

Val Lys Val Pro Glu Lys Leu Asp Pro Ala Ala Ala Ser Ser Ile Thr
130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Val Ser Asn Val Lys
145 150 155 160

Pro Gly Gln Trp Leu Gly Val Phe Gly Ile Gly Gly Leu Gly Asn Leu
165 170 175

Ala Leu Gln Tyr Ala Lys Asn Val Met Gly Ala Lys Ile Val Ala Phe
180 185 190

Asp Ile Asn Asp Asp Lys Leu Ala Phe Ala Lys Glu Leu Gly Ala Asp
195 200 205

Ala Ile Ile Asn Ser Lys Asp Val Asp Pro Val Ala Glu Val Met Lys
210 215 220

Leu Thr Asp Asn Lys Gly Leu Asp Ala Thr Val Val Thr Ser Val Ala
225 230 235 240

Lys Thr Pro Phe Asn Gln Ala Val Asp Val Val Lys Ala Gly Ala Arg
245 250 255

Val Val Ala Val Gly Leu Pro Val Asp Lys Met Asn Leu Asp Ile Pro
260 265 270

Arg Leu Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr
275 280 285

Arg Gln Asp Leu Arg Glu Ala Phe Glu Phe Ala Ala Glu Asn Lys Val
290 295 300

Thr Pro Lys Val Gln Leu Arg Lys Leu Glu Glu Ile Asn Asp Ile Phe
305 310 315 320

Glu Glu Met Glu Asn Gly Thr Ile Thr Gly Arg Met Val Ile Lys Phe
325 330 335

<210> 697

<211> 365

<212> PRT

<213> Apium graveolens

<400> 697

Met Ala Lys Ser Ser Glu Ile Glu His Pro Val Lys Ala Phe Gly Trp

1 5 10 15
Ala Ala Arg Asp Thr Thr Gly Leu Leu Ser Pro Phe Lys Phe Ser Arg
 20 25 30
Arg Ala Thr Gly Glu Lys Asp Val Arg Leu Lys Val Leu Phe Cys Gly
 35 40 45
Val Cys His Ser Asp His His Met Ile His Asn Asn Trp Gly Phe Thr
 50 55 60
Thr Tyr Pro Ile Val Pro Gly His Glu Ile Val Gly Val Val Thr Glu

65 70 75 80
Val Gly Ser Lys Val Glu Lys Val Lys Val Gly Asp Asn Val Gly Ile
 85 90 95
Gly Cys Leu Val Gly Ser Cys Arg Ser Cys Glu Ser Cys Cys Asp Asn
 100 105 110
Arg Glu Ser His Cys Glu Asn Thr Ile Asp Thr Tyr Gly Ser Ile Tyr
 115 120 125
Phe Asp Gly Thr Met Thr His Gly Gly Tyr Ser Asp Thr Met Val Ala

130 135 140
Asp Glu His Phe Ile Leu Arg Trp Pro Lys Asn Leu Pro Leu Asp Ser
145 150 155 160
Gly Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Lys
 165 170 175
Tyr Tyr Gly Leu Asp Lys Pro Gly Thr Lys Ile Gly Val Val Gly Leu
 180 185 190
Gly Gly Leu Gly His Val Ala Val Lys Met Ala Lys Ala Phe Gly Ala

195 200 205
Gln Val Thr Val Ile Asp Ile Ser Glu Ser Lys Arg Lys Glu Ala Leu
210 215 220
Glu Lys Leu Gly Ala Asp Ser Phe Leu Leu Asn Ser Asp Gln Glu Gln
225 230 235 240
Met Lys Gly Ala Arg Ser Ser Leu Asp Gly Ile Ile Asp Thr Val Pro

245 250 255
Val Asn His Pro Leu Ala Pro Leu Phe Asp Leu Leu Lys Pro Asn Gly

260 265 270
Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Phe Glu Leu Pro Val

275 280 285
Phe Ser Leu Leu Lys Gly Arg Lys Leu Leu Gly Gly Thr Ile Asn Gly

290 295 300
Gly Ile Lys Glu Thr Gln Glu Met Leu Asp Phe Ala Ala Lys His Asn

305 310 315 320
Ile Thr Ala Asp Val Glu Val Ile Pro Met Asp Tyr Val Asn Thr Ala

325 330 335
Met Glu Arg Leu Val Lys Ser Asp Val Arg Tyr Arg Phe Val Ile Asp

340 345 350
Ile Ala Asn Thr Met Arg Thr Glu Glu Ser Leu Gly Ala

355 360 365
<210> 698

<211> 336

<212> PRT

<213> Staphylococcus aureus

<400> 698

Met Arg Ala Ala Val Val Thr Lys Asp His Lys Val Ser Ile Glu Asp
1 5 10 15

Lys Lys Leu Arg Ala Leu Lys Pro Gly Glu Ala Leu Val Gln Thr Glu
20 25 30

Tyr Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Ala Asp Phe
35 40 45

Gly Asp Val Thr Gly Val Thr Leu Gly His Glu Gly Ile Gly Lys Val
50 55 60

Ile Glu Val Ala Glu Asp Val Glu Ser Leu Lys Ile Gly Asp Arg Val
65 70 75 80

Ser Ile Ala Trp Met Phe Glu Ser Cys Gly Arg Cys Glu Tyr Cys Thr

85	90	95
Thr Gly Arg Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Thr		
100	105	110
Val Asp Gly Ala Met Ala Glu Gln Val Ile Val Thr Ala Asp Tyr Ala		
115	120	125
Val Lys Val Pro Glu Lys Leu Asp Pro Ala Ala Ala Ser Ser Ile Thr		
130	135	140
Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Val Ser Asn Val Lys		
145	150	155
160		
Pro Gly Gln Trp Leu Gly Val Phe Gly Ile Gly Gly Leu Gly Asn Leu		
165	170	175
Ala Leu Gln Tyr Ala Lys Asn Val Met Gly Ala Lys Ile Val Ala Phe		
180	185	190
Asp Ile Asn Asp Asp Lys Leu Ala Phe Ala Lys Glu Leu Gly Ala Asp		
195	200	205
Ala Ile Ile Asn Ser Lys Asp Val Asp Pro Val Ala Glu Val Met Lys		
210	215	220
Leu Thr Asp Asn Lys Gly Leu Asp Ala Thr Val Val Thr Ser Val Ala		
225	230	235
240		
Lys Thr Pro Phe Asn Gln Ala Val Asp Val Val Lys Ala Gly Ala Arg		
245	250	255
Val Val Ala Val Gly Leu Pro Val Asp Lys Met Asn Leu Asp Ile Pro		
260	265	270
Arg Leu Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr		
275	280	285
Arg Gln Asp Leu Arg Glu Ala Phe Glu Phe Ala Ala Glu Asn Lys Val		
290	295	300
Thr Pro Lys Val Gln Leu Arg Lys Leu Glu Glu Ile Asn Asp Ile Phe		
305	310	315
320		
Glu Glu Met Glu Lys Gly Thr Ile Thr Gly Arg Met Val Ile Lys Phe		
325	330	335

<210> 699

<211> 346

<212> PRT

<213> *Gibberella fujikuroi*

<400> 699

Met Gln Ala Leu Val Gly Ala Glu Thr Gly Gly Tyr Arg Leu Ala Asp

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Asn Val Glu Lys Pro Val Leu Gln Pro Gly Ser Ile Leu Cys His Val

20 25 30

Lys Ala Val Ala Leu Asn Pro His Asp Ala Lys Ile Val Asp Tyr Ser

35 40 45

Asn Val Pro Gly Ala Leu Gly Gly Cys Asp Phe Ala Gly Val Val Val

50 55 60

Glu Ile Gly Asn Gly Val Lys Arg Phe Lys Glu Gly Asp Arg Val Phe

65 70 75 80

Ala Val Thr Phe Gly Met Asn Ala Ser Asp Lys Thr Ala Gly Ala Phe

85 90 95

Thr Gln Tyr Ala Val Ala Thr Glu Asp Leu Ser Cys Leu Ile Pro Glu

100 105 110

Ala Met Ser Phe Thr Glu Ala Cys Ser Met Gly Leu Ala Ile Ala Thr

115 120 125

Ala Gly Leu Ala Leu Phe Gln Thr Pro Gly Leu Gln Leu Ser Met Gln

130 135 140

Gly Gly Asn Gly Glu Ala Val Leu Val Ser Gly Gly Ala Thr Ala Thr

145 150 155 160

Gly Thr Met Ala Ile Gln Phe Leu Arg Ile Ala Gly Tyr Thr Pro Val

165 170 175

Val Thr Cys Ser Pro Ser Asn Asn Ala Leu Cys Glu Ser Phe Gly Ala

180 185 190

Glu Ile Cys Phe Asp Tyr His Ser Pro Thr Cys Gly Ala Asp Ile Arg

195 200 205

Val Gln Thr Gly Asn Lys Leu Arg His Val Leu Asp Cys Val Val Asp

210 215 220
 Ile Ser Thr Met Lys Met Ser Tyr Asp Ala Ile Gly Ser Ser Gly Gly
 225 230 235 240
 Ala Tyr Val Ala Leu Glu Ala Ile Pro Thr Asn Ile Lys Tyr Thr Arg

 245 250 255
 Arg Asp Ile Cys Ala Asn Trp Leu Met Ala Pro Ser Ile Leu Gly Thr
 260 265 270
 Pro Val Asn Lys Lys Gly Ala Tyr Gly Arg Pro Ser Met Pro Glu His
 275 280 285
 Arg Gln Phe Gly Thr Tyr Leu Phe Ala Leu Ala Glu Lys Trp Leu Gln
 290 295 300
 Asp Gly Ser Ile Lys His His Pro Ile Glu Ile Arg Glu Gly Gly Leu

 305 310 315 320
 Arg Ser Ile Arg Glu Gly Ile Asp Asp Leu Arg Arg Gly Asn Val His
 325 330 335
 Ala Lys Lys Leu Val Tyr Pro Leu Ser Ala
 340 345
 <210> 700
 <211> 351
 <212> PRT
 <213> *Marinobacter similis*
 <400> 700
 Met Thr Ala Thr Lys Ala Tyr Ala Ala Gln Ser Ser Thr Ser Gly Met
 1 5 10 15
 Ala Pro His Asp Ile Asp Arg Arg Ser Leu Arg Asn Asp Asp Ile Ala

 20 25 30
 Ile Glu Ile Asp Tyr Cys Gly Val Cys His Thr Asp Ile His Phe Ala
 35 40 45
 Gln Asn Asp Trp Gly Val Thr Gln Tyr Pro Val Val Pro Gly His Glu
 50 55 60
 Ile Val Gly Arg Val Thr Ala Val Gly Pro Gly Val Lys Ala Tyr Gln
 65 70 75 80

Glu Gly Asp Val Val Gly Val Gly Cys Met Val Asp Ser Cys Arg Thr

85 90 95

Cys Ser Ala Cys Glu Ala Gly Leu Glu Gln Tyr Cys Ser Glu Gly Met

100 105 110

Thr Gly Thr Tyr Asn Gly Glu Asp Arg Gln Asp His Ser Ile Thr Phe

115 120 125

Gly Gly Tyr Ser Glu Arg Ile Val Val Ser Glu Arg Phe Val Val Arg

130 135 140

Ile Pro Asp Lys Leu Asp Ile Thr Lys Ala Ala Pro Leu Leu Cys Ala

145 150 155 160

Gly Ile Thr Thr Tyr Ser Pro Leu Arg His Tyr Gly Val Lys Pro Gly

165 170 175

His Lys Val Gly Val Ile Gly Met Gly Gly Leu Gly His Met Gly Val

180 185 190

Lys Phe Ala Lys Ala Leu Gly Ala Glu Val Thr Ile Phe Thr Arg Ser

195 200 205

Glu Ser Lys Val Gly Glu Ala Lys Lys Gln Gly Ala Asp Tyr Val Val

210 215 220

Val Ser Thr Asp Glu Asp Gln Met Ala Ala Ala Ala Glu Thr Phe Asp

225 230 235 240

Phe Met Leu Asp Thr Val Pro Val Gln His Asp Ile Asn Pro Tyr Leu

245 250 255

Asn Cys Leu Ser Tyr Asp Gly Thr His Ile Met Val Gly Leu Leu Glu

260 265 270

Pro Leu Glu Pro Ala Leu Gln Thr Gly Ala Leu Val Phe Lys Arg Arg

275 280 285

Val Leu Ala Gly Ser Leu Ile Gly Gly Met Pro Glu Thr Gln Glu Val

290 295 300

Leu Asp Phe Cys Ala Glu His Asp Ile Ser Cys Asp Val Glu Met Leu

305 310 315 320

Asp Ile His Asn Ile Asn Asp Ala Tyr Glu Arg Met Lys Lys Gly Asp

325 330 335
Val Lys Tyr Arg Phe Val Ile Asp Met Ala Thr Leu Lys Asp Ser

340 345 350