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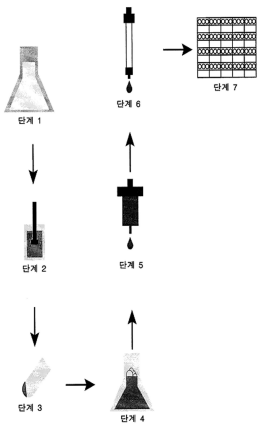
(54) 발명의 명칭 **SLAM 폴리뉴클레오타이드 및 폴리펩타이드 및 이의 용도**

(57) 요 약

본 개시내용은 표면 지질단백질 어셈블리 모듈레이터(SLAM) 폴리펩타이드를 사용하여 표적 단백질(예를 들면, 표면 지질단백질)을, 사이토졸로부터 박테리아 세포의 세포외 표면으로 이동시키는 방법에 관한 것이다. 박테리아 감염염 질환의 예방에서 유용한 백신을 제조하는 방법에서의 SLAM 폴리펩타이드의 사용이 또한 교시된다.

대 표 도



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청구범위

청구항 1

표적 단백질을 포함하는 단리된 숙주 세포의 세포기질에서 세포외 표면으로의 상기 표적 단백질의 수송을 초래하는 방법이되, 하기를 포함하는 방법:

(a) 작동가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

(i) 단리된 숙주 세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

(ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드로서, 서열식별번호: 5, 서열식별번호: 199, 서열식별번호: 273, 서열식별번호: 385, 서열식별번호: 387, 서열식별번호: 1087, 서열식별번호: 1111, 및 서열식별번호: 1181로 구성된 군으로부터 선택되는 폴리뉴클레오타이드 서열, 또는 임의의 전술한 폴리뉴클레오타이드에 의해 인코딩되는 폴리펩타이드와 적어도 90% 동일한 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드 서열을 포함하는, 폴리뉴클레오타이드; 및

(b) 상기 단리된 숙주 세포에 키메라성 폴리뉴클레오타이드를 유입시키고 상기 단리된 숙주 세포를 성장시켜 SLAM 폴리펩타이드를 생산하고, 그로써 상기 단리된 숙주 세포의 세포기질에서 세포외 표면으로 상기 표적 단백질의 수송을 초래하는 단계.

청구항 2

제1항에 있어서, 하기를 포함하는 방법:

(a) 작동가능하게 연결된 성분으로 하기를 포함하는 제2 키메라성 폴리뉴클레오타이드를 제공하는 단계:

(i) 상기 단리된 숙주 세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

(ii) 표적 단백질을 인코딩하는 폴리뉴클레오타이드; 및

(b) 상기 숙주 세포에 키메라성 폴리뉴클레오타이드를 유입시키고 상기 단리된 숙주 세포를 성장시켜 SLAM 폴리펩타이드 및 표적 단백질을 생산하고, 그로써 세포기질에서 세포외 표면으로 표적 단백질의 수송을 초래하는 단계.

청구항 3

제1항 또는 제2항에 있어서, 상기 단리된 숙주 세포가 그램-음성 박테리아 세포인, 방법.

청구항 4

제1항 또는 제2항에 있어서, 상기 단리된 숙주 세포가 병원성 박테리아 세포인, 방법.

청구항 5

제1항 또는 제2항에 있어서, 상기 단리된 숙주 세포가 속 나이세리아, 모락셀라, 악티노바실러스, 헤모필루스, 파스튜렐라, 아시네토박터, 에스케리치아 또는 비브리오에 속하는 박테리아 세포에서 선택된 세포인, 방법.

청구항 6

제5항에 있어서, 상기 단리된 숙주 세포가 종 나이세리아 메닌기티디스, 나이세리아 고노르호아에, 나이세리아 락타미카, 나이세리아 신세라, 클렙시엘라 데니트리피칸스, 모락셀라 카타르할리스, 만헤이미아 하에몰리티카, 악티노바실러스 플레우롭네오모니애, 헤모필루스 솜니, 헤모필루스 인플루엔자, 파스튜렐라 멀토시다, 아시네토박터 바우마니 또는 비브리오 콜레라에 속하는 박테리아 세포에서 선택되는, 방법.

청구항 7

제1항 또는 제2항에 있어서, 상기 SLAM 폴리펩타이드가 상기 단리된 숙주 세포에 천연적으로 존재하지 않는, 방

법.

청구항 8

제1항 또는 제2항에 있어서, 상기 표적 단백질이 상기 단리된 숙주 세포에 천연적으로 존재하는, 방법.

청구항 9

제1항 또는 제2항에 있어서, 상기 표적 단백질이 상기 단리된 숙주 세포에 천연적으로 존재하지 않고, 상기 키메라성 폴리뉴클레오타이드가 상기 표적 단백질을 인코딩하는 폴리뉴클레오타이드를 포함하는, 방법.

청구항 10

제1항 또는 제2항에 있어서, 상기 표적 단백질이 상기 SLAM 폴리펩타이드에 비-공유적으로 결합되는, 방법.

청구항 11

제1항 또는 제2항에 있어서, 상기 표적 단백질이 SLAM 폴리펩타이드에 공유적으로 결합되는, 방법.

청구항 12

제1항 또는 제2항에 있어서, 상기 표적 단백질이 숙주 유기체에서 면역 반응을 불러 일으킬 수 있는 면역원인, 방법.

청구항 13

제1항 또는 제2항에 있어서, 상기 표적 단백질이 병원성 미생물의 외측 표면에 자연적으로 나타난 면역원성 폴리펩타이드, 또는 이것의 면역원성 부분인, 방법.

청구항 14

제12항에 있어서, 상기 면역원이 표면 지질단백질(SLP)인, 방법.

청구항 15

제14항에 있어서, 상기 표면 지질단백질(SLP)이 본원에 제시된 서열식별번호: 696 내지 서열식별번호: 1082, 및 서열식별번호: 1178의 짝수-넘버링된 서열식별번호 중 하나로부터 선택되는 서열을 포함하는, 방법.

청구항 16

제14항에 있어서, 상기 표면 지질단백질(SLP)이 트랜스페린 결합 단백질 B(TbpB), 헤모글로빈-합토글로빈 결합 단백질 A(HpuA), 인자 H 결합 단백질(fHbp), 및 락토페린 결합 단백질(LbpB)에서 선택되는, 방법.

청구항 17

제16항에 있어서,

상기 트랜스페린 결합 단백질 B(TbpB)가 본원에 제시된 서열식별번호: 806, 서열식별번호: 828, 서열식별번호: 868, 서열식별번호: 1094, 및 서열식별번호: 1148 내지 서열식별번호: 1168의 짝수-넘버링된 서열식별번호 중 하나로부터 선택되는 서열을 포함하고;

상기 헤모글로빈-합토글로빈 결합 단백질 A(HpuA)가 본원에 제시된 서열식별번호: 850, 서열식별번호: 924, 서열식별번호: 932, 또는 서열식별번호: 1110으로부터 선택되는 서열을 포함하고;

상기 인자 H 결합 단백질(fHbp)이 본원에 제시된 서열식별번호: 1116 내지 서열식별번호: 1136의 짝수-넘버링된 서열식별번호 중 하나로부터 선택되는 서열을 포함하고;

상기 락토페린 결합 단백질(LbpB)이 본원에 제시된 서열식별번호: 870, 또는 서열식별번호: 1138 내지 서열식별번호: 1146의 짝수-넘버링된 서열식별번호 중 하나로부터 선택되는 서열을 포함하는, 방법.

청구항 18

제1항 또는 제2항에 있어서, 상기 표적 단백질이 서열식별번호: 696 내지 서열식별번호: 1082의 짝수-넘버링된

서열식별번호 중 하나; 서열식별번호: 1094; 서열식별번호: 1100; 서열식별번호: 1116 내지 서열식별번호: 1168의 짝수-넘버링된 서열식별번호 중 하나; 및 서열목록번호: 1178로부터 선택되는 서열을 포함하는, 방법.

청구항 19

제1항 또는 제2항에 있어서, 상기 단리된 숙주 세포가 백신 제형을 제조하는 데 사용되는, 방법.

청구항 20

백신을 제조하는 방법으로, 하기를 포함하는 방법:

(a) 면역원을 생산할 수 있는 단리된 숙주 세포를 선택하는 단계;

(b) 작동가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

(i) 상기 단리된 숙주 세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

(ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드로서, 서열식별번호: 5, 서열식별번호: 199, 서열식별번호: 273, 서열식별번호: 385, 서열식별번호: 387, 서열식별번호: 1087, 서열식별번호: 1111, 및 서열식별번호: 1181로 구성된 군으로부터 선택되는 폴리뉴클레오타이드 서열, 또는 임의의 전술한 폴리뉴클레오타이드에 의해 인코딩되는 폴리펩타이드와 적어도 90% 동일한 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드 서열을 포함하는, 폴리뉴클레오타이드; 및

(c) 상기 키메라성 핵산 서열을 상기 단리된 숙주 세포에 유입시키고 상기 단리된 숙주 세포를 성장시켜 상기 SLAM 폴리펩타이드와 상기 면역원을 생산하는 단계;

(d) 상기 단리된 숙주 세포를 약화시켜 약화된 단리된 숙주 세포를 제조하는 단계; 및

(e) 상기 약화된 단리된 숙주 세포를 사용하여 백신 제형을 제조하는 단계.

청구항 21

제20항에 있어서, 하기를 포함하는 방법:

(a) 작동가능하게 연결된 성분으로 하기를 포함하는 제2 키메라성 폴리뉴클레오타이드를 제공하는 단계:

(i) 상기 단리된 숙주 세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

(ii) 면역원을 인코딩하는 폴리뉴클레오타이드; 및

(b) 상기 단리된 숙주 세포에 키메라성 폴리뉴클레오타이드를 유입시키고 상기 숙주 세포를 성장시켜 SLAM 폴리펩타이드 및 면역원을 생산하는 단계.

청구항 22

제20항 또는 제21항에 있어서, 상기 면역원이 병원성 미생물의 외측 표면 상에 자연적으로 나타나는, 방법.

청구항 23

제20항 또는 제21항에 있어서, 상기 면역원이 표면 지질단백질(SLP)인, 방법.

청구항 24

제23항에 있어서, 상기 표면 지질단백질(SLP)이 본원에 제시된 서열식별번호: 696 내지 서열식별번호: 1082의 짝수-넘버링된 서열식별번호 중 하나로부터 선택된 서열을 포함하는, 방법.

청구항 25

제23항에 있어서, 상기 표면 지질단백질이 트랜스페린 결합 단백질 B(TbpB), 헤모글로빈-합토글로빈 결합 단백질 A(HpuA), 인자 H 결합 단백질(fHbp), 및 락토페린 결합 단백질(LbpB)에서 선택되는, 방법.

청구항 26

제25항에 있어서,

상기 트랜스페린 결합 단백질 B(TbpB)가 본원에 제시된 서열식별번호: 806, 서열식별번호: 828, 서열식별번호: 868, 서열식별번호: 1094, 및 서열식별번호: 1148 내지 서열식별번호: 1168의 짝수-넘버링된 서열식별번호 중 하나로부터 선택되는 서열을 포함하고;

상기 헤모글로빈-합토글로빈 결합 단백질 A(HpuA)가 본원에 제시된 서열식별번호: 850, 서열식별번호: 924, 서열식별번호: 932, 또는 서열식별번호: 1110으로부터 선택되는 서열을 포함하고;

상기 인자 H 결합 단백질(fHbp)이 본원에 제시된 서열식별번호: 1116 내지 서열식별번호: 1136의 짝수-넘버링된 서열식별번호 중 하나로부터 선택되는 서열을 포함하고;

상기 락토페린 결합 단백질(LbpB)이 본원에 제시된 서열식별번호: 870, 또는 서열식별번호: 1138 내지 서열식별번호: 1146의 짝수-넘버링된 서열식별번호 중 하나로부터 선택되는 서열을 포함하는, 방법.

청구항 27

제20항 또는 제21항에 있어서, 상기 표적 단백질이 상기 SLAM 폴리펩타이드에 비-공유적으로 결합되는, 방법.

청구항 28

제20항 또는 제21항에 있어서, 상기 표적 단백질이 상기 SLAM 폴리펩타이드에 공유적으로 결합되는, 방법.

청구항 29

삭제

청구항 30

삭제

청구항 31

삭제

청구항 32

삭제

발명의 설명

기 술 분 야

[0001] 관련 출원에 대한 교차 참조

[0002] 본원은 2016년 2월 10일에 출원된 미국 특허 가출원 번호 62/293,491의 이점을 주장한다. 상기 미국 특허 가출원 번호 62/293,491의 전체 내용이 본 명세서에 참고로 편입되어 있다.

[0003] 발명의 분야

[0004] 본 개시내용은 표면 지질단백질 어셈블리 모듈레이터 폴리펩타이드, 즉 SLAM 폴리펩타이드라고 알려진 폴리펩타이드 부류, 및 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드, 및 이것의 기질, 표면 지질단백질(SLPs)에 관한 것이다. 상기 SLAM 폴리펩타이드는 그램-음성 박테리아 종에서 획득 가능하다. 상기 SLAM 폴리펩타이드 및 폴리뉴클레오타이드는 병원성 박테리아 종, 예컨대, 예를 들어, 나이세리아 속에 속하는 박테리아 종에 의해 야기된 감염성 질환의 예방 및 치료에 유용하다.

배 경 기 술

[0005] 하기 단락은 이어 따라오는 좀 더 상세한 설명을 독자에게 소개하려는 것으로 본 개시내용의 청구된 요지를 규정하거나 또는 제한하기 위한 것이 아니다.

[0006] 병원성 박테리아 종, 예컨대 나이세리아 속에 속하는 박테리아 종은 큰 유행성 질환의 원인 인자이다. 따라서,

예를 들어 수막염이 나이세리아 메닌기티디스에 의해 야기되고, 임질이 나이세리아 고노르호아에에 의해 야기된다. 세계보건기구(WHO)가 2009년에 소위 "수막염 벨트"라 불리는 사하라 이남 아프리카 내의 14개 국가에서 88,000건이 넘는 의심되는 사례를 보고하였고, 이들 중 5,300명이 사망에 이르렀다(WHO 팩트 시트 No 141, 2012년 11월). 북미를 비롯한 다른 곳에서 산발적 수막염 발발이 발생하였다. 임질은 미국 단독으로 연간 820,000건의 신규 사례가 보고되고 있고, 전 세계 100 백만명이 넘는 사람들에게 영향을 주는 것으로 추정된 바 있다. 항생제, 예컨대 암피실린, 테트라사이클린 및 퀴놀론은 나이세리아 감염에 대응하는 치료 선택을 제공하는 데, 이들 항생제에 대한 내성이 점점 더 상당한 우려를 낳고 있다. 나이세리아 감염에 대응하여 보호를 제공하는 백신이 개발된 바 있으나, 혈청군에 따라, 상기 백신의 효능이 다양하기 때문에, 추가 백신에 대한 필요성은 현재 진행형이다. 따라서, 예를 들어, 4cMenB로 알려진 백신(나이세리아 메닌기티디스 혈청군 B에 대한 4성분 백신)의 효능이 확립되어야 하고, 캐나다에서는 소아에 사용이 침습성 수막염균 질환의 최고 위험에 처한 개체에만 권고된다(Robinson JL, Paediatric Child Health, 2014 19(2): 91-94). N. 고노르호아에에 이용가능한 백신은 아직도 없다.

발명의 내용

해결하려는 과제

[0007] 따라서 병원성 나이세리아 종 및 다른 병원성 박테리아 종에 의해 야기된 감염에 대응하는 추가적 치료 및 예방 옵션의 개발이 필요하다.

과제의 해결 수단

[0008] 발명의 요약

[0009] 일 측면에서, 본 개시내용은 표면 지질단백질 어셈블리 모듈레이터(SLAM) 폴리펩타이드로 공지된 폴리펩타이드 부류에 관한 것이다.

[0010] 또 다른 측면에서, 본 개시내용은 숙주세포, 예컨대 병원성 또는 비-병원성 박테리아 세포에서 SLAM 폴리펩타이드의 생산에 관한 것이다.

[0011] 또 다른 측면에서, 본 개시내용은 세포 내에서 상기 세포의 세포기질에서 세포외 표면으로의 특정 표적 단백질의 수송에 관한 것이다.

[0012] 따라서, 일 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 표적 단백질을 포함하는 숙주세포의 세포기질에서 세포외 표면으로의 상기 표적 단백질의 수송을 초래하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0013] (a) 작동가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0014] (i) 하기에서 발현을 제어할 수 있는 폴리뉴클레오타이드:

[0015] 숙주 세포; 및

[0016] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0017] (b) 상기 숙주세포에 키메라성 폴리뉴클레오타이드를 유입시키고 상기 숙주세포를 성장시켜 SLAM 폴리펩타이드를 생산함으로써, 상기 숙주세포의 세포기질에서 세포외 표면으로 상기 표적 단백질의 수송을 초래하는 단계.

[0018] 일부 구현예에서, 상기 숙주세포는 그램-음성 박테리아 세포이다.

[0019] 일부 구현예에서, 상기 숙주세포는 병원성 박테리아 세포이다.

[0020] 일부 구현예에서, 상기 숙주세포는 나이세리아 속, 클렙시엘라, 모락셀라, 만헤이미아, 악티노바실러스, 헤모필루스, 파스튜렐라, 아시네토박터, 에스케리치아 또는 비브리오에 속하는 박테리아 세포에서 선택된 세포이다.

[0021] 일부 구현예에서, 상기 숙주세포는 나이세리아 메닌기티디스 종, 나이세리아 고노르호아에, 나이세리아 락타미카, 나이세리아 신세라, 클렙시엘라 데니트리피칸스, 모락셀라 카타르할리스, 만헤이미아 하에몰리티카, 악티노바실러스 플레우롭네오모니애, 헤모필루스 솜니, 헤모필루스 인플루엔자, 파스튜렐라 멀토시다, 아시네토박터 바우마니, 에스케리치아 콜라이 또는 비브리오 콜레라에 속하는 박테리아 세포에서 선택된다.

[0022] 일부 구현예에서, 상기 SLAM 폴리펩타이드는 상기 숙주세포 내에 천연적으로 존재하지 않는다.

[0023] 일부 구현예에서, 상기 표적 단백질은 상기 숙주세포에 천연적으로 존재한다.

[0024] 일부 구현예에서, 상기 표적 단백질은 상기 숙주세포에 천연적으로 존재하지 않는다.

[0025] 일부 구현예에서, 상기 표적 단백질은 상기 SLAM 폴리펩타이드에 비-공유적으로 결합된다.

[0026] 일부 구현예에서, 상기 표적 단백질은 상기 SLAM 폴리펩타이드에 공유결합된다.

[0027] 일부 구현예에서, 상기 표적 단백질은 숙주 유기체에서 면역 반응을 이끌어낼 수 있는 면역원이다.

[0028] 일부 구현예에서, 상기 표적 단백질은, 병원성 미생물의 외측 표면에 자연적으로 출연하는 면역원성 폴리펩타이드, 또는 이것의 면역원성 부분이다.

[0029] 일부 구현예에서, 상기 표적 단백질은 표면 지질단백질(SLP)이다.

[0030] 일부 구현예에서, 상기 표면 지질단백질(SLP)은 하기의 짝수-넘버링된 서열식별번호들 중 하나에서 선택된 서열을 포함하거나 또는 그것으로 이루어진다: 서열식별번호: 696 내지 서열식별번호: 1082; 서열식별번호: 1094; 서열식별번호: 1100; 짝수-넘버링된 서열식별번호: 1116 내지 서열식별번호: 1168; 및 서열목록번호; 1178(본원에 제시됨).

[0031] 일부 구현예에서, 상기 표면 지질단백질은 트랜스페린 결합 단백질 B(TbpB), 헤모글로빈-합토글로빈 결합 단백질 A(HpuA), 인자 H 결합 단백질(fHbp), 및 락토페린 결합 단백질(LbpB)에서 선택된다.

[0032] 일부 구현예에서, 상기 트랜스페린 결합 단백질 B(TbpB)은 하기에서 선택된 서열을 포함하거나 또는 서열로 이루어진다: 서열식별번호: 806, 서열식별번호: 828, 서열식별번호: 868, 서열식별번호: 1094, 및 서열식별번호: 1148 내지 서열식별번호: 1168(본원에 제시됨)의 짝수-넘버링된 서열식별번호 중 하나; 상기 헤모글로빈-합토글로빈 결합 단백질 A(HpuA)는 하기에서 선택된 서열을 포함하거나 또는 그것으로 이루어진다: 서열식별번호: 850, 서열식별번호: 924, 서열식별번호: 932, 또는 서열식별번호: 1110(본원에 제시됨), 상기 인자 H 결합 단백질(fHbp)은 서열식별번호: 1116 내지 서열식별번호: 1136 (본원에 제시됨)의 짝수-넘버링된 서열식별번호 중 하나에서 선택된 서열을 포함하거나 또는 상기 서열로 이루어지고, 그리고 상기 락토페린 결합 단백질(LbpB)은 하기에서 선택된 서열을 포함하거나 또는 그것으로 이루어진다: 서열식별번호: 870 또는 하기의 짝수-넘버링된 서열식별번호 중 하나: 서열식별번호: 1138 내지 서열식별번호: 1146(본원에 제시됨).

[0033] 일부 구현예에서, 상기 SLAM 폴리펩타이드를 인코딩하는 상기 폴리뉴클레오타이드는 하기 홀수 -넘버링된 서열식별번호 중 하나에서 선택된 서열을 포함하거나 또는 그것으로 이루어진다: 서열식별번호: 1 내지 서열식별번호: 693(본원에 제시됨).

[0034] 일부 구현예에서, 상기 표적 단백질은 하기의 짝수-넘버링된 서열식별번호들 중 하나에서 선택된 서열을 포함하거나 또는 그것으로 이루어진다: 서열식별번호: 696 내지 서열식별번호: 1082, 서열식별번호: 1094; 서열식별번호: 1100; 짝수-넘버링된 서열식별번호: 1116 내지 서열식별번호: 1168; 및 서열목록번호; 1178.

[0035] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 숙주세포의 세포기질에서 세포외 표면으로 표적 단백질의 수송을 초래하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0036] (a) 상기 세포에 천연적으로 존재하는 표적 단백질을 포함하는 숙주세포를 선택하는 단계;

[0037] (b) 작동 가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0038] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0039] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0040] (c) 상기 키메라성 핵산 서열을 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 SLAM 폴리펩타이드를 생산하여, 세포기질에서 세포외 표면으로의 표적 단백질의 수송을 초래하는 단계.

[0041] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 숙주세포의 세포기질에서 세포외 표면으로 표적 단백질의 수송을 초래하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0042] (a) 작동 가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0043] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드;

[0044] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0045] (iii) 표적 단백질을 인코딩하는 폴리뉴클레오타이드; 및

[0046] (b) 상기 키메라성 핵산 서열을 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 상기 SLAM 폴리펩타이드를 생산하고 상기 세포기질에서 상기 세포외 표면으로 상기 표적 단백질의 수송을 초래하는 단계.

[0047] 또 다른 측면에서, 본 개시내용은은 숙주세포의 세포기질에서 세포외 표면으로 표적 단백질의 수송을 초래하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0048] (a) 작동 가능하게 연결된 성분으로 하기를 포함하는 제1 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0049] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0050] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0051] (b) 작동 가능하게 연결된 성분으로 하기를 포함하는 제2 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0052] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0053] (ii) 표적 단백질을 인코딩하는 폴리뉴클레오타이드; 및

[0054] (c) 상기 숙주세포에 제1 및 제2 키메라성 폴리뉴클레오타이드를 유입시키고 상기 숙주세포를 성장시켜 SLAM 폴리펩타이드 및 표적 단백질을 생산하고, 세포기질에서 세포외 표면으로 표적 단백질의 수송을 초래하는 단계.

[0055] 또 다른 측면에서, 본 개시내용은 신규한 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드에 관한 것이다. 따라서, 본 개시내용은 적어도 하나의 구현예에서, 서열식별번호: 1183를 포함하거나 또는 이들로 이루어진 폴리뉴클레오타이드를 제공한다.

[0056] 일부 구현예에서, 상기 폴리뉴클레오타이드는 SLAM 폴리펩타이드를 인코딩하고, 상기 SLAM 폴리뉴클레오타이드는 숙주세포에서 SLAM 폴리펩타이드의 발현을 용이하게 하기 위해 변형되었다.

[0057] 일부 구현예에서, 상기 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 코돈-최적화되었다.

[0058] 일부 구현예에서, 상기 코돈-최적화된 폴리뉴클레오타이드는 서열식별번호: 1113에 제시된 서열을 포함하거나 또는 그것으로 이루어진다.

[0059] 일부 구현예에서, SLAM 폴리펩타이드를 인코딩하는 상기 폴리뉴클레오타이드는 추가로 신호 서열을 포함한다.

[0060] 또 다른 측면에서, 본 개시내용은 신규한 폴리펩타이드에 관한 것이다. 따라서 본 개시내용은 적어도 하나의 구현예에서, 서열식별번호: 1184를 포함하거나 또는 그것으로 이루어진 폴리펩타이드를 제공한다.

[0061] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 백신을 제조하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0062] (a) 면역원을 생산할 수 있는 숙주세포를 선택하는 단계;

[0063] (b) 작동 가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0064] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0065] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0066] (c) 상기 키메라성 핵산 서열을 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 상기 SLAM 폴리펩타이드와 상기 면역원을 생산하는 단계;

[0067] (d) 상기 숙주세포를 약화시켜 약화된 숙주세포를 제조하는 단계; 및

[0068] (e) 상기 약화된 숙주세포를 사용하여 백신 제형을 제조하는 단계.

[0069] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 백신을 제조하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0070] (a) 작동 가능하게 연결된 성분으로 하기를 포함하는 제1 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0071] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드;

[0072] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0073] (b) 작동 가능하게 연결된 성분으로 하기를 포함하는 제2 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0074] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0075] (ii) 표적 단백질을 인코딩하는 폴리뉴클레오타이드; 및

[0076] (c) 상기 제1 및 제2 키메라성 폴리뉴클레오타이드를 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 SLAM 폴리펩타이드와 표적 단백질을 생산하는 단계; 및

[0077] (d) (c)의 세포를 사용하여 백신 제형을 제조하는 단계.

[0078] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 백신을 제조하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0079] (a) 작동가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0080] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드;

[0081] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0082] (iii) 표적 단백질을 인코딩하는 폴리뉴클레오타이드; 및

[0083] (b) 상기 키메라성 폴리뉴클레오타이드를 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 상기 SLAM 폴리펩타이드와 상기 표적 단백질을 생산하는 단계; 및

[0084] (c) (b)의 세포를 사용하여 백신 제형을 제조하는 단계.

[0085] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 병원성 박테리아 감염에 대응하는 백신을 제조하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0086] (a) SLAM 폴리펩타이드를 인코딩하는 핵산 서열을 포함하는 병원성 균주를 제공하는 단계;

[0087] (b) 상기 병원성 균주에서 SLAM 생산을 손상시켜 SLAM이 손상된 병원성 균주를 수득하는 단계; 및

[0088] (c) 상기 SLAM이 손상된 병원성 균주를 사용하여 백신을 제형화하는 단계.

[0089] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 본 개시내용의 방법들 중 임의의 것에 따라 제조된 백신 제제를 제공한다.

[0090] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 숙주 유기체에 면역력을 제공하기 위한 본 개시내용의 임의의 방법에 따라 제조된 백신 제제의 용도를 제공한다.

[0091] 일부 구현예에서, 상기 백신 제제는 박테리아 유기체에 의해 매개된 감염성 질환에 대한 보호를 제공한다.

[0092] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 병원성 박테리아 종에 의해 감염된 환자의 치료에 사용하기 위한 후보 화합물을 식별하기 위한 스크리닝 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0093] (a) 시험 화합물을 제공하는 단계;

[0094] (b) 기능성 검정에서, 병원성 박테리아 종에서 SLAM 폴리펩타이드의 기능과 관련하여 상기 시험 화합물의 영향과 효과와 대조군의 영향을 비교하는 단계; 및

[0095] (c) SLAM 폴리펩타이드의 원상태 기능에 영향을 미치는 시험 화합물을 식별하는 단계.

[0096] 일부 구현예에서, 상기 병원성 박테리아 종은 나이세리아 속에 속한다.

[0097] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, SLAM 폴리펩타이드에 의해 세포의 세포기질에서 세포외 표면으로 수송될 수 있는 표적 단백질을 식별하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0098] (a) 하기를 포함하는 게놈 뉴클레오타이드 서열을 제공하는 단계

[0099] (i) SLAM 폴리펩타이드를 인코딩하는 제1 뉴클레오타이드 서열; 및

[0100] (ii) 폴리펩타이드를 인코딩하기에 충분히 길고 상기 제1 뉴클레오타이드 서열에 자연적으로 부착된 제2 뉴클레오타이드 서열;

[0101] (b) 상기 제2 뉴클레오타이드 서열을 평가하여 상기 제2 뉴클레오타이드 서열 내 폴리펩타이드 인코딩 서열을

식별하는 단계; 및

[0102] (c) 폴리펩타이드 인코딩 서열을 사용하여 SLAM 폴리펩타이드를 포함하는 숙주세포에서 폴리펩타이드를 발현시켜서 상기 단백질이 상기 숙주세포의 세포기질에서 세포외 표면으로 수송되었는지 여부를 판단함으로써, 상기 단백질이 표적 단백질인지 여부를 식별하는 단계.

[0103] 일부 구현예에서, 상기 제1 뉴클레오타이드 서열은 서열식별번호 1 내지 서열식별번호: 695(본원에 제시됨)의 홀수-넘버링된 서열식별번호 중 임의의 하나에서 선택된 서열을 포함한다.

[0104] 본 개시내용의 다른 특징 및 이점은 하기 상세한 설명으로 분명해질 것이다. 그러나, 개시내용의 사상 및 범위 내에서 다양한 수정 및 변형이 당해 분야의 숙련가에 분명할 것이기 때문에 상세한 설명은 상기 개시내용의 바람직한 구현예이되, 단지 주어진 예시임이 이해되어야 한다.

도면의 간단한 설명

[0105] 본 개시내용은 그것의 도면과 관련하여 기재된 이하 제공 단락에 존재한다. 본원에 제공된 도면은 설명하기 위한 것으로 본 개시내용을 제한하려는 의도는 없다.

도 1은 SLAMs의 정제를 위한 방법론을 개략적으로 나타낸 다이어그램을 도시한다. 단계 1: 5H3을 함유한 플라스미드로 전환된 세포를 원하는 광학 밀도에 도달되기까지 37° C에서 성장시켰다. 이 시점에서, IPTG의 첨가로 발현을 유도한다. 단계 2: 밤새 성장 후, 원심분리로 세포를 수확한다. 그러고 나서, 리소자임 및 DNAse의 존재하에 초음파 처리로 세포를 용해한다. 단계 3: 상기 용해물의 막 분획을 초원심 분리를 통해 단리한다. 단계 4: 막 펠렛을 재현탁하고, 50mM 인산칼륨(pH 7.5, 3% Elugent 및 PMSF) 중 상기 막에서 막 단백질을 밤새 추출한다. 단계 5: 상기 추출 용액을 니켈-NTA 칼럼에 장입한다. 0.6^ C8E4 함유 완충액으로 상기 칼럼에서 5H3이 용출되기 전에 이미다졸 양을 늘려가며 상기 칼럼을 세정한다. 단계 6: 추가 정제 및 세제 교환을 위해 겔여과 칼럼 상에 5H3을 함유한 농축된 분획을 장입한다. 단계 7: 5H3 분획을 풀링 및 농축시키고, 상기 단백질을 후속적인 결정 스크린에 사용한다.

도 2는 SLAM1 정제 및 결정화의 다양한 단계의 개요를 보여준다. 도 2a: S200 칼럼을 사용한 크기-제외 크로마토그래피(SEC). 도 2b 쿠마씨 염색된 SDS-PAGE를 사용하여 SLAM1을 함유한 피크를 분석하고 추가로 농축시킨 후, 상업적으로 입수가능한 스크린을 사용하여 결정화 시도를 위해 사용하였다. 도 2c는 SLAM1에 대한 초기 결정 적중물(hits)을 보여준다.

도 3은 다양한 박테리아 종에서 다양한 SLAM 폴리펩타이드 동족체의 계통발생적 트리 및 계통발생적 관계를 보여준다. 그룹 1(옅은 박스, 맨 위)의 SLAM 동족체는 나이세리아 속 및 모락셀라 카타르할리스에 속하는 반면, 그룹 2(보통 회색, 중간)는 감마-프로테오박테리아의 파스튜렐라세아에 계열에서 유래된 상이한 구성원을 함유한다. 그룹 3(짙은 녹색, 바닥)은 나이세리아 샤예가니만 함유한다.

도 4는 SLAM2 정제 및 결정화의 다양한 단계들의 개요를 보여준다. 도 4a: 정제를 위해 사용된 구성체는 N-말단 pelB 서열(단백질 국재화용) 및 6XHis 태그(NiNTA 정제용)를 함유한다. 도 4b: NiNTA 정제 후 수집된 상이한 분획이 용출된 분획이 SLAM2를 함유함을 보여준다. 도 4c: 분획의 웨스턴 블랏이 SLAM2의 기대된 몰 중량을 갖는 His 태그의 존재를 확인한다. 끓인 분획과 끓이지 않은 분획을 대상으로 시험하였다. 도 4d: NiNTA 정제 후, S200 칼럼을 사용하는 크기-제외 크로마토그래피(SEC)를 사용하여 샘플을 추가로 정제하였다. 상기 도면은 SEC 운행에서 프로파일을 보여준다. SLAM2를 함유한 피크를 추가로 농축시키고, 상업적으로 입수가능한 스크린을 사용하여 결정화 시도를 위해 사용하였다. 도 4e: SLAM2에 대한 초기 결정 적중물(hits)을 보여준다.

도 5는 SLAM 1 폴리펩타이드의 N-말단 및 C-말단부(도 5a), SLAM1으로 전환된 나이세리아 메닌기티디스 녹아웃 균주 및 이것의 일부분, 그리고 유세포측정을 사용한 표면 지질단백질의 전좌의 평가에서 수득된 결과들(도 5b) 및 프로테이나제 K 소화 결과들(도 5c)을 보여준다

도 6은 SLPs와 함께 E. 콜리에서 SLAM 1의 발현 이후 수득된 결과들을 보여준다. 정량적 형광(히스토그램) 및 전좌를 보여주는 웨스턴 블랏을 보여준다. TbpB를 사용하여 수득된 결과들을 보여준다(도 6.a), LbpB(도 6b) 및 fHbp(도 6c). 히스토그램은 인간 트랜스페린 또는 SLP 특정 항체로 인큐베이션하고, 이어서 2차 형광 분자로 인큐베이션한 후, 각각의 샘플에 대해 측정된 평균 형광 강도를 표시한다.

도 7은 SLAM이 손상된 나이세리아 균주의 평가에서 수득된 결과들을 보여준다. 도 7a는 파라포름알데하이드(PFA)로 고정되거나 또는 SDS로 용해되어, 니트로셀룰로스 상에서 발견되고 α-TbpB 항체로 탐색된 N. 메닌기티

디스 세포로 이루어진 고상 결합 검정을 보여준다. ΔSLAM/tn5는 트랜스포존 삽입을 통해 수득된 SLAM 결핍 세포의 최초 균주를 지칭한다. ΔSLAM은 상기 SLAM 열린 해독틀(ORF)을 카나마이신 저항 카세트로 대체함으로써 수득된 N. 메닌기티디스에서의 SLAM의 녹아웃을 기술한다. 도 7b는 Nm 세포가 SLAM이 결핍된(ΔSLAM) 것인 경우에만 TbpB, LbpB 및 fHbp의 열화를 보여주는 프로테이나제 K 소화 검정을 나타낸다. SLPs을 단독으로 및 SLAM과 함께 발현하는 N. 메닌기티디스 세포를 프로테이나제 K로 인큐베이팅하였고, 웨스턴 블랏을 사용하여 프로테아제 소화의 존재 및 부재(+/-) 하에 모든 세 SLPs 수치의 수준을 검출하였다. 유세포측정을 사용하여, ΔSLAM 세포가 상기 세포 표면 상에 TbpB(도 7c) 또는 fHbp(도 7d)를 표현할 수 없음을 확인하였다. 형광을 제공하기 위해 파이코에리트린에 연결된 2차 α-토끼 항체로 인큐베이션한 후 TbpB 및 fHbp에 대한 항체를 사용하여 표면 노출된 SLPs를 결합시켰다. BD FACS Calibur의 FL2 검출기를 사용하여 각각의 샘플의 평균 형광 강도(MFI)를 측정하였다. 녹아웃 세포에서 유래된 신호와 비교하기 위해, 야생형 세포에서 수득된 신호를 100%로 설정하였다. 오차 막대는 세 가지 실험에서의 평균 표준 오차(SEM)를 나타낸다. 도 7e에 다양한 균주로의 마우스 감염의 결과를 도시하였다. 복강내 주사를 통해 야생형 N. 메닌기티디스 균주 B16B6(TbpB(ΔtbpB)의 녹아웃이 있는 B16B6 또는 nmb0313 Δslam의 녹아웃이 있는 B16B6)의 1 x 10^6 CFU로 마우스를 감염시키고, 감염 48시간 전부터 감염 48시간 후에 이르기까지 12시간마다 생존 및 질환 증상에 대해 모니터링하고, 감염 3시간 후에 추가로 모니터링하였다. Mantel-Cox 로그 순위 시험(GraphPad Prism 5)에 의해 생존에서 통계적인 차이를 평가하였다(*p<0.05, n.s.는 유의미하지 않음을 뜻함).

도 8은 본 개시내용에 따라 사용될 수 예시적인 미생물을 포함하는 계통발생적 트리를 보여준다. 언급된 박테리아 종에서의 SLAM 단백질의 예상 개수가 괄호에 나타나 있다.

도 9는 그램-음성 박테리아 종 전반에 걸쳐 SLAM 계열 단백질의 존재를 보여준다. 도 9a는 두 가지 도메인: 테트라트리코펩타이드 반복체를 함유한 주변세포질 N-말단 도메인(Ntd) 및 막 결합된 14-가닥 배럴 도메인(DUF560이라 불림)을 보유한 N. 메닌기티디스 SLAM1의 도메인 구조를 보여준다. 도 9b는 프로테오박테리아에서 SLAM 단백질의 분포를 보여준다. 프로테오박테리아 내 주요 박테리아 계열을 나타내는 55종에서 유래된 16S-RNA 서열을 사용하여 프로테오박테리아의 계열 트리를 만들었다. SLAM 동족체와 함께 적어도 하나의 종을 함유한 계열이 흑색점들로 강조되었다. SLAM 동족체가 프로테오박테리아의 모든 분기군에서 발견되었다.

도 10은 에스케리치아 콜라이의 모락셀라 카타르할리스 및 헤모필루스 인플루엔자에서 유래된 SLAM 및 TbpB 쌍의 전좌를 보여준다. 도 10a는 M. 카타르할리스 및 H. 인플루엔자에서의 SLAM 및 TbpB 유전자 클러스터를 보여준다. 수행된 생물정보학 분석에서, SLAM이 두 가지 인간 병원체 모두에서 공지된 트랜스페린 결합 표면 지질단백질 TbpB에 인접함이 밝혀졌다. 도 10b는 이와 같은 연구에 사용된 E. 콜리 전좌 검정의 개략도를 보여준다. 간단히, SLAM 및 TbpB 유전자를 E. 콜리 C43(DE3) 세포에서 발현시켰다. 상기 세포를 R-파이코에리스린(PE)에 연결된 바이오티닐화된 인간 트랜스페린 및 스트렙타비딘으로 표지하였다. 유세포측정을 사용하여 TbpB의 표면 출연(display)를 정량화하였다. 도 10c는 SLAM과 함께(흑색으로 도시) 또는 SLAM 없이(회색으로 도시) 수득된 M. 카타르할리스 TbpB(McTbpB) 및 H. 인플루엔자 TbpB(HiTbpB)의 유세포측정 프로파일을 보여준다. SLAM의 존재하에 더 높은 신호를 관측하였고, 이것은 SLPs의 효과적인 표면 발현을 위한 SLAM에 대한 의존도를 나타낸다. 도 10d는 평균 형광 강도를 사용하여 M. 카타르할리스 및 H. 인플루엔자에서 유래된 TbpB 동족체에 대한 평균 형광 블롯을 보여준다 원-웨이 ANOVA를 사용하여 통계적 유의성을 판단하였다(***은 $p \leq 0.001$을 의미한다).

도 11은 파스튜렐라 멀토시다에서 SLAM-의존적 표면 지질단백질의 식별을 보여준다. 도 11a는 P. 멀토시다 균주 Pm70에서 SLAM 유전자 클러스터를 보여준다. 우리의 생물정보학 검색에서 PM1515(흑색으로 도시)를 SLAM 동족체로 식별하였다. PM1514(회색 도시)에는 가설 단백질이라고 주석이 달렸다. PM1514는 추정 리포박스(ITAC) 모티프로 끝나는 신호 펩티다아제 II 절단 부위를 함유한다. 도 11b는 PM1514가 SLAM-의존적 SLP인지 여부를 조사하기 위해 전좌 검정을 위해 만든 P. 멀토시다 유전자 구성체를 보여준다. 간단히, PM1514를 C-말단 Flag-태그(PM1514-Flag)로 클로닝하고, PM1515를 N-말단 His-태그 및 pelB 신호 서열로 클로닝하고, PM1515-PM1514-Flag를 PM1515 및 PM1514 영역 둘 다로 클로닝하였다. 도 11c는 도 11b에 기술된 세 가지 구성체가 모두 E. 콜리 C43(DE3) 세포에서 발현되고, α-Flag 항체 및 R-파이코에리스린(PE)에 연결된 마우스 2차 항체로 표지된 P. 멀토시다 구성체의 유세포측정 프로파일을 보여준다. PM1514-Flag(옅은 회색), PM1515 및 PM1514-Flag(흑색) 및 PM1515-PM1514-Flag(짙은 회색)의 유세포측정 프로파일이 보여진다. 도 11d는 P. 멀토시다 구성체의 평균 형광 강도(MFI)를 사용하여 정량화된 평균 형광 강도 블롯을 보여준다. 원-웨이 ANOVA를 사용하여 통계적 유의도를 결정하였고, 여기서 ***는 $p \leq 0.001$를 나타낸다.

도 12는 전좌 모티프가 TbpB 상에 존재하는지 여부의 확인을 보여준다. 도 12a는 이와 같은 연구에서 사용된 N.

메닌기티디스 TbpB 및 HpuA 구성체를 보여주는데, 여기에 야생형 TbpB, 야생형 HpuA, TbpB N-엽, TbpB C-엽, 및 HpuA(Nlobe_HpuA)에 융합된 TbpB N-엽이 포함된다. 도 12b는 α-TbpB 및 토끼-FITC 항체로의 표지 이후 N. 메닌기티디스 TbpB 및 N. 메닌기티디스 SLAM1의 전장 또는 개별 엽을 발현하는 E. 콜리 C43(DE3) 세포의 유세포측정에 의해 정량화된 TbpB의 N- 및 C-엽의 전좌 효율을 보여준다. 도 12c, 12d 및 도 12e는 α-TbpB, α-HpuA, 및 바이오티닐화된 인간 트랜스페린 각각을 갖는 Nlobe_HpuA의 전좌 효율을 보여준다. 유세포측정을 사용하여, E. 콜리의 표면으로의 Nlobe-HpuA의 전좌를 가능하게 하는 SLAM1 및 SLAM2의 능력을 시험하였다. α α-HpuA를 사용하여 HpuA를 검출하는 반면, -TbpB 및 바이오티닐화된 인간 트랜스페린을 사용하여 TbpB N-엽을 검출하였다. 평균 형광 강도 블롯이 도시되었는데, 이것은 TbpB C-엽과 HpuA의 교체가 구성체의 특이성을 SLAM1에서 SLAM2로 바꿈을 강조한다. 원-웨이 ANOVA를 사용하여 통계적 유의도를 결정하였는데, 여기서 ***는 $p \leq 0.001$을, ****는 $p \leq 0.0001$을 나타내고, n.s.는 유의미하지 않음을 나타낸다.

도 13은 SLAM-의존적 표면 지질단백질의 C-말단 가닥 두 개가 표면 출연(display)를 위해 보존되고 요구됨이 보여준다. 도 13a는 SLAM-의존적 SLPs에서 발견된 단백질 도메인의 일반적인 구조를 보여준다. 이와 같은 계열의 단백질은 가요성 핸들 도메인 및 8-가닥 배럴 도메인을 함유한다. 상기 배럴 도메인은 모든 추정 SLAM-의존적 SLPs에서 보존된다. 도 13b는 N. 메닌기티디스 균주 B16B6(하기의 PDB ID)에서 유래된 TbpB의 구조에 따라 상기 가닥이 넘버링된 N. 메닌기티디스 TbpB 유래 배럴 도메인의 개략도를 보여준다: 4QQ1). 폴리알라닌 돌연변이에 의해 돌연변이된 가닥은 B22, B23, B30 및 B31로 표현된다. 도 13c 및 도 13d는 4가지 상이한 베타-배럴 가닥에서 TbpB 야생형 단독, SLAM1 및 TbpB 야생형, 또는 SLAM1 및 폴리알라닌 돌연변이를 함유하는 TbpB 돌연변이체 중 하나를 발현하는 E. 콜리 C43(DE3) 세포의 전좌 효율을 보여준다. 세포를 α-TbpB 및 바이오티닐화된 인간 트랜스페린으로 표지하였고, 평균 형광 강도 블롯은 TbpB C-엽 배럴의 마지막 2개의 가닥에서의 돌연변이가 TbpB의 표면 출연(display)를 방지함을 밝혀주었다. α-TbpB 및 α-His로의 웨스턴 블랏 분석을 수행하여 TbpB C-엽 돌연변이체 및 SLAM1 각각의 발현을 확인하였다. 도 13e는 회색으로 강조된 보존된 잔기들이 있는 SLAM-의존적 SLPs의 C-말단 베타-배럴의 마지막 2개의 가닥의 다중 서열 정렬을 보여준다. 도 13f는 TbpB의 C-엽 구조에서 마지막 두 베타-배럴 가닥 상에 보존된 잔기들의 오버레이를 보여준다. 배럴 밖의 잔기들이 서로 멀리 떨어져 있는 반면, 배럴 도메인에 있는 잔기들이 서로를 마주보는 가운데, 2개의 가닥이 서로 마주보는 것이 보여진다. 상기 보존된 잔기들은 배럴 도메인의 중심에서 함께 무리를 이룬다. 원-웨이 ANOVA를 사용하여 통계적 유의도를 결정하였는데, 여기서 ***은 $p \leq 0.001$를, ****는 $p \leq 0.0001$를, 그리고 n.s.는 유의미하지 않음을 나타낸다.

도 14는 악티노박테르 바우마니에서 SLAM-의존적 표면 지질단백질의 식별을 보여준다. 도 14a는 A. 바우마니 균주 LAC4에서 SLAM 유전자 클러스터를 보여준다. AbSLAM(회색으로 도시)은 생물정보학 검색에서 SLAM 동족체로 식별되었다. AbSLP(흑색으로 도시)는 가설 단백질이라고 주석이 붙었다. 도 14b는 AbSLP가 Slam-의존적 SLP인지 여부를 조사하기 위해 전좌 검정을 위해 만든 A. 바우마니 유전자 구성체를 보여준다. 간단히, AbSLP를 C-말단 Flag-태그(AbSLP-Flag)로 클로닝하였고, AbSLAM을 N-말단 His-태그 및 pelB 신호 서열로 클로닝하였다. 도 14b(오른쪽)는 A. 바우마니 구성체의 유세포측정 프로파일을 보여주되, 기술된 두 구성체는 E. 콜리 C43(DE3) 세포에서 발현되었고 α-Flag 항체 및 R- 파이코에리스린(PE)에 연결된 마우스 2차 항체로 표지되었다. 도 14c는 형성된 바 있는 AbSLP 결정(왼쪽) 및 AbSLP의 확인된 결정 구조의 그림 다이어그램을 보여준다. 도 14d는 A. 바우마니에서의 PK 셰이빙 검정을 보여준다.

발명을 실시하기 위한 구체적인 내용

[0106] 각각의 청구된 요지의 구현예의 예를 제공하기 위해 다양한 조성물 및 방법이 하기에 기재된다. 하기에 기재된 구현예는 어떤 것도 임의의 청구된 요지를 제한하지 않으며, 임의의 청구된 요지는 아래에 기재된 것들과 다른 방법, 공정, 조성물 또는 시스템을 다룰 수 있다. 상기 청구된 요지는 하기에 기재된 임의의 하나의 조성물, 방법, 시스템 또는 공정의 모든 특징을 갖는 조성물 또는 방법에, 또는 하기에 기재된 다중 또는 모든 조성물, 시스템 또는 방법의 일반적인 특징들에 제한되지 않는다. 하기에 기재된 조성물, 시스템, 방법 또는 공정은 임의의 청구된 요지의 구현예가 아닐 가능성이 있다. 본 문서에서 청구되지 않은, 하기에 기재된 조성물, 시스템, 방법 또는 공정에서 개시된 임의의 요지는 또 다른 보호성 기기, 예를 들어, 진행중인 특허 출원의 요지일 수 있어서, 출원인, 발명자들 또는 소유자들은 본 문서의 개시내용에 의한 그와 같은 요지를 포기, 부인 또는 공공에 헌정할 의사가 없다. 모든 공보, 특허 및 특허 출원은 각각의 개별 공보와 마찬가지로 동일한 수준으로 그 전문이 본원에 참고로 편입되었다.

[0107] 용어들 및 정의

[0108] 달리 정의되지 않는 한, 본원에 사용된 모든 기술 및 과학 용어들은 본 개시내용과 관련이 있는 당해 분야의 숙련가에 의해 통상적으로 이해되는 바와 동일한 의미를 갖는다. 하기 용어들은 하기 의미를 갖는다고 이해되어야 한다.

[0109] 본원에 상호교환적으로 사용된 용어들 "표면 지질단백질 어셈블리 모듈레이터", "SLAM", "SLAM 단백질", 및 "SLAM 폴리펩타이드"는 임의의 그리고 모든 SLAM 단백질을 지칭하는데, 이것은 짝수-넘버링된 서열식별번호: 2 내지 서열식별번호: 694 및 서열식별번호: 1184 중 임의의 하나에 제시된 것을 포함하거나: , 및 (i) 본원에 제시된 임의의 SLAM 단백질을 구성하는 아미노산 서열에 실질적으로 동일하고;(ii) 적어도 중간 정도로 엄격한 조건 하에 본원에 제시된 임의의 SLAM 단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있거나, 또는 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에 본원에 제시된 임의의 SLAM 단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있는, 핵산 서열에 의해 인코딩된 아미노산 잔기의 서열을 포함하는 것들을 포함한다. 용어들은 추가로 임의의 SLAM 전구체 폴리펩타이드를 포함한다.

[0110] 용어 "표면 지질단백질"은 짝수-넘버링된 서열식별번호: 696 내지 서열식별번호: 1082, 서열식별번호: 1094, 서열식별번호: 1100 및 짝수-넘버링된 서열식별번호: 1116 내지 서열식별번호: 1168, 및 서열목록번호; 1178 (본원에 제시됨) 중 하나에 제시된 것들을 포함하는 임의의 및 모든 표면 지질단백질을 지칭하고, 및 (i) 본원에 제시된 임의의 표면 지질단백질을 구성하는 아미노산 서열과 실질적으로 동일하고; (ii) 적어도 중간 정도로 엄격한 조건 하에 본원에 제시된 임의의 표면 지질단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있는, 또는 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에 본원에 제시된 임의의 표면 지질단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있는 핵산 서열에 의해 인코딩된 아미노산 잔기의 서열을 포함한 것을 지칭한다. 용어 표면 지질단백질은 또한 하기 식별번호에 제시된 표면 리포박스 서열 모티프를 포함하는 폴리펩타이드를 지칭하고: 1170 및 서열식별번호: 1174 및 (i) 본원에 제시된 임의의 표면 리포 박스 서열 모티프를 구성하는 아미노산 서열과 실질적으로 동일하거나; 또는 (ii) 적어도 중간 정도로 엄격한 조건 하에 본원에 제시된 임의의 표면 리포 박스 서열 모티프를 인코딩하는 임의의 핵산 서열로 혼성화할 수 있거나, 또는 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에서 본원에 제시된 임의의 표면 리포 박스 서열 모티프를 인코딩하는 임의의 핵산 서열로 혼성화할 수 있는 핵산 서열에 의해 인코딩된 아미노산 잔기의 서열을 포함하는 것을 지칭한다.

[0111] 본원에 상호교환적으로 사용된 용어들 "트랜스페린 결합 단백질 B", "TbpB 단백질", "TbpB 폴리펩타이드" 및 "TbpB"는 서열식별번호: 806, 서열식별번호: 828, 서열식별번호: 868, 서열식별번호: 1094에서 선택된 서열, 및 짝수-넘버링된 서열식별번호: 1148 내지 서열식별번호: 1168 (본원에 제시됨) 중 하나에 제시된 것을 비롯한 임의의 및 모든 TbpB 단백질을 지칭하고, 및 (i) 본원에 제시된 임의의 TbpB 단백질을 구성하는 아미노산 서열과 실질적으로 동일하거나; (ii) 적어도 중간 정도로 엄격한 조건하에 본원에 제시된 임의의 TbpB 단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있거나, 또는 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에서 본원에 제시된 임의의 TbpB 단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있는 핵산 서열에 의해 인코딩된 아미노산 잔기의 서열을 포함하는 것을 지칭한다.

[0112] 본원에서 상호교환적으로 사용된 용어들 "락토페린 결합 단백질", "LbpB 단백질", "LbpB 폴리펩타이드" 및 "LbpB"는 서열식별번호: 870에서 선택된 서열 또는 본 명세서 6에서 제시된 짝수-넘버링된 서열식별번호: 1138 내지 서열식별번호: 1146 (본원에 제시됨) 중 하나에 제시된 것들을 비롯한 임의의 및 모든 LbpB 단백질을 지칭하고, 및 (i) 본원에 제시된 임의의 LbpB 단백질을 구성하는 아미노산 서열과 실질적으로 동일하거나; (ii) 적어도 중간 정도로 엄격한 조건 하에서 본원에 제시된 임의의 LbpB 단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있거나 또는, 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에서 본원에 제시된 임의의 LbpB 단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있는 핵산 서열에 의해 인코딩된 아미노산 잔기의 서열을 포함하는 것들을 지칭한다.

[0113] 본원에서 상호교환적으로 사용된 용어들 "인자 H 결합 단백질", "fHbp 단백질", fHbp 폴리펩타이드" 및 "fHbp"는 짝수-넘버링된 서열식별번호: 1116 내지 서열식별번호: 1136 (본원에 제시됨) 중 하나에서 선택된 서열을 비롯한 임의의 및 모든 fHbp 단백질을 지칭하고, 및 (i) 본원에 제시된 임의의 fHbp 단백질을 구성하는 제시된 아미노산 서열과 실질적으로 동일하거나; (ii) 적어도 중간 정도로 엄격한 조건 하에서 본원에 제시된 임의의 fHbp 단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있거나, 또는, 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에서 본원에 제시된 임의의 fHbp 단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있는 핵산 서열에 의해 인코딩된 아미노산 잔기의 서열을 포함하는 것들을 지칭한다.

[0114] 본원에서 상호교환적으로 사용된 용어들 “헤모글로빈-합토글로빈 결합 단백질 A”, “HpuA 단백질”, “HpuA 폴리펩타이드” 및 “HpuA”는 서열식별번호: 850, 서열식별번호: 924, 서열식별번호: 932, 또는 서열식별번호: 1110에 제시된 것들을 비롯하여 임의의 및 모든 SLAM 단백질을 지칭하고 및 (i) 본원에 제시된 임의의 HpuA 단백질을 구성하는 아미노산 서열과 실질적으로 동일하거나; (ii) 적어도 중간 정도로 엄격한 조건 하에서 본원에 제시된 임의의 HpuA 단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있거나, 또는, 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에서 본원에 제시된 임의의 HpuA 단백질을 인코딩하는 임의의 핵산 서열로 혼성화할 수 있는 핵산 서열에 의해 인코딩되는 아미노산 잔기의 서열을 포함하는 것들을 지칭한다.

[0115] 본원에 상호교환적으로 사용된 용어들 “표면 지질단백질 어셈블리 모듈레이터를 인코딩하는 폴리뉴클레오타이드”; “SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드”; 및 SLAM 단백질을 인코딩하는 폴리뉴클레오타이드는 SLAM 폴리펩타이드를 인코딩하는 임의의 및 모든 폴리뉴클레오타이드, 예컨대 임의의 SLAM 폴리펩타이드 및 SLAM 전구체를 인코딩하는 임의의 핵산 서열, 예컨대 서열식별번호: 1 및 서열식별번호: 3에 제시된 폴리뉴클레오타이드를 지칭한다. 본 명세서에서 사용된 바와 같이 “SLAM 전구체”는 E. 콜리 및 다른 그램-음성 박테리아 종의 세포질 막을 가로질러 폴리펩타이드 사슬의 수출을 용이하게 하는 N-말단 신호 서열을 추가로 포함하는 SLAM 분자를 지칭한다. SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 (i) 본원에 제시된 SLAM 폴리펩타이드 서열과 실질적으로 동일한 폴리펩타이드를 인코딩하거나; 또는 (ii) 적어도 중간 정도로 엄격한 혼성화 조건 하에서 본원에 제시된 임의의 SLAM 폴리뉴클레오타이드로 혼성화하거나 또는, 동의어 코돈의 사용 없이 적어도 중간 정도로 엄격한 조건 하에서 그와 같이 혼성화하곤 하는 임의의 및 모든 리뉴클레오타이드를 추가로 포함한다.

[0116] 용어 “표면 지질단백질을 인코딩하는 폴리뉴클레오타이드”는 표면 지질단백질, 예컨대 임의의 표면 지질단백질을 인코딩하는 임의의 및 모든 폴리뉴클레오타이드, 예컨대 서열식별번호: 695 내지 서열식별번호: 1081, 및 서열식별번호: 1177(본원에 제시됨)를 비롯하여 홀수-넘버링된 서열식별번호에 제시된 폴리뉴클레오타이드를 지칭한다. 표면 지질단백질을 인코딩하는 폴리뉴클레오타이드는 (i) 본원에 제시된 표면 지질단백질 서열과 실질적으로 동일한 단백질을 인코딩하거나; 또는 (ii) 적어도 중간 정도로 엄격한 혼성화 조건 하에서 본원에 제시된 임의의 표면 지질단백질 폴리뉴클레오타이드로 혼성화하거나, 또는 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에서 이와 같이 혼성화하곤 하는 임의의 및 모든 폴리뉴클레오타이드를 추가로 포함한다.

[0117] 본원에서 상호교환적으로 사용될 수 있는 용어들 “TbpB를 인코딩하는 폴리뉴클레오타이드”, “TbpB 단백질을 인코딩하는 폴리뉴클레오타이드” 및 “TbpB 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드”는 TbpB 단백질, 예컨대 임의의 TbpB 단백질을 인코딩하는 임의의 및 모든 폴리뉴클레오타이드, 예컨대 서열식별번호: 1147에 제시된 폴리뉴클레오타이드를 지칭한다. 표면 지질단백질을 인코딩하는 폴리뉴클레오타이드는 (i) 본원에 제시된 표면 지질단백질 서열과 실질적으로 동일한 단백질을 인코딩하거나; 또는 (ii) 적어도 중간 정도로 엄격한 혼성화 조건 하에서 본원에 제시된 임의의 표면 지질단백질 폴리뉴클레오타이드로 혼성화하거나, 또는 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에서 이와 같이 혼성화하곤 하는 임의의 및 모든 폴리뉴클레오타이드를 추가로 포함한다.

[0118] 본원에서 상호교환적으로 사용될 수 있는 용어들 “LbpB를 인코딩하는 폴리뉴클레오타이드”, “LbpB 단백질을 인코딩하는 폴리뉴클레오타이드” 및 “LbpB 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드”는 LbpB 단백질, 예컨대 임의의 LbpB 단백질을 인코딩하는 임의의 및 모든 폴리뉴클레오타이드, 예컨대 서열식별번호: 869에 제시된 폴리뉴클레오타이드를 지칭한다. 표면 지질단백질을 인코딩하는 폴리뉴클레오타이드는 (i) 본원에 제시된 표면 지질단백질 서열과 실질적으로 동일한 단백질을 인코딩하거나; 또는 (ii) 적어도 중간 정도로 엄격한 혼성화 조건 하에서 본원에 제시된 임의의 표면 지질단백질 폴리뉴클레오타이드로 혼성화하거나, 또는 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에서 이와 같이 혼성화하곤 하는 임의의 및 모든 폴리뉴클레오타이드를 추가로 포함한다.

[0119] 본원에서 상호교환적으로 사용될 수 있는 용어들 “fHbp를 인코딩하는 폴리뉴클레오타이드”, “fHbp 단백질을 인코딩하는 폴리뉴클레오타이드” 및 “fHbp 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드”는 fHbp 단백질, 예컨대 임의의 fHbp 단백질을 인코딩하는 임의의 및 모든 폴리뉴클레오타이드, 예컨대 서열식별번호: 1115에 제시된 폴리뉴클레오타이드를 지칭한다. 표면 지질단백질을 인코딩하는 폴리뉴클레오타이드는 (i) 본원에 제시된 표면 지질단백질 서열과 실질적으로 동일한 단백질을 인코딩하거나; 또는 (ii) 적어도 중간 정도로 엄격한 혼성화 조건 하에서 본원에 제시된 임의의 표면 지질단백질 폴리뉴클레오타이드로 혼성화하거나, 또는 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에서 이와 같이 혼성화하곤 하는 임의의 및 모든 폴리뉴클레

오타이드를 추가로 포함한다.

[0120] 본원에서 상호교환적으로 사용될 수 있는 용어들 “HpuA를 인코딩하는 폴리뉴클레오타이드”, “HpuA 단백질을 인코딩하는 폴리뉴클레오타이드” 및 “HpuA 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드”는 HpuA 단백질, 예컨대 임의의 HpuA 단백질을 인코딩하는 임의의 및 모든 폴리뉴클레오타이드, 예컨대 서열식별번호: 931에 제시된 폴리뉴클레오타이드를 지칭한다. 표면 지질단백질을 인코딩하는 폴리뉴클레오타이드는 (i) 본원에 제시된 표면 지질단백질 서열과 실질적으로 동일한 단백질을 인코딩하거나; 또는 (ii) 적어도 중간 정도로 엄격한 혼성화 조건 하에서 본원에 제시된 임의의 표면 지질단백질 폴리뉴클레오타이드로 혼성화하거나, 또는 동의어 코돈의 사용 없이, 적어도 중간 정도로 엄격한 조건 하에서 이와 같이 혼성화하곤 하는 임의의 및 모든 폴리뉴클레오타이드를 추가로 포함한다.

[0121] 용어 “실질적으로 동일한”은 두 개의 폴리펩타이드 서열이 바람직하게는 적어도 50% 동일한, 더 바람직하게는 적어도 85% 동일한, 가장 바람직하게는 적어도 95% 동일한, 예를 들어 96%, 97%, 98% 또는 99% 동일한 것을 의미한다. 2개의 폴리펩타이드 서열 사이의 동일성 백분율을 판단하기 위해, 그와 같은 2개의 서열의 아미노산 서열이 예를 들어 Needleman 및 Wunsch의 정렬 방법을 사용하여 정렬된다(Needleman SB, Wunsch CD.1970.두 단백질의 아미노산 서열에서 유사성을 탐색하는 데 적용가능한 일반적 방법.Journal of molecular biology 48: 443-453)(Smith 및 Waterman에 의해 개정됨)(Smith TFaMSW.1981.Comparison of Biosequences.Advances in Applied Mathematics 2: 482-489), 그래서 상기 두 서열 사이의 최고차수의 일치가 수득되고, 상기 두 서열 사이의 동일한 아미노산의 개수가 결정된다. 2개의 폴리펩타이드를 정확하게 정렬하기 위한 바람직하고 광범위하게 적용가능한 방법은 Clustal W 알고리즘를 수반하는데(Thompson JD, Higgins DG, Gibson TJ.1994.CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice.Nucleic acids research 22: 4673-4680.), 이것은 BLOSUM 62 평점 매트릭스와함께 활용되고(Henikoff S, Henikoff JG.1992.Amino acid substitution matrices from protein blocks.Proc Natl Acad Sci U S 89: 10915-10919) 이것은 갭 열림 페널티 10과 갭 연장 패널티 0.1을 사용한다. 이것은 두 서열 사이의 높은 평점 정렬의 식별을 가능하게 하되, 적어도 상기 두 서열 중 하나의 총 길이 중 적어도 50%가 상기 정렬에 관여된다. 2 개의 정렬된 아미노산 서열 사이의 백분율 동일성을 계산하는 방법은 일반적으로 당해기술에서 인식되고, 예를 들어, 하기를 포함한다: Carillo 및 Lipton(Carrillo H, 및 D.Lipman.1989.생물학에서 다중 서열 정렬 문제(The Multiple Sequence Alignment Problem in Biology). SIAM Journal on Applied Mathematics 48: 1073-1082)에 의해 기술된 것, 및 컴퓨터를 이용한 분자 생물학(Computational Molecular Biology), Lesk, e.d.Oxford University Press, New York, 1988, Biocomputing: Informatics and Genomics Projects에서 기술된 것들.일반적으로, 그와 같은 계산을 위해 컴퓨터 프로그램이 이용된다. 이와 관련하여 사용될 수 있는 컴퓨터 프로그램은 비제한적으로 하기를 포함한다: GCG(Devereux J, Haeberli P, Smithies O.1984.A comprehensive set of sequence analysis programs for the VAX.Nucleic acids research 12: 387-395), BLASTP, BLASTN 및 FASTA(Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ.1990.Basic local alignment search tool.Journal of Molecular Biology 215: 403-410).

[0122] “적어도 중간 정도로 엄격한 혼성화 조건”이란 용액에서 두 개의 상보적 핵산 분자 사이에서 선택적 혼성화를 촉진하는 조건이 선택됨을 의미한다. 혼성화는 핵산 서열 분자의 모두 또는 일부에 일어날 수 있다. 상기 혼성화 부분은 전형적으로 길이가 적어도 15(예를 들어 20, 25, 30, 40 또는 50) 뉴클레오타이드이다. 당해 분야의 숙련가는 핵산 듀플렉스, 또는 하이브리드의 안정성이 Tm(나트륨 함유 완충액에서, 나트륨 이온 농도 및 온도의 함수(Tm=81.5 ℃.-16.6(Log10 [Na+])+0.41(%(G+C)-600/l), 또는 유사한 방정식)에 의해 결정됨을 이해할 것이다. 따라서, 하이브리드 안정성을 결정하는 세척 조건에서 매개변수는 나트륨 이온 농도 및 온도이다. 공지된 핵산 분자와 유사하나 동일하지는 않은 분자를 식별하기 위해, 1% 불일치 Tm에서 약 1 ℃ 감소를 초래하는 것으로 추정될 수 있는데, 예를 들어 >95% 동일성을 갖는 핵산 분자를 추구하는 경우, 최종 세정 온도는 약 5 ℃ 감소할 것이다. 이들 고려사항들을 기반으로, 당해 분야의 숙련가는 쉽게 적절한 혼성화 조건을 선택할 수 있을 것이다. 바람직한 구현예에서, 엄격한 혼성화 조건이 선택된다. 예로써 하기 조건들이 엄격한 혼성화를 달성하기 위해 이용될 수 있다: Tm(상기 방정식 기반) -5 ℃에서 5× 염화나트륨/나트륨 시트레이트(SSC)/5×덴하르트 용액/1.0% SDS에서 혼성화 및, 이어서 60° C에서 0.2×SSC/0.1% SDS의 세척. 중간 정도로 엄격한 혼성화 조건은 42° C에서 3×SSC의 세척 단계를 포함한다. 그러나 대안적인 완충액, 염 및 온도를 사용하여 동등한 엄격성이 달성될 수 있음이 이해된다. 혼성화 조건과 관련된 추가의 안내는 아래에서 발견할 수 있다: Green and Sambrook, Molecular Cloning, a Laboratory Manual, Cold Spring Harbor Laboratory Press, 2012 (32).

[0123] 본 명세서에서 사용된 용어 “키메라성”은 폴리뉴클레오타이드의 문맥에서, 자연적으로 연결되지 않는 적어도

2종의 연결된 폴리뉴클레오타이드를 지칭한다. 키메라성 핵산 폴리뉴클레오타이드는 상이한 천연 기원의 연결된 폴리뉴클레오타이드를 포함한다. 예를 들어, 나이세리아 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드에 연결된 E. 콜리 박테리아 프로모터를 구성하는 폴리뉴클레오타이드는 키메라성으로 간주된다. 게다가, 키메라성 폴리뉴클레오타이드는 동일한 천연 기원을 가질 수 있으나 자연적으로 연결되지는 않는다. 더욱이, 비-자연 발생 폴리뉴클레오타이드 벡터는 키메라성이다. 예를 들어, 특별한 세포-유형에서 수득된 프로모터를 구성하는 폴리뉴클레오타이드는 동일한 세포-유형에서 수득되나, 상기 프로모터를 구성하는 폴리뉴클레오타이드에 정상적으로 연결되지 않는 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드에 연결될 수 있다. 키메라성 폴리뉴클레오타이드는 또한 임의의 비-자연 발생 폴리뉴클레오타이드에 연결된 임의의 자연 발생 폴리뉴클레오타이드를 포함하는 폴리뉴클레오타이드를 포함한다.

[0124] 본 명세서에서 사용된 용어 “세포기질”은 세포, 예를 들어 박테리아 세포의 내부, 일반적으로 수성 부분을 지칭하고, 상기 세포기질 내에 존재할 수 있는 모든 세포 성분을 포함하되, 구체적으로 상기 세포의 세포외 표면은 제외한다.

[0125] 본 명세서에서 사용된 용어 “세포외 표면”은 세포의 외인성 환경에서 그것의 세포질 부분을 분리하는 세포의 세포 표면 구조를 지칭하는 것이다. 상기 세포 표면 구조는 단백질 및/또는 그 안에 포매된 리포폴리사카라이드를 갖는 하나 이상의 포스포지질 막을 포함할 수 있다.

[0126] 본 명세서에서 사용된 용어 “숙주 유기체”는 인간 및 비-인간 척추동물 동물, 예컨대 비제한적으로, 소, 돼지, 말, 쥣과, 갯과, 고양이, 물고기, 양, 염소, 유인원 및 조류 동물을 지칭한다.

[0127] 본원에서 상호교환적으로 사용되는 용어들 “면역원” 및 “면역원성 조성물”은 그것의 가장 넓은 의미로 숙주 유기체에서 면역 반응을 자극하여 세포 면역원-특이 면역 반응, 또는 체액성 항체 반응을 일으키는 하나 이상의 에피토프를 함유하는 분자를 지칭하기 위해 사용된다. 면역원은 단백질, 폴리펩타이드, 펩타이드 및 면역원성 단백질 단편을 포함한다.

[0128] 본원에서 상호교환적으로 사용되는 용어들 “백신” 및 “백신 조성물”은 면역원을 함유하는 임의의 약제학적 조성물을 지칭하되, 상기 조성물은 숙주 유기체에서 질환 또는 병태를 예방하거나 또는 치료하기 위해 사용될 수 있다. 상기 용어들은 따라서 하위단위 백신, 즉, 자연계에서 상기 면역원이 관련된 전체의 유기체에서 별도 및 별개인 면역원 함유 백신 조성물을 아우르고, 추가로, 생 백신을 포함한다.

[0129] 본 명세서에서 사용된 정도의 용어들, 예컨대 “실질적으로”, “본질적으로” “약” 및 “대략”은 최종 결과가 유의미하게 바뀌지 않을 정도인, 수식되는 용어의 합리적인 편차의 양을 의미함에 유의해야 한다. 이들 정도를 나타내는 용어들은 상기 편차가 이것이 수식하는 용어의 의미를 무효화하지 않는 한 상기 수식된 용어의 편차를 포함하는 것으로 해석되어야 한다.

[0130] 본 명세서에서 사용된 바와 같이, 표현 “및/또는”은 포괄적인 “또는”을 나타내는 것이다. 즉, “X 및/또는 Y”는 예를 들어, X 또는 Y 또는 둘 모두를 의미하는 것이다. 추가 예로서, “X, Y, 및/또는 Z”는 X 또는 Y 또는 Z 또는 이들의 임의의 조합을 의미하는 것이다.

[0131] 본 명세서 및 첨부된 청구항들에서 사용된 단수 형태 “a”, “an”, 및 “the”는 내용에서 달리 명확히 지시하지 않는 한, 복수의 지시대상을 포함한다. 따라서, 예를 들어, “면역원”의 언급은 2종 이상의 그와 같은 제제의 혼합물을 포함하고, “폴리펩타이드”의 언급은 2종 이상의 폴리펩타이드의 혼합물의 언급을 포함하고, “세포”의 언급은 그와 같은 2종 이상의 세포, 및 기타 동종의 것을 포함한다.

[0132] 일반적인 실행

[0133] 위에서 언급된 바와 같이, 본 개시내용은 그램-음성 박테리아 종에서 수득가능한 또는 수득된 폴리펩타이드 및 폴리뉴클레오타이드에 관한 것으로, 주목할 만한 점은 폴리펩타이드가 표면 지질단백질 어셈블리 모듈레이터, 즉 SLAM 단백질로 알려진 단백질 부류에 속한다는 점이다.

[0134] 본 개시내용의 SLAM 단백질을 인코딩하는 폴리뉴클레오타이드는 숙주세포에서 SLAM 단백질의 발현 및 생산에 사용될 수 있다. 숙주세포에서 그와 같은 SLAM 단백질의 발현은, 놀랍게도, 상기 숙주세포에 존재하는 또 다른 단백질(이하 통칭 표적 단백질)을 상기 숙주세포의 세포질 부분에서 상기 숙주세포의 세포외 표면으로 전좌시킬 수 있다.

[0135] 더욱이, SLAM 단백질을 인코딩하는 폴리뉴클레오타이드는 병원성 박테리아 종, 예를 들어, 나이세리아에 속하는

박테리아 종에 의한 감염의 예방을 위해 유용한 백신 제형을 제조하는 데 사용될 수 있다.

[0136] 더욱이, SLAM 단백질을 인코딩하는 폴리뉴클레오타이드 및 SLAM 단백질은 병원성 박테리아 종에 감염된 환자의 치료에 유용한 화합물을 식별하는 검정에 사용될 수 있다.

[0137] 따라서, 일 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 표적 단백질을 포함하는 숙주세포의 세포기질에서 세포외 표면으로의 상기 표적 단백질의 수송을 초래하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0138] (a) 작동가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0139] (i) 하기에서 발현을 제어할 수 있는 폴리뉴클레오타이드:

[0140] 숙주 세포; 및

[0141] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0142] (b) 상기 키메라성 핵산 서열을 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 SLAM 폴리펩타이드를 생산함으로써, 상기 숙주세포의 세포기질에서 세포외 표면으로의 상기 표적 단백질의 수송을 초래하는 단계.

[0143] 본원에 따른 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 SLAM 단백질을 인코딩하는 폴리뉴클레오타이드를 포함하는 임의의 박테리아 종 또는 균주, 예컨대 특히, 임의의 그램 음성 박테리아 종, 예컨대 프로테오박테리아의 문에 속하는 임의의 박테리아 종, 및 알파-프로테오박테리아, 베타-프로테오박테리아, 감마-프로테오박테리아 및 델타-프로테오박테리아 부류에 속하는 임의의 박테리아 종에서 수득될 수 있다.

[0144] 일부 구현예에서, SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 알파-프로테오박테리아 내 계열, 예를 들어 스핑고모나다세아에, 라이조비알레스 및 로도박테라세아에 계열에 속하는 박테리아 종에서 수득될 수 있다. 이들 각각의 계열에 속하는 예시적인 박테리아 속 및 종은 도 8 및 도 9에 제공된 모든 종이다.

[0145] 일부 구현예에서, SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 베타-프로테오박테리아 내 계열, 예를 들어 나이세리아세아에, 버르홀더리아레스 및 로다시클라세아에의 계열에 속하는 박테리아 종에서 수득될 수 있다. 이들 각각의 계열에 속하는 예시적인 박테리아 속 및 종은 도 8 및 도 9에 제공된 모든 종이다.

[0146] 일부 구현예에서, SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 감마-프로테오박테리아 내의 계열, 예를 들어 파스튜렐라세아에, 슈도모노달레스, 엔테로박테리아세아에, 비브리오나세아에, 크산토모나다세아에, 카디오박테리아세아에 및 메틸로파가의 계열에 속하는 박테리아 종에서 수득될 수 있다. 이들 각각의 계열에 속하는 예시적인 박테리아 속 및 종은 도 8 및 도 9에 제공된 모든 종이다.

[0147] 일부 구현예에서, SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 델타-프로테오박테리아 내 계열, 예를 들어 데설포비브리오나케애의 계열에 속하는 박테리아 종에서 수득될 수 있다. 이와 같은 계열에 속하는 예시적인 박테리아 속 및 종이 도 8 및 도 9에 제공되었다.

[0148] 일부 구현예에서, SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 나이세리아 메닌기티디스 종, 나이세리아 고노르호아에, 나이세리아 락타미카, 나이세리아 신세라, 클렙시엘라 데니트리피칸스, 모락셀라 카타르할리스, 만헤이미아 하에몰리티카, 악티노바실러스 플레우롭네오모니애, 헤모필루스 솜니, 헤모필루스 인플루엔자, 파스튜렐라 멀토시다, 아시네토박터 바우마니 또는 비브리오 콜레라에 속하는 박테리아 종에서 수득될 수 있다.

[0149] 일부 구현예에서, SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 서열식별번호: 1에서 시작하는 본원에 제시된 홀수- 넘버링된 서열식별번호 중 임의의 하나를 포함하거나 또는 그것으로 이루어진 폴리뉴클레오타이드이고, 서열식별번호: 693에서 끝난다.

[0150] 일부 구현예에서, SLAM 폴리펩타이드는 서열식별번호에서 시작하는 짝수-넘버링된 서열식별번호: 2의 임의 중 하나를 포함하는 또는 그것으로 이루어진 폴리펩타이드이고, 서열식별번호: 694에서 끝난다.

[0151] 본 개시내용의 일부 측면에 따라, SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 숙주세포에서 SLAM 폴리펩타이드의 발현을 제어할 수 있는 폴리뉴클레오타이드에 연결된다. 상기 숙주세포 임의의 세포, 예컨대 임의의 진핵 세포, 예를 들어 동물 세포 또는 식물 세포, 또는 미생물 세포, 예컨대 진균 세포 또는 박테리아 세포일 수 있다.

[0152] 일부 구현예에서, 상기 숙주세포는 박테리아 세포이다.

[0153] 일부 구현예에서, 상기 숙주세포는 그램-음성 박테리아 세포이다.

[0154] 일부 구현예에서, 상기 숙주세포는 나이세리아 속, 클렙시엘라, 모락셀라, 만헤이미아, 악티노바실러스, 헤모필루스, 파스튜렐라, 아시네토박터, 에스케리치아 또는 비브리오에 속하는 박테리아 세포에서 선택된 세포이다.

[0155] 일부 구현예에서, 상기 숙주세포는 나이세리아 메닌기티디스 속, 나이세리아 고노르호아에, 나이세리아 락타미카, 나이세리아 신세라, 클렙시엘라 데니트리피칸스, 모락셀라 카타르할리스, 만헤이미아 하에몰리티카, 악티노바실러스 플레우롭네오모니애, 헤모필루스 솜니, 헤모필루스 인플루엔자, 파스튜렐라 멀토시다, 아시네토박터 바우마니 또는 비브리오 콜레라에 속하는 박테리아 세포에서 선택된다.

[0156] 바람직한 구현예에서, 상기 숙주세포는 나이세리아 속, 예컨대 나이세리아 메닌기티디스 및 나이세리아 고노르호아에, 또는 에스케리치아 콜라이에 속하는 박테리아 세포에서 선택된다.

[0157] 본 개시내용의 일 측면에 따라, 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드는 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드에 연결된다. 따라서, 일 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드에 연결된 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드를 추가로 제공한다.

[0158] 본원에 사용될 수 있는 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드에는 숙주세포에서 폴리펩타이드의 발현을 제어할 수 있는 임의의 전사 프로모터가 포함된다. 일반적으로, 미생물 숙주가 본원의 내용에 따라 선택된 경우, 미생물 세포에서 수득된 프로모터가 사용되는 반면, 진핵생물 숙주가 선택되는 경우, 진핵 프로모터가 선택된다. 숙주세포에서 발현을 제어할 수 있는 추가의 폴리뉴클레오타이드 성분에는 전사 종결자, 인핸서 및 기타 동종의 것이 포함되고, 이들 모두는 본 개시내용의 키메라성 폴리뉴클레오타이드에 포함될 수 있다.

[0159] 본 개시내용에 따르면, 본 개시내용의 키메라성 폴리뉴클레오타이드는 바람직하게는 상기 숙주세포에서 SLAM 폴리펩타이드의 양호한 발현을 보장하는 발현 벡터에 포함된다. 따라서, 본 개시내용은 일 구현예에서, 작동가능하게 연결된 성분으로 하기를 포함하는 재조합 발현 벡터를 포함한다:

[0160] (i) 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0161] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드

[0162] 여기서 상기 발현 벡터는 숙주세포에서의 발현에 적합하다. 용어 "숙주세포에서의 발현에 적합한"은 상기 재조합 발현 벡터가 숙주세포에서의 발현을 달성하기 위해 요구되는 유전 인자에 연결된 본 개시내용의 키메라성 핵산 서열을 포함함을 의미한다. 이와 관련하여 상기 발현 벡터에 포함될 수 있는 유전 인자에는 전사 종결 영역, 마커 유전자를 인코딩하는 하나 이상의 핵산 서열, 하나 이상의 복제의 기원, 및 기타 동종의 것이 포함된다. 당해 분야의 숙련가에게 알려진 바와 같이, 예를 들어 프로모터를 전사의 5' 에서 3' 방향으로 코딩 서열에 연결시킴으로써, 상기 유전 인자가 작동가능하게 연결된다. 바람직한 구현예에서, 상기 발현 벡터는 숙주세포의 게놈에서 벡터 또는 이것의 부분의 통합을 위해 요구되는 유전 인자를 추가로 포함한다. 본 개시내용과 관련하여, 상기 발현 벡터는 마커 유전자를 추가로 함유할 수 있다. 본 개시내용에 따라 사용될 수 있는 마커 유전자에는 비-전환된 세포와 전환된 세포의 구별을 허용하는 모든 유전자, 예컨대 모든 선택가능한 및 선별가능한 마커 유전자가 포함된다. 마커 유전자는 저항 마커, 예컨대 예를 들어, 카나마이신 또는 암피실린에 대한 항생제 내성 마커일 수 있다. 육안 검사를 통해 형질전환체를 식별하기 위해 이용될 수 있는 선별가능한 마커에는 예를 들어, β-갈락토시다아제, β-글루쿠로니다제(GUS)(U.S.특허 번호 5,268,463 및 5,599,670) 및 녹색 형광 단백질(GFP)(Niedz RP, Sussman MR, Satterlee JS.1995.Green Fluorescent Protein - an in-Vivo Reporter of Plant Gene-Expression.Plant Cell Rep 14: 403-406), 또는 다른 단백질 태그, 예를 들어 도 11 및 도 13에서 나타낸 바와 같은 폴리-히스티딘 태그 또는 Flag 태그가 포함된다.

[0163] 본 개시내용의 일 측면에 따라, SLAM을 인코딩하는 자연 발생 폴리뉴클레오타이드는 변형될 수 있다. 따라서 상기 자연 발생 폴리뉴클레오타이드는 숙주세포에서 SLAM 폴리펩타이드의 발현을 향상시키기 위해, 예를 들어 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드 서열을 코돈 최적화함으로써, 변형될 수 있다. 따라서, 본 개시내용은 SLAM 폴리펩타이드를 인코딩하는 코돈 최적화된 폴리뉴클레오타이드, 예컨대 서열식별번호: 1113에 제시된 폴리뉴클레오타이드를 제공한다. SLAM을 인코딩하는 폴리뉴클레오타이드는 발현을 용이하게 하기 위한 신호 서열을 포함하기 위해 추가로 변형될 수 있다. 신호 서열을 인코딩하는 예시적인 폴리뉴클레오타이드가 서열식별번호: 1179에 제시되고, 상기 상응하는 폴리펩타이드 신호 서열이 서열식별번호: 1180에 제시된다. 따라서 본 개시내용은 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드에 작동가능하게 연결된 미생물 신호 서

열을 인코딩하는 키메라성 폴리뉴클레오타이드 뿐만 아니라, 상기 폴리뉴클레오타이드, 예컨대 서열식별번호: 1181 및 서열식별번호: 1182에 제시된 폴리뉴클레오타이드 및 폴리펩타이드에 의해 인코딩된 폴리펩타이드를 추가로 포함한다.

[0164] 특히 편리하게 사용될 수 있는 한 가지 숙주세포는 에스케리치아 콜리이다. E. 콜리 벡터의 제조는 통상적으로 공지된 기술 예컨대 제한 소화, 결찰, 결찰-독립적인 클로닝, 겔 전기영동, DNA 서열분석, 폴리머라제 연쇄 반응(PCR), 및 다른 방법들을 사용하여 달성될 수 있다. 다양한 클로닝 벡터가 본 발명자들이 개발한 바 있는 맞춤형 벡터를 비롯한 재조합 발현 벡터를 제조하기에 요구되는 필요한 단계를 수행하는 데 이용 가능하다. E. 콜리에서 기능성이 있는 복제 시스템을 갖춘 벡터들에, 벡터 예컨대 벡터의 pUC 또는 pET 시리즈 등이 속한다. 전형적으로, 이들 클로닝 벡터는 전환된 세포의 선택을 허용하는 마커를 함유한다. 폴리뉴클레오타이드는 예를 들어 제한 및 결찰 효소를 사용하여 이들 벡터에 도입될 수 있고, 상기 벡터는 반응능 세포를 제조함으로써, 전기천공에 의해 또는 당해기술자에 잘 알려진 다른 방법에 의해 E. 콜리에 도입될 수 있다. E. 콜리는 적절한 배지, 예컨대 Luria-액체배지에서 성장되어, 수확될 수 있다. 재조합 발현 벡터는 세포의 수확 및 용해 시 상기 세포에서 쉽게 회수될 수 있다. 또한, 재조합 벡터의 제조 및 재조합 유기체의 성장과 관련된 일반적인 안내는 아래에서 발견될 수 있다: 예를 들어: Sambrook 등, Molecular Cloning, a Laboratory Manual, Cold Spring Harbor Laboratory Press, 2001, Third Ed.

[0165] 재조합 SLAM 폴리펩타이드의 생산은 균주의 성장 전반에 걸쳐 발생하거나, 또는 상당한 바이오매스를 달성하기 위한 성장 기간 후, 예를 들어 유도성 프로모터, 예컨대 lacZ 프로모터를 사용하여, 발현의 유도에 의해 달성될 수 있다.

[0166] 본원에 있어서, 일부 구현예에서, 상기 SLAM 폴리펩타이드는 후속적으로 다른 숙주세포 성분에서 회수, 단리 및 분리된다. 따라서 본 개시내용은 추가 구현예에서, 숙주세포에서 SLAM 폴리펩타이드를 발현시키는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0167] (a) 작동가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0168] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0169] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0170] (b) 상기 키메라성 핵산 서열을 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 SLAM 폴리펩타이드를 생산하는 단계; 및

[0171] (c) 상기 SLAM 폴리펩타이드를 상기 숙주세포에서 회수하는 단계.

[0172] SLAM 단백질 회수는 다양한 상이한 단백질 정제 기술, 예컨대, 예를 들어 금속-킬레이트 크로마토그래피, 이온 교환 크로마토그래피, 크기 배제 크로마토그래피, 친화성 크로마토그래피, 소수성 상호작용 크로마토그래피, 역상 크로마토그래피, 겔 여과 등에 의해 영향을 받을 수 있다. 더 나아가, 단백질 정제와 관련된 일반적인 안내는 예를 들어 아래에 발견될 수 있다: Protein Purification: Principles, High Resolution Methods, and Applications Janson J-C. 2013.Protein Purification: Principles, High Resolution Methods, and Application, vol. 54.Wiley.명세서에서 사용된 용어 “회수된”은 바와 같이 상기 폴리펩타이드가 다소간 순수한 형태로 수득됨을 의미한다. “실질적으로 순수한”은 상기 면역원성 단백질이 다른 숙주세포 성분에서 분리되었음을 의미한다. 본원에 있어서, 상기 면역원성 단백질은 적어도 95% 순수하고, 더 바람직하게는 적어도 96%, 97%, 98% 또는 99% 순수하다.

[0173] 또 다른 측면에서, 본 개시내용은 신규한 SLAM 폴리펩타이드에 관한 것이다. 따라서 본 개시내용은 적어도 하나의 구현예에서, 서열식별번호: 1184를 포함하거나 또는 이들로 이루어진 SLAM 폴리펩타이드, 또는 이것과 실질적으로 동일한 폴리펩타이드를 제공한다.

[0174] 또 다른 측면에서, 본 개시내용은 신규한 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드에 관한 것이다. 따라서, 본 개시내용은 적어도 하나의 구현예에서, 서열식별번호: 1183를 포함하거나 또는 이들로 이루어진 폴리뉴클레오타이드를 제공한다.

[0175] 상기 숙주세포와 관련하여, 상기 SLAM 폴리펩타이드는 거기에 천연적으로 존재하는 SLAM 폴리펩타이드일 수 있고, 따라서 일부 구현예에서, 상기 숙주세포에서 SLAM 폴리펩타이드의 생산은 상기 세포에서 SLAM 폴리펩타이드 단백질 농도의 조절을 초래할 수 있고, 예를 들어, 상기 세포에서 SLAM 폴리펩타이드 농도는 키메라성 폴리펩타이드 서열의 도입의 결과로 증가할 수 있다. 다른 구현예에서, 상기 생산된 SLAM 폴리펩타이드는 상기 숙주세포

에 천연적으로 존재하지 않는다.

[0176] 상기 표적 단백질은 숙주세포의 세포기질에서 세포외 표면으로의 수송을 요구할 수 있는 임의의 단백질, 폴리펩타이드 또는 펩타이드일 수 있다. 본 명세서에서 사용된 용어 “세포외 표면”은 세포의 세포 표면 구조를 지칭하는 것으로, 이것은 세포의 외인성 환경에서 그것의 세포질 부분을 분리한 것이다. 상기 세포 표면 구조는 단백질 및/또는 그 안에 포매된 리포폴리사카라이드를 갖는 하나 이상의 포스포지질 막을 포함할 수 있다. 그램-음성 박테리아에서, 상기 세포외 표면 구조는 내부 인지질 이중층 막 및, 수성 주변세포질 구획에 의해 서로 분리된 외부 인지질 이중층 막을 포함한다. 숙주세포의 세포기질에서 세포외 표면으로의 수송 시, 상기 표적 단백질은 상기 세포의 세포외 표면 구조와 잘 조화되고 상호작용한다. 이와 같은 상호작용은 상기 세포의 외인성 환경에 상기 표적 단백질의 적어도 일부분의 노출로 이어질 수 있다.

[0177] 적어도 일부 구현예에서, 상기 표적 단백질은 숙주 유기체에서 면역 반응을 불러 일으킬 수 있는 면역원성 단백질이다.

[0178] 적어도 일부 구현예에서, 상기 표적 단백질은 병원성 미생물의 외측 표면 상에 자연적으로 나타나는 면역원성 폴리펩타이드, 또는 이것의 면역원성 부분이다.

[0179] 적어도 일부 구현예에서, 상기 면역원성 단백질은 표면 지질단백질(SLP) 또는 이것의 부분이다.

[0180] 적어도 일부 구현예에서, 상기 표면 지질단백질(SLP)은 하기의 짝수-넘버링된 서열식별번호: 서열식별번호: 696 내지 서열식별번호: 1082, 서열식별번호: 1094, 서열식별번호: 1100 및 짝수-넘버링된 서열식별번호: 1116 내지 서열식별번호: 1168, 및 서열목록번호; 1178(본원에 제시됨) 중 하나 이상에서 선택된 폴리펩타이드 서열 또는 이것의 부분을 포함하거나 또는 이들로 이루어진다.

[0181] 적어도 일부 구현예에서, 상기 표면 지질단백질(SLP)은 서열식별번호: 695에서 시작된 짝수-넘버링된 서열식별번호들 중 하나에서 선택된 폴리뉴클레오타이드에 의해 인코딩된 폴리펩타이드 서열 또는 이것의 부분을 포함하거나 또는 이들로 이루어지고, 서열식별번호: 1081(본원에 제시됨)에서 끝난다.

[0182] 적어도 일부 구현예에서, 상기 표적 단백질은 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드 서열에 인접한 박테리아 게놈 상에 위치한 표면 지질단백질이다.

[0183] 적어도 일부 구현예에서, 상기 면역원성 단백질은 표면 지질단백질, 또는 이들의 면역원성 부분인데, 이들은, 일부 구현예에서, 하기 서열식별번호: 1148를 포함하는 TbpB 폴리펩타이드를 포함하는, 트랜스페린 결합 단백질 B(TbpB), 일부 구현예에서, 서열식별번호: 932를 포함하는 HpuA 폴리펩타이드를 비롯한 헤모글로빈-합토글로빈 결합 단백질 A(HpuA), 일부 구현예에서, 서열식별번호: 1116를 포함하는 fHbp 폴리펩타이드를 비롯한 인자 H 결합 단백질(fHbp) 및, 일부 구현예에서, 서열식별번호: 1138를 포함하는 LbpB 폴리펩타이드를 비롯한 락토페린 결합 단백질(LbpB)로 구성된 군으로부터 선택된다.

[0184] 적어도 일부 구현예에서, 상기 트랜스페린 결합 단백질 B(TbpB)는 서열식별번호: 1149를 포함하거나 또는 이들로 이루어진 폴리뉴클레오타이드 서열에 의해 인코딩된다.

[0185] 적어도 일부 구현예에서, 상기 락토페린 결합 단백질 B(LbpB)가 서열식별번호: 869를 포함하거나 또는 이들로 이루어진 폴리뉴클레오타이드 서열에 의해 인코딩된다.

[0186] 적어도 일부 구현예에서, 상기 인자 H 결합 단백질(fHbp)이 서열식별번호: 1115를 포함하거나 또는 이들로 이루어진 폴리뉴클레오타이드 서열에 의해 인코딩된다: .

[0187] 적어도 일부 구현예에서, 상기 헤모글로빈-합토글로빈 결합 단백질 A(HpuA)이 서열식별번호: 923를 포함하거나 또는 이들로 이루어진 폴리뉴클레오타이드 서열에 의해 인코딩된다.

[0188] 적어도 일부 구현예에서, 상기 표적 단백질은 2종 이상의 표면 지질단백질 또는 이것의 일부분들을 포함하는 융합 단백질이다. 일부 구현예에서, 상기 표적 단백질은 서열식별번호: 696 내지 서열식별번호: 1082, 및 서열식별번호: 1178(본원에 제시됨)에서 선택된 적어도 2종의 지질단백질들에서 수득된 둘 이상의 폴리펩타이드, 또는 이들의 일부분들을 포함하는 융합 단백질이다. 추가 구현예에서, 상기 표적 단백질은 트랜스페린 결합 단백질(TbpB), 락토페린 결합 단백질(LbpB), 인자 H 결합 단백질(fHbp) 및 헤모글로빈-합토글로빈 결합 단백질(HpuA) 중 적어도 2종에서 수득된 부분을 포함하는 융합 폴리펩타이드이다. 일부 구현예에서, 상기 표적 단백질은 제2 표면 지질단백질의 면역원성 부분에(N-말단 또는 C-말단에서) 융합된 제1 표면 지질단백질을 포함하는 융합 폴리펩타이드이다. 특정 구현예에서, 상기 표적 단백질은 서열식별번호: 1102에 제시된 융합 폴리펩타이드이다.

본 개시내용에 따른 표적 단백질로 융합 폴리펩타이드의 용도의 실행이 실시예 9에 추가로 설명되었다.

[0189] 일반적으로, TbpB 펩타이드의 일부분이 사용되는 이것의 구현예에서, 이와 같은 일부분은 하기를 포함한다: 적어도 (i) TbpB 신호 펩타이드 지질-박스, 예컨대 고착 펩타이드(서열식별번호: 1170), 및/또는 (ii) TbpB 폴리펩타이드의 C-말단 도메인 (서열식별번호: 1098).

[0190] *표적 단백질의 실질적인 개수는 본 개시내용에서 제공되는데, 신규한 표적 단백질이 본 개시내용의 목적에서 벗어나지 않으면서 본 개시내용에 따라 발견 및 사용될 수 있다. 따라서 본 개시내용은 상기 표적 단백질과 관련하여 제한되도록 의도된 것이 아니고, 임의의 표적 단백질은 본 개시내용의 신규한 방법을 실행하기 위해 사용될 수 있다. 일 구현예에서, 신규한 표적 단백질을 발견하기 위해, SLAM 폴리펩타이드를 인코딩하는 게놈 영역에 바로 인접한 게놈 영역이 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드 서열의 존재에 대해 탐색될 수 있고, 임의의 확인된 폴리펩타이드는 표적 단백질로서 평가될 수 있다. 따라서, 또 다른 측면에 따르면, 본 개시내용은 적어도 하나의 구현예에서, SLAM 폴리펩타이드에 의해 세포의 세포기질에서 세포외 표면으로 수송될 수 있는 표적 단백질을 식별하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0191] (a) 하기를 포함하는 게놈 뉴클레오타이드 서열을 제공하는 단계

[0192] (i) SLAM 폴리펩타이드를 인코딩하는 제1 뉴클레오타이드 서열; 및

[0193] (ii) 폴리펩타이드를 인코딩하기에 충분히 길고 상기 제1 뉴클레오타이드 서열에 자연적으로 부착된 제2 뉴클레오타이드 서열;

[0194] (b) 상기 제2 뉴클레오타이드 서열을 평가하여 상기 제2 뉴클레오타이드 서열 내 폴리펩타이드 인코딩 서열을 식별하는 단계; 및

[0195] (c) 폴리펩타이드 인코딩 서열을 사용하여 SLAM 폴리펩타이드를 포함하는 숙주세포에서 폴리펩타이드를 발현시켜서 상기 단백질이 상기 숙주세포의 세포기질에서 세포외 표면으로 수송되었는지 여부를 판단함으로써, 상기 단백질이 표적 단백질인지 여부를 식별하는 단계.

[0196] 전술한 내용에 따라, SLAM 폴리펩타이드를 인코딩하는 임의의 게놈 뉴클레오타이드 서열이 제공될 수 있다.

[0197] 일부 구현예에서, 임의의 미생물 게놈, 예컨대, 예를 들어, 나이세리아 속, 클렙시엘라, 모락셀라, 만헤이미아, 악티노바실러스, 헤모필루스, 파스튜렐라, 아시네토박터, 에스케리치아 및 비브리오에 속하는 박테리아 종의 게놈에서 유래된 게놈 뉴클레오타이드 서열이 제공된다. 상기 게놈 뉴클레오타이드 서열은, 제1 및 제2 뉴클레오타이드 서열이 자연적으로 부착된 경우, 및 추가로 상기 제2 뉴클레오타이드 서열이 폴리펩타이드를 인코딩하는 뉴클레오타이드 서열을 포함하기에 충분히 긴 경우, 그 길이가 다양할 수 있고, 전체 게놈 또는 이것의 부분 또는 단편을 나타낼 수 있다.

[0198] 일부 구현예에서, 상기 제1 뉴클레오타이드 서열은 홀수-넘버링된 서열식별번호 1 내지 서열식별번호: 695중 임의의 하나에서 선택된 서열을 포함한다.

[0199] 일반적으로, 제1 뉴클레오타이드 서열의 양면 중 한쪽 또는 양면 모두에 부착될 수 있는(즉 상기 SLAM 인코딩 서열 관련 5’ 또는 3’) 상기 제2 뉴클레오타이드 서열은 제1 뉴클레오타이드 서열에서 적어도 100 뉴클레오타이드 연장된다. 상기 제2 뉴클레오타이드 서열은 또한 더 길 수 있는데, 예를 들어, 길이가 적어도 250 뉴클레오타이드, 적어도 500 뉴클레오타이드, 적어도 1,000 뉴클레오타이드, 적어도 2,000 뉴클레오타이드 또는 적어도 5,000 뉴클레오타이드일 수 있다. 일부 구현예에서, 상기 게놈 뉴클레오타이드 서열은 시각적으로 뉴클레오타이드 서열 정보를 표시할 수 있는 매체, 예컨대 컴퓨터 스크린, 정제 스크린 또는 휴대용 디바이스, 또는 종이 상에 뉴클레오타이드 서열의 인쇄 상에 존재하는 뉴클레오타이드 서열의 시각적 표현이다. 게놈 뉴클레오타이드 서열을 수득하기 위해, 미생물 유기체에서 그것의 단리 시 폴리뉴클레오타이드가 제공될 수 있고, 상기 폴리뉴클레오타이드의 서열은 당해기술에 잘 알려진 뉴클레오타이드 서열분석용 기술을 사용하여 결정될 수 있고, 상기 수득된 뉴클레오타이드 서열이 이어서 평가를 위해 시각적으로 표시될 수 있다. 상기 뉴클레오타이드 서열은 당해 기술에 잘 알려진 기법 및 방법을 사용하여 열린 해독틀 및 코딩 영역 폴리펩타이드 인코딩 서열의 존재에 대해 평가 및 분석될 수 있으며, 이에는 핵산 서열 번역을 할 수 있는 컴퓨터 소프트웨어가 포함되고, 예컨대 ExPASy (Gasteiger, E.;Gattiker, A; Hoogland, C; Ivanyi, I; Appel, RD; Bairoch, A(2003)가 포함된다. "ExPASy: The proteomics server for in-depth protein knowledge and analysis".Nucleic Acids Research.31(13): 3784-8). 제2 핵산 내 폴리펩타이드 인코딩 서열의 확인 시, 상기 폴리펩타이드 인코딩 서열을 포함하는 유전적 구성체가 숙주세포에서의 발현을 위해 제조 및 사용되어 상기 폴리펩타이드가 상기 숙주세

포의 세포기질에서 세포외 표면으로 수송되었는지 여부를 확인할 수 있다 유전적 구성체는 폴리펩타이드 인코딩 뉴클레오타이드 서열을 그것의 천연 공급원 미생물 유기체에서 단리하고 그것을 발현에 적합한 발현 벡터 숙주 세포에 유입시킴으로써, 제조될 수 있다. 일부 구현예에서, 상기 폴리펩타이드 인코딩 뉴클레오타이드 서열은 게놈 뉴클레오타이드 서열을 포함하거나 또는 이들로 이루어진다. 상기 발현 벡터는 이어서 숙주세포에 유입될 수 있다. 상기 숙주세포는 일부 구현예에서, 세포 안에 천연적으로 존재할 수 있거나, 또는 다른 구현예에서, 상기 숙주세포에서 재조합으로 발현될 수 있는 SLAM 폴리펩타이드를 포함하는 세포이다. 상기 폴리펩타이드 인코딩 뉴클레오타이드 서열이 유전자 서열을 포함하거나 또는 이들로 이루어진 구현예에서, 상기 폴리펩타이드 인코딩 뉴클레오타이드 서열과 SLAM 폴리펩타이드를 인코딩하는 뉴클레오타이드 서열이 상기 숙주세포에 동시에 유입될 수 있다. 일부 구현예에서, 상기 숙주세포는 에스케리치아 콜리 세포이다. 상기 숙주세포의 성장 시, 그리고 상기 숙주세포에서 표적 단백질의 발현 시, 상기 폴리펩타이드가 상기 숙주세포의 세포외 표면으로 수송되어 상기 세포외 표면과 결합하는 경우, 상기 폴리펩타이드는 표적 단백질이다. 본 개시내용의 전술한 구현예는 하기의 실시예 8 내지 및 10에서 상세히 기술된다.

[0200] 적어도 일부 구현예에서, 상기 표적 단백질은 상기 숙주세포에 천연적으로 존재한다. 따라서, 본 개시내용은 숙주세포의 세포기질에서 세포외 표면으로의 상기 숙주세포에 천연적으로 존재하는 표적 단백질의 수송을 초래하는 방법을 추가로 포함하되, 상기 방법은 하기를 포함한다:

[0201] (a) 상기 세포에 천연적으로 존재하는 표적 단백질을 포함하는 숙주세포를 선택하는 단계;

[0202] (b) 작동 가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0203] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0204] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0205] (c) 상기 키메라성 핵산 서열을 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 SLAM 폴리펩타이드를 생산하여, 세포기질에서 세포외 표면으로의 표적 단백질의 수송을 초래하는 단계.

[0206] 적어도 일부 구현예에서, 상기 표적 단백질은 나이세리아 메닌기티디스, 나이세리아 고노르호아에, 나이세리아 락타미카, 나이세리아 신세라, 클렙시엘라 데니트리피칸스, 모락셀라 카타르할리스, 만헤이미아 하에몰리티카, 악티노바실러스 플레우롭네오모니애, 헤모필루스 솜니, 헤모필루스 인플루엔자, 파스튜렐라 멀토시다, 아시네토박터 바우마니 또는 비브리오 콜레라에로 이루어진 박테리아 군에서 선택된 병원성 박테리아 종의 세포에 천연적으로 존재한다.

[0207] 적어도 일부 구현예에서, 상기 표적 단백질은 비-공유 방식으로 상기 SLAM 폴리펩타이드와 상호작용 및 조화를 이룬다. 상기 SLAM 폴리펩타이드와 상기 표적 단백질 사이의 비-공유 상호작용은 상기 SLAM 폴리펩타이드와 상기 표적 단백질을 포함하는 헤테로이량체성 단백질 복합체의 형성을 야기할 수 있다. 상기 상호작용은 예를 들어 일정한 기간 동안 상기 세포기질에서 유래된 상기 표적 폴리펩타이드의 상기 세포기질에서 세포외 표면으로의 수송을 허용할 정도로 충분한 일시적 상호작용이거나, 또는 상기 세포의 세포외 막으로의 상기 표적 폴리펩타이드의 수송 시 상기 SLAM 폴리펩타이드와 상기 표적 단백질 사이의 비-공유 상호작용이 유지되는 좀 더 장기적인 상호작용일 수 있다.

[0208] 적어도 일부 구현예에서, 상기 표적 단백질은 숙주세포에 천연적으로 존재하지 않는다. 따라서, 본 개시내용은 적어도 하나의 구현예에서, 숙주세포의 세포기질에서 세포외 표면으로의 표적 단백질의 수송을 초래하는 방법을 추가로 제공하되, 상기 방법은 하기를 포함한다:

[0209] (a) 작동 가능하게 연결된 성분으로 하기를 포함하는 제1 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0210] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0211] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0212] (b) 작동 가능하게 연결된 성분으로 하기를 포함하는 제2 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0213] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0214] (ii) 표적 단백질을 인코딩하는 폴리뉴클레오타이드; 및

[0215] (b) 상기 제1 및 제2 키메라성 폴리뉴클레오타이드를 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 SLAM 폴리펩타이드 및 표적 단백질을 생산하는 단계.

[0216] 적어도 일부 구현예에서, 상기 표적 단백질은 상기 SLAM 폴리펩타이드에 공유결합된다. 따라서, 본 개시내용은 적어도 하나의 구현예에서, 숙주세포의 세포기질에서 세포외 표면으로의 표적 단백질의 수송을 초래하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0217] (a) 작동 가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0218] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드;

[0219] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0220] (iii) 표적 단백질을 인코딩하는 폴리뉴클레오타이드; 및

[0221] (b) 상기 키메라성 핵산 서열을 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 SLAM 폴리펩타이드를 생산하고 세포기질에서 세포외 표면으로의 표적 단백질의 수송을 초래하는 단계.

[0222] 적어도 일부 구현예에서, 상기 키메라성 폴리뉴클레오타이드는 바람직하게는 펩타이드 결합을 통해, 표적 단백질의 N-말단과 SLAM 폴리펩타이드의 C-말단의 공유 연결을 초래하는 방식으로 구성된다.

[0223] 적어도 일부 구현예에서, 상기 키메라성 폴리뉴클레오타이드는 바람직하게는 펩타이드 결합을 통해, SLAM 폴리펩타이드의 N-말단과 표적 단백질의 C-말단의 공유 연결을 초래하는 방식으로 구성된다.

[0224] 적어도 일부 구현예에서, 상기 키메라성 폴리뉴클레오타이드는 상기 SLAM 폴리펩타이드의 일부분의 제거 및 상기 표적 폴리펩타이드로의 그것의 대체를 초래하는 방식으로 구성된다. 일부 구현예에서, 상기 키메라성 폴리뉴클레오타이드는 상기 SLAM 폴리펩타이드의 N-말단의 적어도 1, 2, 3, 4, 5, 6, 7, 8, 9, 또는 10 아미노산 잔기의 제거 및 상기 표적 단백질로의 그와 같은 잔기(들)의 대체를 야기하는 방식으로 구성된다. 일부 구현예에서, 상기 키메라성 폴리뉴클레오타이드는 상기 SLAM 폴리펩타이드의 C-말단의 적어도 1, 2, 3, 4, 5, 6, 7, 8, 9, 또는 10 아미노산 잔기의 제거 및 표적 단백질로의 잔기(들)의 대체를 초래하는 방식으로 구성된다. 일부 구현예에서, 상기 키메라성 폴리뉴클레오타이드는 상기 SLAM 폴리펩타이드의 폴리펩타이드 서열 내에 상기 표적 단백질의 삽입을 초래하는 방식으로 구성된다. 일부 구현예에서, 상기 키메라성 폴리뉴클레오타이드는 상기 SLAM 폴리펩타이드 내에 표적 단백질의 삽입 및 상기 표적 단백질에 의한 SLAM 폴리펩타이드의 적어도 1, 2, 3, 4, 5, 6, 7, 8, 9, 또는 10 아미노산 잔기(들)의 대체를 초래하는 방식으로 구성된다.

[0225] 적어도 일부 구현예에서, SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드는 실질적으로 절단될 수 있다. SLAM 폴리펩타이드의 N-말단부가 제거되어 12 - 14 외막 스패닝(spanning) 가닥들로 이루어진 C-말단 도메인 β-배럴도메인으로만 이루어진 절단된 SLAM 폴리펩타이드가 획득될 수 있다는 점이 주목할 만하다. 표적 단백질의 수송을 초래하기 위해 본원에서 사용될 수 있는 절단된 SLAM 폴리펩타이드의 예가 서열식별번호: 1111 및 서열식별번호: 1112에 제시되었다.

[0226] 본원의 또 다른 측면에 따르면, 본 개시내용은 특정 구현예에서, 백신을 제조하는 방법을 제공한다. 따라서, 본 개시내용은 추가로 적어도 하나의 구현예에서, 백신을 제조하는 방법을 추가로 제고하되, 상기 방법은 하기를 포함한다:

[0227] (a) 면역원을 생산할 수 있는 숙주세포를 선택하는 단계

[0228] (b) 작동 가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0229] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0230] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0231] (c) 상기 키메라성 핵산 서열을 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 상기 SLAM 폴리펩타이드와 상기 면역원을 생산하는 단계; 및

[0232] (d) 상기 숙주세포를 약화시켜 약화된 숙주세포를 제조하는 단계; 및

[0233] (e) 상기 약화된 숙주세포를 포함하는 백신 제형을 제조하는 단계.

[0234] 일부 구현예에서, 상기 숙주세포는 미생물 세포이다.

[0235] 일부 구현예에서, 상기 숙주세포는 병원성 미생물 세포이다.

[0236] 일부 구현예에서, 상기 숙주세포는 감염성 질환을 매개하는 병원성 미생물 세포이다.

[0237] 적어도 하나의 구현예에서, 상기 숙주세포는 나이세리아 메닌기티디스, 나이세리아 고노르호아에, 나이세리아 락타미카, 나이세리아 신세라, 클렙시엘라 데니트리피칸스, 모락셀라 카타르할리스, 만헤이미아 하에몰리티카, 악티노바실러스 플레우롭네오모니애, 헤모필루스 솜니, 헤모필루스 인플루엔자, 파스튜렐라 멀토시다, 아시네토박터 바우마니 및 비브리오 콜레라에로 이루어진 세포 군에서 선택된 세포이다. 상기 면역원은 상기 숙주세포에 천연적으로 존재할 수도 있고, 또는 상기 숙주세포에서 재조합으로 발현될 수도 있다. 감쇠를 달성하기 위해, 상기 세포는, SLAM 단백질과 면역원의 생산 시, 더 이상 감염될 수 없는 방식으로 처리된다. 전형적으로 이것은 박테리아 세포의 열사(heat-killing)에 의해 또는 외막 소포의 형성에 의해 달성된다. 감쇠 기술은 일반적으로 당해 분야의 숙련가에게 공지된 것으로, 예를 들어, 하기에서 발견될 수 있다: 약화된 나이세리아 메닌기티디스로 균주로의 예방접종은 생 수막염균으로의 면역반응의 초래를 방지한다 Li Y, Sun YH, Ison C, LevineMM, Tang CM.Infect Immun. 2004 Jan; 72(1): 345-51.Li Y, Zhang Q, Winterbotham M, Mowe E, Gorringe A, Tang CM.생 나이세리아 락타미카를 이용한 면역화는 수막염균 면역반응에서 마우스를 보호하고, 혈청 살균 항체를 유도할 수 있다. Infect Immun. 2006;74(11): 6348-55.Dalseg R, Wedege E, Holst J, Haugen I L, Høiby E A, Haneberg B.그룹 B 수막염균에서 유래된 외막 소포는 마우스에 비강내로 들어갈 때 면역원성이 강하다. Vaccine. 1999;17: 2336-2345.

[0238] 적어도 일부 구현예에서, 본 개시내용은 백신을 제조하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0239] (a) 작동 가능하게 연결된 성분으로 하기를 포함하는 제1 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0240] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드;

[0241] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0242] (b) 작동 가능하게 연결된 성분으로 하기를 포함하는 제2 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0243] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드; 및

[0244] (ii) 표적 단백질을 인코딩하는 폴리뉴클레오타이드; 및

[0245] (c) 상기 제1 및 제2 키메라성 폴리뉴클레오타이드를 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 SLAM 폴리펩타이드와 표적 단백질을 생산하는 단계; 및

[0246] (d) (c)의 세포를 포함하는 백신 제형을 제조하는 단계.

[0247] 적어도 일부 구현예에서, 본 개시내용은은 백신을 제조하는 방법을 제공하되, 상기 방법은 하기를 포함한다:

[0248] (a) 작동 가능하게 연결된 성분으로 하기를 포함하는 키메라성 폴리뉴클레오타이드를 제공하는 단계:

[0249] (i) 상기 숙주세포에서 발현을 제어할 수 있는 폴리뉴클레오타이드;

[0250] (ii) SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드; 및

[0251] (iii) 표적 단백질을 인코딩하는 폴리뉴클레오타이드; 및

[0252] (c) (b) 상기 키메라성 폴리뉴클레오타이드를 상기 숙주세포에 유입시키고 상기 숙주세포를 성장시켜 상기 SLAM 폴리펩타이드와 상기 표적 단백질을 생산하는 단계; 및

[0253] (b)의 세포를 포함하는 백신 제형을 제조하는 단계.

[0254] 적어도 일부 구현예에서, 본 개시내용은 병원성 박테리아 감염에 대한 백신을 제조하는 방법을 추가로 제공하되, 상기 방법은 하기를 포함한다:

[0255] (a) SLAM 폴리펩타이드를 인코딩하는 핵산 서열을 포함하는 병원성 균주를 제공하는 단계;

[0256] (b) 상기 병원성 균주에서 SLAM 생산을 손상시켜 SLAM이 손상된 병원성 균주를 수득하는 단계; 및

[0257] (c) 상기 SLAM이 손상된 병원성 균주를 사용하여 백신을 제형화하는 단계.

[0258] 바람직한 구현예에서, 상기 병원성 균주는 나이세리아 메닌기티디스, 나이세리아 고노르호아에, 나이세리아 락타미카, 나이세리아 신세라, 클렙시엘라 데니트리피칸스, 모락셀라 카타르할리스, 만헤이미아 하에몰리티카, 악티노바실러스 플레우롭네오모니애, 헤모필루스 솜니, 헤모필루스 인플루엔자, 파스튜렐라 멀토시다, 아시네토박터 바우마니 또는 비브리오 콜레라의 균주이다.

[0259] 적어도 일부 구현예에서, 상기 병원성 균주는 나이세리아 속에 속하는 균주이다. 전술한 내용에 따르면, 임의의 박테리아 나이세리아 균주가 사용될 수 있다. 나이세리아 균주를 손상시키기 위해, 임의의 방법이 사용될 수 있다. 바람직하게는, SLAM 폴리펩타이드를 인코딩하는 게놈 폴리뉴클레오타이드 서열의 감쇠 또는 녹아웃을 초래하기 위한 방법이, 예를 들어 트랜스포존 돌연변이 유발에 의해 사용된다. 따라서 바람직한 구현예에서, SLAM이 손상된 나이세리아 균주가, SLAM 폴리펩타이드가 실질적으로 전혀 생산되지 않는 방식으로 게놈 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드에 이미 돌연변이가 일어난 나이세리아 균주이고, 이와 같은 돌연변이에는 SLAM 폴리펩타이드를 인코딩하는 폴리뉴클레오타이드의 제거가 포함될 수 있다.

[0260] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 손상된 게놈 SLAM 폴리뉴클레오타이드 서열을 포함하는 병원성 균주를 제공한다. 용어 “손상된 게놈 SLAM 폴리뉴클레오타이드 서열을 포함하는 균주”는 실질적인 양의 SLAM 폴리펩타이드를 생산할 수 없는 균주를 의미한다. 일부 구현예에서, 상기 병원성 균주는 나이세리아 균주이다. 여기에는 열린 해독틀이 이미 차단된 폴리뉴클레오타이드를 포함하는 균주가 포함되고, SLAM 단백질의 발현을 조절하는 균주는 기능적이지 않고, 상기 용어에는 게놈 SLAM을 인코딩하는 폴리뉴클레오타이드 서열이 이미 제거된 균주가 추가로 포함된다. 따라서 상기 개시내용은 SLAM 폴리펩타이드를 인코딩하는 게놈 폴리뉴클레오타이드 서열이 부족한 돌연변이체 병원성 균주를 추가로 포함한다. 바람직한 구현예에서, 상기 돌연변이된 병원성 균주는 나이세리아 균주이다. 전술한 내용에 따르면, 원상태 균주와 비교할 때, 돌연변이 균주는 적어도 하나의 SLAM 폴리펩타이드를 인코딩하는 게놈 폴리뉴클레오타이드가 없는 것이다. 바람직한 구현예에서, 상기 돌연변이체 나이세리아 균주는 나이세리아 메닌기티디스 균주 또는 나이세리아 고노르호아에 균주이다.

[0261] 본 개시내용의 특정 측면에 따르면, 백신 제제가 제조된다. 상기 백신은 숙주 유기체, 예컨대 임의의 인간 및 비-인간 동물, 예를 들어 비제한적으로 임의의 소, 돼지, 말, 쥣과, 갯과, 고양이, 물고기, 양, 염소, 유인원 및 조류 동물에 투여하기 위해 사용될 수 있다. 따라서, 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 본 개시내용의 임의의 방법에 따라 제조된 백신을 제공한다.

[0262] 또 다른 측면에서, 본 개시내용은 적어도 하나의 구현예에서, 숙주 유기체에 면역력을 제공하기 위한 본 개시내용의 임의의 방법에 따라 제조된 백신 제제의 용도를 제공한다.

[0263] 일부 구현예에서, 상기 백신 제제는 박테리아 유기체 나이세리아 속, 클렙시엘라, 모락셀라, 악티노바실러스, 헤모필루스, 파스튜렐라, 아시네토박터 또는 비브리오 콜레라에 속하는 박테리아 유기체에 의해 매개된 감염성 질환에 대한 면역력을 숙주 유기체에 주기 위해 사용될 수 있다.

[0264] 일부 구현예에서, 상기 백신 제제는 나이세리아 메닌기티디스 종, 나이세리아 고노르호아에, 나이세리아 락타미카, 나이세리아 신세라, 클렙시엘라 데니트리피칸스, 모락셀라 카타르할리스, 만헤이이아 하에몰리티카, 악티노바실러스 플레우롭네오모니애, 헤모필루스 솜니, 헤모필루스 인플루엔자, 파스튜렐라 멀토시다, 아시네토박터 바우마니 또는 비브리오 콜레라에 속하는 박테리아 유기체에 의해 매개된 감염성 질환에 대한 면역력을 숙주 유기체에 주기 위해 사용될 수 있다.

[0265] 적어도 본 개시내용의 일부 구현예에서, 상기 백신은 인간에게 투여된 경우, 나이세리아 박테리아, 현저히 나이세리아 메닌기티디스 및 나이세리아 고노르호아에에 의한 감염을 방지한다. 본원에 따르면, 본 개시내용의 방법들을 사용하여 제조된 세포를 사용하여 백신 제형들이 제조될 수 있다. 일부 구현예에서, 상기 백신 제형은 약화된 세포를 사용하여 제조될 수 있다. 다른 구현예에서, 상기 세포는 특정 분획, 예를 들어 단백질 분획 또는 막이 수득되어 백신을 제조하는 데 사용되는 공급원으로 사용될 수 있다. 본 개시내용의 백신 제제는 바람직하게는 추가로 비히클, 부형제 및 보조 물질, 예컨대 습윤제 또는 유화제, pH 완충 물질 및 기타 동종의 것을 포함한다. 이들 비히클, 부형제 및 보조 물질은 일반적으로 수령 개체에서 면역 반응을 일으키지 않고, 과도한 독성 없이 투여될 수 있는 약제이다. 약제학적으로 허용가능한 부형제에는 비제한적으로, 액체 예컨대 물, 염수, 폴리에틸렌글리콜, 하이알루론산, 글리세롤 및 에탄올이 포함된다. 상기 부형제에는 약제학적으로 허용가능한 염, 예를 들어 무기산 염 예컨대 하이드로클로라이드, 포스페이트, 설페이트, 및 기타 동종의 것; 및 유기산 염 예컨대 아세테이트, 프로피오네이트, 벤조에이트, 및 기타 동종의 것이 또한 포함된다. 비록 요구사항은 아니지만, 상기 제제는 특히 본 개시내용의 폴리펩타이드를 안정화시키기 위해 안정화제로 작용하는 약제학적으로 허용가능한 부형제를 함유하는 것이 또한 바람직하다. 펩타이드용 안정화제로 작용하는 적합한 캐리어의 예에는, 비제한적으로, 약품 등급의 덱스트로스, 수크로스, 락토스, 소르비톨, 이노시톨, 덱스트란, 및 기타 동종의 것이 포함된다. 다른 적합한 캐리어에는 다시 한 번 비제한적으로, 전분, 셀룰로스, 나트륨 또는 인산칼슘, 시트르산, 글리신, 폴리에틸렌 글리콜(PEGs), 및 이들의 조합이 포함된다. 한 개체서 면역 반응을 증가시키기 위해, 본원에 제공된 조성물은 바람직하게는 아쥬반트, 예컨대 약리적 제제, 사이토카인 등을 추가로 포함한다. 적합

한 아쥬반트에는 본 개시내용의 면역원성 폴리펩타이드에 대한 상기 개체의 면역 반응을 향상시키는 임의의 물질이 포함된다. 아쥬반트의 비-제한적인 예에는 사이토카인, 예를 들어, IL-1, IL-2, IL-12, IL-6이 포함되고, 추가로 무기 염, 예를 들어 알루미늄 수산화물, 알루미늄 포스페이트, 및 인산칼슘; 오일 에멀젼, 예를 들면, 광유, MF59, QS-21, Montamide ISA51 및 ISA-720; Isocoms, 예를 들면 ISCOMATRIX; 미생물 유도체, 예를 들면, MPLA, 대식세포-활성 단백질-2, 바이로좀, LT/CT, CpG; 천연 폴리머, 예를 들면 다당류; 및 합성 폴리머, 예를 들면 폴리무수물 및 폴리에스테르가 포함되고, 상기는 Wilson-Welder 등 (Wilson-Welder JH, Torres MP, Kipper MJ, Mallapragada SK, Wannemuehler MJ, Narasimhan B.2009.Vaccine Adjuvants: Current Challenges and Future Approaches.J Pharm Sci-Us 98: 1278-1316)에서 검토된 바와 같다. 아쥬반트는 예를 들어, 단백질 또는 다른 거대분자로서 약화된 세포의 투여와 동시에, 그 전에 또는 그 이후에 투여될 수 있다.

[0266] 본 개시내용은 또한 병원성 박테리아 종에 의해 감염을 가지고 있는 환자의 치료에 사용하기 위한 후보 화합물을 식별하는 스크리닝 방법을 추가로 제공하되, 상기 방법은 하기를 포함한다:

[0267] (a) 시험 화합물을 제공하는 단계;

[0268] (b) 기능성 검정에서 병원성 박테리아 종에서 SLAM 폴리펩타이드의 원상태 기능에 미치는 시험 화합물의 영향과 대조군을 비교하는 단계; 및

[0269] (c) SLAM 폴리펩타이드의 원상태 기능에 영향을 미치는 시험 화합물을 식별하는 단계.

[0270] 바람직한 구현예에서, 상기 병원성 박테리아 종은 나이세리아 속에 속한다.

[0271] 전술한 내용에 따르면, 화합물은 나이세리아 감염 환자를 치료하는 데 그것의 유용성에 대해 평가될 수 있다. 전형적으로 이것은 시험하고자 하는 하나 이상의 화합물을 제공함으로써 그리고 기능성 검정의 성능에 의해 달성된다. 상기 검정은 바람직하게는 시험관내 검정이고, 다중 화합물이 동시에 평가되도록 구성될 수 있다. 상기 기능성 검정은 SLAM 폴리펩타이드의 원상태 기능에 미치는 영향을 검출할 수 있는 임의의 검정일 수 있다. 예를 들어, 상기 검정은 상기 화합물의 존재 하에 표적 단백질의 세포 표면으로의 수송의 평가, 주목할 만한 것은 음성 대조군(예를 들어 유해하지 않은 화합물) 또는 양성 대조군(즉, SLAM 단백질의 기능에 영향을 미치는 공지된 화합물)의 존재 하의 수송의 비교를 수반할 수 있다. 따라서 예를 들어, SLAM 폴리펩타이드의 원상태 기능에 영향을 미치는 화합물을 선택할 때 TbpB 수송이 모니터링될 수 있고, 상기 선택된 화합물의 추가 평가는 인간에 상기 화합물의 투여를 비롯한 시험관내 또는 생체내 시험에서 상기 화합물의 시험을 포함할 수 있다.

[0272] 이하에서 본 개시내용의 방법을 수행하는 특정 구현예 뿐만 아니라 본 개시내용의 조성물을 나타내는 구현예의 실시예들이 제공된다. 하기 실시예들은 단지 설명하기 위해 제공되고, 본 개시내용의 범위를 어떤 식으로든 제한하려는 것은 아니다.

[0273] 실시예

[0274] 실시예 1 -SLAM 폴리펩타이드(SLAM 1)를 인코딩하는 폴리뉴클레오타이드의 단리

[0275] N.men-B16B6 게놈 DNA의 시험관내 전좌를 EZ: TN<KAN2> 트랜스포존 키트(Epicentre)을 사용하여 수행하였다. 100㎕ 반응물에서 초음파처리된 DNA(1-6 kb) 대략 400ng을 전위효소 10 ㎕와 혼합하고, 37 ° C에서 2시간 동안 인큐베이션하였다. EZTN5-정지 용액을 첨가하고 70 ° C에서 10분 동안 인큐베이션하였다. 에탄올 침전에 의한 농축 후, 상기 DNA를 하기로 보수하였다: T4 DNA 폴리머라제 및 T4 리가제(V. pelicic, S.Morelle, D.Lampe, X.Nassif, Journal of Bacteriology, 182: 5391(Oct 1, 2000)).

[0276] 하기에 의해 B16B6에 트랜스포존을 유입시켰다: 스폿 전환(T.H.Dillard 등 Surg.Obes.Rel.Dis. 9: 269(Jan 1, 2013)).간단히, 상기 반응 혼합물을 뇌 심장 주입(BHI) 플레이트에 스폿팅하였고, 여기서 N.men-B16B6 콜로니를 사용하여 스폿을 비롯한 전체 플레이트에 줄무늬를 넣었다. 상기 플레이트를 5% CO_2 하의 37° C에서 8시간 동안 또는 콜로니가 나타날 때까지, 인큐베이션하였다. 상기 스폿들에서 성장된 수막염균을 카나마이신(80㎍/mL)을 함유한 BHI 플레이트에 플레이팅하고, 밤새 인큐베이션하였다. 트랜스포존 돌연변이체를 미세적정 플레이트로 수집하고 6시간 동안 액체 BHI에서 성장시킨 후, 20% 글리세롤을 함유한 BHI 중에서 -80° C로 동결시켰다.

[0277] 닷 블랏(dot blot)으로 표면 TbpB의 존재에 대해 트랜스포존 돌연변이체를 선별하였다. 전체의 세포를 PBS 중 2% 포름알데하이드로 고정시키고, 니트로셀룰로스에 스폿팅하고, 5% 탈지유로 차단하고, 토끼 항-TbpB 항체와 함께 인큐베이션하였다. 표면 TbpB를 보이지 않은 돌연변이체는 하기에 의해 서열분석된다: RATE PCR(T.F.Ducey, Dyer D., Epicentre Forum 9,(2002)) 또는 스플린커렛 PCR(C.J. Potter, L.Luo, PLoS ONE 5,

e10168(Jan 1, 2010)). RATE PCR의 경우, 3 단계 PCR 반응을 위해 게놈 DNA를 단일 프라이머(inv1 또는 inv2)와 혼합하였는데, 상기 3단계는 1차 엄격한 어닐링 온도, 2차 낮은 어닐링 온도 및 3차 엄격한 어닐링 온도로 이루어진다. Kan F 또는 Kan R 프라이머로 수득한 생성물을 서열분석하였다. 스플린커렛 PCR의 경우, 게놈 DNA를 제한 효소들(BstY1, BglII, 또는 HindIII)로 별도로 소화시킴으로써, 스플린커렛 올리고뉴클레오타이드에 결찰될 수 있는 점성 말단을 생산한다. 수득한 생성물은 2개의 내포된 PCR가 TN5 삽입 및 스플린커렛 사이에서 유전자 서열을 증폭시키기 위해 사용된다. 상기 생성물은 또 다른 내포된 프라이머에 의한 서열분석에 사용된다. 전술한 접근법을 사용하여, 서열식별번호: 385로 명시된 SLAM 1을 인코딩하는 폴리뉴클레오타이드를 수득하였다.

[0278] 하기 플라스미드 구성체를 위해 제한 없는 클로닝을 이용하였다(F van den Ent, J. Lowe, Journal of Biochemical and Biophysical Methods (Jan 1, 2006)). 간단히, NMB0313 ORF를 카나마이신 카세트로 대체하기 위해, NMB0313을 함유하는 ~2500bp 단편과 NMB0313의 상류방향 및 하류 방향의 500bp를 F1(pUC19OmpU476RF) 및 R1(pUC19-OmpURev)을 사용하여 pUC19로 클로닝하였다. EZ: TN 트랜스포존 키트에서 유래된 KAN2를 프라이머 F2(F-RF-OmpUdKan) 및 R2(R-RF-OmpUdKan)을 사용하여 증폭시켰고, 수득한 메가프라이머를 사용하여 2차 RF 반응에서 NMB0313 ORF를 대체하였다. WT B16B6에서 스폿 전환을 위해 수득한 플라스미드를 사용하였다. 카나마이신(80㎍/mL)을 함유한 BHI 플레이트 상에서 녹아웃을 선택하고, NMB0313의 옆에 있는 프라이머를 사용하여 PCR에 의해 확인하였다.

[0279] NMB0313 유전자를 pGCC4의 PacI/FseI 부위로 클로닝함으로써 상보성 벡터 pSLAM를 구성하였는데(I.J. Mehr, C.D. Long, C.D. Serkin, H.S. Siefert, Genetics, 154, 523 (Feb 1,2000))(Gift from H.Siefert), 프라이머 F3(F-RF-pGOmpU) 및 R3(R-RF-pGOmpU)을 사용하였다. His 태그를 함유하는 인산화된 프라이머 F4(F-OmpU-HIS phos) 및 R4(R-OmpU-HIS phos)로 상기 전체의 벡터를 증폭시키고 상기 생성물을 결찰함으로써, 상기 신호 펩타이드 뒤에 HIS 태그를 삽입하였다. 녹아웃 및 트랜스포존 돌연변이체를 에리트로마이신(30 ㎍/mL) 플레이트 상에서 스폿 전환 및 선택에 의해 pSLAM으로 보완하였다. NMB0313의 삽입을 PCR에 의해 확인하였다. 1mM IPTG BHI 플레이트 상에 콜로니를 성장시킴으로서 발현을 유도하였고, 항-HIS 웨스턴으로 검증하였다.

[0280] 실시예 2 -제1 SLAM 폴리펩타이드(SLAM 1)의 정제

[0281] 도 1에 설명된 바와 같이, SLAM 폴리펩타이드를 정제하였다. NMB0313 및 그것의 동족체를 pET26으로 클로닝하였고, N-말단 pelB 신호 펩타이드에 이어서 절단불가능 7X His 태그로 발현시켰다. 상기 플라스미드는 E. 콜리 BL21-C43 세포로 전환시키고, 50 ㎍/mL 카나마이신으로 Luria-액체배지(LB)에서 37°C로 OD_{600}이 0.8이 될 때까지 성장시켰고, 이 시점에 이소프로필 β-D-1-티오갈락토피라노시드(IPTG)를 최종 농도가 1mM가 되도록 첨가하여 단백질 발현을 유도하였다. 추가의 18시간 동안 37°C에서 세포를 성장시켰고 4000 x g의 원심분리로 수확하였다. 상기 세포를 세정하고, 세포 5g당 세포용해 완충액 100mL(50mM 인산칼륨, pH 7.5 및 0.2mM PMSF)에 재현탁시켰다. 리소자임 및 DNase의 존재 하에, 얼음 위에서 30초 펄스 4개로 초음파처리에 의해, 세포 용해를 수행하였다. 미용해된 세포는 20분 동안 10,000 x g의 원심분리에 의해 제거하였다. 그러고 나서, 상기 용해물을 1시간 동안 95,834 x g으로 원심 분리하여 막 분획을 단리하였다. 상기 펠렛을 세정하여 용해된 세포 5g 당 50 mL의 추출 완충액(50mM 인산칼륨, pH 7.5 및 3% Elugent(밀리포어)에 재현탁시켰다. 밤새 4°C에서 추출을 수행하였다. 95,834 xg에서 40분 동안 원심분리를 한 후, 상기 가용화된 단백질을 0.45㎛ 필터에 통과시키고, 완충액 A(50mM 인산칼륨, 0.6% C_8E_4 (Affymetrix))로 평형을 이룬 1mL Ni-NTA 수지 칼럼(GE) 상에 장입하였다. 완충액 A를 완충액 B(50mM 인산칼륨, 0.6% C_8E_4, 400mM 이미다졸)와 혼합하여 이미다졸 구배를 만들었다. 상기 칼럼을 20mM, 60mM 및 80mM 이미다졸로 세정하고, 원하는 단백질을 260mM 이미다졸에서 용출하였다. SDS-PAGE에 의해 순도를 확인하고, 크기 배제 크로마토그래피에 의해 20mM HEPES, pH 8, 150mM NaCl, 0.6% C_8E_4에서 평형이 유지된 24 mL Superdex-200(GE)으로 추가 정제를 달성하였다. 5H3 NMB0313을 함유한 단일 피크를 Sephadex-200에서 수집하였고, 50kDa 농축기(밀리포어)를 사용하여 6 mg/mL로 농축시켰다. 결과는 도 2에 도시하였다.

[0282] 실시예 3 - SLAM 2를 비롯한 SLAM 폴리펩타이드를 인코딩하는 다른 폴리뉴클레오타이드

[0283] Blastp 탐색을 수행하였는데, SLAM1 단백질 서열(서열식별번호: 385)을 템플레이트로 사용하였다. 그러고 나서, 상기 결과물을 여과하여 동일한 유기체의 다중 균주에서 유래된 SLAM 타격을 제거하였고 최상부 타격을 유지시켰다. Geneious R7(생체물질, http: //www.geneious.com/)을 사용하여 다중 서열 정렬s 및 계통발생적 트리(이웃 결합) 구성을 수행하였다. 내재된 부트스트랩 모듈을 사용하여 상기 트리를 100회 반복 샘플링하였다. SLAM 적중물을 함유하는 게놈의 각각에서 fHBP, TbpB 및 LbpB 동족체를 탐색하여 상기 계통발생적 트리에

첨가하였다. 상기 계통발생적 트리를 도 3에 도시하였다. 도 3과 관련하여, SLAM 동족체(박테리아 게놈의 BLAST 탐색에 의해 확인됨)는 세 그룹으로 무리를 이루었다. 그룹 1(옅은 회색, 맨위)의 SLAM 동족체는 나이세리아 속 및 모락셀라 카타르할리스에 속하는 반면, 그룹 2(중간 회색, 중간)는 감마-프로테오박테리아의 파스튜렐라세아에 계열에서 유래된 상이한 구성원을 함유한다. 그룹 3(짙은 회색, 바닥)은 오로지 나이세리아 샤예가니를 함유한다. 상기 트리는 명료성을 위해 축약하였고; 단일 종에서 유래된 다중 적중물을 포함하지 않으며, 부트스트랩 값을 제거하였다. 게놈에 TbpB, LbpB, 또는 fHbp 동족체를 보유한 종은 각각 원, 정사각형 및 삼각형으로 표시하였다. 나이세리아 메닝자이티데스의 제2 SLAM 폴리펩타이드, SLAM 2의 폴리뉴클레오타이드 서열이 서열식별번호: 387처럼 본원에 제시되었다.

[0284] 실시예 4 -제2 SLAM 폴리펩타이드(SLAM2)의 정제

[0285] 나이세리아 메닝자이티데스의 제2 SLAM 폴리펩타이드(SLAM 2; 서열식별번호: 387)를 실시예 2에 추가로 기재된 바와 같은 방법을 사용하여 정제하였다. 도 4는 수득된 결과를 보여준다.

[0286] 실시예 5 -온전한 및 절단된 SLAM 1 폴리펩타이드를 사용한 표면 지질단백질 전좌

[0287] 나이세리아 메닌기티디스 SLAM 녹아웃 균주 Δmnb0313를 사용하여 표면 지질단백질(SLPs)의 전좌를 평가하였다. SLAM 폴리펩타이드의 전장 SLAM 폴리펩타이드 및 N-말단 및 C-말단부를 사용하였다. 상기 N-말단 및 C-말단부가 도 5 a에 도시되었다. 유세포측정(도 5b) 및 프로테이나제 K 소화(도 5c) 실험은 상기 SLAM 녹아웃 균주에서 관측된 SLP 전좌 결함이 오직 C-말단 β-배럴 도메인(아미노산 204~488)으로 구조될 수 있음을 드러낸다. SLAM의 N-말단 도메인(Ntd)(아미노산 32~203)은 임의의 SLP 전좌 활성을 제공하지 않는다. 각각의 샘플에 대한 평균 형광 강도를 측정하였고, 야생형 세포에서 수득된 세포를 녹아웃 및 단일 도메인 보체 세포에서 유래된 신호들과의 비교를 위해 100%로 설정하였다. 오차 막대는 세 가지 실험에서의 평균 표준 오차(SEM)를 나타낸다. A *는 $p<0.05$에서 유의미하게 상이한 결과를 가리킨다.

[0288] 실시예 6 -E. 콜리에서 SLAM 및 표면 지질단백질, TbpB, LbpB 및 fHbp의 공발현

[0289] 나이세리아 메닌기티디스 혈청형 B 균주 B16B6의 게놈에서 유래된 TbpB 및 NMB0313 유전자를 증폭시켰다. 나이세리아 메닌기티디스 혈청형 B 균주 MC58에서 유래된 LbpB 유전자를 증폭시켰다. 전장 TbpB를 제한 없는 클로닝을 사용하여 pETDuet의 다중 클로닝 부위 2에 삽입하였다((F van den Ent, J. Lowe, Journal of Biochemical and Biophysical Methods (Jan 1, 2006)).). NMB0313을 pET26에 삽입하였는데, 여기서 상기 원상태 신호 펩타이드는 pelB의 그것으로 대체하였다. 이들 벡터 상에서 부위-지향 돌연변이유발 및 제한 없는 클로닝을 사용하여 각각돌연변이 및 절단을 수행하였다. 벡터 쌍을 E. 콜리 C43으로 전환하고, 카나마이신(50 μg/mL) 및 암피실린(100 μg/mL)으로 보충된 LB 우무평판에서 밤새 성장시켰다.

[0290] M. 카타르할리스 균주 O35E 및 H. 인플루엔자 균주 86-028NP의 게놈에서 유래된 tbpB 유전자를 증폭시키고, 상기와 같이 제한 없는 클로닝에 의해 pET52b 플라스미드로 클로닝하였다. 제한 없는 클로닝을 사용하여 상응하는 SLAMs(M. 카타르할리스 SLAM 1, H. 인플루엔자 SLAM1)을 pET26b에 삽입하였다. 6His-태그를 상기와 같이 pelB 및 성숙한 SLAM 서열 사이에 삽입하였다. 상기와 같이, 벡터를 E. 콜리 C43으로 전환시켰다.

[0291] 4000g에서 원심분리에 의해 세포를 수확하고, 1mL PBS로 2회 세정하여 임의의 잔존하는 성장 배지를 제거하였다. 그러고 나서, 세포를 0.05~0.1 mg/mL 바이오티닐화된 인간 트랜스페린(Sigma-aldrich T3915-5MG), α-TbpB(M. 카타르할리스 및 H. 인플루엔자의 경우, 토끼 혈청에서 1: 200 희석; N. 메닌기티디스의 경우, 토끼 혈청에서 1: 10000 희석), 또는 α-LbpB(J.Lemieux에서 수득된 토끼 혈청에서 1: 10000 희석) 또는 a-fHbp(하기에서 수득된 마우스에서 1: 5000 희석: D. Granoff) 중 하나로 1.5시간 동안 4°C에서 인큐베이션하고, 이어서 PBS 1mL로 2회 세정하였다. 그러고 나서, 상기 세포를 25ug/mL의 R-파이코에리트린이 접합된 스트렙타비딘(0.5 mg/ml Cedarlane) 또는 R-파이코에리트린이 접합된 항-토끼 IgG(스톡 0.5 mg/ml Rockland)로 1.5시간 동안 4°C에서 인큐베이션하였다. 그런 다음, 상기 세포를 1 mL PBS로 세정하고 200uL 고정액(PBS + 2% 포름알데하이드)에 재현탁시키고 20분 동안 방치하였다. 마지막으로, 세포를 1mL PBS로 2회 세정하고, 5 mL 폴리스티렌 FACS 튜브로 전달하였다. Becton Dickinson FACSCalibur를 사용하여 PE 형광에 대하여 각각의 샘플의 PE 형광을 측정하였다. FLOWJO 소프트웨어를 사용하여 상기 결과를 분석하여 각각의 샘플에 대한 평균 형광 강도(MFI)로 제시하였다. N. 메닝티디스 실험의 경우, 모든 샘플을 야생형 형광 신호를 100%로 정규화함으로써 야생형 균주와 비교하였다. 오차 막대는 세 차례 실험을 통틀어 평균 표준 오차(SEM)를 나타낸다. GraphPad Prism 5 소프트웨어를 사용하여 통계적으로 분석된 결과를 플롯팅하였다. 도 6에 도시된 결과는 SLPs, TbpB(도 6a),LbpB(도 6b)및 fHbp(도 6C)에 대한 것으로, SLAM이 E. 콜리에서 세 가지 SLP 폴리펩타이드 모두의 전좌를 초래함을 입증

한다. 도 10에 나타난 결과는 M. 카타르할리스(도 10c)에서 유래된 TbpB의 E. 콜리 중 H. 인플루엔자(도 10d)에서의 전좌는 요구된 SLAM 단백질의 공-발현을 요구함을 입증한다(Slam은 나이세리아에서 지질화된 발병력 인자의 표면 출연(display)를 위해 요구되는 외막 단백질이다). Hooda Y, Lai CC, Judd A, Buckwalter CM, Shin HE, Gray-Owen SD, Moraes TF.Nat Microbiol.2016 Feb 29;1: 16009).

[0292] 실시예 7 -손상된 SLAM 유전자를 포함하는 나이세리아 균주의 발병력의 감소

[0293] 패혈증 모델링을 수행하였는데, 이는 하기에 기재된 것과 같았다: Gorringe A.R., Reddin, K.M., Voet P. and Poolman J.T. (Methods Mol. Med. 66, 241 (Jan 1, 2001)) and Johswich, K.O. 등 (Infect.Immun.80, 2346(Jul 1, 2012)). 8-주령 C57BL/6 마우스(Charles River Laboratories) 6마리의 집단에 복강내 주사를 통해 N. 메닌기티디스 균주 B16B6, B16B6 Δtbpb, 또는 B16B6 Δnmb0313(N=2 독립적인 실험)을 접종하였다. 접종물을 제조하기 위해, 감염용 균주를 GC 한천에서 밤새 성장시키고, 37° C에서 10mL의 뇌 심장 주입(BHI) 배지에서 교반하면서 재현탁한 후, 4시간 동안 성장시켰다. 배양물을 각각의 최종 500μl 접종물이 $1x10^6$ 콜로니 형성 단위 및 10 mg 인간 홀로-트랜스페린을 함유하도록 조정하였다. 감염 48시간 전부터 감염 48시간 후에 이르기까지 적어도 12시간마다 중량, 임상 증상 및 균혈증에서의 변화에 대해 마우스를 모니터링하였다. 하기 임상 증상의 중증도를 기반으로 0~2의 척도로 마우스를 채점하였다: 털 상태, 자세, 눈 및 코의 모습, 숨쉬기, 탈수, 설사, 정당한 이유 없는(unprovoked) 행동 및 정당한 이유가 있는(provoked) 행동.종점 기준에 도달한 동물을 인도적으로 안락사하였다. 동물 실험을 토론토 대학의 동물 윤리학 검토위원회(Animal Ethics Review Committee)에 준거하여 수행하였다.

[0294] 도 7은 수득된 결과를 보여준다. 도 7a는 파라포름알데하이드(PFA)로 고정시킨 또는 SDS로 용해시킨, 그리고 니트로셀룰로스 상에 스폿팅하여 및 α-TbpB 항체로 탐색된 N.men 세포로 이루어진 고상 결합 검정을 보여준다. ΔSLAM/tn5는 트랜스포존 삽입을 통해 수득된 SLAM이 결핍된 세포의 최초 균주를 지칭한다. ΔSLAM은 SLAM ORF를 카나마이신 저항 카세트로 대체함으로써 수득된 나이세리아 메닌기티디스에서 SLAM의 녹아웃을 기술한다. 도 7b는 Nm 세포가 SLAM이 결핍된(ΔSLAM) 것인 경우에만 TbpB, LbpB 및 fHbp의 열화를 보여주는 프로테이나제 K 소화 검정을 나타낸다. 개별 SLPs을 단독으로 그리고 SLAM과 함께 발현하는 Nm 세포를 프로테이나제 K로 인큐베이션하였고, 웨스턴 블랏를 사용하여 프로테아제 소화(-/+)가 있거나 없을 때 세 가지 SLPs의 수치의 수준을 검출하였다. 유세포측정을 사용하여 ΔSLAM 세포가 상기 세포 표면에 TbpB(도 7c) 또는 fHbp(도 7d)를 출연시킬 수 없음을 확인하였다. TbpB 및 fHbp에 대한 항체를 사용하여 표면 노출된 SLPs를 결합시키고 이어서파이코에리트린에 연결된 α-토끼 항체로 인큐베이션함으로써 형광을 제공하였다. BD FACS Calibur의 FL2 검출기를 사용하여 각각의 샘플의 평균 형광 강도(MFI)를 측정하였다. 녹아웃 세포에서 유래된 신호와 비교하기 위해, 야생형 세포에서 수득된 신호를 100%로 설정하였다. 오차 막대는 세 가지 실험에서의 평균 표준 오차(SEM)를 나타낸다. 도 7e에 다양한 균주로의 마우스 감염의 결과를 도시하였다. 복강내 주사를 통해 야생형 N. 메닌기티디스 균주 B16B6(TbpB(ΔtbpB)의 녹아웃이 있는 B16B6 또는 nmb0313 Δslam의 녹아웃이 있는 B16B6)의 1×10^6 CFU로 마우스를 감염시키고, 감염 48시간 전부터 감염 48시간 후에 이르기까지 12시간마다 생존 및 질환 증상에 대해 모니터링하고, 감염 3시간 후에 추가로 모니터링하였다. Mantel-Cox 로그 순위 시험(GraphPad Prism 5)에 의해 생존에서 통계적인 차이를 평가하였다(*$p<0.05$, n.s.는 유의미하지 않음을 뜻함). 이들 결과는 nmb0313 Δslam 균주의 녹아웃으로 감염된 마우스에서 감염 후 사망률에서의 주목할 만한 감소를 보여준다.

[0295] 실시예 8: 파스튜렐라 멀토시다에서 신규한 SLAM-의존적 표면 지질단백질의 식별

[0296] SLAM 동족체가 식별된 주어진 박테리아 종에 대한 게놈을 선택할 때, 완전하게 서열분석된 게놈을 함유한 게놈을 참조하는 것이 선호된다. 나이세리아에 밀접하게 관련된 종부터 좀 더 멀리 관련된 종에 이르기까지 반복적인 Blast 탐색을 사용하여 SLAM 동족체를 식별하였다. 이들 종에서 식별된 SLAM 동족체들 각각에 대해, 상응하는 게놈 기록(NCBI 게놈)을 사용하여 그것의 상응하는 기능성 주석과 함께 상류방향에 그리고 하류방향에 존재하는 유전자를 식별하였다(NCBI 단백질 데이터베이스, Ensembl 박테리아). 그 어떤 사례에서도, 콘티그의 시작점 또는 단부에 너무 가까워서 SLAM 유전자의 상류방향 또는 하류방향에 존재할 것으로 예상되는 유전자는 없었고, 따라서 이들 서열은 무시되었다.

[0297] 하기에 대해 이웃한 유전자를 분석하였다: 1) N-말단 리포 박스 모티프(LipoP, SignalP를 사용하여 예상됨), 및 2) 용질 결합 단백질, Tbp-유사(InterPro 서명: IPR 또는 IPR011250), 또는 pagP-베타 배럴(InterPro 서명: IPR011250) 접힌 부분(fold). 그들이 이들 요소를 함유한 경우, 우리는 잠재적인 SLAM-의존적 표면 지질단백질로서 인접한 유전자를 식별하였다.

[0298] 추정 SLAM(PM1515, 서열식별번호: 1087)을 검색물로서 나이세리아 SLAM을 사용하여 파스튜렐라 멀토시다에서 식별하였다. 상기 추정 SLAM(PM1515, 서열식별번호: 1087)은 미공지된 기능을 갖는 하기의 새로 예상된 지질단백질 유전자에 인접해있다: (PM1514, 서열식별번호: 1083)(도 11a). 상기 추정 SLAM은 N. 메닌기티디스 SLAM1에 32% 동일성을 나타내는 반면, 상기 SLP는 공지된 SLAM-의존적 나이세리아 SLPs에 어떤 서열 유사성도 보이지 않았다.

[0299] 상기 추정 SLAM(PM1515, 서열식별번호: 1087) 및 그것의 인접한 지질단백질(PM1514, 서열식별번호: 1083)을 이전에 기재된 바와 같이 pET26b 및 pET52b로 각각 클로닝하고, E. 콜리 C43으로 전환하여 카나마이신(50ug/ml) 및 암피실린(100ug/ml)으로 보충된 LB 한천 상에서 밤새 성장시켰다.

[0300] 세포를 오토-유도 배지에서 18시간 동안 37C에서 성장시키고, 그런 다음 수확하여 1mM MgCl2를 함유한 PBS로 2회 세정하고, α-Flag(1: 200, Sigma)로 1시간 동안 4C에서 표지하였다. 그러고 나서, 상기 세포를 1mM MgCl2를 함유한 PBS로 2회 세정하고, 그런 다음 R-PE 접합된 α-마우스 IgG(25ug/mL, Thermo Fisher Scientific)로 1시간 동안 4C에서 표지하였다. 염색 후, 세포를 2% 포름알데하이드에서 20분 동안 고정시키고, 1mM MgCl2를 함유한 PBS로 추가 세정하였다. Becton Dickinson FACSCalibur으로 유세포측정을 수행하고, FLOWJO 소프트웨어를 사용하여 상기 결과를 분석하였다. 적어도 세 가지 복제물을 사용하여 평균 형광 강도(MFI)를 계산하고, 이를 사용하여 추정 SLAM(PM1515)를 함유하거나 또는 이것이 부재한 균주에서 지질단백질의 표면 노출을 비교하여, 도 11c 및 도 11d에 도시하였다. PM1514는 E. 콜리의 표면에서 검출될 수 있는데, 이것은 하기를 서술한다: i) SLAM은 SLPs를 식별하기 위해 사용될 수 있고; 및 ii) SLAM은 상기 세포의 표면으로의 이들 SLPs의 전좌를 위해 요구된다 - 따라서 "SLAM-의존적 표면 지질단백질"이라 불리는 단백질의 부류를 식별할 수 있다. 정제된 PmSLP(PM1514)에 대항하여 항체를 육성하였고, 상기 단백질은 PK 셰이빙 검정을 통해 파스튜렐라 멀토시다의 표면 상에 존재함이 밝혀졌다.

[0301] 실시예 9: SLAM-의존적 표면 지질단백질의 전좌 모티프의 식별 및 SLAM 특이성에서의 역할.

[0302] 사용된 최소 도메인 및 도메인 스왑 구성체는 pETDUET HpuA(서열식별번호: 1099), TbpB N-엽(서열식별번호: 1095), TbpB C-엽(서열식별번호: 1097), 및 TbpB N-엽-HpuA(서열식별번호: 1101)이었다. 상기 성숙한 HpuA을 증폭시켜 TbpB의 신호 펩타이드를 갖는 프레임에 삽입하였고, 동시에 pETDUET TbpB에서의 TbpB 유전자의 나머지를 대체함으로써 제한 없는 클로닝을 사용하여 pETDUET HpuA를 형성하였다. 앵커 펩타이드(아미노산 1~40), TbpB(아미노산 41~331)의 N-엽 및 TbpB의 C-엽 (아미노산 332~579)을 N. 메닌기티디스 균주 B16B6 TbpB 구조(PDB ID 4QQ1)를 기반으로 분석하였다. 역 클로닝을 사용하여 N-엽 구성체를 클로닝하고, 템플레이트로 pETDUET TbpB를 사용하여 TbpB의 N 및 C 엽 사이에 정지 코돈을 삽입하였다. TbpB의 C-엽 구성체를 제한 없는 클로닝을 사용하여 클로닝하고, pETDUET TbpB N-엽에 TbpB N-엽을 삽입하는 동시에 대체하였다. 상기 C-엽을 앵커 펩타이드가 있는 프레임에 삽입하였다. 제한 없는 클로닝에 의해 pETDUET TbpB N-엽의 N-엽이 있는 프레임에 HpuA(아미노산 2-엔드)를 삽입함으로써 융합 구성체 pETDUET TbpB N-엽-HpuA을 클로닝하였다. 템플레이트로 pETDUET TbpB를 사용하여 FastCloning으로 Poly-Ala 돌연변이를 형성하였다. SLAM1 또는 SLAM2 중 하나를 함유한 벡터를 사용하였다.

[0303] 플라스미드 E. 콜리 C43(DE3) 세포로 전환하여 오토-유도 배지에서 18시간 동안 37C에서 성장시켰다. 세포를 수확하고, 1mM MgCl2를 함유한 PBS로 2회 세정하고, α-TbpB 항체(1: 200, 토끼 혈청) 또는 바이오티닐화된 인간 트랜스페린(0.05mg/ml, Sigma) 중 하나로 1시간 동안 4C에서 표지하였다. 그러고 나서, 상기 세포를 1mM MgCl2를 함유한 PBS로 2회 세정하고 그런 다음, R-FITC 접합된 α-토끼 IgG(25ug/ml, Thermo Fisher Scientific)로 1시간 동안 4C에서 표지하였다. 염색 후, 세포를 2% 포름알데하이드에서 20분 동안 고정시키고, 1mM MgCl2를 함유한 PBS로 추가 세정하였다. Becton Dickinson FACSCalibur으로 유세포측정을 수행하고, FLOWJO 소프트웨어를 사용하여 상기 결과를 분석하였다. 적어도 세 가지 복제물을 사용하여 평균 형광 강도를 계산하고, 이를 사용하여 상이한 균주 사이의 주어진 SLP의 표면 노출을 비교하였다. E. 콜리의 표면으로의 SLAM1 의존적 전좌를 위해 TbpB의 C-엽이 요구(도 12b)되는 것으로 보이는 반면, 상기 N-엽은 상당한 역할을 하는 것으로 보이지 않는다. 추가로, TbpB N-엽에 융합된 HpuA의 사용은 SLAM 의존성을 SLAM1에서 SLAM2로 이동시킨다(도 12c~e).

[0304] 상기 방법을 사용하여, 표면 지질단백질의 표면 출연(display)에서의 중요성에 대해 8개 베타-배럴 가닥 중 4개를 탐색하였다. N. 메닌기티디스 TbpB의 하기의 베타-배럴 가닥 2개의 돌연변이: 가닥 B30(서열식별번호: 1107) 및 B31(서열식별번호: 1109)는 TbpB의 표면 발현을 위해 요구되는 것으로 나타났다(도 13c 및 도 13d).

[0305] N. 메닌기티디스, N. 고노르호아에, M. 카타르할리스, H. 인플루엔자, 및 A. 플레우로뉴모니아에에서 유래된 TbpB의 C-엽, N. 메닌기티디스 및 N. 락타미카에서 유래된 LbpB 및 N. 메닌기티디스, N. 고노르호아에, 및 K.

데니트리피칸스에서 유래된 HpuA의 C-엽의 8-가닥 배럴 도메인의 마지막 2개의 가닥에서 다중 서열 정렬을 수행하였다. 도 13e에 나타낸 바와 같이, 가닥 B30은 보존된 [L/M]GGx[F/I/V] 서열을 갖는 것으로 나타났고, 가닥 B31은 보존된 ϕx[A/T/V]FG[A/G] 서열을 갖는 것으로 보인다.

[0306] 실시예 10: 악티노박테르 바우마니에서 신규한 SLAM-의존적 표면 지질단백질의 식별

[0307] A. 바우마니는 기회성 병원체이고, 중환자나 면역저하또는 기저 질환을 가진 환자에게서 질환을 유발시킨다(Camp, C. & Tatum, O.L.Lab.Med. 41, 649-657(2010)). A. 바우마니는 다양한 임상 징후 예컨대 폐렴, 패혈증 및 요로 감염을 일으킨다. 전투 지역 병원에서 연조직 감염을 일으키는 것으로 악명을 얻은 바 있다. 다중-약물 내성 A. 바우마니는 A. 바우마니가 병상에서 사용된 많은 항생제에 내성이 있기 때문에 치료하는 의사들에게 상당한 도전을 제기하고, 인간 건강을 위협한다(Camp, C. & Tatum, O.L.Lab.Med. 41, 649-657(2010)).

[0308] 하기의 최초 쿼리 서열로서 NmSLAM으로 반복적인 blast 탐색을 사용하여 A. 바우마니 중 유전자 클러스터에서 SLAM-유사 단백질(AbSLAM)을 식별하였다(도 14a): (서열식별번호: 1177 및 1178). 이와 같은 유전자 클러스터가 Antunes 등에 의해 초기에 발견되었으나, 철 수득에 관여되는 유전자를 탐색하면서, 상기 SLAM 유전자에 가설 단백질이라고 잘못된 주석을 달았었다(Antunes, L.C. S., Imperi, F., Towner, K.J. & Visca, P.Res.Microbiol. 162, 279-284(2011)). 상기 SLAM 유전자에 인접하여 미공지된 기능의 지질단백질을 인코딩하는 유전자(AbSLP)가 있다. 이와 같은 예측은 상기 단백질의 N-말단에 리포 박스 모티프(LVAC)의 존재에 의해 뒷받침된다.

[0309] 우리는 유세포측정을 사용하여 AbSLP가 E. 콜리에서 외인성으로 발현될 수 있고, AbSLAM와 공발현될 때에만 세포 표면에 자리잡음을 실증한 바 있다(도 14b). 더욱이, AbSLP의 구조는 X-선 결정학에 의해 해결하였다(도 14c). AbSLP는 8 역평행 β-가닥 및 C-말단 8 가닥 β-배럴로 이루어진 N-말단 β-핸들로 구성된다. 상기 구조는 AbSLP가 공지된 SLAM-의존적 SLPs(TbpB, LbpB, HpuA)(도 1b~c 및 도 2)의 구조와 높은 구조적 유사성을 갖는 헴(heme) 결합 단백질임을 보여준다. SLAM으로 AbSLP를 발현시킴으로써, E. 콜리에서의 AbSLP의 표면 출연(display)이 유발된다(도 14b). AbSLP에 대한 항체를 육성하였고, 이것은 AbSLP가 프로테이나제 K 셰이빙에 의해 A. 바우마니(LAC4)의 표면 상에 위치됨을 설명한다(도 14d).

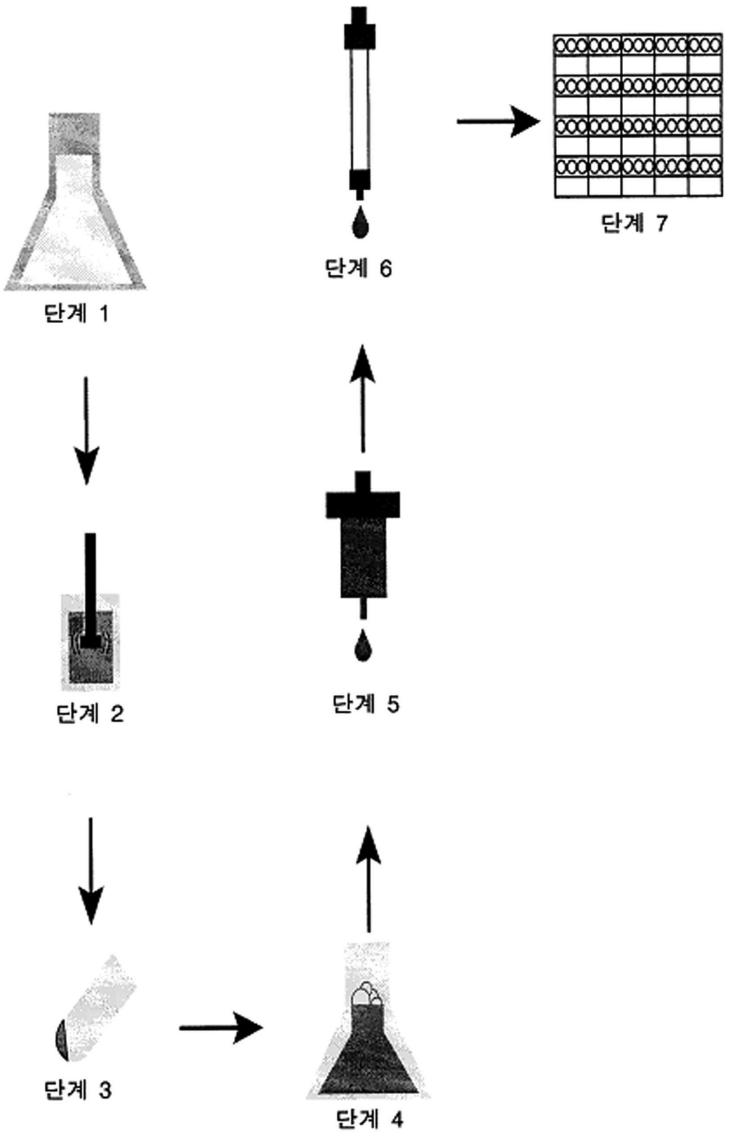
[0310] 인접한 SLAM 유전자의 존재에 의한 신규한 SLP AbSLP의 발견은 상기 SLAM 유전자에 인접하게 위치한 잠재적인 백신 항원 SLPs를 식별하기 위한 SLAM의 유용성을 기술한다.

[0311] 본 개시내용이 현재 바람직한 예라고 간주되는 것과 관련하여 기재되었으나, 본 개시내용이 개시된 실시예에 제한되지 않음이 이해되어야 한다. 반대로, 본 개시내용은 첨부된 청구항들의 사상 및 범위 내에 포함된 다양한 변형 및 동등한 장치들을 다루도록 의도된 것이다.

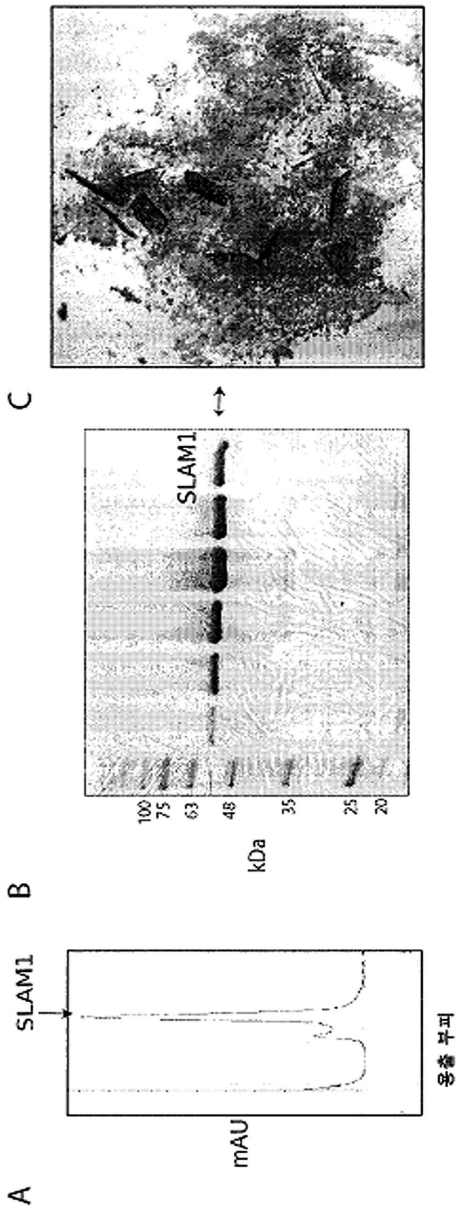
[0312] 모든 공보, 특허 및 특허 출원은 각각의 개별 공보, 특허 또는 특허 출원이 구체적으로 그리고 개별적으로 그 전문이 참고로 편입되었음이 시사된 것과 같이, 그 전문이 참고로 본원에 편입되었다.

도면

도면1



도면2



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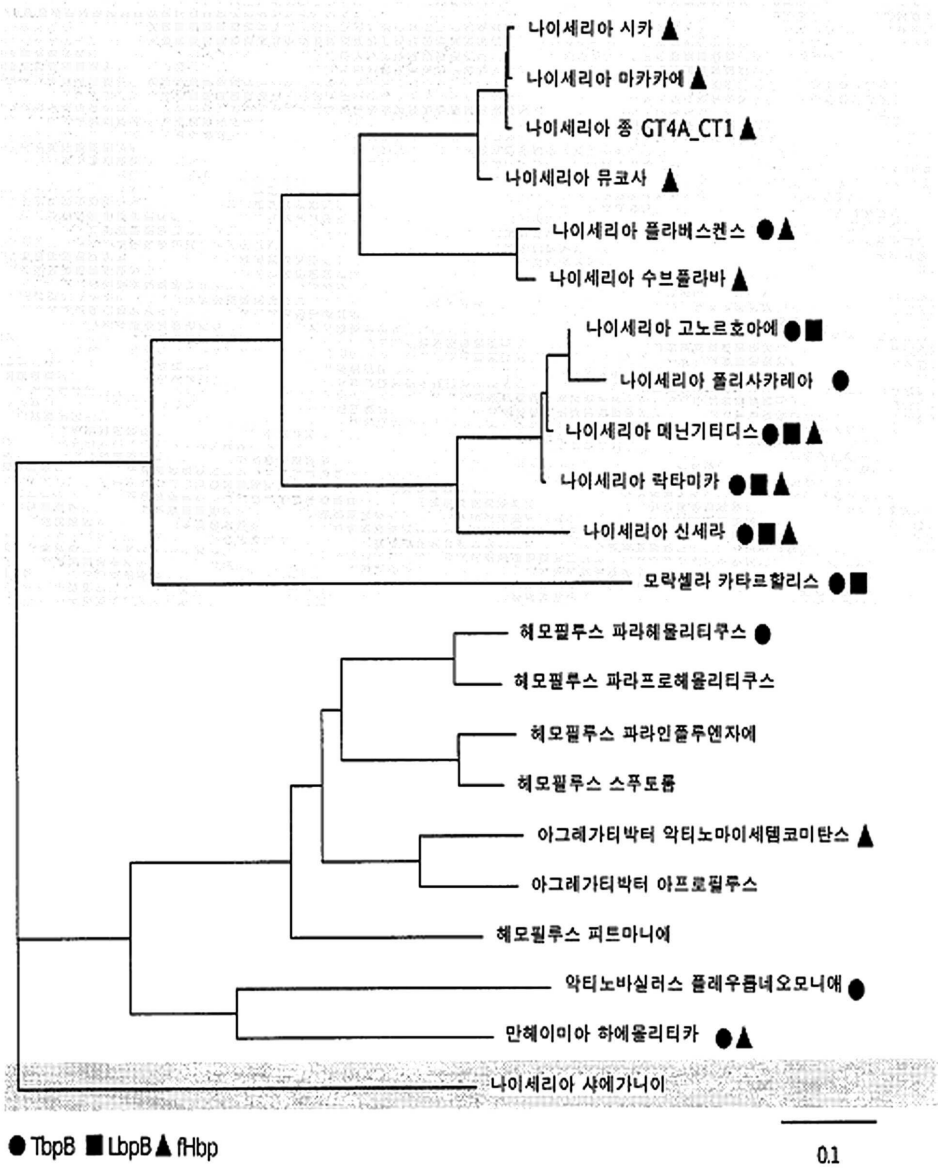
나이세리아 시카
나이세리아 마카카에
나이세리아 종 GT4A_CT1
나이세리아 뮤코사
나이세리아 플라버스켄스
나이세리아 수브플라바
나이세리아 고노르호아에
나이세리아 폴리사카레아
나이세리아 메닌기티디스
나이세리아 락타미카
나이세리아 신세락
모락셀라 카타르할리스
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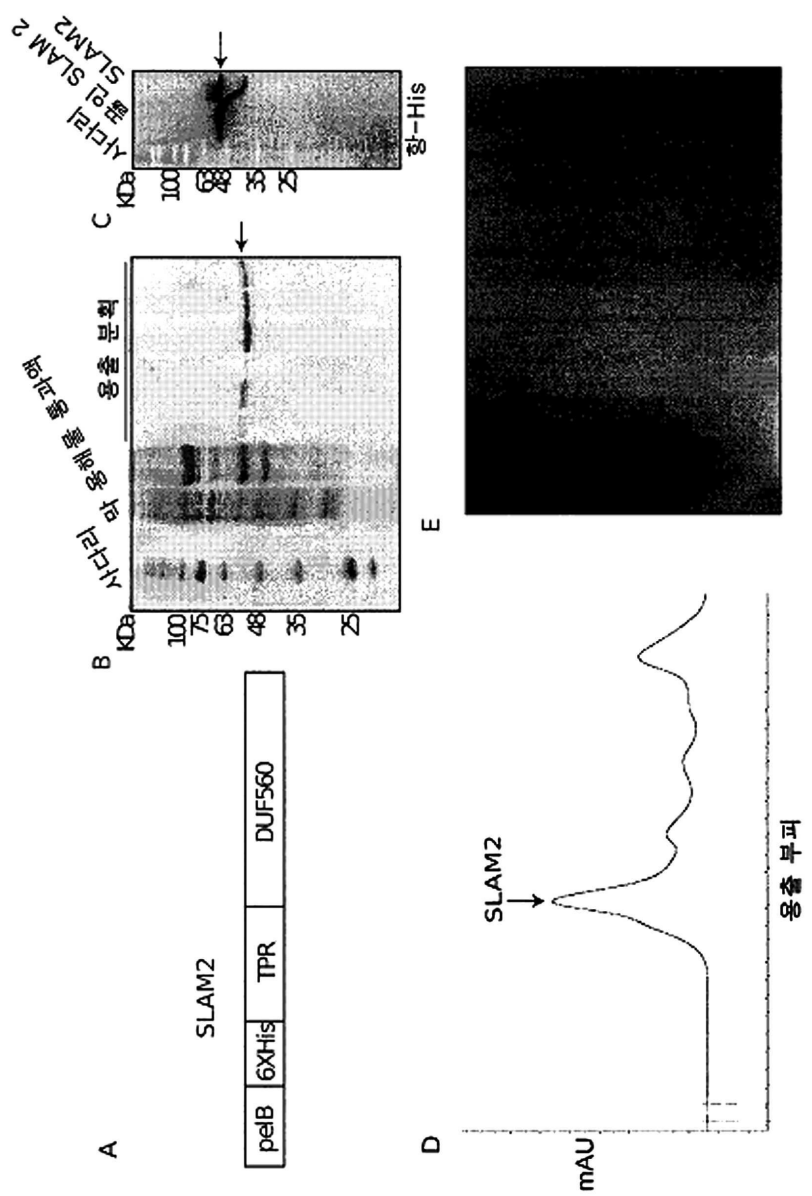
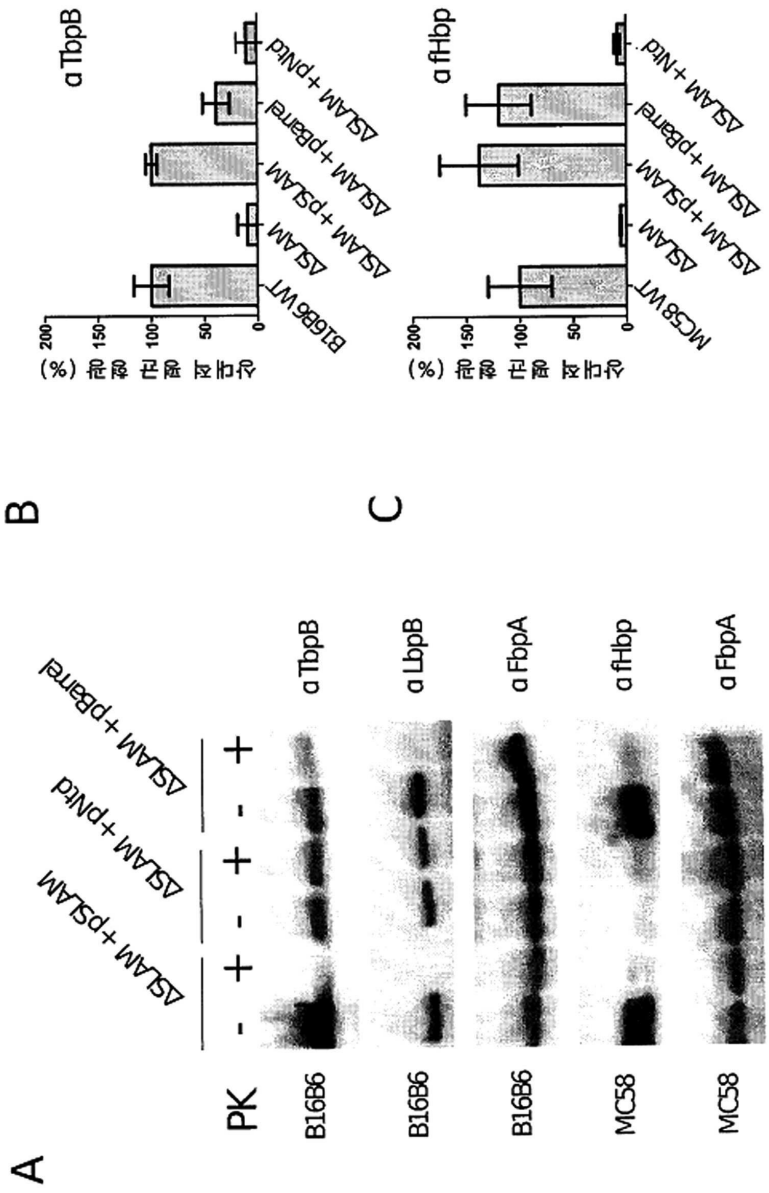
헤모필루스 파라프로헤몰리티쿠스
헤모필루스 파라인플루엔자에
헤모필루스 스푸토룸
아그레가티박터 악티노마이세템코미탄스
아그레가티박터 아프로필루스
헤모필루스 피르마니에
악티노바실러스 플레우룸네오모니애
만헤이미아 하에몰리티카
나이세리아 샤에가니이
TbpB LbpB fHbp
0.1

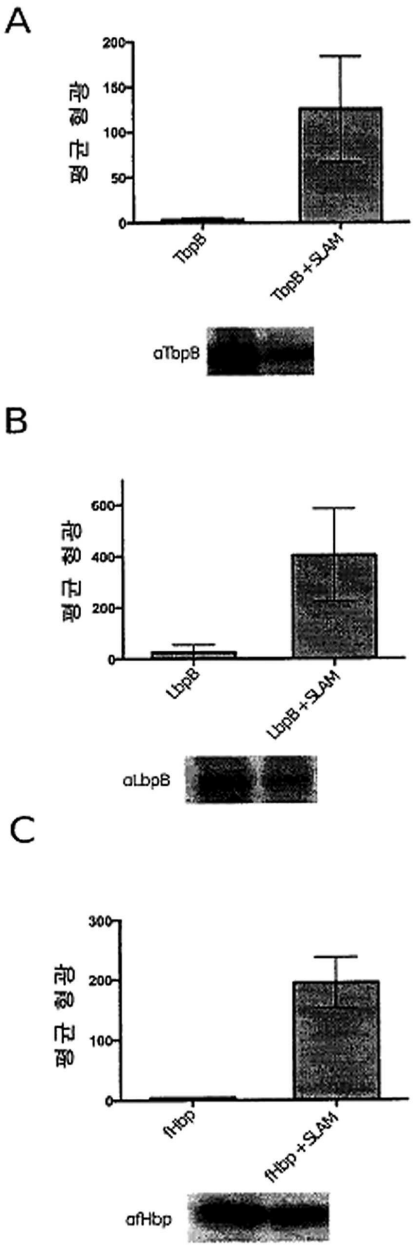
도면4


A
SLAM2
pelB
6XHis
TPR
DUF560
B
KDa
100
75
63
48
35
25
용출 분획
C
KDa
100
63
48
35
25
항-His
D
SLAM2
mAU
용출 부피
E

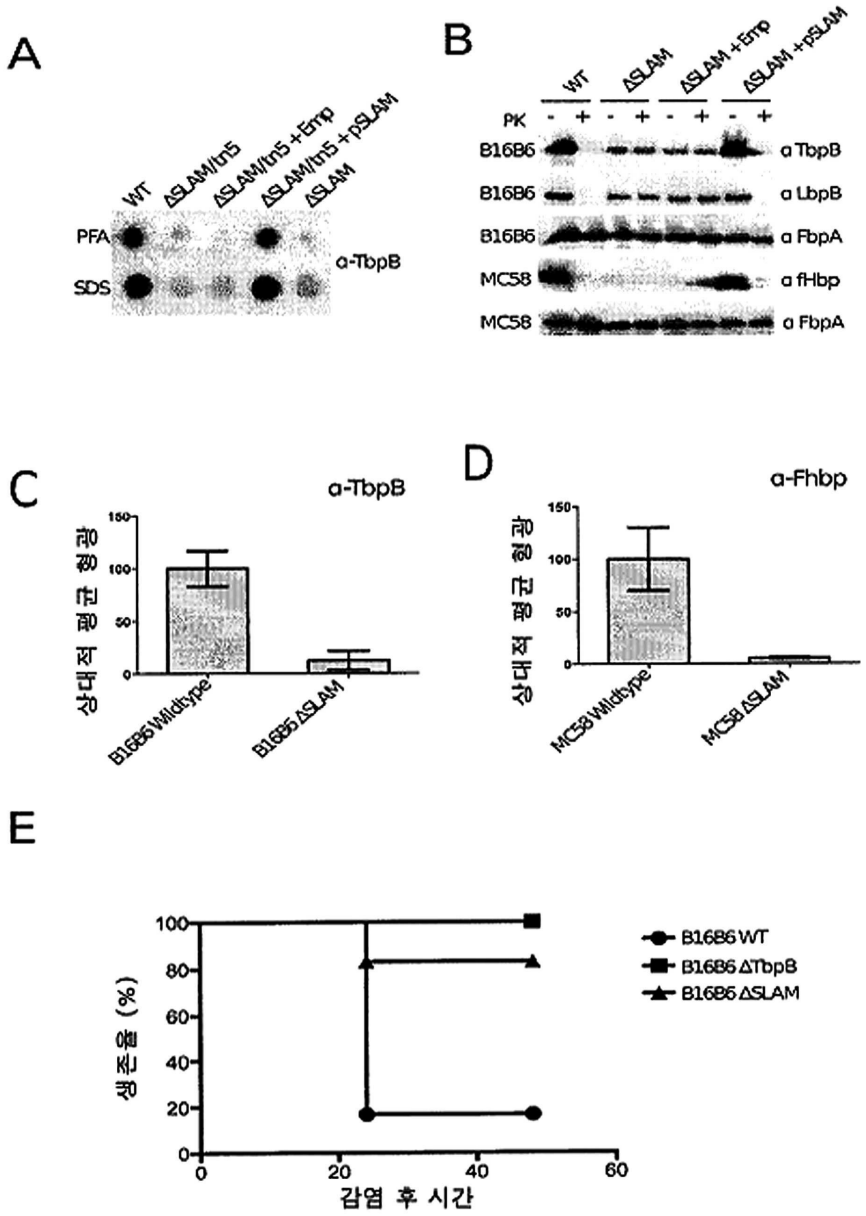
도면5


A
PK
B16B6
B16B6
B16B6
MC58
MC58
- + - + - +
ΔSLAM+pSLAM
ΔSLAM+pNid
ΔSLAM+pBenr
αTbpB
αLbpB
αFbpA
αfHbp
αFbpA
B
αTbpB
상대적 평균 형광 (%)
200
150
100
50
0
B16B6 WT
ΔSLAM
ΔSLAM+pSLAM
ΔSLAM+pBenr
ΔSLAM+pNid
C
αfHbp
상대적 평균 형광 (%)
200
150
100
50
0
MC58 WT
ΔSLAM
ΔSLAM+pSLAM
ΔSLAM+pBenr
ΔSLAM+Nid

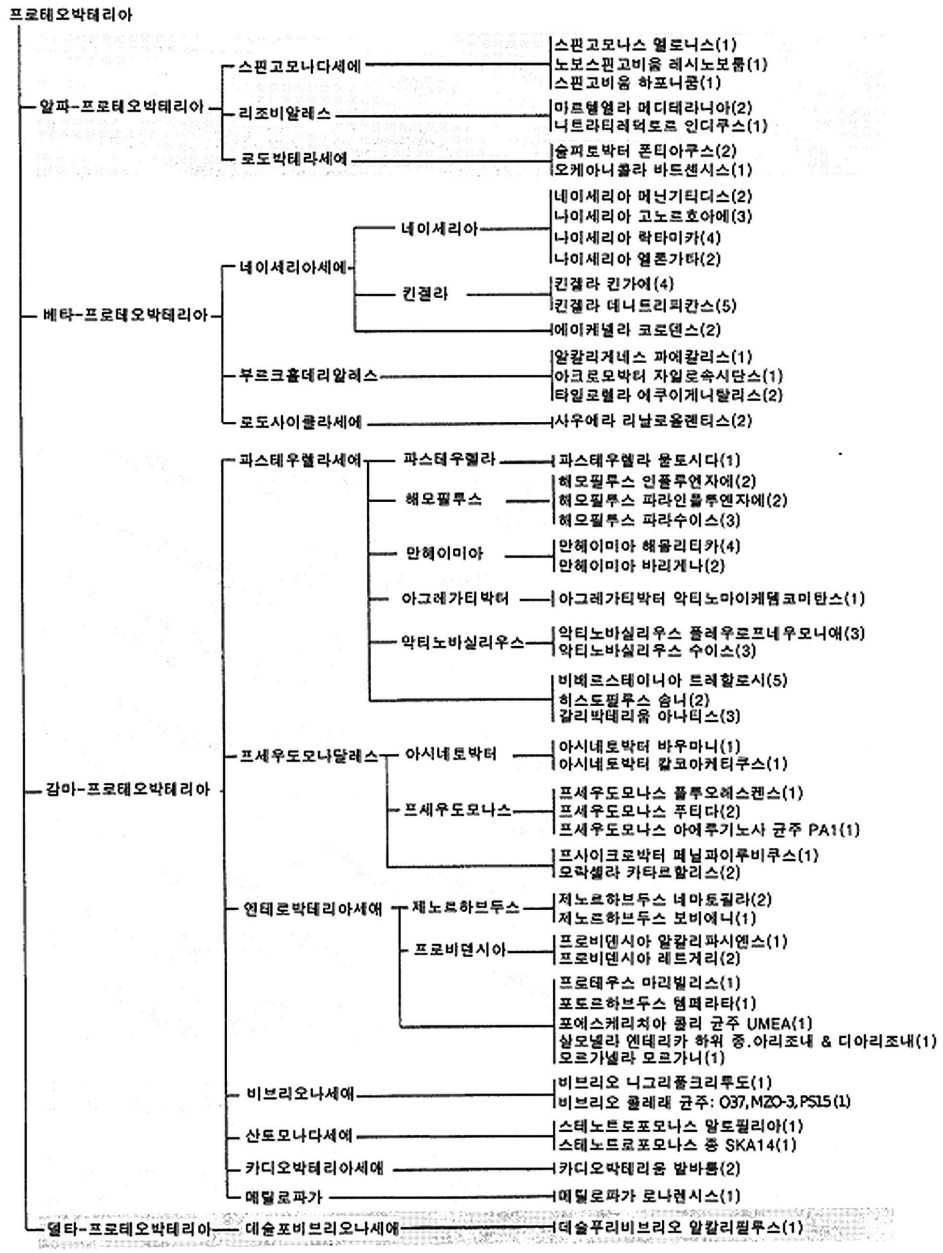
도면6


A
200
150
100
50
0
평균 형광
TbpB
TbpB+SLAM
αTbpB
B
600
400
200
0
평균 형광
LbpB
LbpB+SLAM
αLbpB
C
300
200
100
0
평균 형광
fHbp
fHbp+SLAM
αfHbp

도면7


A
WT
ΔSLAM/tn5
ΔSLAM/tn5 +Emp
ΔSLAM/tn5 +pSLAM
ΔSLAM
PFA
SDS
α-TbpB
B
WT
ΔSLAM
ΔSLAM +Emp
ΔSLAM +pSLAM
PK - + - + - + - +
B16B6
α TbpB
B16B6
α LbpB
B16B6
α FbpA
MC58
α fHbp
MC58
α FbpA
C
α-TbpB
상대적 평균 형광
150
100
50
0
B16B6 Wildtype
B16B6 ΔSLAM
D
α-Fhbp
상대적 평균 형광
150
100
50
0
MC58 Wildtype
MC58 ΔSLAM
E
생존율 (%)
100
80
60
40
20
0
0
20
40
60
감염 후 시간
B16B6 WT
B16B6 ΔTbpB
B16B6 ΔSLAM

도면8


프로테오박테리아
알파-프로테오박테리아
스핀고모나다세에
스핀고모나스 엘로니스(1)
노보스핀고비움 레시노보룸(1)
스핀고비움 하포니쿰(1)
리조비알레스
마르텔엘라 메디테라니아(2)
니트라티레덕토르 인디쿠스(1)
로도박테라세에
슬퍼로박터 폰티아쿠스(2)
오케아니콜라 바드센시스(1)
베타-프로테오박테리아
네이세리아세에
네이세리아
네이세리아 메닌기티디스(2)
나이세리아 고노르호아에(3)
나이세리아 락타미카(4)
나이세리아 엘존가타(2)
킨젤라
킨젤라 킨가에(4)
킨젤라 데니트리피칸스(5)
에이케넬라 코로덴스(2)
부르크홀데리알레스
알칼리게네스 파에칼리스(1)
아크로모박터 자일로속시단스(1)
타일로엘라 에쿠이게니탈리스(2)
로도사이클라세에
사우에라 리날로올렌티스(2)
감마-프로테오박테리아
파스테우렐라세에
파스테우렐라
파스테우렐라 물토시다(1)
헤모필루스
헤모필루스 인플루엔자에(2)
헤모필루스 파라인플루엔자에(2)
헤모필루스 파라수이스(3)
만헤이미아
만헤이미아 헤몰리티카(4)
만헤이미아 바리게나(2)
아그레가티박터
아그레가티박터 악티노마이케템코미탄스(1)
악티노바실리우스
악티노바실리우스 플레우로프네우모니애(3)
악티노바실리우스 수이스(3)
비베르스테이니아 트레할로시(5)
히스토필루스 솜니(2)
갈리박테리움 아나티스(3)
프세우도모나달레스
아시네토박터
아시네토박터 바우마니(1)
아시네토박터 칼코아케티쿠스(1)
프세우도모나스
프세우도모나스 플루오레스켄스(1)
프세우도모나스 푸티다(2)
프세우도모나스 아에루기노사 균주 PA1(1)
프시이크로박터 페닐파이루비쿠스(1)
오락셀라 카타르할리스(2)
엔테로박테리아세애
제노르하브두스
제노르하브두스 네마토필라(2)
제노르하브두스 보비에니(1)
프로비덴시아
프로비덴시아 알칼리파시엔스(1)
프로비덴시아 레트게리(2)
프로테우스 마리빌리스(1)
포토르하브두스 템페라타(1)
포에스케리치아 콜리 균주 UMEA(1)
살모넬라 엔테리카 하위 종.아리조내 & 디아리조내(1)
모르가넬라 모르가니(1)
비브리오나세애
비브리오 니그리풀크리투도(1)
비브리오 콜레래 균주: O37,MZO-3,PS15(1)
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스테노트로포모나스 말도필리아(1)
스테노드로포모나스 종 SKA14(1)
카디오박테리아세애
카디오박테리움 발바룸(2)
메틸로파가
메틸로파가 로나렌시스(1)
델타-프로테오박테리아
데술포비브리오나세애
데술푸리비브리오 알칼리필루스(1)

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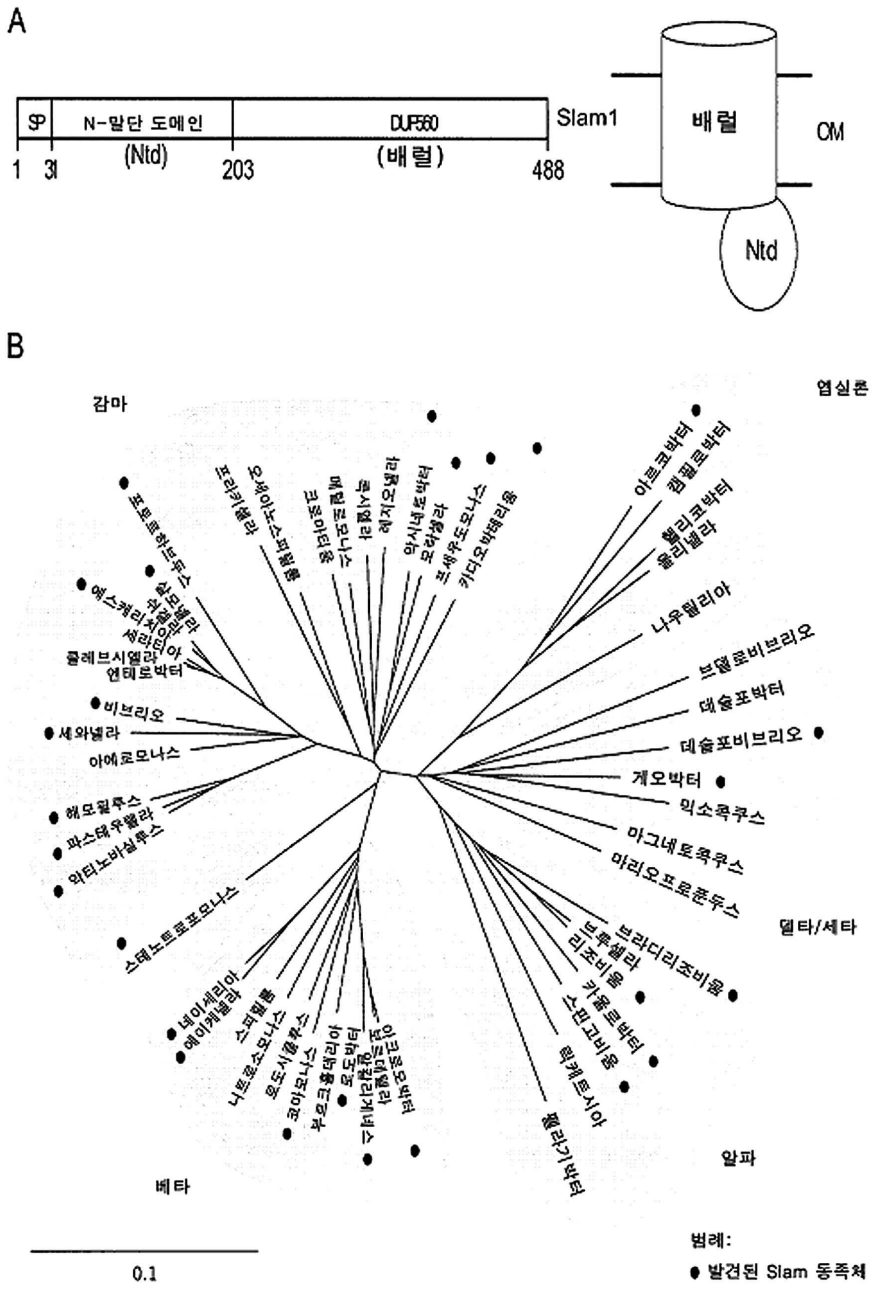
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SP
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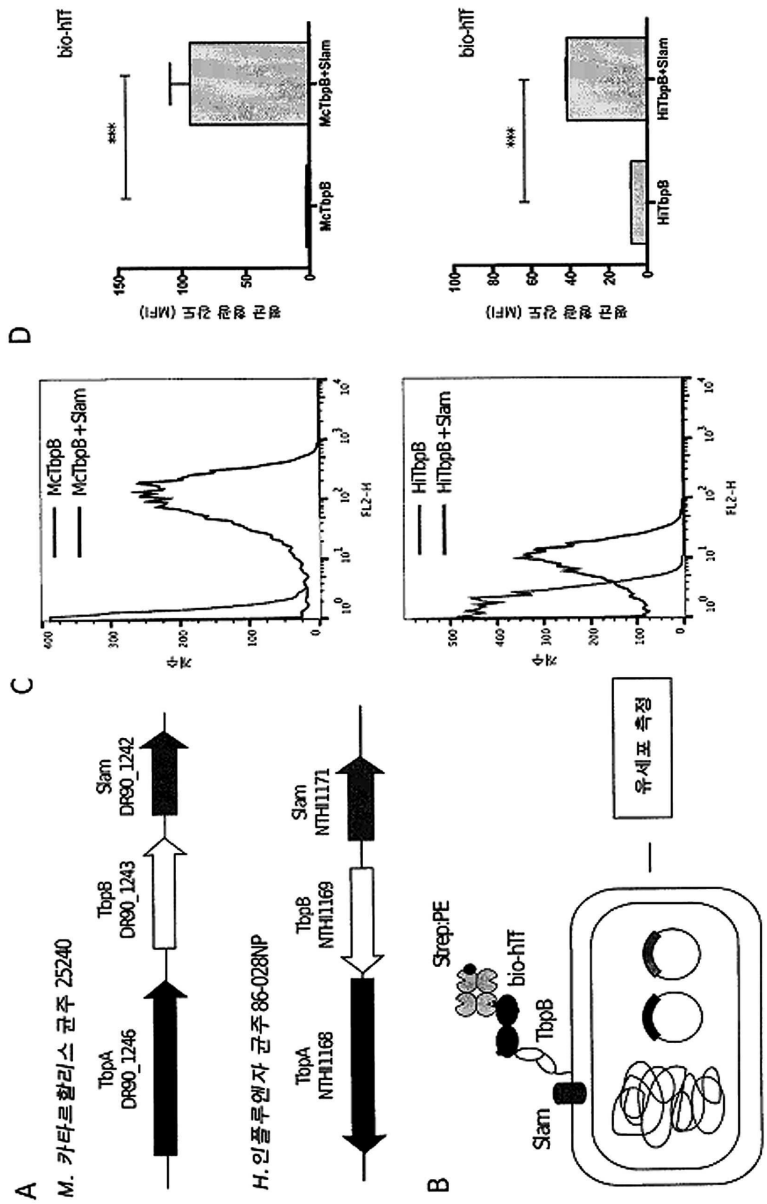
(Ntd)
DUF560
(배럴)
Slam1
1
31
203
488
배럴
OM
Ntd
B
감마
엡실론
베타
델타/세타
알파
0.1
범례:
발견된 Slam 동족체

도면10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Slam DR90_1242
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TbpA NTHI1168
TbpB NTHI1169
Slam NTHI1171
B
Strep:PE
bio-hTf
TbpB
Slam
유세포 측정
C
McTbpB
McTbpB+Slam
HiTbpB
HiTbpB+Slam
FL2-H
수치
D
bio-hTf
***
McTbpB
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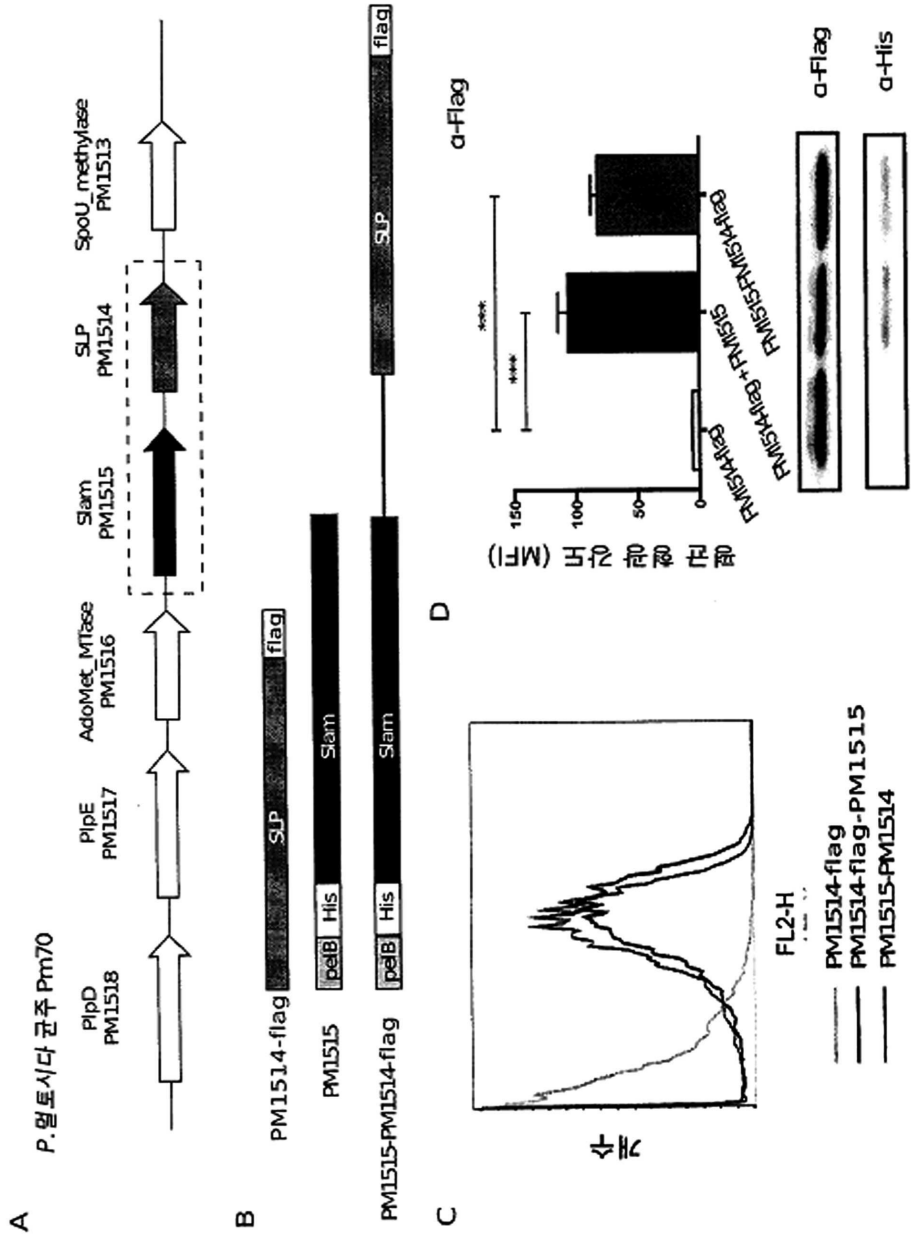
평균 형광 강도 (MFI)

도면11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Slam PM1515
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SpoU_methylase PM1513
B
PM1514-flag
SLP
flag
PM1515
pelB
His
Slam
PM1515-PM1514-flag
C
개수
FL2-H
PM1514-flag
PM1514-flag-PM1515
PM1515-PM1514
D
α-Flag
평균 형광 강도 (MFI)
150
100
50
0
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***
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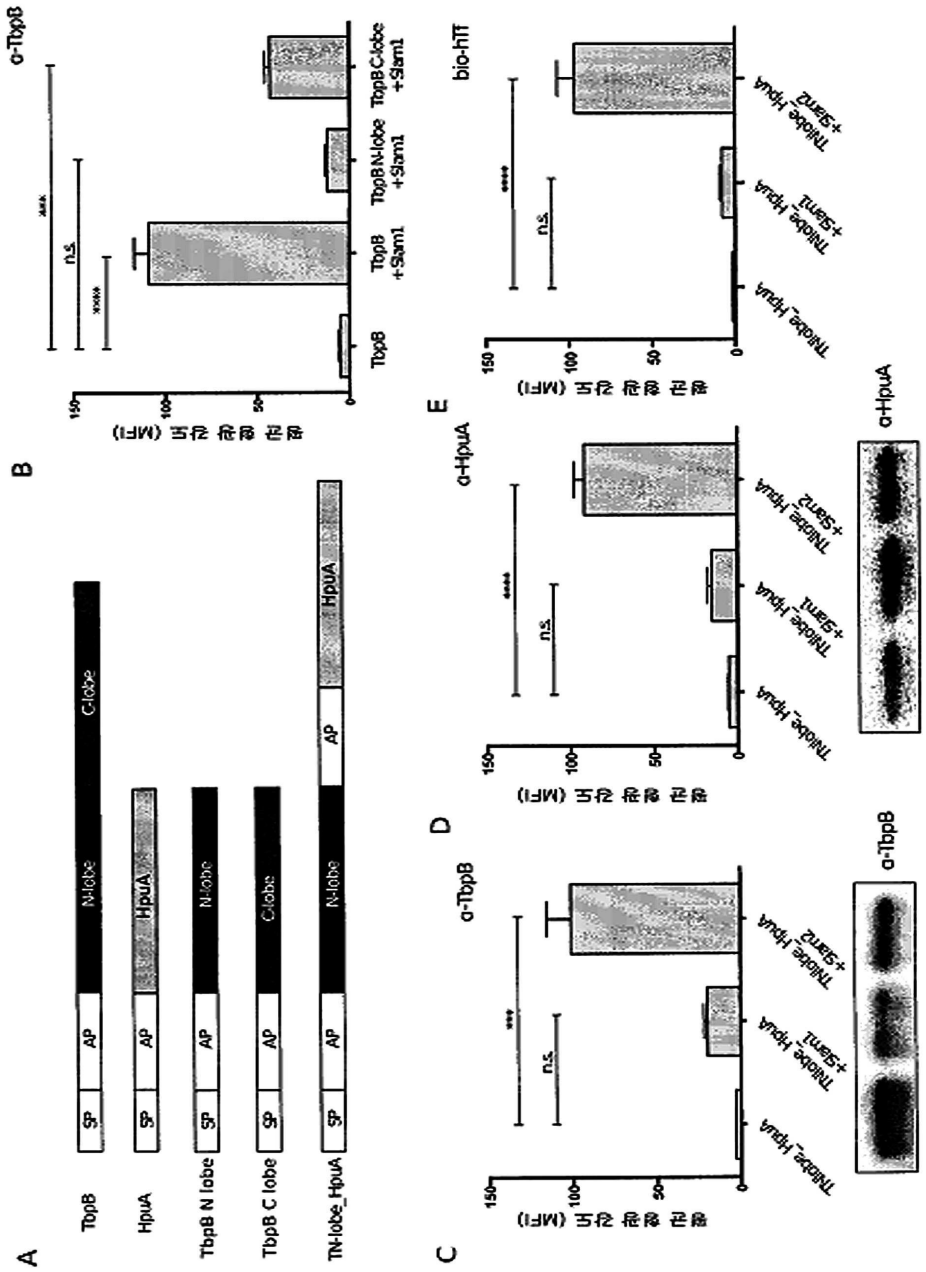
α-Flag
α-His

도면12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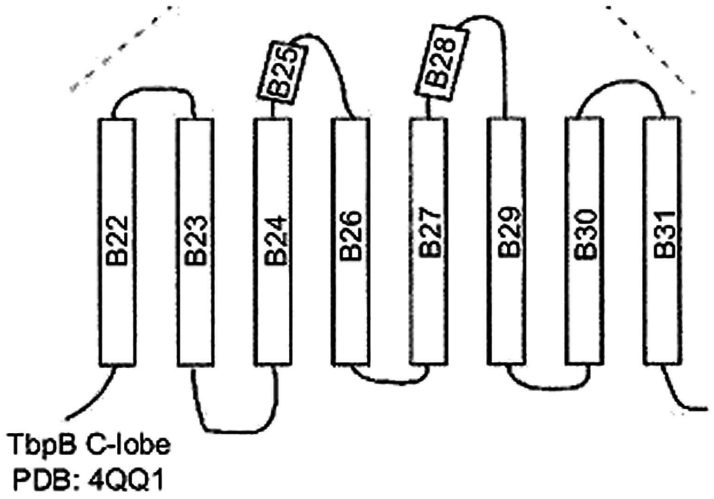
TbpB
HpuA
TbpB N lobe
TbpB C lobe
TN-lobe_HpuA
SP
AP
N-lobe
C-lobe
HpuA
B
α-TbpB
평균 형광 강도 (MFI)
TbpB
TbpB +Slam1
TbpB N-lobe +Slam1
TbpB C-lobe +Slam1
n.s
****
***
C
α-TbpB
TN-lobe_HpuA
TN-lobe_HpuA +Slam1
TN-lobe_HpuA +Slam2
D
α-HpuA
E
bio-hTf

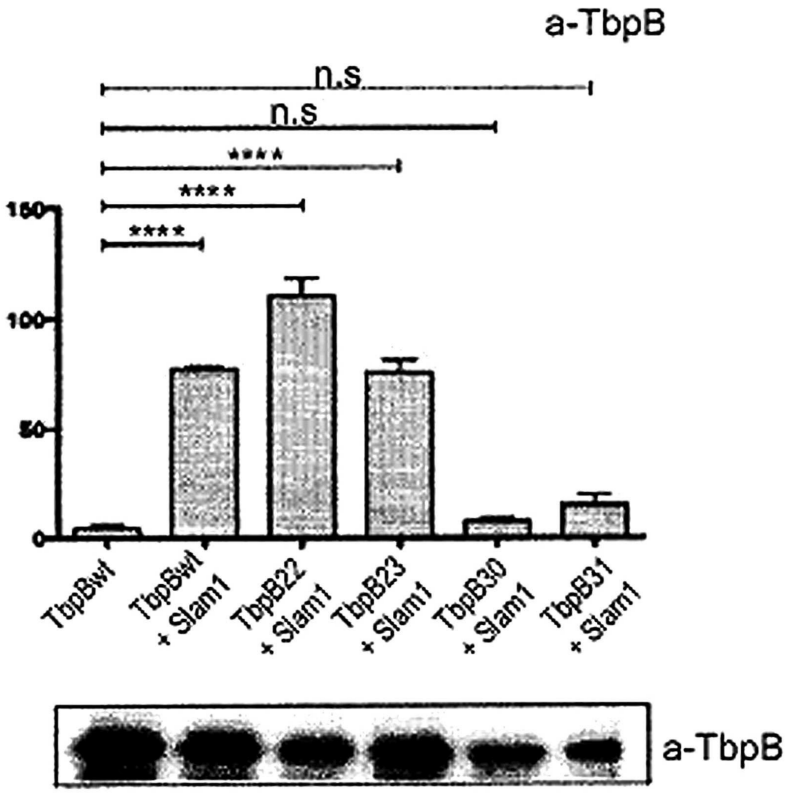
도면13a


핸들 도메인
6베타 가닥
가변형
배럴 도메인
8베타 가닥
보존형

도면13b


B22
B23
B24
B25
B26
B27
B28
B29
B30
B31
TbpB C-lobe
PDB: 4QQ1

도면13c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n.s
n.s
****
****
****
150
100
50
0
TbpBwt
TbpBwt + Slam1
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TbpB23 + Slam1
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a-TbpB

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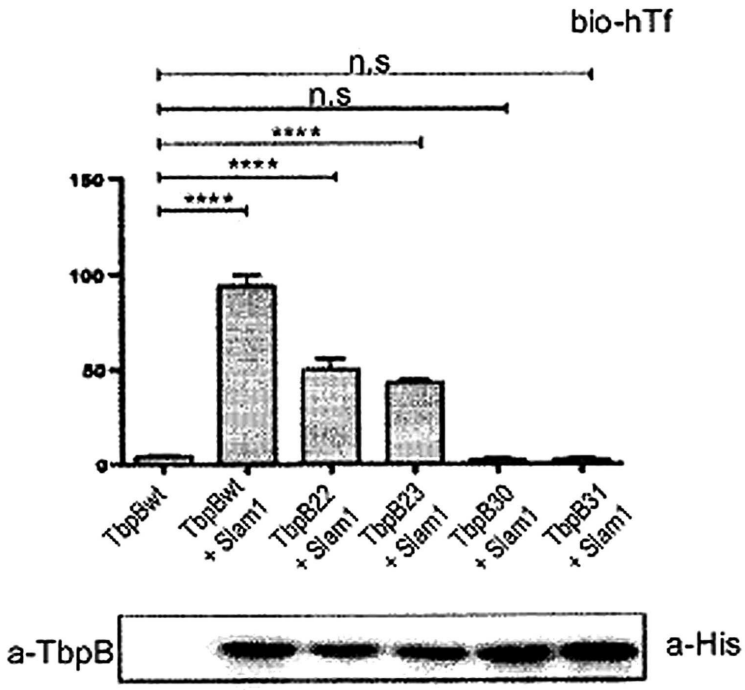

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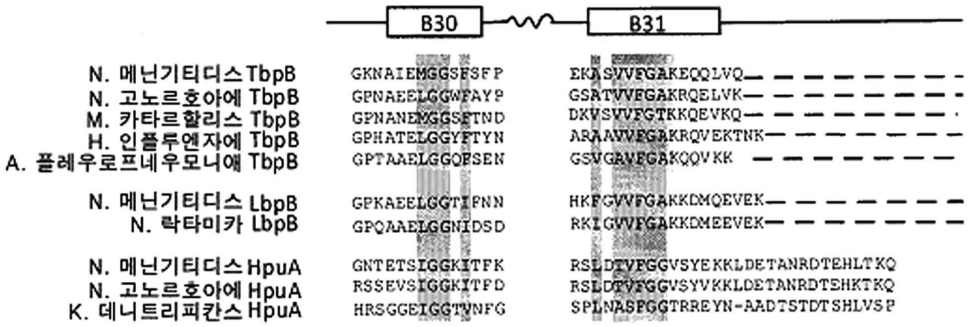

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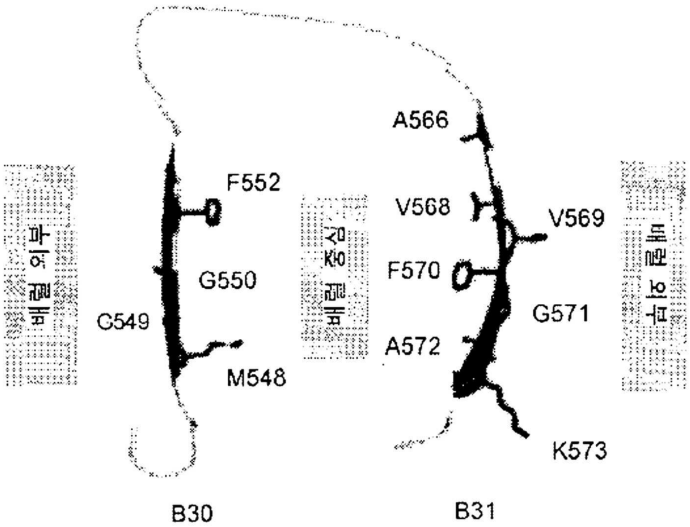

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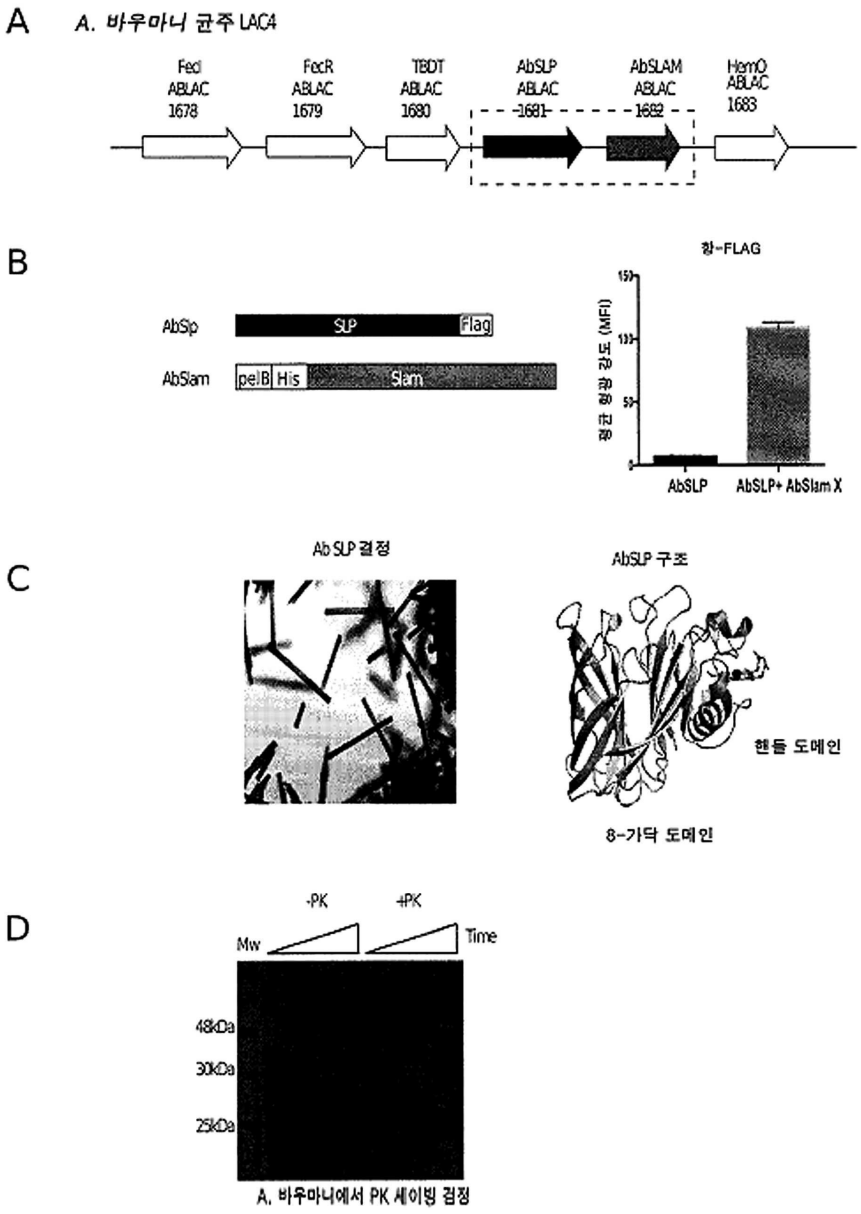

서 열 목 록

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<150> US 62/293,491

<151> 2016-02-10

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gatagcgata atgcctatca gcgtaaaaat cttcgtttgg gctgggtgca ggaatggccg 1200

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50 55 60

Lys Glu Glu Leu Ala Lys His Pro Asp Leu Ile Ile Arg Gly Leu Ile
65 70 75 80

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85 90 95

Leu Tyr Gln Asn Leu Pro Gln Gln Asp Pro Phe Leu Leu Ala Trp Ala
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Glu Ala Ile Ile Ala Thr Lys Gln Gly Asn Tyr Ser Arg Ala Val Gln
115 120 125

Glu Tyr Arg Thr Leu Phe Ala Gln Arg Pro Asp Ile Leu Gln Leu Arg
130 135 140

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Gly Lys Tyr Tyr Trp Asp Asn Lys Lys Tyr Asn Glu Phe Asn Ala Arg
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Ile Gly Ala Gly Leu Gly Tyr Gln Thr Ala Asn Thr Glu Val Val Leu
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Leu Pro Phe Thr Glu Arg Arg Trp Tyr Ser Gly Gly Ser Ser Gly Ser
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Asp Ala Met Lys Gln Phe Ser Lys Asn Ser Gly Val Arg Phe Glu Leu
305 310 315 320
Ser His Trp Phe His Lys Met Trp Gln Ile Ser Thr Ala Leu Glu Tyr
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Leu Gly Ile Ser Thr Arg Ile Ser Leu Ala Tyr Ala Arg Arg Thr Tyr
405 410 415
Asn Asn Ile Asp Phe Phe Ser Ile Arg Gln Lys Asn Asn Glu Tyr Gln
420 425 430

Ala Ala Leu Thr Val Trp His Arg Asn Leu Tyr Phe Leu Gly Ile Thr
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Pro Lys Leu Thr Trp Ser Tyr Gln Lys Asn Asp Ser Asn His Pro Phe
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tctattacca aaaaagaact ggcaaaacga ccggatttaa ttattcgcgg gttgattccg 240

gcggtgctgc agaataatac ggaagcggtg gaattgctgt tgccgttata ccaaaatctg 300

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cctctacgtt atcaattagc acacgtattg tttttaaata atgataacga agcggcaaaa 480

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35 40 45

Gln Val Glu Lys Thr Ala Asp Asn Lys His Ile Leu Ser Ile Thr Lys
50 55 60

Lys Glu Leu Ala Lys Arg Pro Asp Leu Ile Ile Arg Gly Leu Ile Pro
65 70 75 80

Ala Val Leu Gln Asn Asn Thr Glu Ala Val Glu Leu Leu Leu Pro Leu
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Tyr Gln Asn Leu Pro Gln Gln Asp Pro Phe Leu Leu Ala Trp Ala Glu
100 105 110

Ala Ile Ile Ala Thr Lys Gln Gly Asn Tyr Ser Arg Ala Val Gln Glu
115 120 125

Tyr Arg Thr Leu Phe Ala Gln Arg Pro Asp Ile Leu Pro Leu Arg Tyr
130 135 140

Gln Leu Ala His Val Leu Phe Leu Asn Asn Asp Asn Glu Ala Ala Lys
145 150 155 160

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

His Val Ile Asp Gln Tyr Leu Thr Ala Ile Asn Gln Arg Asp Gln Trp
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Arg Ile Ser Gly Gly Ile Ser Phe Leu Asn Glu Ser Asn Val Asn Asn
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Ala Pro Lys Ala Gly Thr Arg Ile Gly Gly Trp Gln Ala Trp Gln Arg
210 215 220

Glu Ser Ala His Gly Leu Ser Tyr Tyr Leu Gly Ser Glu Lys Lys Trp

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Ser Leu Pro Lys Asn Ile Phe Ala Lys Phe Ile Trp Asp Gly Gln Gly

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Lys Tyr Tyr Trp Asp Asn Lys Lys Tyr Asn Glu Phe Asn Ala Arg Val

260 265 270

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

275 280 285

Pro Phe Thr Glu Arg Arg Trp Tyr Ser Gly Gly Ser Ser Gly Ser Asp

290 295 300

Ala Met Lys Gln Phe Ser Lys Asn Ser Gly Val Arg Phe Glu Leu Ser

305 310 315 320

Tyr Trp Phe His Lys Met Trp Gln Ile Ser Thr Ala Leu Glu Tyr Gly

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Glu Gln Arg Tyr Val Lys Arg Lys His Leu Asn Gly Asn Asn Tyr Leu

340 345 350

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

355 360 365

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

370 375 380

Tyr Gln Arg Lys Asn Leu Arg Leu Gly Trp Val Gln Glu Trp Pro Leu

385 390 395 400

Gly Ile Ser Thr Arg Ile Ser Leu Ala Tyr Ala Arg Arg Thr Tyr Asn

405 410 415

Asn Ile Asp Phe Phe Ser Ile Arg Gln Lys Asn Asn Glu Tyr Gln Ala

420 425 430

Gly Leu Thr Val Trp His Arg Asn Leu Tyr Phe Leu Gly Ile Thr Pro

435 440 445

Lys Leu Thr Trp Ser Tyr Gln Lys Asn Asp Ser Asn His Pro Phe Tyr

450 455 460

Arg Tyr Asp Lys Asn Arg Ile Tyr Leu Glu Met Ser Lys Thr Phe

465 470 475

<210> 5

<211> 1491

<212> DNA

<213> A. baummannii SLAM 1

<400> 5

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caattacaac aacaaggcac cattcgtgac accgagaaac tgcccagtat ccgtattaat 180

ggccaaattt acgcggtaga acaaaatccg gatgatctgg ccaaagcgct atatctggcg 240

gtcatgcaaa agcaatgggg caatgctgcg atttacttaa aacactatca gcagtatcaa 300

ggctatgatc aggctttaac cgattttgcc gaagcggcct tggcgcgcgc tcagggaaag 360

ctcaaattag ccgaacaaaa atttcaaagc agtcttaatc aacaacccaa taatctgatt 420

tgtgaactcg agttagcgcg cgtgctgttt gaacagcaga agaataaaca agcagcacgc 480

ctttttacat cgattcagga caagctaggg cagagcaatg gtgcaatgat cccaccagaa 540

gtgcaacaaa cgattgatct gttcgtcaaa gcacttgatc agcgagattc gtggcaaggc 600

agtgtcgcaa ttggcccatc ctatgccaca aatctgaata gttcttcgga acaaagcaaa 660

acatggacgt tgtatggcat tgatgacaag ggcaaggcga ctccaattca ggaaattacc 720

cgcggcagcc ccaaagcagc atcagcaaca gggattgact atgaggccag tctaatcaag 780

cgcttttcgc tttcgggcaa tcatggcatt tccttacgcg gtttagcatt tgggcaatcc 840

tatgctgatc atgcgctcta taacgaatcc accctgaata tcaatgcagg ctatagtttt 900

tttgatttaa aaaatcaaat caccattgca ccgctatttg agcacaaacg ttatgccaat 960

gatggtttat acaatgcatg gggggcacgt actgaatgga tgcgatttct agcaccagac 1020

aaagccttca agcttgaagc tgaaatcaag gatctggact atcaaaagta taaaaacctа 1080

gatggtaaag aaagctcggc aatgtttaca ttctggaaaa ttctaccgca gcaatggaca 1140

ctttttagcg gactggatgt actggatcat gacacccagg aaaaatatat ggcggcttat 1200

cagcaacaag gcatccgtct aggactgagc aaatcctgga aagcaggttt gaataccacg 1260

ctattaacct cataccgctg gcggcagttt gaccgctacg tcgagacctt tgctgcacgt 1320

cgccatgatt ttgaacagaa ctataccctg gttgtacaaa tgccacggtt taagttttat 1380

ggtatgacgc cgaatttgac ctatcgctac aaccataatg acagtaatgt cgactggctc 1440

tattcctacg ataaacacaa tatcagctta aagctggaac atcgttttta g 1491

<210> 6

<211> 496

<212> PRT

<213> A. baummannii SLAM 1

<400> 6

Met Lys Lys Thr Leu Leu Cys Cys Val Ile Leu Leu Ala Ala Ser Ser
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Leu Tyr Ala Asp Asp Glu Thr Gln Leu Arg Leu Asn Gln Ser Leu Asp
20 25 30

Gln Asn Leu Phe Gln Gln Gln His Gln Leu Gln Gln Gln Gly Thr Ile
35 40 45

Arg Asp Thr Glu Lys Leu Pro Ser Ile Arg Ile Asn Gly Gln Ile Tyr
50 55 60

Ala Val Glu Gln Asn Pro Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Gly Asn Ala Ala Ile Tyr Leu Lys His Tyr
85 90 95

Gln Gln Tyr Gln Gly Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Ala
100 105 110

Ala Leu Ala Arg Ala Gln Gly Lys Leu Lys Leu Ala Glu Gln Lys Phe
115 120 125

Gln Ser Ser Leu Asn Gln Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu
130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Gln Ala Ala Arg
145 150 155 160

Leu Phe Thr Ser Ile Gln Asp Lys Leu Gly Gln Ser Asn Gly Ala Met
165 170 175

Ile Pro Pro Glu Val Gln Gln Thr Ile Asp Leu Phe Val Lys Ala Leu
180 185 190

Asp Gln Arg Asp Ser Trp Gln Gly Ser Val Ala Ile Gly Pro Ser Tyr
195 200 205

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

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

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

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

450 455 460

Asn Leu Thr Tyr Arg Tyr Asn His Asn Asp Ser Asn Val Asp Trp Leu
465 470 475 480
Tyr Ser Tyr Asp Lys His Asn Ile Ser Leu Lys Leu Glu His Arg Phe
485 490 495

<210> 7

<211> 1491

<212> DNA

<213> A. baylyi SLAM 1

<400> 7

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cagtttcacg agcagggaac cattcgtagt accgagcaat taccaaaact tcaaattaat 180

ggacaagaat acagtattga acaaaaccag aatgatcttg ccaaggcgtt atatttggca 240

gtcatgcaaa aacagtggct caaagccacg gtttatttag aacattataa gaaatatgtt 300

ggctacgatc gggctttaac cgactttgcc gaaggggcag ttgcacgttc tcagggtcaa 360

ctgaaattgg ctgaacaaaa atttcaaagc agcctaaaac aacaacctca taatttaatt 420

tgtgaacttg agttagcgcg cgtgctgttt gaacaacaga aaaataagga agcagcacgc 480

ctttttattt ccattcaaga tcaacttaaa caaagtgacc ctgcggtaat cccgtctgga 540

gttttaacca cagtgaatac ttttgttcag gcattaaaag aacgagactc ttggcaaggc 600

tcggtttcag cgggttatac ctatgtcagt aatttaaata gttcttctga acagagtaaa 660

acatggacgc tttatggcaa agatagtaac ggtaatatta tcccaattga gcaagttacc 720

cgtgggacgc ctaaagctga atcggcaacg ggtttagatt acgaagccag tcttataaaa 780

cgctatgcga ttaaggggca tcatggcgtg gctttacgtg cgctggcgtt tggacagtcc 840

tataacgacc acgcggcatt taatgaatct accgttaaca ttaatgctgg ctacagctac 900

tttgacttaa aaaatcaaat tggggtgagt ccgctttttg aacataaacg ttatggcaat 960

gatggccttt acaatgcgtg gggcgcgcgt gccgagtgga tgcattttat ctcagcagat 1020

aaagccttca agcttgaagc tgagagtaaa gatttaaatt atcagaaata taaaacccta 1080

gatggggtag aaagttcagc ttttgttact ttctggaaaa tcctcccaaa tcagtggacc 1140

gtttttagtg gtttagacgt agtcgaccat tcgacccaag aaaaatatat ggctgcatac 1200

cagcagcaag gtgtgcggtt gggcttaagc aaatcttgga gcacaggatt taataccact 1260

ttgctgagtt cttatcgttg gcgtatgttt gataaatatg cagaaacttt cttagctcgt 1320

cgtcatgatt ttgaacagaa ctataccttt gtcgtgcaaa tgccgcgctt tgagttttat 1380

ggcatgacgc ctaatttaac ctatcgctat aaccataata aaagcaatgt cgattggctc 1440

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<210> 8

<211> 496

<212> PRT

<213> A. baylyi SLAM 1

<400> 8

Met Lys Arg Thr Leu Leu Cys Cys Leu Thr Leu Leu Ser Cys Pro Phe
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Leu Tyr Ala Asp Glu Asp Thr Gln Leu Arg Leu Asn Gln Ser Leu Asp
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Gln Thr Leu Leu Gln Glu Gln Arg Gln Phe His Glu Gln Gly Thr Ile
35 40 45

Arg Ser Thr Glu Gln Leu Pro Lys Leu Gln Ile Asn Gly Gln Glu Tyr
50 55 60

Ser Ile Glu Gln Asn Gln Asn Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Leu Lys Ala Thr Val Tyr Leu Glu His Tyr
85 90 95

Lys Lys Tyr Val Gly Tyr Asp Arg Ala Leu Thr Asp Phe Ala Glu Gly
100 105 110

Ala Val Ala Arg Ser Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe
115 120 125

Gln Ser Ser Leu Lys Gln Gln Pro His Asn Leu Ile Cys Glu Leu Glu
130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Glu Ala Ala Arg
145 150 155 160

Leu Phe Ile Ser Ile Gln Asp Gln Leu Lys Gln Ser Asp Pro Ala Val
165 170 175

Ile Pro Ser Gly Val Leu Thr Thr Val Asn Thr Phe Val Gln Ala Leu
180 185 190

Lys Glu Arg Asp Ser Trp Gln Gly Ser Val Ser Ala Gly Tyr Thr Tyr
195 200 205

Val Ser Asn Leu Asn Ser Ser Ser Glu Gln Ser Lys Thr Trp Thr Leu
210 215 220

Tyr Gly Lys Asp Ser Asn Gly Asn Ile Ile Pro Ile Glu Gln Val Thr
225 230 235 240

Arg Gly Thr Pro Lys Ala Glu Ser Ala Thr Gly Leu Asp Tyr Glu Ala
245 250 255

Ser Leu Ile Lys Arg Tyr Ala Ile Lys Gly His His Gly Val Ala Leu
260 265 270

Arg Ala Leu Ala Phe Gly Gln Ser Tyr Asn Asp His Ala Ala Phe Asn
275 280 285

Glu Ser Thr Val Asn Ile Asn Ala Gly Tyr Ser Tyr Phe Asp Leu Lys
290 295 300

Asn Gln Ile Gly Val Ser Pro Leu Phe Glu His Lys Arg Tyr Gly Asn
305 310 315 320

Asp Gly Leu Tyr Asn Ala Trp Gly Ala Arg Ala Glu Trp Met His Phe
325 330 335

Ile Ser Ala Asp Lys Ala Phe Lys Leu Glu Ala Glu Ser Lys Asp Leu
340 345 350

Asn Tyr Gln Lys Tyr Lys Thr Leu Asp Gly Val Glu Ser Ser Ala Phe
355 360 365

Val Thr Phe Trp Lys Ile Leu Pro Asn Gln Trp Thr Val Phe Ser Gly
370 375 380

Leu Asp Val Val Asp His Ser Thr Gln Glu Lys Tyr Met Ala Ala Tyr
385 390 395 400

Gln Gln Gln Gly Val Arg Leu Gly Leu Ser Lys Ser Trp Ser Thr Gly
405 410 415

Phe Asn Thr Thr Leu Leu Ser Ser Tyr Arg Trp Arg Met Phe Asp Lys

420 425 430

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

<210> 9
<211> 1491
<212> DNA
<213> A. beijerinckii SLAM 1
<400> 9

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caactacaac aacaaggcac aattcgtgat accgagaaac tacccagtat tcttatcaat 180
ggccaaattt ttgcggtaga gaaaaatcag gatgatttgg caaaagctct gtatttggca 240
gtcatgcaaa aacaatgggg caatgctgcg gtttatttaa agcattatca gcaatatcaa 300
gactatgatc aggctttaac tgattttgcc gaaggggcat tggcacgtgc tcaggggcaa 360

ctcaaattag ccgagcaaaa atttcaaagc agtctcaata aacaacccaa taatctgatt 420
tgtgaactag agttagcgcg cgtgctgttt gaacagcaga agaacaaaga agcagcacgc 480
ctttttacat caattcaaaa caaactggga cagagtgatc gtgcggtgat accgccagaa 540
gtagaacaaa cggttaatct gttcgtcaaa gcactcgatc agcgggattc atggcaaggc 600
agtgtcgcga taggtccatc ctatgccaca aatctgaata gttcttctga acaaagtaaa 660
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cgtggcagcc ctaaagcagc atcagcaaca ggtatggact atgaaaccag tttaatgaaa 780

cgcttttctc tctacggcaa tcatggggtt tccttacgtg ggttagctta tggacaatct 840
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gacggtttat ataatgcatg gggtgtacgt gctgaatgga tgcgatttat tgccgcagac 1020

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gatggtaaag aaagctcagc gatgttcacg ttttggaaga ttctacccaa gcaatggaca 1140

ttatttagtg gactagacgt gcttgatcat gacactcaag aaaaatatat ggcggcctat 1200

caacaacaag gggtccgttt agggttgagg aagtcttgga atgttgggtt gaataccact 1260

ttattcactt cgtatcgctg gcggcagttt gatcgctatg ctgaaagtct agaagcccgt 1320

cgtcatgatt ttgaacaaaa ttataccttt gttgtacaga tgcctcgatt taaattttat 1380

ggtgtgacgc caaaccttac ttatcgttat aaccaaaaca gtagcaatgt ggattggttg 1440

tattcttatg agaaacataa tgttagcttg aagcttgagc atcgttttta g 1491

<210> 10

<211> 496

<212> PRT

<213> A. beijerinckii SLAM 1

<400> 10

Met Lys Arg Thr Leu Leu Cys Cys Leu Thr Leu Leu Ala Ala Ser Ser

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Leu Tyr Ala Asp Asp Asp Thr Gln Leu Arg Leu Asn Gln Ser Leu Asp

20 25 30

Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Thr Ile

35 40 45

Arg Asp Thr Glu Lys Leu Pro Ser Ile Leu Ile Asn Gly Gln Ile Phe

50 55 60

Ala Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala

65 70 75 80

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

85 90 95

Gln Gln Tyr Gln Asp Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly

100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe

115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu

130 135 140

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

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

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

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

385 390 395 400

Gln Gln Gln Gly Val Arg Leu Gly Leu Arg Lys Ser Trp Asn Val Gly

405 410 415

Leu Asn Thr Thr Leu Phe Thr Ser Tyr Arg Trp Arg Gln Phe Asp Arg

420 425 430

Tyr Ala Glu Ser Leu Glu Ala Arg Arg His Asp Phe Glu Gln Asn Tyr

435 440 445

Thr Phe Val Val Gln Met Pro Arg Phe Lys Phe Tyr Gly Val Thr Pro

450 455 460

Asn Leu Thr Tyr Arg Tyr Asn Gln Asn Ser Ser Asn Val Asp Trp Leu

465 470 475 480

Tyr Ser Tyr Glu Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 11

<211> 1491

<212> DNA

<213> A. bereziniae SLAM 1

<400> 11

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aaactactca aatcagatga tcccaaaaaa gaccaagcat taccgaatct gatcatacaa 180

ggtcaggaat atatggtgaa ggatgaaccc gcagaagttg cttatgcgct ttatttggca 240

gtgatgcaaa aacaatggca tgtcgcttta cgttatttag aaaaatataa aaaatttcca 300

aattatgatc aggctttgac tgaattcgct gaaggcgtca tggcacgaac acagggaaat 360

ttaagcttag ctgaaagtaa actacaacac agtctaaaga ttcaatccaa taatttaatg 420

actcagcttg agctggcgcg tgtctacacc gaacaacaaa aaaatcagca aggactacag 480

ttatttcagc agattcaatc tcaattaact atgtctaacg atcctactgc tcaaggtatt 540

cttcaaactg tagagatgta tcttaaagga cttaaacaac gtgatgcatg gcaaggttct 600

ttagcttttg gttcacgtta tgccaataat atcaataacg cttcggataa atacgacatc 660

gtgacctatt acggtattga cccagaaacc aaggaagtcg tgcctgtcga acaattaaag 720

cgaggtacac cagatgcgat cagtgcccaa ggtctggatt atgaagccac tttaaccaag 780

cgttggtcac tttctgggca gcatggtatt gctttacgtg gattattcta tggtcaagtt 840

tacccagatc agacagatta taatgaatta acttttaatt taaatgcggg ttatagtttt 900

tataatgaac gtaatcaagt cttggttgct cctgtatttg aacataaata ctatgcacat 960

gatccactct acaatgctta tgggttaaga ggcgagtgga tgcgctttat ttccaacgat 1020

aaagccgtca agttagaggc tgaaatgaaa gatatgaact attctcagta taaggggcag 1080

aatggcacgg aatactcagt ctattcaact ttttggaaaa ttttaccaaa aaactggacc 1140

ttatttggtg gactcgattt cgttgaccat aatacccaag agcaatattt cacagcatat 1200

caacaacaag gcatacgttt agggttgtcc aaaaatttta ccgcaggctt taacaccaat 1260

ttatttagtt cttttcgttg gcgtcaattt gataaattta cgcctgtatt agagactagg 1320

cgacatgatt ttgaacaaaa ctataccttg attttaagtg caccgcgttg ggccttttac 1380

ggtttaacac caaatctcac ttatcaatat aatcaaaata acagtaatgt agagtggttg 1440

tattcttatg ataaacacaa tatcagctta aagttagaac atcgttttta a 1491

<210> 12

<211> 496

<212> PRT

<213> A. bereziniae SLAM 1

<400> 12

Met Lys Lys Ile Val Leu Leu Gly Val Val Val Leu Cys Gly Glu Ser

1 5 10 15

Val Tyr Ala Ala Asp Asp Thr Ser Ile Arg Leu Asn Gln Glu Ile Ser

20 25 30

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

35 40 45

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

50 55 60

Met Val Lys Asp Glu Pro Ala Glu Val Ala Tyr Ala Leu Tyr Leu Ala

65 70 75 80

Val Met Gln Lys Gln Trp His Val Ala Leu Arg Tyr Leu Glu Lys Tyr

85 90 95

Lys Lys Phe Pro Asn Tyr Asp Gln Ala Leu Thr Glu Phe Ala Glu Gly

100 105 110

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

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

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

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

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

        355                 360                 365
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Ser Thr Phe Trp Lys Ile Leu Pro Lys Asn Trp Thr Leu Phe Gly Gly

370 375 380

Leu Asp Phe Val Asp His Asn Thr Gln Glu Gln Tyr Phe Thr Ala Tyr

385 390 395 400

Gln Gln Gln Gly Ile Arg Leu Gly Leu Ser Lys Asn Phe Thr Ala Gly

405 410 415

Phe Asn Thr Asn Leu Phe Ser Ser Phe Arg Trp Arg Gln Phe Asp Lys

420 425 430

Phe Thr Pro Val Leu Glu Thr Arg Arg His Asp Phe Glu Gln Asn Tyr

435 440 445

Thr Leu Ile Leu Ser Ala Pro Arg Trp Ala Phe Tyr Gly Leu Thr Pro

450 455 460

Asn Leu Thr Tyr Gln Tyr Asn Gln Asn Asn Ser Asn Val Glu Trp Leu

465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Ile Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 13

<211> 1491

<212> DNA

<213> A. calcoaceticus SLAM 1

<400> 13

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cagtttcacg agcagggaac cattcgtagc accgagcaat taccaaaact tcaaattaat 180

ggacaagaat atagtgttga gcaaaacccg aatgatcttg ccaaggcgct atatctggca 240

gtcatgcaaa aacagtggct caaagccacg gtttatttag aacattataa aaaatatgtt 300

ggctacgatc gggctttaac cgactttgcc gaaggggcag ttgcacgttc tcagggtcaa 360

ctgaaattgg ctgaacaaaa atttcaaagc agcctaaaac aacaatctaa taacttaatt 420

tgtgaacttg agttagcgcg cgtgctgttt gaacaacaga agaataagga agcagcacgc 480

ctttttattt ccattcaaga caaacttaaa caaagtgacc ctgcggtaat cccgtctggg 540

gttttaacaa cagtgaatac ttttgttcag gcattaaaaa aacgagactc ttggcaaggc 600

tcggtttcag ctggttacac ctatgtcagt aatttaaata gttcttctga acaaagcaaa 660

acatggacgc tttatggcag agatagtgac ggtaatatta tcccaattga gcaagtcacc 720

cgtggaactc caaaagccga atcggcaacg ggtttagatt acgaagccag tctgattaaa 780
cgctatgcga ttgagggtca tcatggcgtg gctttacgtg cgttggcttt tggacagtcc 840
tataacgacc acgcggcatt taatgaatct actattaaca ttaatgcagg ctatagctac 900
tttgacttaa aaaatcaaat tggggtgagt ccgctttttg aacataaacg ttatggcaat 960
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gtttttggtg gtttagatgt agtcgaccat tcgacccaag aaaaatatat ggctgcatac 1200
cagcagcaag gtgtgcggtt gggcttaagc aaatcttgga gcacaggatt taacaccact 1260
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ggcatgacgc ctaatttaac ctaccgttat aaccataata aaagtaatgt cgattggctg 1440
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<210> 14
<211> 496
<212> PRT
<213> A. calcoaceticus SLAM 1

<400> 14

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

Ser Val Glu Gln Asn Pro Asn Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80
Val Met Gln Lys Gln Trp Leu Lys Ala Thr Val Tyr Leu Glu His Tyr
85 90 95

Lys Lys Tyr Val Gly Tyr Asp Arg Ala Leu Thr Asp Phe Ala Glu Gly
100 105 110
Ala Val Ala Arg Ser Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe
115 120 125

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

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

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

Asp Gly Leu Tyr Ser Ala Trp Gly Ala Arg Ala Glu Trp Met His Phe
325 330 335
Ile Ser Ala Asp Lys Ala Phe Lys Leu Glu Ala Glu Arg Lys Asp Leu

340 345 350

Asn Tyr Gln Lys Tyr Lys Thr Leu Asp Gly Val Glu Ser Ser Ala Phe

355 360 365

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

370 375 380

Leu Asp Val Val Asp His Ser Thr Gln Glu Lys Tyr Met Ala Ala Tyr

385 390 395 400

Gln Gln Gln Gly Val Arg Leu Gly Leu Ser Lys Ser Trp Ser Thr Gly

405 410 415

Phe Asn Thr Thr Leu Leu Ser Ser Tyr Arg Trp Arg Leu Phe Asp Lys

420 425 430

Tyr Ala Glu Thr Phe Leu Ala Arg Arg His Asp Phe Glu Gln Asn Tyr

435 440 445

Thr Val Val Val Gln Met Pro Arg Phe Glu Phe Tyr Gly Met Thr Pro

450 455 460

Asn Leu Thr Tyr Arg Tyr Asn His Asn Lys Ser Asn Val Asp Trp Leu

465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Ile Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 15

<211> 1464

<212> DNA

<213> A. capsulatus SLAM 1

<400> 15

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gatactacag aacaaaaaat ttccgaccat ttaaacgatt tacgaagcca aacggaagta 120

gcgattgaat ctcgtattca aaagccggtt gctcgttcac ttcctcaatc aaccgttcag 180

caaaaaaagc ttccaagtat gagcaaagag gagttcgcta agcgaccaga tttaatttca 240

aatgcgcttg ttttagcatt acatcaatct aattctgata cggttaattt tctttattcg 300

ttttatagca aactgccagc acaataccaa gacccgatta tggttaagtg gtcggaagct 360

attttagccc gtcaaaaagg cgactacagt accgccattg ctctctatcg agaaatatta 420

gccgaacatt caggcttagg ctctgctcgt ttacagcttg ctgtagcatt atttgagaac 480

aatgaattag aagccgccga agatcaattc caaaaaatac gcgcagaaaa tccgcctgcc 540
cagattaaag atgttatcga tcaatatatt gccgcaatcg taaataaaga tcgatgggta 600
ttttccggtg gattcactta tttaaacgat ccgaatatta ataacgcccc gaaatctggc 660
accacttacg gacaatggag cgcaccgaaa tccgaatccg cacaagggat cggctttaac 720
ttctatgctg gcaagaaatg gtcttgggga aataatttct ataatgaatt ccgtctaagc 780
agtaacggaa aatattattg gaataacaaa aaatataatg aagtcagcgc aagaggaagc 840
cttggtttag gctatcaaac cgctcgcttt aatatggcta ttcttccttt tatggaacaa 900

acactttatg ctggcggttc gaacagtagc aacagtttaa aacgattctc aaaaacaagc 960
ggcgcaacat tagaaaccag ttactggatc tcaccgaaat ggcaatggga atcaaactat 1020
gaatatgccg aacaacgtta tatggatcgt aaacatttaa atggtagcta ccatttcgtt 1080
tcaagtggct taacttatct tgccagtgca aaacaatatt ggtttactaa tataaactac 1140
aaccgcacag caactcgaga taaggatgac agttatatcc gccgcggaat cgcgcttggc 1200
tggggacaag aatggccatt cggtctatca acacgattaa gtgttaacta tgcacaaaaa 1260
aattacaaag caccaatgcc aatctttggc attacacaac gtaataaaga atacggtgta 1320

tcattaagtc tatggcatcg tgccatacat tattggggta ttacacctcg cctaacgtat 1380
agctttaata aagtaaaaag taatcacgca ttctatagct acgataaaca ccgtattttt 1440
gtggagttta gcaaacgctt ctag 1464

<210> 16
<211> 487
<212> PRT
<213> A. capsulatus SLAM 1
<400> 16

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

Asp Leu Arg Ser Gln Thr Glu Val Ala Ile Glu Ser Arg Ile Gln Lys
35 40 45
Pro Val Ala Arg Ser Leu Pro Gln Ser Thr Val Gln Gln Lys Lys Leu
50 55 60

Pro Ser Met Ser Lys Glu Glu Phe Ala Lys Arg Pro Asp Leu Ile Ser
65 70 75 80
Asn Ala Leu Val Leu Ala Leu His Gln Ser Asn Ser Asp Thr Val Asn
85 90 95

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

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

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

Arg Phe Asn Met Ala Ile Leu Pro Phe Met Glu Gln Thr Leu Tyr Ala
290 295 300
Gly Gly Ser Asn Ser Ser Asn Ser Leu Lys Arg Phe Ser Lys Thr Ser

305 310 315 320

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

325 330 335

Glu Ser Asn Tyr Glu Tyr Ala Glu Gln Arg Tyr Met Asp Arg Lys His

340 345 350

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

355 360 365

Ser Ala Lys Gln Tyr Trp Phe Thr Asn Ile Asn Tyr Asn Arg Thr Ala

370 375 380

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

385 390 395 400

Trp Gly Gln Glu Trp Pro Phe Gly Leu Ser Thr Arg Leu Ser Val Asn

405 410 415

Tyr Ala Gln Lys Asn Tyr Lys Ala Pro Met Pro Ile Phe Gly Ile Thr

420 425 430

Gln Arg Asn Lys Glu Tyr Gly Val Ser Leu Ser Leu Trp His Arg Ala

435 440 445

Ile His Tyr Trp Gly Ile Thr Pro Arg Leu Thr Tyr Ser Phe Asn Lys

450 455 460

Val Lys Ser Asn His Ala Phe Tyr Ser Tyr Asp Lys His Arg Ile Phe

465 470 475 480

Val Glu Phe Ser Lys Arg Phe

485

<210> 17

<211> 1443

<212> DNA

<213> A. capsulatus SLAM 2

<400> 17

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gcttatgcag agcagcaaat taatacacct gaaaagaata tggaaattgc taaattactt 120

aaagaatcca aaaaattacc tgaattagtt atagatacgg cagaaaatat tcaattttcc 180

gttcaaggtt tattcagtaa taaagtattg agcgaacaat tactcaatca tgcaatagaa 240

acaggtaacc tttcttctat tgaatactta ttggcgattt atcgtcaatt tcccgatacc 300

gatcctgttt taattctttt tgcacaggca caaattgcca aaatacagca acaatatacg 360

aaggcaagca agttataccg tgacatattg gcactaaaac cggaacttac gcccgttcgc 420

atacagcttg ccatcgtgtt atttcaatct caacaggaca aggcggctaa agagcagttt 480

gaaaaagctt tgagcgagcc gcaacttccc attgatattg aacaattgat tcatctttat 540

ttacaagcgc tggaacaacg taatacgtgg cagctttcat taagcgctaa ttatttgcga 600

gaagacaatg taaataatgt ttcaggcgaa cgatatattg aaaataccgc ctttataaaa 660

ggcgagagta tgttgccgca aaaagcacag gggatcggtt attactttgg tttagagcgt 720

gatatcaatt tatggaatgc ccattatttg catatcgaaa atagtttata cggcaaaagt 780

tactgggatc agcatgatta cgatgatatt accaatcgct tatcgttagg ctatgtacat 840

aaaggctcac agcaacgctt tgcgattttg ccgttttatg aacagcaatg gtatggtggt 900

catcgatata agcgcagtaa tggcagcaga atagaattta atcgttggct aacgtcaaat 960

tggcaatttt caacggctgc agagtatgct cggaatttct attcaaatag cccaagttta 1020

aacggtaaga gtaagttagc ttcactaacg atgttatggc gcgctagtcc tcgtacttat 1080

ttttatttag gtgcggatta cgctcaagaa cgcactaaag ttcgtcatta cagctatgac 1140

ttaaaaatag cccgtatcgg ttggggacaa gaatggcatt ggggaatatc ttctcgttta 1200

agcttttcag cctctaagcg agagtataag gataatcttt cgctcggttc ggtttttcat 1260

ttcgacaggc ggcgtgaaga ccgaatctat catatcaatg caaccgtttg gaaaagagat 1320

tggcatttat gggggattac cccaaagctc aattatcact ggaaaaaaca acgtagcaat 1380

tttgtaagcc tttattctta ctcggataaa agtatcaaca taatactgga aaaaactttt 1440

taa 1443

<210> 18

<211> 480

<212> PRT

<213> A. capsulatus SLAM 2

<400> 18

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Arg Val Gly Val Ala Tyr Ala Glu Gln Gln Ile Asn Thr Pro Glu Lys
20 25 30

Asn Met Glu Ile Ala Lys Leu Leu Lys Glu Ser Lys Lys Leu Pro Glu

35 40 45

Leu Val Ile Asp Thr Ala Glu Asn Ile Gln Phe Ser Val Gln Gly Leu

50 55 60

Phe Ser Asn Lys Val Leu Ser Glu Gln Leu Leu Asn His Ala Ile Glu

65 70 75 80

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

85 90 95

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

100 105 110

Ala Lys Ile Gln Gln Gln Tyr Thr Lys Ala Ser Lys Leu Tyr Arg Asp

115 120 125

Ile Leu Ala Leu Lys Pro Glu Leu Thr Pro Val Arg Ile Gln Leu Ala

130 135 140

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

145 150 155 160

Glu Lys Ala Leu Ser Glu Pro Gln Leu Pro Ile Asp Ile Glu Gln Leu

165 170 175

Ile His Leu Tyr Leu Gln Ala Leu Glu Gln Arg Asn Thr Trp Gln Leu

180 185 190

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

195 200 205

Gly Glu Arg Tyr Ile Glu Asn Thr Ala Phe Ile Lys Gly Glu Ser Met

210 215 220

Leu Pro Gln Lys Ala Gln Gly Ile Gly Tyr Tyr Phe Gly Leu Glu Arg

225 230 235 240

Asp Ile Asn Leu Trp Asn Ala His Tyr Leu His Ile Glu Asn Ser Leu

245 250 255

Tyr Gly Lys Ser Tyr Trp Asp Gln His Asp Tyr Asp Asp Ile Thr Asn

260 265 270

Arg Leu Ser Leu Gly Tyr Val His Lys Gly Ser Gln Gln Arg Phe Ala

275 280 285

Ile Leu Pro Phe Tyr Glu Gln Gln Trp Tyr Gly Gly His Arg Tyr Lys
290 295 300

Arg Ser Asn Gly Ser Arg Ile Glu Phe Asn Arg Trp Leu Thr Ser Asn
305 310 315 320

Trp Gln Phe Ser Thr Ala Ala Glu Tyr Ala Arg Asn Phe Tyr Ser Asn
325 330 335

Ser Pro Ser Leu Asn Gly Lys Ser Lys Leu Ala Ser Leu Thr Met Leu
340 345 350

Trp Arg Ala Ser Pro Arg Thr Tyr Phe Tyr Leu Gly Ala Asp Tyr Ala
355 360 365

Gln Glu Arg Thr Lys Val Arg His Tyr Ser Tyr Asp Leu Lys Ile Ala
370 375 380

Arg Ile Gly Trp Gly Gln Glu Trp His Trp Gly Ile Ser Ser Arg Leu
385 390 395 400

Ser Phe Ser Ala Ser Lys Arg Glu Tyr Lys Asp Asn Leu Ser Leu Gly
405 410 415

Ser Val Phe His Phe Asp Arg Arg Arg Glu Asp Arg Ile Tyr His Ile
420 425 430

Asn Ala Thr Val Trp Lys Arg Asp Trp His Leu Trp Gly Ile Thr Pro
435 440 445

Lys Leu Asn Tyr His Trp Lys Lys Gln Arg Ser Asn Phe Val Ser Leu
450 455 460

Tyr Ser Tyr Ser Asp Lys Ser Ile Asn Ile Ile Leu Glu Lys Thr Phe
465 470 475 480

<210> 19

<211> 1488

<212> DNA

<213> A. faecalis SLAM 1

<400> 19

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caagccaacg acgacgatac gcgccgactt ctgaatcaaa tcgaccgcaa tctgaacgaa 120

cgtgaacgct cccatttagt ggaagaaacc ccgcccgatg gggacccatc ggccctgatc 180

accatcaacg gcacaaccta tagcgtcgat gccacgctga ctgatctgga accggccatt 240

tatgtcgcca tcaatctgca gcagtgggcc aaggtggatc agtttgtaga aaagtatcag 300

gagctgcccg gccacaaccc tgccttggtg ctgatggctc aaggggtggt ggcccgtagc 360

aaggacaatc acagcctggc gatcagcaag ctgcgccggg ctcaggaaag cgatcccact 420

atgatgcgcg ccaagctgga gctggcccgc gtactgttcg aggactatca atccagcgaa 480

gccaaggagc tgttcagcca gatttcctct accggtattc ctgatgaagt gcgactcgtg 540

atcgaaggct tccagggtgc cctgcaagac cgcaatgcct ggcacggttc tgcctcgatt 600

ggcttgggct acaacagcaa tatcaataaa gaaaacggac agcaagacac cttctttacc 660

tgttatttct ttgggtgctt tccgtcggtg cgcaagatgc cggacccggt caaatccacg 720

gccatggtct acgacctgac cttgaaccgg cgcttccagc taagcggcaa ccacaatctg 780

cttctgcgcg gcctgagcta cggcaatctg tacgacaagc ataaggaagc caagcccaag 840

aacatttatt acagcgacaa caccagcatt atttacgcgg gctacaacta tcaggacgct 900

aaaaacgatc tgtcgattac gcccttgttc gagaacaatt acaccaaccg tcgcaccagc 960

tatcagtcct ggggcgggcg cgtggactgg aagcacaatc ttagcgacag gctgcaagtg 1020

ggcgtgaatg cccagcataa gagcctgtcc tacaaaggcg atttacggca gtactttgaa 1080

ggcgtcaaag agaaccagat aggcttgtac ggctcgtatc tgattgacgc caaaaccgta 1140

gtctacgggg gcctgaatta cacccgcaat ctgcagtctc agcaaaccgc gcaaagccgc 1200

agctatatgg cgaacctggg aatttacagg gcctttgatg caggctttaa catcaacgcc 1260

acggcactgt accggcagac ccgtcacgat gcccaagact tgttcctggg tgggctgcgc 1320

aaggaccgcc agcagattta tatcctgaac gtgggcatgc cacgctttgc gttccaaggc 1380

attacgccca atctgtatct gaagcacacc ttcaacaaca gcaacatcga ctgggctttc 1440

aaatacaagc aaaccgaagt cgcgctgaag ctggaaaagc ggttttaa 1488

<210> 20

<211> 495

<212> PRT

<213> A. faecalis SLAM 1

<400> 20

Met His Gly Arg Ala Leu Pro Leu Leu Cys Leu Leu Leu Ala Met Ala

1 5 10 15

Ser Ser Ala Val Gln Ala Asn Asp Asp Asp Thr Arg Arg Leu Leu Asn

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Gln Ile Asp Arg Asn Leu Asn Glu Arg Glu Arg Ser His Leu Val Glu
        35                  40                  45

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

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

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

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

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

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

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

<210> 21
<211> 1449
<212> DNA

<213> A. gerneri SLAM 1

<400> 21

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ttaccgacga tggtcattga tggcgaaaaa atagaagtga agaaaaatag caatgaactt 180

ggacgagctt tatacattgc agtgatgcaa aaacaatggc aagcagccag tatatatttg 240

gaacattatt taaaactaaa cgatcatgat ccctctttgg tttattttgc acaaggtgct 300

ttgcaacgtg tgcaaggcaa cttgtctcaa gcagagcatg attttaaaca ggcactagat 360

ttacagccgc aaaatgcgat gatcaaattg gagttggcac gactctatac cgaaagacaa 420

aaaaataatg aagctaaaca gctctttgaa caagttaaac atcaattggg ggatacagtc 480

gatcctacgc tgttaaatat tcatcatgcg attgatatat atctagatgg tttgaaaaaa 540

cgtgatgctt ggcagggttc tatcaatttg ggtatacgtt atgcaaccaa tatcaatagt 600

gcgaccgaga aaacaacaac ttggacgaca tttggcaaag accaaaatgg caatattatt 660

ccgatacaaa ttacacgcgg tacacctgat ccaattgatg cgacagcctt tgattatgag 720

ggaactttga gtaaacgatg gtcactgcaa gaaaatcatg gcttggcact taaagccttt 780

gcttatggcc gtgtttttga tgggcataaa gattttaatg aaatgacact caatctaaat 840

gcagggtata gctttcaaaa tcaacgtaat caaatcttag tcgcccctgt ttatgagcat 900

agacgttata gcaatgaaac attttcaaat gcttggggcg ggcatttaga gtggatgcat 960

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aaatattcga ctcaaagtgg tcttgaaagt tcggtctata gcactttctg gaaagtatta 1080

cctcagaact ggacagtctt tactggtctg gattttacgg atcatcgaag caaagaaaaa 1140

atctttaatc aataccaaca gcaaggcata cgttttggat tttccaaaca atggaatact 1200

ggttttaatg caacagcatt tagttctttt cgatggcgtc aatatgcaac acaaaatcaa 1260

gttttaggcg gtgaacgccg tcatgatttt gaacaaaact atacagtggt actgtcagca 1320

cctcgatggc aattttatgg tgtgattcca aatttgactt atcaatataa taacaacctg 1380

agtaatattg attggctcta tagctacgac aaacacaatg taagtttaag gctcgagtat 1440

cggttttaa 1449

<210> 22

<211> 482

<212> PRT

<213> A. gerneri SLAM 1

<400> 22

Met Ser Ser Ser Ile Leu His Ala Ala Asp Asp Asp Thr Arg Phe Arg

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Leu Gln Gln Gln Lys Gln Asp Gln Leu Pro Thr Met Val Ile Asp Gly

35 40 45

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

50 55 60

Tyr Ile Ala Val Met Gln Lys Gln Trp Gln Ala Ala Ser Ile Tyr Leu

65 70 75 80

Glu His Tyr Leu Lys Leu Asn Asp His Asp Pro Ser Leu Val Tyr Phe

85 90 95

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

100 105 110

His Asp Phe Lys Gln Ala Leu Asp Leu Gln Pro Gln Asn Ala Met Ile

115 120 125

Lys Leu Glu Leu Ala Arg Leu Tyr Thr Glu Arg Gln Lys Asn Asn Glu

130 135 140

Ala Lys Gln Leu Phe Glu Gln Val Lys His Gln Leu Gly Asp Thr Val

145 150 155 160

Asp Pro Thr Leu Leu Asn Ile His His Ala Ile Asp Ile Tyr Leu Asp

165 170 175

Gly Leu Lys Lys Arg Asp Ala Trp Gln Gly Ser Ile Asn Leu Gly Ile

180 185 190

Arg Tyr Ala Thr Asn Ile Asn Ser Ala Thr Glu Lys Thr Thr Thr Trp

195 200 205

Thr Thr Phe Gly Lys Asp Gln Asn Gly Asn Ile Ile Pro Ile Gln Ile

210 215 220

Thr Arg Gly Thr Pro Asp Pro Ile Asp Ala Thr Ala Phe Asp Tyr Glu

225 230 235 240

Gly Thr Leu Ser Lys Arg Trp Ser Leu Gln Glu Asn His Gly Leu Ala

245 250 255

Leu Lys Ala Phe Ala Tyr Gly Arg Val Phe Asp Gly His Lys Asp Phe

260 265 270

Asn Glu Met Thr Leu Asn Leu Asn Ala Gly Tyr Ser Phe Gln Asn Gln

275 280 285

Arg Asn Gln Ile Leu Val Ala Pro Val Tyr Glu His Arg Arg Tyr Ser

290 295 300

Asn Glu Thr Phe Ser Asn Ala Trp Gly Gly His Leu Glu Trp Met His

305 310 315 320

Phe Leu Gly His Asp Lys Ala Phe Lys Leu Glu Thr Glu Ile Lys Asp

325 330 335

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

340 345 350

Tyr Ser Thr Phe Trp Lys Val Leu Pro Gln Asn Trp Thr Val Phe Thr

355 360 365

Gly Leu Asp Phe Thr Asp His Arg Ser Lys Glu Lys Ile Phe Asn Gln

370 375 380

Tyr Gln Gln Gln Gly Ile Arg Phe Gly Phe Ser Lys Gln Trp Asn Thr

385 390 395 400

Gly Phe Asn Ala Thr Ala Phe Ser Ser Phe Arg Trp Arg Gln Tyr Ala

405 410 415

Thr Gln Asn Gln Val Leu Gly Gly Glu Arg Arg His Asp Phe Glu Gln

420 425 430

Asn Tyr Thr Val Val Leu Ser Ala Pro Arg Trp Gln Phe Tyr Gly Val

435 440 445

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

450 455 460

Trp Leu Tyr Ser Tyr Asp Lys His Asn Val Ser Leu Arg Leu Glu Tyr

465 470 475 480

Arg Phe

<210> 23

<211> 1491

<212> DNA

<213> A. guillouiae SLAM 1

<400> 23

atgaaaaaaa tagtattgct tggtgccgta ttgcagtgtg gacaatgtgt ttatgcagcg 60

gatgatacca gtatcaggtt aaatcaggaa attagccaac agcaatatca aaatgataag 120

aaactactca aatcagaaga ccctaagaac acacaagcat taccgaatct gatcatacaa 180

ggtcaagaat atgtggttaa ggatgaaccc gcagaagtcg catatgcact ttacttggca 240

gtgatgcaaa aacaatggca agtggcttta agctatcttg aaaaatataa aaaatttcca 300

aattatgatc aggctttgac tgagttcgct gagggcgtca tggcacgaac acaggggaat 360

ttaagtttag ctgagagtaa acttaaacat agcctagaga ttcaatccaa taatttaatg 420

acccaacttg agctggctcg tgtctacacc gaacaacaaa aaaatcagca aggtcaacag 480

ttattcctgc agattcaatc tcaactggct ctgtctacag atcctgctgc ccaaggtatt 540

ggtcaaaccg tagagatgta tctcaaaggg cttaaacaac gagatgaatg gcatggttca 600

ttggcgtttg gttcacgtta tgccagtaat gttaataatg cttccgataa atacgacatc 660

attacgtatt atggcattga ccctgagact aagaaggtcg ttcctattga acaagtaaag 720

cgtggcacac ctgacgcgat cagtgcgcaa ggtttggatt atgaagcgac cttaactaaa 780

cgatggtcgc tttctggaca acatggtatt gcattgcgtg gattattcta tggtcaagtt 840

tatccagagc agacagatta taatgaatta acttttaact taaatgcggg ttatagttat 900

tacaacgaac gtaatcaaat cttgatagca cccgtatttg aacataaata ctatgcccac 960

gacccgctgt atagtgccta tgggttaagg ggcgagtgga tgcgttttat ctctaacgac 1020

aaagctgtca agttagaagc cgaaatcaaa gatataaatt attcccagta taaaggccaa 1080

gatggcgtgg aatattcagt ctattcaacc ttttggaaaa ttttaccgag aaactggacg 1140

ctatttggcg gactggattt tgtcgaccat aatacccaag aacaatattt tacggcttat 1200

caacaacaag tcgtgcgttt gggcctttcc aaaaactttg actcaggttt taacgcaaat 1260

ttatttagtt ctttccgttg gcgtcaattt gataaattta ctccagtgtt ggaggctaga 1320

cgacatgatt ttgaacaaaa ttatacttta attctaagtg caccacgctg ggctttttat 1380

ggtttaacac ctaatctcac ttatcaatat aatcaaaata acagcaatgt agagtggcta 1440

tattcttatg ataaacacaa tgtcagttta aagctggagc atcggttcta a 1491

<210> 24

<211> 496

<212> PRT

<213> A. guillouiae SLAM 1

<400> 24

Met Lys Lys Ile Val Leu Leu Gly Ala Val Leu Gln Cys Gly Gln Cys
1 5 10 15

Val Tyr Ala Ala Asp Asp Thr Ser Ile Arg Leu Asn Gln Glu Ile Ser
20 25 30

Gln Gln Gln Tyr Gln Asn Asp Lys Lys Leu Leu Lys Ser Glu Asp Pro
35 40 45

Lys Asn Thr Gln Ala Leu Pro Asn Leu Ile Ile Gln Gly Gln Glu Tyr
50 55 60

Val Val Lys Asp Glu Pro Ala Glu Val Ala Tyr Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Gln Val Ala Leu Ser Tyr Leu Glu Lys Tyr
85 90 95

Lys Lys Phe Pro Asn Tyr Asp Gln Ala Leu Thr Glu Phe Ala Glu Gly
100 105 110

Val Met Ala Arg Thr Gln Gly Asn Leu Ser Leu Ala Glu Ser Lys Leu
115 120 125

Lys His Ser Leu Glu Ile Gln Ser Asn Asn Leu Met Thr Gln Leu Glu
130 135 140

Leu Ala Arg Val Tyr Thr Glu Gln Gln Lys Asn Gln Gln Gly Gln Gln
145 150 155 160

Leu Phe Leu Gln Ile Gln Ser Gln Leu Ala Leu Ser Thr Asp Pro Ala
165 170 175

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

Gln Arg Asp Glu Trp His Gly Ser Leu Ala Phe Gly Ser Arg Tyr Ala
195 200 205

Ser Asn Val Asn Asn Ala Ser Asp Lys Tyr Asp Ile Ile Thr Tyr Tyr
210 215 220

Gly Ile Asp Pro Glu Thr Lys Lys Val Val Pro Ile Glu Gln Val Lys
225 230 235 240

Arg Gly Thr Pro Asp Ala Ile Ser Ala Gln Gly Leu Asp Tyr Glu Ala
245 250 255

Thr Leu Thr Lys Arg Trp Ser Leu Ser Gly Gln His Gly Ile Ala Leu
260 265 270

Arg Gly Leu Phe Tyr Gly Gln Val Tyr Pro Glu Gln Thr Asp Tyr Asn
275 280 285

Glu Leu Thr Phe Asn Leu Asn Ala Gly Tyr Ser Tyr Tyr Asn Glu Arg
290 295 300

Asn Gln Ile Leu Ile Ala Pro Val Phe Glu His Lys Tyr Tyr Ala His
305 310 315 320

Asp Pro Leu Tyr Ser Ala Tyr Gly Leu Arg Gly Glu Trp Met Arg Phe
325 330 335

Ile Ser Asn Asp Lys Ala Val Lys Leu Glu Ala Glu Ile Lys Asp Ile
340 345 350

Asn Tyr Ser Gln Tyr Lys Gly Gln Asp Gly Val Glu Tyr Ser Val Tyr
355 360 365

Ser Thr Phe Trp Lys Ile Leu Pro Arg Asn Trp Thr Leu Phe Gly Gly
370 375 380

Leu Asp Phe Val Asp His Asn Thr Gln Glu Gln Tyr Phe Thr Ala Tyr
385 390 395 400

Gln Gln Gln Val Val Arg Leu Gly Leu Ser Lys Asn Phe Asp Ser Gly
405 410 415

Phe Asn Ala Asn Leu Phe Ser Ser Phe Arg Trp Arg Gln Phe Asp Lys
420 425 430

Phe Thr Pro Val Leu Glu Ala Arg Arg His Asp Phe Glu Gln Asn Tyr
435 440 445

Thr Leu Ile Leu Ser Ala Pro Arg Trp Ala Phe Tyr Gly Leu Thr Pro
450 455 460

Asn Leu Thr Tyr Gln Tyr Asn Gln Asn Asn Ser Asn Val Glu Trp Leu

465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 25

<211> 1491

<212> DNA

<213> A. gyllenbergii SLAM 1

<400> 25

atgaaaagaa aattgctgtg ctgtttgatt ttattggcga attcatcact ctacgcagat 60

gatgagacac aactgcgcct gaatcaaaac ttggatcaga atttattaca acaacagcac 120

caactacaac aacaaggggc aattcggagc accgatgaac taccgaatat tgtgattaat 180

ggtcaagtat ttgaggttga gaagaaccaa gatgatcttg caaaagcttt atatttggcg 240

gtcatgcaaa agcaatgggg taatgctgct gtttatctaa agcattatca acaatatgat 300

ggctatgacc aagcattaac agattttgcc gagggagcat tggctcgtgc gcaaggccaa 360

ctcaaattag ccgaacaaaa atttcaaagc agcctcaata aacaaccgaa taaccttatt 420

tgtgaacttg agttagcgcg cgtgctgttt gaacagcaga agaacaaaca agcagcacgc 480

ctttttacat cgattcaaaa caaattgggg cagagtgatc gtggtgtgat tccaccagag 540

gttgaacaaa cggttaatct gtttgtcaaa gcacttgatc aacgtgatgc atggcaaggc 600

agtgtcgcaa ttggtccatc ctatgccacg aatctgaata gttcttctga acaaagcaaa 660

gtatggacgc tatatggctt tgacaaagat ggtaaggtca ttcctgttag agaaattacc 720

cgcagtagcc ctaaagctga gtcggcaaca ggtgtggact atgaagccag tttaatgaaa 780

cgcttttctc tgtatggcaa tcatgggctc tccttacgtg gtttggctta tggacagtct 840

tatgacgatc gtgccgactt taatgaatcc actctcaata tcaatgctgg ctatagtttt 900

tttgatttaa aaaatcaaat caccattgca ccgttatttg agcacaaacg ttatgccaat 960

gatggcctat acaatgcttg gggcgcgcgc gcagaatgga tgcgattcat ttccgctgat 1020

aaagcactca agcttgaagc tgaaatcaaa gatttaaatt atcaaaaata taagacccta 1080

gatggtaaag aaagttcagc tatgctgacc ttttggaaga ttctacctga acaatggacc 1140

ttatttggtg gcttggatgt cttagatcat gatacccaag aagaatacat ggcggcgtac 1200

cagcaacaag gtgttcgttt aggtctgagt aaaccgtgga gtgctggctt taataccact 1260

ttattcagtt tgtatcgttg gcgacagttt gatcgttacg tggcggcatt tcaaacacgc 1320

cgtcaagatt ttgagcaaaa ctacaccttt gtgttgcaaa tgcctcgttt caaattctat 1380

ggtgtgacgc cgaatctaac ctatcgctat aaccgtaata acagcaatgt ggattggtta 1440

tattcctatg acaaacacaa tgtcagccta aaactagagc accgttttta g 1491

<210> 26

<211> 496

<212> PRT

<213> A. gyllenbergii SLAM 1

<400> 26

Met Lys Arg Lys Leu Leu Cys Cys Leu Ile Leu Leu Ala Asn Ser Ser

1 5 10 15

Leu Tyr Ala Asp Asp Glu Thr Gln Leu Arg Leu Asn Gln Asn Leu Asp

20 25 30

Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Ala Ile

35 40 45

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

50 55 60

Glu Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala

65 70 75 80

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

85 90 95

Gln Gln Tyr Asp Gly Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly

100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe

115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu

130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Gln Ala Ala Arg

145 150 155 160

Leu Phe Thr Ser Ile Gln Asn Lys Leu Gly Gln Ser Asp Arg Gly Val

165 170 175

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

180 185 190

Asp Gln Arg Asp Ala Trp Gln Gly Ser Val Ala Ile Gly Pro Ser Tyr

195 200 205

Ala Thr Asn Leu Asn Ser Ser Ser Glu Gln Ser Lys Val Trp Thr Leu

210 215 220

Tyr Gly Phe Asp Lys Asp Gly Lys Val Ile Pro Val Arg Glu Ile Thr

225 230 235 240

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

245 250 255

Ser Leu Met Lys Arg Phe Ser Leu Tyr Gly Asn His Gly Leu Ser Leu

260 265 270

Arg Gly Leu Ala Tyr Gly Gln Ser Tyr Asp Asp Arg Ala Asp Phe Asn

275 280 285

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

290 295 300

Asn Gln Ile Thr Ile Ala Pro Leu Phe Glu His Lys Arg Tyr Ala Asn

305 310 315 320

Asp Gly Leu Tyr Asn Ala Trp Gly Ala Arg Ala Glu Trp Met Arg Phe

325 330 335

Ile Ser Ala Asp Lys Ala Leu Lys Leu Glu Ala Glu Ile Lys Asp Leu

340 345 350

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

355 360 365

Leu Thr Phe Trp Lys Ile Leu Pro Glu Gln Trp Thr Leu Phe Gly Gly

370 375 380

Leu Asp Val Leu Asp His Asp Thr Gln Glu Glu Tyr Met Ala Ala Tyr

385 390 395 400

Gln Gln Gln Gly Val Arg Leu Gly Leu Ser Lys Pro Trp Ser Ala Gly

405 410 415

Phe Asn Thr Thr Leu Phe Ser Leu Tyr Arg Trp Arg Gln Phe Asp Arg

420 425 430

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

435 440 445

Thr Phe Val Leu Gln Met Pro Arg Phe Lys Phe Tyr Gly Val Thr Pro

450 455 460

Asn Leu Thr Tyr Arg Tyr Asn Arg Asn Asn Ser Asn Val Asp Trp Leu

465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 27

<211> 1488

<212> DNA

<213> A. haemolyticus SLAM 1

<400> 27

atgaaaaaaa cactgatgtg ttgcctgata ttactgagtt gtccatattt atatgctgac 60

gatgatacgc aactacgtct aaatcagagc ctagatcaac atttattaca acagcaaaga 120

gaacttcaaa aacaaggtac gattcgcagc actgaggaat tacccgatat tcatatcaat 180

ggaaaagtgt atgtggtcga gaaaaaccaa gatgatttag ccaaagcttt atatctcgct 240

gtaatgcaaa agcaatggac gaatgttcaa atttatctga cgcattatca acaatatcct 300

gattatgatc aggcgttaac tgattttgca gaagcagcct tggcacgtac ccaagggcaa 360

ttaaaattag ctgaacaaaa attccaaagc agtttaaata aacaaccgaa caatctaatt 420

tgtgaactcg agttagcgcg tgtgctgttt gaacaacaga agaacaaaga ggcagcacac 480

ctttttataa cgattcaaaa taaattgaaa caaagtgatc acagtgtcat tccgccagaa 540

gtacaaaaaa cggttcagct tttcgtcaaa gcgcttgctc aacgagatgc atggcaaggt 600

tctattgcta taggtccgac ttatgcgagt aatctaaaca gttcatcaga acaaagtaaa 660

acttggacgc tgtatggcat ggataaagat ggcaacatta tcccagctca aattacacga 720

ggaagtccaa aagcagtttc agcaaatggt atagattatg acgcaagcct aatcaaacgt 780

ttttccatca aagaaaatca tggcgttgca ctacgtgctc tagcttatgg acagtcctac 840

gataaccaaa gcaattataa cgaatccacc atcaacgtaa atgcaggtta tagctattat 900

gatttaaaaa accaaattaa tttcagccca ctatttgaac acaaacgtta tggcaacgag 960

agtttgtacg atgcttgggg cgggcggatt gaatggatgc gatttatttc gggcgataaa 1020

gcactcaaac ttgaagcaga aattaaagat tttgattacc acacctataa aacactcaat 1080

gggcaagagc gttcggtact ggcgactttt tggaaaattt tactagaaca atggacatta 1140

tttggtggac tcgacctcct tgatcgttcg acacaagaac aatatatcgc ggcttaccag 1200

caacaaggaa ttcgtctagg tataagtaaa ccatggaata ttggaattca tacaacatta 1260

ttaagtactt atcgttggcg acaatttgat aaatacgcaa aggtttatga agcaagacga 1320

catgattttg aacaaaatta tacgtttgtt gtgcaaatgc cacgcttcaa attttatggc 1380

gtaacaccga atttaacgta tcgttataac cacaatgata gcaatgtgga ttggttgtac 1440

acctatgaca agcacaatgt cagcctgaaa ctcgaacacc gtttctag 1488

<210> 28

<211> 495

<212> PRT

<213> A. haemolyticus SLAM 1

<400> 28

Met Lys Lys Thr Leu Met Cys Cys Leu Ile Leu Leu Ser Cys Pro Tyr
1 5 10 15

Leu Tyr Ala Asp Asp Asp Thr Gln Leu Arg Leu Asn Gln Ser Leu Asp
20 25 30

Gln His Leu Leu Gln Gln Gln Arg Glu Leu Gln Lys Gln Gly Thr Ile
35 40 45

Arg Ser Thr Glu Glu Leu Pro Asp Ile His Ile Asn Gly Lys Val Tyr
50 55 60

Val Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Thr Asn Val Gln Ile Tyr Leu Thr His Tyr
85 90 95

Gln Gln Tyr Pro Asp Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Ala
100 105 110

Ala Leu Ala Arg Thr Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe
115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu
130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Glu Ala Ala His
145 150 155 160

Leu Phe Ile Thr Ile Gln Asn Lys Leu Lys Gln Ser Asp His Ser Val

165 170 175

Ile Pro Pro Glu Val Gln Lys Thr Val Gln Leu Phe Val Lys Ala Leu

180 185 190

Ala Gln Arg Asp Ala Trp Gln Gly Ser Ile Ala Ile Gly Pro Thr Tyr

195 200 205

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

210 215 220

Tyr Gly Met Asp Lys Asp Gly Asn Ile Ile Pro Ala Gln Ile Thr Arg

225 230 235 240

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

245 250 255

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

260 265 270

Ala Leu Ala Tyr Gly Gln Ser Tyr Asp Asn Gln Ser Asn Tyr Asn Glu

275 280 285

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

290 295 300

Gln Ile Asn Phe Ser Pro Leu Phe Glu His Lys Arg Tyr Gly Asn Glu

305 310 315 320

Ser Leu Tyr Asp Ala Trp Gly Gly Arg Ile Glu Trp Met Arg Phe Ile

325 330 335

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

340 345 350

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

355 360 365

Thr Phe Trp Lys Ile Leu Leu Glu Gln Trp Thr Leu Phe Gly Gly Leu

370 375 380

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

385 390 395 400

Gln Gln Gly Ile Arg Leu Gly Ile Ser Lys Pro Trp Asn Ile Gly Ile

405 410 415

His Thr Thr Leu Leu Ser Thr Tyr Arg Trp Arg Gln Phe Asp Lys Tyr

420 425 430

Ala Lys Val Tyr Glu Ala Arg Arg His Asp Phe Glu Gln Asn Tyr Thr

435 440 445

Phe Val Val Gln Met Pro Arg Phe Lys Phe Tyr Gly Val Thr Pro Asn

450 455 460

Leu Thr Tyr Arg Tyr Asn His Asn Asp Ser Asn Val Asp Trp Leu Tyr

465 470 475 480

Thr Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 29

<211> 1191

<212> DNA

<213> A. insuavis SLAM 1

<400> 29

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gcgctgctgc gccacgatgg gcgcctagcc gaggccatcg cgctttaccg ccagttgatc 120

gcgcgacatc ccgacctgga ctacgtcaga ctggaactag ccaccatgct gatggaggac 180

cgccaattcg cgcaatccga cgccgagctg gccgacctgc gcctggcatc gctggagccg 240

gcggcgcagc gcagcgtgat gcagtaccgg caggcgctgg agcagcaacg ccgctggaat 300

ttccgcctgg gcgcgggcac cgtctacagc gacaacgtca actcggccaa ccgcgatccg 360

atgttgtatc tgccggtcgc gacgcggcgc gggccactgt gggtgccatt cgccaagagc 420

cgggatgccc tgcccaaatc ggattggggc ttgaagtaca gcggcagcgc caatgtcgag 480

cgcaatctcg gcggacacca ctactacacg ctgggcgcgg atatcgatgg caccgcctac 540

cgcgtgcagc gcgactacag cgaccgcgcc ctgacgctgc gcggcggcta caagtggcag 600

gacgccacgc gttggttcgc cgcgacgccg caggcgggcc gcagctggat gggcagccgg 660

cgctacagcc acaaccacgg catgagcctg gaatacggtt ggcggccaac gcccgggtgg 720

caattgatgg gggcctggct atggctcaag cgcggctatg acgaccgcgc ctacgccgcc 780

tacgacggcc acctggaggt gctgtcgttg acggcgatcc gcgtcttctc gccggcgctg 840

ctggcctacg gcagcgttgg cctgcagcgc gaggcagtgg cggcgggcga gtacagctat 900

cgcttcccct gggcacagct cggcgtgatc aagaccttcg ggcgggtgct cggcgcgcgc 960

ttgagcgccc gctatggccg ccagtcgtat aaggcgccct acgccctgtt cctgaaccag 1020

cggcggcacg attatgaatt gcgcgtggac gcttcggtct ggacgccgga tttcacgatc 1080

gccggcctcg aaccgaagct gagcctcagc tacctcaagg tcaccagcga cttgcccatg 1140

tatgcgcggg acagaaccga ggtcagcctg atgttggaga aacggttctg a 1191

<210> 30

<211> 396

<212> PRT

<213> A. insuavis SLAM 1

<400> 30

Met Arg Phe Tyr Pro Trp Met Ala Gly Val Asp Pro Ile Leu Arg Asp
1 5 10 15

Tyr Val His Gly Ala Leu Leu Arg His Asp Gly Arg Leu Ala Glu Ala
20 25 30

Ile Ala Leu Tyr Arg Gln Leu Ile Ala Arg His Pro Asp Leu Asp Tyr
35 40 45

Val Arg Leu Glu Leu Ala Thr Met Leu Met Glu Asp Arg Gln Phe Ala
50 55 60

Gln Ser Asp Ala Glu Leu Ala Asp Leu Arg Leu Ala Ser Leu Glu Pro
65 70 75 80

Ala Ala Gln Arg Ser Val Met Gln Tyr Arg Gln Ala Leu Glu Gln Gln
85 90 95

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

Val Asn Ser Ala Asn Arg Asp Pro Met Leu Tyr Leu Pro Val Ala Thr
115 120 125

Arg Arg Gly Pro Leu Trp Val Pro Phe Ala Lys Ser Arg Asp Ala Leu
130 135 140

Pro Lys Ser Asp Trp Gly Leu Lys Tyr Ser Gly Ser Ala Asn Val Glu
145 150 155 160

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

165 170 175

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

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

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

Leu Ser Tyr Leu Lys Val Thr Ser Asp Leu Pro Met Tyr Ala Arg Asp
370 375 380
Arg Thr Glu Val Ser Leu Met Leu Glu Lys Arg Phe
385 390 395

<210> 31

<211> 1332

<212> DNA

<213> A. mimigardefordensis SLAM 1

<400> 31

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cgcacgttgc gactcggtgc cgccgaattg tcccgttatc ccgggctgct tttcaaggtg 120

ctgttacagg cgctttcggc caatcaggaa gaggtcgtgc tgaaattatt accgtattat 180

cggcagcagc ctgacgccga tgcccgcctg attcagtggg gagaggcgat gatggcacgc 240

agacaacggc gttatgacga gtcgatccgg atgtatcgcg atacgctcgc gcgtgaaccg 300

cagaacctgc cggtgcgcat gcaactggct acgactctgt ttctgaacca tgaggacgag 360

gcggcgctgg accagttcga gcggattcgc gccatgaatt tacccgcttc ggcaacacat 420

gcagtgaatc gttatattga ggctgttcac caacgggatc aatgggacat cagcggcggg 480

ctgtcgtata tccgggatga taacgtcaac aatgctccca ggccggatac aacgctttat 540

ggttttcgtg catgggagcc ggaatccgcc tccggtgcac aataccggat acaactgggg 600

cgccgcttgc ctctgcgaaa ccaatactat aaccgtgttg atatcgagac cggtggcaag 660

cagtacttct caaatcgaca atatagtgaa tcgaatgcaa ctgtcagttg gtcgctcggc 720

gggcagaccg gtaaccgcga tattcgtttg ggcccgatgt acgaaaagaa gtggtatgca 780

ggcgggcggg caacgagcga ttctctgaaa caatattccg cctttaccgg gctggcgctg 840

caggccagtt actggttcaa ttcacactgg cagtggcgca cgcaactgca atgggggcgg 900

gagcgcttta atcgccaatc gtacctggat ggaaccacgt tgctctggtc gaacacagct 960

ttctatctga gcagtgcagc ccggttctgg aatgccgggg tggattatta tcgcaagggc 1020

gcccgggaca aggcgcatgc tttccacttg tggaacgcac gggcagggtg gggccaggac 1080

tggccgctgg gaatatcgac ttatttacag atcagttata gccagcgcaa atacgagggg 1140

taccggctgt ttcttgcgca aaggcagaaa aacaaggaaa ccgttgcgca gttgtcagtc 1200

tggcaccgtg gtctgcactt tctcggcttt acgccgcgcc tgacgttcag ttatcaatcc 1260

gtgcgtagca atcatgcctt ttaccagttc gataaatccc gcgtctttgt tgacgtgagc 1320

cgacggtttt ga 1332

<210> 32

<211> 443

<212> PRT

<213> A. mimigardefordensis SLAM 1

<400> 32

Met Val Ser Pro Leu Arg Asp Glu Pro Gly Asn Gly Ala Asp Thr Ala
1 5 10 15
Met Arg Thr Pro Arg Thr Leu Arg Leu Gly Ala Ala Glu Leu Ser Arg
20 25 30
Tyr Pro Gly Leu Leu Phe Lys Val Leu Leu Gln Ala Leu Ser Ala Asn
35 40 45
Gln Glu Glu Val Val Leu Lys Leu Leu Pro Tyr Tyr Arg Gln Gln Pro
50 55 60

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

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

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

245 250 255

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

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

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

<210> 33
<211> 1401

<212> DNA
<213> A. minor SLAM 1
<400> 33
atgaaaaaat acttatccct tatccttttt attcccctag ttgcaaacgc agcccccgaa 60

ttggaaatca aacctgccaa gccaacattg ccaacacaag cggttatttt ttcagaaaaa 120

tcagcaaata atggggaaat cactttaacc caagagctga tcagtaaccc tgaacttact 180

cgtcaaatgt taaatcgggc gattgatagc cgacaatttc atttattgcc tgagctggtg 240

cagatttatc aacaaacgcc taatcctgat ttggtgctga ttgattatgc caacggcatt 300

attttggcaa gtcaggggga ttataaaacg gcaatcgatc tctatcgtgg cattattgcg 360

aagcatccta attttcagcc tgtgcgtttt cgtttagcac aaatgttgtt tgaagatcgg 420

caaaatgaag ccgcacttgc gcaatttcgt aagctacaag cggacggatt accgccacaa 480

attgcaaatg gggtggaaca atatattgct gccattcaga aacgttcggg ttggtcattc 540

gactttggtg tgaattattt gcacgaaagc aatgttaata atgcttcaag ctcgccttat 600

gttcgagtgg ggaatgtacc gtttaagaaa acggaagaat cattaccgca atcagcaaat 660

gggttgagct atcatctaaa tttggctaag aattggaatg ttagcggatc ccattatcta 720

catttcgaga accaatttag cggaaaatcc tattgggata atcatcaatt tgacgatcag 780

caaaaccgtt caagtcttgg ctatcaatat caaaatgctc aaagtcgtct tgctttttg 840

ccttattatg aaatgcgttg gtatggtaat catcgctaca atcacggcta tggtgttcgg 900

ggagaagtag agcattggct tacatcacaa tggcagcttt ctacggctgg tgaaatgggc 960

aaactcaaac atcggggcga aaatcagctt gcagatagta cgacattatt tggttctgct 1020

acgttactct acgcctttga tgcgaaaagt tatctctatg gtggtgtaga tttgttgcga 1080

gatcggacgt tagaacgttc tttagcctca aaacgttata cagggcgaat tggttggggg 1140

caagaatggt ggggcggaat ttccagccgt attcagctca gttatggcaa acgtaaattt 1200

gaccaagctc accgcatttt taatcaaatt cgtcaagata gggagttagg tttgaatgtt 1260

acactttggc atcgtaacct gcatttctgg gggattacgc cgaaaatcag ttatcaatat 1320

cagcgtgtaa attccaattt agcggatctt tattcgtata aacgaaatcg agtttatttg 1380

agttttgaga aaacgtttta a 1401

<210> 34

<211> 466

<212> PRT

<213> A. minor SLAM 1

<400> 34

Met Lys Lys Tyr Leu Ser Leu Ile Leu Phe Ile Pro Leu Val Ala Asn

1 5 10 15

Ala Ala Pro Glu Leu Glu Ile Lys Pro Ala Lys Pro Thr Leu Pro Thr

20 25 30

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

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

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

His Leu Asn Leu Ala Lys Asn Trp Asn Val Ser Gly Ser His Tyr Leu
225 230 235 240
His Phe Glu Asn Gln Phe Ser Gly Lys Ser Tyr Trp Asp Asn His Gln
245 250 255
Phe Asp Asp Gln Gln Asn Arg Ser Ser Leu Gly Tyr Gln Tyr Gln Asn
260 265 270

Ala Gln Ser Arg Leu Ala Phe Leu Pro Tyr Tyr Glu Met Arg Trp Tyr
275 280 285

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

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

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

<210> 35

<211> 1437

<212> DNA

<213> A. minor SLAM 2

<400> 35

atgaaaaaat ctgcccaaat cttaccgctt gtgttgttca gtttgccaat tttggcaaat 60

ccagccgata acactgagca aaaactgcaa aatgtggcta aaccgcaagc cccacaaaaa 120

tcattacctg atgcaacaaa tcataccgca agcaaagtgg tggatattac tgaagcggag 180

ttattacaaa attactctct cacacaacat ttgctttctg aggcaattta cactcgacaa 240

gcgggctttt taagccaaat tcttgcaatt tatcagaaat ttctacagcg agatttaatt 300

ttagaaaaat ttgctcaagc aaaattatat ggtttaaatg agcagtattc gcctgccatt 360

gcccttttatc gtgaaattct cgctgaaaag ccggatttaa atgcggtacg ggttgagttg 420

gcgattttac tctttcgaac taaacagaat aatgctgcgc tagaccaatt taacaaagcc 480

aaaagtgttg aaaacctccc ggcaccggta gccgatttaa ttgatgccta taccggcgca 540

atcaataagc aagatgagtg gcagtttggc gcgtctgttt attatgtaaa tacacacaac 600

gtcaataaca cctccgatgc gacagaaatt gaaaataccg gctatgttaa aggtgaagga 660

atgaagcctc gttcagctaa aggatttggc tttaatgcag atatttcacg agattttaac 720

ttatttagta gccattattt aagttttgaa aataatgctt acggtaaaat ttattggaat 780

agccacgaag atgatgatat aagcaatcgt actttattag ggtatagtta taaaacggtt 840

gatggtcaat tccgtttact gccatttttt gaaaaacgtt cggtaggtaa tcagtcgtat 900

cgccgtacaa ggggggcgcg agccgaatgg aattattggt ttaacccaaa ttggcaaatc 960

tcaacagcgc ttgagtatgg taaacagaat aattatgaca gcacagctca agacggctca 1020

accaaattag cctcagcgac cttgctttgg ttgcgcaacc ctcagcaatt cttctatttg 1080

ggaagcgact ttaatcgtga agatgtaaaa gtgaaacaat atggctcaga caccaaaagc 1140

gtacgtttag gctggggaca agaatggaat ttatggggct tatccacccg cttgaacctg 1200

tcatttatga aacgggatta taaagatatt gctaaattag gtggtttttt atcgctcggc 1260

aaggtaaggg aagataaggt ttactcttca agtttaacct tatggaaacg ggattggcat 1320

ttatggaata ttacacctaa attacaattt agttggaaaa aatatgacag caacctacca 1380

acactctatt cctacacgga caaaaacata aatttgttgt ttgaaacgag gttttaa 1437

<210> 36

<211> 478

<212> PRT

<213> A. minor SLAM 2

<400> 36

Met Lys Lys Ser Ala Gln Ile Leu Pro Leu Val Leu Phe Ser Leu Pro

1 5 10 15

Ile Leu Ala Asn Pro Ala Asp Asn Thr Glu Gln Lys Leu Gln Asn Val
20 25 30
Ala Lys Pro Gln Ala Pro Gln Lys Ser Leu Pro Asp Ala Thr Asn His

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

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

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

225 230 235 240
Leu Phe Ser Ser His Tyr Leu Ser Phe Glu Asn Asn Ala Tyr Gly Lys
245 250 255
Ile Tyr Trp Asn Ser His Glu Asp Asp Asp Ile Ser Asn Arg Thr Leu

260 265 270

Leu Gly Tyr Ser Tyr Lys Thr Val Asp Gly Gln Phe Arg Leu Leu Pro

275 280 285

Phe Phe Glu Lys Arg Ser Val Gly Asn Gln Ser Tyr Arg Arg Thr Arg

290 295 300

Gly Ala Arg Ala Glu Trp Asn Tyr Trp Phe Asn Pro Asn Trp Gln Ile

305 310 315 320

Ser Thr Ala Leu Glu Tyr Gly Lys Gln Asn Asn Tyr Asp Ser Thr Ala

325 330 335

Gln Asp Gly Ser Thr Lys Leu Ala Ser Ala Thr Leu Leu Trp Leu Arg

340 345 350

Asn Pro Gln Gln Phe Phe Tyr Leu Gly Ser Asp Phe Asn Arg Glu Asp

355 360 365

Val Lys Val Lys Gln Tyr Gly Ser Asp Thr Lys Ser Val Arg Leu Gly

370 375 380

Trp Gly Gln Glu Trp Asn Leu Trp Gly Leu Ser Thr Arg Leu Asn Leu

385 390 395 400

Ser Phe Met Lys Arg Asp Tyr Lys Asp Ile Ala Lys Leu Gly Gly Phe

405 410 415

Leu Ser Leu Gly Lys Val Arg Glu Asp Lys Val Tyr Ser Ser Ser Leu

420 425 430

Thr Leu Trp Lys Arg Asp Trp His Leu Trp Asn Ile Thr Pro Lys Leu

435 440 445

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

450 455 460

Tyr Thr Asp Lys Asn Ile Asn Leu Leu Phe Glu Thr Arg Phe

465 470 475

<210> 37

<211> 1296

<212> DNA

<213> A. minor SLAM 3

<400> 37

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acacttgaag agcaattaaa gcaagctact taccaaaata atagcggtca aattcaatct 120

ttactttacc aatatcaaca gcagcctcag caagatttga cattaaagtc ttatgcagaa 180

gctaagctag ccgctttaca gcataactat gacgttgcta ttcgtattta ccgaaaaata 240

ttgagcgaac gacctgaact aaattcaatt cgaatggaat tggcaaaagt actctttgcc 300

gatcgacaag atagcgcagc aagagtgcag tttgataaag tgaaaagtgt caaaaatcta 360

ccgtcttcgg cataccaact tattgaacgt tatattgatg ctctcaattc cagaaatagt 420

tggcaatttg atgcgagcat ttcctatctt aaaacggata atgtcgaaaa tgtttcatca 480

tcttcagtca ttgaaaatac aggatttgta aaaggtgcag gaatgttgcc gcaaaaagca 540

cagggttttg cctataattt gggtataaat cgtgatttta atctaatagg ttcacattat 600

ctcggcgtga gtaatgaaac ctacggcaaa acctattggg ataaccacca atatgacgat 660

ctctttagcc gtacttttat cggttatgct tacaaaaaga atgatacgac tttgcgatta 720

caaccctttt atgaaaaacg ctggtatgga ggcaattcat ttcattggtc aaatggcgca 780

gaaatcagtt acagtttttg gctttcacaa aattggcaaa gccaaaccgc acttgaatat 840

gaaaaacgcc gttttttcaa agataacccg caggcaggga atattcgaac agcttcaaca 900

acgttgattt ggtatcgaaa ccccgaacaa atttttttatc tcggagcagc tttttctcag 960

caacgcttac aagagcgaca atacagctct gatattcaga atttacgttt aggttggttg 1020

caagaatacg cttttggaat ttcaacaaaa ttaaatctct cttttactca tcgtcaattt 1080

aaagatcaag cgatactggg aggtatcttg ccattaagca aaactcgcca agatcagatt 1140

tattcggttt ttgcacaagt gtggaaacga gattggcatt tatggggtat tacacctaaa 1200

ttaaatttgg aatggcgtaa gcagaaaagt aatttggata cgctttattc ctataaaatg 1260

cataacgtta cactcgcttt tgaaaagact ttctaa 1296

<210> 38

<211> 431

<212> PRT

<213> A. minor SLAM 3

<400> 38

Met Arg Ser Phe Phe Leu Leu Ala Leu Cys Cys Ser Asn Ile Val Phe

1 5 10 15

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

20 25 30

Asn Asn Ser Gly Gln Ile Gln Ser Leu Leu Tyr Gln Tyr Gln Gln Gln
35 40 45

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

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

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

Gln Pro Phe Tyr Glu Lys Arg Trp Tyr Gly Gly Asn Ser Phe His Trp
245 250 255
Ser Asn Gly Ala Glu Ile Ser Tyr Ser Phe Trp Leu Ser Gln Asn Trp
260 265 270
Gln Ser Gln Thr Ala Leu Glu Tyr Glu Lys Arg Arg Phe Phe Lys Asp

275 280 285

Asn Pro Gln Ala Gly Asn Ile Arg Thr Ala Ser Thr Thr Leu Ile Trp

290 295 300

Tyr Arg Asn Pro Glu Gln Ile Phe Tyr Leu Gly Ala Ala Phe Ser Gln

305 310 315 320

Gln Arg Leu Gln Glu Arg Gln Tyr Ser Ser Asp Ile Gln Asn Leu Arg

325 330 335

Leu Gly Trp Leu Gln Glu Tyr Ala Phe Gly Ile Ser Thr Lys Leu Asn

340 345 350

Leu Ser Phe Thr His Arg Gln Phe Lys Asp Gln Ala Ile Leu Gly Gly

355 360 365

Ile Leu Pro Leu Ser Lys Thr Arg Gln Asp Gln Ile Tyr Ser Val Phe

370 375 380

Ala Gln Val Trp Lys Arg Asp Trp His Leu Trp Gly Ile Thr Pro Lys

385 390 395 400

Leu Asn Leu Glu Trp Arg Lys Gln Lys Ser Asn Leu Asp Thr Leu Tyr

405 410 415

Ser Tyr Lys Met His Asn Val Thr Leu Ala Phe Glu Lys Thr Phe

420 425 430

<210> 39

<211> 1386

<212> DNA

<213> A. nasoniae SLAM 1

<400> 39

atgctctttt ttgttatgga ataaaaaatg actaacagga aacgattaat tataatccta 60

tttatttctt atttttttca tataaaatta actatcgcta attcattgat aataaataat 120

acacaaatga ataaaataaa taataaaaat tatattaata atatttttat tgctattaat 180

aaaaaagatt ggcatcaagt tgaagattat ttaaatcaat taataataag taattatcac 240

gataagagtt taatctattt tattcagggt tgtttatcat ataaaaatcg agagcctcaa 300

tctgctatgc actatttatc ccaggcgata ataataaatc ctcattttac gcgtgccaag 360

ctcgatttaa gttatattta tattgaaaac cgaatttatc ataaagcaaa gttattatta 420

aatgaattaa tagcacagca agatttacct gacctggtta agaaaaaaat aaaatatctt 480

ctcactgtgg ttaataataa aaatcctttc tttgccacac tttcactagg ttaccaccta 540

accgataatc tgaataaatc gcctggtagc ccagcagagt gcttacaaaa aaatagtgct 600

ggcgattgcc gattaactcg taaaatgcca aaaaaaatta cttcatcagg cttttcttta 660

ttcggtatga cccaacaggc atttatgttg caagagcctc atgcggtttt tattcgccta 720

atggcaaatg gtcaaatcta tcggcaaaac aatacctata atggatataa agccaatatt 780

tatgctggct accattttca atcctcatac cattatttat tagccggccc cttattgggt 840

tatgaacaag gggaagaaga tccaaatgct tatgaaatag ggggaaaaat tgagtggcgt 900

tatcgtcctg atatagccgc taaattagat tttgtcctaa atcaccaatt taaatggaaa 960

gactattacc aaggacaaca taataatggc ctgaagcatg aaatttcttt ttccattaat 1020

tatcctctta acaatattga ttggtatctc tctttgggtt cttctcaaca tttccatcaa 1080

tggcaaataa acgattatca ccgctatgat attggcggtg gcgttaaatt taagtcatta 1140

ccttatctag aaaccagttt ttcatcactt tggaatcaac atcaatttaa acactttgat 1200

aaccgattag gcgctatgcg gcgtgataca gaatggatct atgcaattaa attaaaacta 1260

accataaaaa ttattggctt cacaccctct attacctttt ttcatcgcaa gaataatagc 1320

aatgtcggct ggctttatcg ctatcaaaaa aacgatctac aactcaattt tgaacgttat 1380

ttttga 1386

<210> 40

<211> 461

<212> PRT

<213> A. nasoniae

<400> 40

Met Leu Phe Phe Val Met Glu Ile Lys Met Thr Asn Arg Lys Arg Leu

1 5 10 15

Ile Ile Ile Leu Phe Ile Ser Tyr Phe Phe His Ile Lys Leu Thr Ile

20 25 30

Ala Asn Ser Leu Ile Ile Asn Asn Thr Gln Met Asn Lys Ile Asn Asn

35 40 45

Lys Asn Tyr Ile Asn Asn Ile Phe Ile Ala Ile Asn Lys Lys Asp Trp

50 55 60

His Gln Val Glu Asp Tyr Leu Asn Gln Leu Ile Ile Ser Asn Tyr His

65 70 75 80

Asp Lys Ser Leu Ile Tyr Phe Ile Gln Gly Cys Leu Ser Tyr Lys Asn

85 90 95

Arg Glu Pro Gln Ser Ala Met His Tyr Leu Ser Gln Ala Ile Ile Ile

100 105 110

Asn Pro His Phe Thr Arg Ala Lys Leu Asp Leu Ser Tyr Ile Tyr Ile

115 120 125

Glu Asn Arg Ile Tyr His Lys Ala Lys Leu Leu Leu Asn Glu Leu Ile

130 135 140

Ala Gln Gln Asp Leu Pro Asp Leu Val Lys Lys Lys Ile Lys Tyr Leu

145 150 155 160

Leu Thr Val Val Asn Asn Lys Asn Pro Phe Phe Ala Thr Leu Ser Leu

165 170 175

Gly Tyr His Leu Thr Asp Asn Leu Asn Lys Ser Pro Gly Ser Pro Ala

180 185 190

Glu Cys Leu Gln Lys Asn Ser Ala Gly Asp Cys Arg Leu Thr Arg Lys

195 200 205

Met Pro Lys Lys Ile Thr Ser Ser Gly Phe Ser Leu Phe Gly Met Thr

210 215 220

Gln Gln Ala Phe Met Leu Gln Glu Pro His Ala Val Phe Ile Arg Leu

225 230 235 240

Met Ala Asn Gly Gln Ile Tyr Arg Gln Asn Asn Thr Tyr Asn Gly Tyr

245 250 255

Lys Ala Asn Ile Tyr Ala Gly Tyr His Phe Gln Ser Ser Tyr His Tyr

260 265 270

Leu Leu Ala Gly Pro Leu Leu Gly Tyr Glu Gln Gly Glu Glu Asp Pro

275 280 285

Asn Ala Tyr Glu Ile Gly Gly Lys Ile Glu Trp Arg Tyr Arg Pro Asp

290 295 300

Ile Ala Ala Lys Leu Asp Phe Val Leu Asn His Gln Phe Lys Trp Lys

305 310 315 320

Asp Tyr Tyr Gln Gly Gln His Asn Asn Gly Leu Lys His Glu Ile Ser

325 330 335

Phe Ser Ile Asn Tyr Pro Leu Asn Asn Ile Asp Trp Tyr Leu Ser Leu

340 345 350

Gly Ser Ser Gln His Phe His Gln Trp Gln Ile Asn Asp Tyr His Arg

355 360 365

Tyr Asp Ile Gly Gly Gly Val Lys Phe Lys Ser Leu Pro Tyr Leu Glu

370 375 380

Thr Ser Phe Ser Ser Leu Trp Asn Gln His Gln Phe Lys His Phe Asp

385 390 395 400

Asn Arg Leu Gly Ala Met Arg Arg Asp Thr Glu Trp Ile Tyr Ala Ile

405 410 415

Lys Leu Lys Leu Thr Ile Lys Ile Ile Gly Phe Thr Pro Ser Ile Thr

420 425 430

Phe Phe His Arg Lys Asn Asn Ser Asn Val Gly Trp Leu Tyr Arg Tyr

435 440 445

Gln Lys Asn Asp Leu Gln Leu Asn Phe Glu Arg Tyr Phe

450 455 460

<210> 41

<211> 1491

<212> DNA

<213> A. oleivorans SLAM 1

<400

> 41

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gaagacacac agcttcgtct caatcaaagc ttggaccaaa cgcttttaca agaacagcgc 120

cagtttcacg agcagggaac cattcgtagt accgagcaat taccaaaact tcaaattaat 180

ggacaagaat atagtgttga gcaaaatccg aatgatcttg ccaaggcgtt atatttggca 240

gtcatgcaaa aacagtggct caaagccacg gtttatttag aacattataa aaaatatgtt 300

ggctacgatc gggctttaac cgactttgcc gaaggggcag ttgcacgttc tcagggtcaa 360

ctgaaattgg ctgaacaaaa atttcaaagc agcctaaaac aacaacctca taatttaatt 420

tgtgaacttg agttagcgcg cgtgctgttt gaacaacaga agaataagga agcagcacgc 480

ctttttattt ccattcaaaa ccaactgaaa caaagtgacc ctgcggtaat cccatctggg 540

gttttaacaa cagtgaatac ctttgttcaa gcattaaaaa aacgagactc ttggcaaggc 600

tcggtttcag cgggttatac ctatgtcagt aatttaaata gttcgtctga acagagcaaa 660

acatggacac tttatggcag agatagtgaa ggtaatatta tcccagttag ggaagttact 720

cgtggaactc ctaaagctga gtcggcaacg ggtttagatt acgaagccag tctgattaaa 780

cgctatgcga ttaaggggca tcatggcgtg gctttacgtg cgctggcgtt tggacagtcc 840

tataacgacc acgcggcatt taatgaatct accatcaaca ttaatgcagg ctacagctac 900

tttgacttaa aaaatcaaat tggggtgagt ccgctttttg aacataaacg ttatggcaat 960

gatggtcttt acaatgcctg gggtgcgcgt gccgagtgga tgcattttat ctctgcagat 1020

aaagctttca agcttgaagc tgagagtaaa gatttaaatt atcagaaata taaaacccta 1080

gatggggtag aaagctcagc ttttgctact ttctggaaga tttttccaga ccagtggact 1140

gtttttggtg gtttagatgt agtcgaccat tcgacccaag aaaaatatat ggctgcctac 1200

cagcagcaag gtatgcggtt gggcttaagc aaatcttgga gtacaggatt taacactact 1260

ttgctgagtt cttaccgttg gcgtcagttt gataaatatg cggaaacttt cttagcacgc 1320

cgtcatgatt ttgaacagaa ctatactttt gttgtgcaaa tgccgcgctt tgagttttat 1380

ggcatgacgc ctaatttaac ctaccgctat aaccataata aaagtaatgt cgattggctg 1440

tattcctacg ataaacacaa cattagcctc aagcttgagc atcgttttta g 1491

<210> 42

<211> 496

<212> PRT

<213> A. oleivorans SLAM 1

<400> 42

Met Lys Arg Thr Leu Leu Cys Cys Leu Thr Leu Leu Ser Cys Pro Phe
1 5 10 15

Leu Tyr Ala Asp Glu Asp Thr Gln Leu Arg Leu Asn Gln Ser Leu Asp
20 25 30

Gln Thr Leu Leu Gln Glu Gln Arg Gln Phe His Glu Gln Gly Thr Ile
35 40 45

Arg Ser Thr Glu Gln Leu Pro Lys Leu Gln Ile Asn Gly Gln Glu Tyr
50 55 60

Ser Val Glu Gln Asn Pro Asn Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

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

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

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

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

325 330 335

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

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

Asn Leu Thr Tyr Arg Tyr Asn His Asn Lys Ser Asn Val Asp Trp Leu
465 470 475 480
Tyr Ser Tyr Asp Lys His Asn Ile Ser Leu Lys Leu Glu His Arg Phe
485 490 495

<210> 43
<211> 1323
<212> DNA
<213> A. oryzae SLAM 1
<400> 43

gtgaaagtca aaaaatccgt attgaatgtc tgcgccgtcc tgtcgttgct gggctgcggc 60
gccgcctggg gggccgatgc caccctgggc caggccggac gcctgctgga aagcggcaag 120
ggcagcgaag cctatgtcct gctggaaagc ctggagcccg aacgggccgg ggaaatcgaa 180

tacgacctgc tgctggggct ggccgccctg gaggcgggcc agaacacccg ggcggtcttc 240
gccctggaac gggtgctggc ccaggaaccg aacaacgccc gggcccgggc cgagattgcc 300

cgggcctatc tggccctggg cgagaccaag aatgcccgcc gcgagttcga gaatgtgcgc 360

agcatgggcg tgccggccga agtgggcagc accatcgagc gtttcctggc agcagtggag 420

cgcctggagg acgaagcccg cacccaggtc cgcggctatc tggagctggg tctgggcatc 480

gacagcaacg tcaacagcgg caccagccgc ggcgagtacg ccattccctt cttcggcggc 540

tggatgttcc cggtcggcag cggcgccaag gaaaacggtg acaccttcac caacgtggcc 600

ggcggcatca atttccgcac tcccctgcag gccggcctgg ccgtcaccgg tggtgccgcc 660

ttctcccagc gcctcaacag caacgatacc gatttcgaca acggcagctg ggacgccaat 720

ctgggcctga ccaaggcggt ggacaagaac cagtattccc ttgccctcca ggccagcacc 780

ttccgcctca acggcgagcg ctaccgggac gccatgggct tcaccggcca atggcagcac 840

aactacgact cccgcaacca ggccagcctc tacctccagt acgccagcct cacctacccg 900

ggccaggcga tccgcaacac ggaccgtttc gtcgtcggcg gcgcctacgc ccacgccttc 960

cgcgaggggc aggtcatcta cggcggcgcc tacgtgggca ccgagatgga gaagaacgag 1020

ctggccacct tcatgggcca cgacctggtg ggcgtgcgca tcggcggcca gatggacttg 1080

gccccgcgct gggtcggctt tgccaacgcc aatctggaac agcgccgcta ccacggcagc 1140

gacccttct tcctcagcat ccgccaggac ctgcaggcca atatcaacgt gggggccaat 1200

ttcagtccca gccgggaatg gcacatcacg ccccagttca gctatacccg caacgactcc 1260

aacctgaccc tcaacgatta ccaccgccag gtggtctccg ttaccgtccg tcgcgatttc 1320

tga 1323

<210> 44

<211> 440

<212> PRT

<213> A. oryzae SLAM 1

<400> 44

Met Lys Val Lys Lys Ser Val Leu Asn Val Cys Ala Val Leu Ser Leu
1 5 10 15

Leu Gly Cys Gly Ala Ala Trp Gly Ala Asp Ala Thr Leu Gly Gln Ala
20 25 30

Gly Arg Leu Leu Glu Ser Gly Lys Gly Ser Glu Ala Tyr Val Leu Leu
35 40 45

Glu Ser Leu Glu Pro Glu Arg Ala Gly Glu Ile Glu Tyr Asp Leu Leu
50 55 60

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

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

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

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

305 310 315 320

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

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

<210> 45
<211> 1521
<212> DNA
<213> A. paragallinarum SLAM 1

<400> 45
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ttaccaagct atgcagatga aaatgcagaa caatctctgc aactgtggca agactcccaa 120
caaaaaatca atcaacaacg aaaagaaacg gcattattca cagcctcaaa tcagcaagaa 180
aatgaaatca ccttagatgg acaatctttt tctgtggcaa atactgaagc cgatgtaggg 240
caagcgcttt atattgcggt aaatcagcaa ctttggcatt atgcagaaaa gtttttacag 300
caatatcgcc aatttcctca acataaaaaa gaacttgtat ggtttgcaca aggagcgctc 360
gcccgtcaac gtggagagtt ggctaaggcg gaaactgaat atcaaaaatt attacaatct 420

gaacctgatt ttttacgggg acaattagat ttagcacgca ttctatttga aaataaaaag 480
aataaagaag ccagcaaatt gttttctcag cttgttcaaa tgccattacc caatgaagtg 540

agcacattat taaaggaata tttacaagtt ttaaaagagc gggagcaatg gcacggtgga 600

ttacgtgtgg gttaccgcta tcaaaaaaat atcaatcaat cctcagaaca ttatcgctgc 660

ctattatttt ctggcacaac ttgcatcgtt gaacgcgctg cccctaaagc gattaacgca 720

aaaggttggg gatatgagct tagcctaaat aaaaaattta atttaacagg gcatcacgga 780

ataaatattt atttcaatag cgaaggacaa tattatccaa cggctcgaca atataatgat 840

accacattta aaacttatat tggatacgct tttcaagatg cgaaaaaaga gctcgttatc 900

gccccacttt ttaaatatga atggtatgcc aataagcgtt attatcacgc ttttggggta 960

catttagaat ggatgcattc tcttttaaaa aaacattttc tcaatgtgca atttgaacaa 1020

aaacatttgt tttataatgc tggttacagt gcgatagata aagcggacat ttcttcttta 1080

tatgccagtt ggtattacac tcctaccaat aacactacat tatttactgg gttcgatggg 1140

atataccgca aagttaaaga gaaaacaaat agctataaaa tgctgggggc gagatttggg 1200

ctttatcatc aatttaatga aaaattagat ctgaccttgc ttgcttcgat aaaaagcacc 1260

cgttacttgc agcacaatgc tattttagaa acaaaaagaa aagataatca ctttatttat 1320

caagcgattt tgtcttttcc caatgtgttt tataaaggga taacacccaa tgtaatcatc 1380

aaaagaacac ataatcatag caatgtagat tggctttatt cttataagca aactgaatta 1440

caatttaatg taagttttgt ttttcaagcc ttactttctc gcatagaaaa agcagcgcta 1500

aaaagggatt ttagtgctta a 1521

<210> 46

<211> 506

<212> PRT

<213> A. paragallinarum SLAM 1

<400> 46

Met Leu Lys Pro Met Lys Lys Ser Phe Leu Ile Leu Leu Ser Val Ala

1 5 10 15

Phe Leu Thr Ala Leu Pro Ser Tyr Ala Asp Glu Asn Ala Glu Gln Ser

20 25 30

Leu Gln Leu Trp Gln Asp Ser Gln Gln Lys Ile Asn Gln Gln Arg Lys

35 40 45

Glu Thr Ala Leu Phe Thr Ala Ser Asn Gln Gln Glu Asn Glu Ile Thr

50 55 60

Leu Asp Gly Gln Ser Phe Ser Val Ala Asn Thr Glu Ala Asp Val Gly

65 70 75 80

Gln Ala Leu Tyr Ile Ala Val Asn Gln Gln Leu Trp His Tyr Ala Glu

85 90 95

Lys Phe Leu Gln Gln Tyr Arg Gln Phe Pro Gln His Lys Lys Glu Leu

100 105 110

Val Trp Phe Ala Gln Gly Ala Leu Ala Arg Gln Arg Gly Glu Leu Ala

115 120 125

Lys Ala Glu Thr Glu Tyr Gln Lys Leu Leu Gln Ser Glu Pro Asp Phe

130 135 140

Leu Arg Gly Gln Leu Asp Leu Ala Arg Ile Leu Phe Glu Asn Lys Lys

145 150 155 160

Asn Lys Glu Ala Ser Lys Leu Phe Ser Gln Leu Val Gln Met Pro Leu

165 170 175

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

180 185 190

Glu Arg Glu Gln Trp His Gly Gly Leu Arg Val Gly Tyr Arg Tyr Gln

195 200 205

Lys Asn Ile Asn Gln Ser Ser Glu His Tyr Arg Cys Leu Leu Phe Ser

210 215 220

Gly Thr Thr Cys Ile Val Glu Arg Ala Ala Pro Lys Ala Ile Asn Ala

225 230 235 240

Lys Gly Trp Gly Tyr Glu Leu Ser Leu Asn Lys Lys Phe Asn Leu Thr

245 250 255

Gly His His Gly Ile Asn Ile Tyr Phe Asn Ser Glu Gly Gln Tyr Tyr

260 265 270

Pro Thr Ala Arg Gln Tyr Asn Asp Thr Thr Phe Lys Thr Tyr Ile Gly

275 280 285

Tyr Ala Phe Gln Asp Ala Lys Lys Glu Leu Val Ile Ala Pro Leu Phe

290 295 300

Lys Tyr Glu Trp Tyr Ala Asn Lys Arg Tyr Tyr His Ala Phe Gly Val

305 310 315 320

His Leu Glu Trp Met His Ser Leu Leu Lys Lys His Phe Leu Asn Val

325 330 335

Gln Phe Glu Gln Lys His Leu Phe Tyr Asn Ala Gly Tyr Ser Ala Ile

340 345 350

Asp Lys Ala Asp Ile Ser Ser Leu Tyr Ala Ser Trp Tyr Tyr Thr Pro

355 360 365

Thr Asn Asn Thr Thr Leu Phe Thr Gly Phe Asp Gly Ile Tyr Arg Lys

370 375 380

Val Lys Glu Lys Thr Asn Ser Tyr Lys Met Leu Gly Ala Arg Phe Gly

385 390 395 400

Leu Tyr His Gln Phe Asn Glu Lys Leu Asp Leu Thr Leu Leu Ala Ser

405 410 415

Ile Lys Ser Thr Arg Tyr Leu Gln His Asn Ala Ile Leu Glu Thr Lys

420 425 430

Arg Lys Asp Asn His Phe Ile Tyr Gln Ala Ile Leu Ser Phe Pro Asn

435 440 445

Val Phe Tyr Lys Gly Ile Thr Pro Asn Val Ile Ile Lys Arg Thr His

450 455 460

Asn His Ser Asn Val Asp Trp Leu Tyr Ser Tyr Lys Gln Thr Glu Leu

465 470 475 480

Gln Phe Asn Val Ser Phe Val Phe Gln Ala Leu Leu Ser Arg Ile Glu

485 490 495

Lys Ala Ala Leu Lys Arg Asp Phe Ser Ala

500 505

<210> 47

<211> 1566

<212> DNA

<213> A. pittii SLAM 1

<400> 47

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caggtttatt gttttatgaa acgaacgctt ttgtgctgtc tgacattgtt gagttgtcca 120

ttttatatg ccgacgaaga cacacagctt cgtctcaatc aaagcttgga ccaaacactt 180

ttacaagaac agcgccagtt tcacgagcag ggaaccattc gtagtaccga gcaattacca 240

aaacttcaaa ttaatggaca agaatatagt gttgagcaaa atccgaatga tcttgccaag 300

gcgttatatt tggcagtcat gcaaaaacag tggctcaaag ccacggttta tttagaacat 360

tataaaaaat atgttggcta cgatcgggct ttaaccgact ttgccgaagg ggcagttgca 420

cgttctcagg gtcaactgaa attggctgaa caaaaatttc aaagcagctt aaaacaacaa 480

cctcataatt taatttgtga acttgagtta gcgcgcgtgc tgtttgaaca acagaaaaat 540

aaggaagcag cacgcctttt tatttccatt caagaccaac tgaaacaaag tgatcccgct 600

gttattcctt ctggggtttt aacaacagtg aataccttg tccaagcatt aaaaaaacga 660

gactcttggc aaggctcgat ttcagcgggt tatacctatg ttagtaattt aaatagttcg 720

tctgaacaaa gcaaaacatg gacgctttat ggcaaagata gtgacggtaa tattatccca 780

attgagcaag ttacccgtgg gacccctaaa gctgaatcgg caacggggtt agattacgaa 840

gccagtctga ttaaacgcta tgcgattaag gggcatcatg gcatggcttt acgtgcactg 900

gcgtttggac agtcctataa cgaccacgcg gcatttaatg aatctaccat taacattaat 960

gcaggctaca gctactttga cttaaaaaat caaattgggg tgagtccgct atttgaacat 1020

aaacgttatg gcaatgatgg tctttacaat gcctggggtg cgcgtgccga gtggatgcat 1080

tttatctctg cagataaagc tttcaagctt gaggctgaga gtaaagattt aaattatcag 1140

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ccagaccagt ggacttttt tggtggtcta gatgtgctcg accattcgac ccaagaaaaa 1260

tacatggctg cctaccaaca gcaaggtgtg cgattgggct taagcaaatc ttggagtaca 1320

ggatttaata ccactttgct gagttcttat cgttggcgcc tgtttgataa atacgcagaa 1380

actttcttag ctcgtcgtca tgattttgaa caaaactata cccttgttgt gcaaatgccg 1440

cgctttgagt tttatggcat gacgcctaat ttaacctatc gctataacca taataaaagc 1500

aatgttgatt ggctgtattc ctacgataaa cacaacatta gtctcaagct tgagcatcgt 1560

ttttag 1566

<210> 48

<211> 521

<212> PRT

<213> A. pittii SLAM 1

<400> 48

Met Gln Lys Glu Ser Lys Tyr Val Gly Ser Phe Cys Phe Trp Ala Phe

1 5 10 15

Ala Trp Leu Leu Gln Val Tyr Cys Phe Met Lys Arg Thr Leu Leu Cys

20 25 30

Cys Leu Thr Leu Leu Ser Cys Pro Phe Leu Tyr Ala Asp Glu Asp Thr

35 40 45

Gln Leu Arg Leu Asn Gln Ser Leu Asp Gln Thr Leu Leu Gln Glu Gln

50 55 60

Arg Gln Phe His Glu Gln Gly Thr Ile Arg Ser Thr Glu Gln Leu Pro

65 70 75 80

Lys Leu Gln Ile Asn Gly Gln Glu Tyr Ser Val Glu Gln Asn Pro Asn

85 90 95

Asp Leu Ala Lys Ala Leu Tyr Leu Ala Val Met Gln Lys Gln Trp Leu

100 105 110

Lys Ala Thr Val Tyr Leu Glu His Tyr Lys Lys Tyr Val Gly Tyr Asp

115 120 125

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

130 135 140

Gln Leu Lys Leu Ala Glu Gln Lys Phe Gln Ser Ser Leu Lys Gln Gln

145 150 155 160

Pro His Asn Leu Ile Cys Glu Leu Glu Leu Ala Arg Val Leu Phe Glu

165 170 175

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

180 185 190

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

195 200 205

Thr Val Asn Thr Phe Val Gln Ala Leu Lys Lys Arg Asp Ser Trp Gln

210 215 220

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

225 230 235 240

Ser Glu Gln Ser Lys Thr Trp Thr Leu Tyr Gly Lys Asp Ser Asp Gly

245 250 255

Asn Ile Ile Pro Ile Glu Gln Val Thr Arg Gly Thr Pro Lys Ala Glu

260 265 270

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

275 280 285

Ile Lys Gly His His Gly Met Ala Leu Arg Ala Leu Ala Phe Gly Gln

290 295 300

Ser Tyr Asn Asp His Ala Ala Phe Asn Glu Ser Thr Ile Asn Ile Asn

305 310 315 320

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

325 330 335

Leu Phe Glu His Lys Arg Tyr Gly Asn Asp Gly Leu Tyr Asn Ala Trp

340 345 350

Gly Ala Arg Ala Glu Trp Met His Phe Ile Ser Ala Asp Lys Ala Phe

355 360 365

Lys Leu Glu Ala Glu Ser Lys Asp Leu Asn Tyr Gln Lys Tyr Lys Thr

370 375 380

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

385 390 395 400

Pro Asp Gln Trp Thr Phe Phe Gly Gly Leu Asp Val Leu Asp His Ser

405 410 415

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

420 425 430

Gly Leu Ser Lys Ser Trp Ser Thr Gly Phe Asn Thr Thr Leu Leu Ser

435 440 445

Ser Tyr Arg Trp Arg Leu Phe Asp Lys Tyr Ala Glu Thr Phe Leu Ala

450 455 460

Arg Arg His Asp Phe Glu Gln Asn Tyr Thr Leu Val Val Gln Met Pro

465 470 475 480

Arg Phe Glu Phe Tyr Gly Met Thr Pro Asn Leu Thr Tyr Arg Tyr Asn

485 490 495

His Asn Lys Ser Asn Val Asp Trp Leu Tyr Ser Tyr Asp Lys His Asn

500 505 510

Ile Ser Leu Lys Leu Glu His Arg Phe

515 520

<210> 49

<211> 1470

<212> DNA

<213> A. pleuropneumoniae SLAM 1

<400> 49

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attgcggaag atcttccaca aaaaatttcc gatcgcttgg atgatcaacg cgtgcagacg 120

gaagtcacta gaccgcgcaa tattgagaat ccgattcgtc atgctcacgt ttcacaaccg 180

actaaagccg ctaaacaaat atcaatgaca aaagaggaat tgattcaacg accggattta 240

ctgtccaacg cacttaatct tgccctctta cagggcaatg ccgaaaccgt cgctttccta 300

ttcccgcttt accgacaaat tccgatacaa taccaagacc ccggttttat aaaatggtct 360

aaagcagtta ttgctcgcca tcacggtaat tatagcgaag ccattcgtca ttaccgcgaa 420

atccttgcga tgtattcgga agcgaccgcc gctcgtttac agctcgccgt ttcgcttttt 480

gaaaataacg aattggaagc ggcggaagat caatttgaaa aagtccgctc cgataacgtt 540

cccgatgaaa ttaaggcgct tgtcgataaa tatatcgccg ctatcgcaca gcgagataga 600

tggacgtttt ccggcggcat gacttatctc aatgatccga atatcaataa tgcaccgaaa 660

gcaggaacca cctacggtaa ctggattgcg ccgaaatcgg aatcggcaca aggaatcggt 720

tttaatttta atatcggtaa aaaatggtct tggggtaacg gtttttataa cgaattgcgc 780

ttgaatacga gcggtaaata ttattggaat aataaaaaat ataacgaagt aagcggaaga 840

ggcagtttag ggttaggcta tcaaaacgct cgctatgacg ttactcttct accgtttatg 900

gaacaaacct tatatgcagg cggttctaaa aataacgaat cggttaaacg tttttctaaa 960

gcgagcggcg caacgcttga aaccagctat tggctttctc ctcaatggca atggaatacc 1020

aactacgagt atgccgaagt ccgctatatg gatcgtaaac atctgaacgg taattatcat 1080

ttcgtttcaa gcggcttaac ttatcttgcc aatgccaaac agtattggtt cggtaatcta 1140

aattacaatc gtaccgcgac acgagataaa gacaatagct atgtacgtcg aggcattagc 1200

ttaggttggg gacaagaatg gggcttagga ctttcaaccc gcatatcgct tagctatgcg 1260

caaaaaaatt ataaagcgcc gcttcctatt ttcggcgtga cacaacgtaa caaagaatac 1320

ggcatcaaca ccagtatttg gcatagagcc attcactatt ggggaatcac accccgctta 1380

acttatagct tcaataaagt aaaaagtagc cacgtctttt acagctacga taaacaccga 1440

gtctttattg aatttagcaa acgcttctaa 1470

<210> 50

<211> 489

<212> PRT

<213> A. pleuropneumoniae SLAM 1

<400> 50

Met Lys Met Arg Phe Lys Leu Phe Ile Thr Thr Phe Ala Gly Leu Ala

1 5 10 15

Ala Leu Pro Val Ile Ala Glu Asp Leu Pro Gln Lys Ile Ser Asp Arg

20 25 30

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

35 40 45

Glu Asn Pro Ile Arg His Ala His Val Ser Gln Pro Thr Lys Ala Ala

50 55 60

Lys Gln Ile Ser Met Thr Lys Glu Glu Leu Ile Gln Arg Pro Asp Leu

65 70 75 80

Leu Ser Asn Ala Leu Asn Leu Ala Leu Leu Gln Gly Asn Ala Glu Thr

85 90 95

Val Ala Phe Leu Phe Pro Leu Tyr Arg Gln Ile Pro Ile Gln Tyr Gln

100 105 110

Asp Pro Gly Phe Ile Lys Trp Ser Lys Ala Val Ile Ala Arg His His

115 120 125

Gly Asn Tyr Ser Glu Ala Ile Arg His Tyr Arg Glu Ile Leu Ala Met

130 135 140

Tyr Ser Glu Ala Thr Ala Ala Arg Leu Gln Leu Ala Val Ser Leu Phe

145 150 155 160

Glu Asn Asn Glu Leu Glu Ala Ala Glu Asp Gln Phe Glu Lys Val Arg

165 170 175

Ser Asp Asn Val Pro Asp Glu Ile Lys Ala Leu Val Asp Lys Tyr Ile

180 185 190

Ala Ala Ile Ala Gln Arg Asp Arg Trp Thr Phe Ser Gly Gly Met Thr

195 200 205

Tyr Leu Asn Asp Pro Asn Ile Asn Asn Ala Pro Lys Ala Gly Thr Thr

210 215 220

Tyr Gly Asn Trp Ile Ala Pro Lys Ser Glu Ser Ala Gln Gly Ile Gly

225 230 235 240

Phe Asn Phe Asn Ile Gly Lys Lys Trp Ser Trp Gly Asn Gly Phe Tyr

245 250 255

Asn Glu Leu Arg Leu Asn Thr Ser Gly Lys Tyr Tyr Trp Asn Asn Lys

260 265 270

Lys Tyr Asn Glu Val Ser Gly Arg Gly Ser Leu Gly Leu Gly Tyr Gln

275 280 285

Asn Ala Arg Tyr Asp Val Thr Leu Leu Pro Phe Met Glu Gln Thr Leu

290 295 300

Tyr Ala Gly Gly Ser Lys Asn Asn Glu Ser Val Lys Arg Phe Ser Lys

305 310 315 320

Ala Ser Gly Ala Thr Leu Glu Thr Ser Tyr Trp Leu Ser Pro Gln Trp

325 330 335

Gln Trp Asn Thr Asn Tyr Glu Tyr Ala Glu Val Arg Tyr Met Asp Arg

340 345 350

Lys His Leu Asn Gly Asn Tyr His Phe Val Ser Ser Gly Leu Thr Tyr

355 360 365

Leu Ala Asn Ala Lys Gln Tyr Trp Phe Gly Asn Leu Asn Tyr Asn Arg

370 375 380

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

385 390 395 400

Leu Gly Trp Gly Gln Glu Trp Gly Leu Gly Leu Ser Thr Arg Ile Ser

405 410 415

Leu Ser Tyr Ala Gln Lys Asn Tyr Lys Ala Pro Leu Pro Ile Phe Gly

420 425 430

Val Thr Gln Arg Asn Lys Glu Tyr Gly Ile Asn Thr Ser Ile Trp His

435 440 445

Arg Ala Ile His Tyr Trp Gly Ile Thr Pro Arg Leu Thr Tyr Ser Phe

450 455 460

Asn Lys Val Lys Ser Ser His Val Phe Tyr Ser Tyr Asp Lys His Arg

465 470 475 480

Val Phe Ile Glu Phe Ser Lys Arg Phe

485

<210> 51

<211> 1416

<212> DNA

<213> A. pleuropneumoniae SLAM 2

<400> 51

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agtacaccta gccaaataga acatatcgct aaaccaacat cggcaccctt acagcttgca 120

gtggaacaat cgtctcgcca cattttaac gaagctgaat tacgtgctaa tcaggcatta 180

accgaaaaat tactcagcca agctatctat actcgccagc tcactaatat ggaaaaactg 240

gtgataattt atcaagattt taaccaaatt gacccaattt tattgcgcta tgctcaaggt 300

aaaatcgcgc tacttaaagg aaattattca caagctattc gagagtttcg cactattctt 360

gctaaacaac ctgaactaaa taccgtacga attgaactgg caattgcatt actacatgat 420

caacaaacga atgcggcaag tgaacaattc gataaagcta aaagtgccga aaacctacct 480

tataaagtgc agcaactgat tgaacagtat cagcaatatc tggagaaaaa acaagcttgg 540

aagttcaatt tctctgccca ctatgtacgg gatggtaata tcaataacac atccaaacaa 600

actgaaattg agcataccgg ctatgtgaaa cagcctaacc tgttaccaca aactgcgcac 660

ggaattcact attcttttgg actacaaaga gattttaacc tacttggctc gcattacctt 720

agtttcgata atcaaacgca gggggaactt tattgggata atcatgacta cgatgaaatc 780

accaatcgcg ctttgtttgg ctatgcttac aaaaagtcac accaaaccac ccgcgtattg 840

ccattttatg aaaaacgctg gaaacatcat caatcagaac gctggacaaa cggattaagg 900

ctagaacatg catattggct ttctattcac tggcaacttg ctactgcatt cgagtatggg 960

aaaaaacgct atttcgacca gcacatttac aatggcagct ataaacttgc ttcagctacc 1020

ctactctggc tacgtaatcc gcaacagttt ttctttattg gtaccgattt caaccgagat 1080

aaaaccgtat tgaaacaaca tagttctgat accaaaagct tacgtttcgg ctggcagcag 1140

gaatggcaaa cacttggatt atcaagccgc ctgacccttg cttacaccga cagacattat 1200

aaagacactg cggtgctggg tggcaaactt aatctaggta aaattcgcca tgaccgtgtg 1260

aacagcatta atcttaccct ttggaaacga gattggcatt ggttagggct tacacccaaa 1320

ctgcaacttg gctatgctaa acatcatagc aacttaccaa gcctatatgc ttacacggat 1380

aaaaatgcga atctgatcat cgaaagtcgt ttttaa 1416

<210> 52

<211> 471

<212> PRT

<213> A. pleuropneumoniae SLAM 2

<400> 52

Met Lys Lys Phe Thr Leu Leu Phe Phe Phe Pro Thr Leu Leu Phe Ala
1 5 10 15

Gln Asp Pro Asn Ser Thr Pro Ser Gln Ile Glu His Ile Ala Lys Pro
20 25 30

Thr Ser Ala Pro Leu Gln Leu Ala Val Glu Gln Ser Ser Arg His Ile
35 40 45

Phe Asn Glu Ala Glu Leu Arg Ala Asn Gln Ala Leu Thr Glu Lys Leu
50 55 60

Leu Ser Gln Ala Ile Tyr Thr Arg Gln Leu Thr Asn Met Glu Lys Leu
65 70 75 80

Val Ile Ile Tyr Gln Asp Phe Asn Gln Ile Asp Pro Ile Leu Leu Arg
85 90 95

Tyr Ala Gln Gly Lys Ile Ala Leu Leu Lys Gly Asn Tyr Ser Gln Ala
100 105 110

Ile Arg Glu Phe Arg Thr Ile Leu Ala Lys Gln Pro Glu Leu Asn Thr
115 120 125

Val Arg Ile Glu Leu Ala Ile Ala Leu Leu His Asp Gln Gln Thr Asn
130 135 140

Ala Ala Ser Glu Gln Phe Asp Lys Ala Lys Ser Ala Glu Asn Leu Pro
145 150 155 160

Tyr Lys Val Gln Gln Leu Ile Glu Gln Tyr Gln Gln Tyr Leu Glu Lys

165 170 175

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

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

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

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

His Asp Arg Val Asn Ser Ile Asn Leu Thr Leu Trp Lys Arg Asp Trp
420 425 430

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

<210> 53

<211> 1284

<212> DNA

<213> A. pleuropneumoniae SLAM 3

<400> 53

atgaaatcaa tacctttttat tctgtctgtg cttcccacaa cgcttttagc ggaaactatt 60
tctacaccaa aaccagtctt ttttgaggat aaatccgatc atctaaaacc ggcggaattt 120

gcaaaaagtt caccgaattt aaccgctgat accccgatat ttacaccaac cgaacaagcg 180
aatttggatc aaaccattac ctctttattg atcaataaac agtggaaagc cttaaaaatc 240
gcattagaac gttatgtaaa acagacgaat tttgatccga ttttatatcg ttatgcaaaa 300
ggagcgatgt tacgcgcgga acaagattat gacggagcga tcgagcttta ccaacaaatt 360
ttacagaccc aaccgcagtt agcttatcca cgtttcgatt tgggcgtaat gttgtttgaa 420
aataaacaat atcgtgaagc gaaacagcaa ttaaacaaag caagaaaatc tcttgatccg 480
caaatgcagc cgttagttga acgttatttg caagcaatgg cagagcgtca aaattggcaa 540

ccggatgcag aattgcaata tacacaaacc gataatgtga ataatgcgtc tagtgaacga 600
gaagttgaaa tcggggttta cgattctgtg gtgtacatta ttgggataat caagattaca 660
gcgaaaaatc gttatacggt tcttttggtt atcgtaaaca ttctgcatta caatcttggg 720
gcattttgcc gttctttgaa caaaactggc ttgcttctcc acgttatagc aaaaatttcg 780
gggcaaatgc tgagttccgc cgtcagctta atcgcctttt ccaccaattt caaccacaca 840
caaaaacgtt atgccgatga aaatattgca cagcgttata acggttatat caatggggta 900
tccgcttcat taagctatac tgccaatccg aattgggtga tgtttggtgg tgtagaactt 960

agcaaagatc gcactaaaga taaggcagaa acctcaactc gtaagggaat taatatcggt 1020
acgctagtgc gttatggcga tgttgtgagc cgagtcagtt tgcgttatgt aaagcgtcat 1080

ttcttggcgg ataactttta tttcccgaaa aaacgcattg atgacgaata cagcgtaaat 1140

gccagcctgt ggcataacca aattcaatgg caaggttttg tgccaaaatt aaattatcgt 1200

tatcgtaaaa ttgacagcaa tattgccgct ttttatagcc gttcgagcag tgaatggttt 1260

atgacggtag aaaagaattg gtag 1284

<210> 54

<211> 427

<212> PRT

<213> A. pleuropneumoniae SLAM 3

<400> 54

Met Lys Ser Ile Pro Phe Ile Leu Ser Val Leu Pro Thr Thr Leu Leu
1 5 10 15

Ala Glu Thr Ile Ser Thr Pro Lys Pro Val Phe Phe Glu Asp Lys Ser
20 25 30

Asp His Leu Lys Pro Ala Glu Phe Ala Lys Ser Ser Pro Asn Leu Thr
35 40 45

Ala Asp Thr Pro Ile Phe Thr Pro Thr Glu Gln Ala Asn Leu Asp Gln
50 55 60

Thr Ile Thr Ser Leu Leu Ile Asn Lys Gln Trp Lys Ala Leu Lys Ile
65 70 75 80

Ala Leu Glu Arg Tyr Val Lys Gln Thr Asn Phe Asp Pro Ile Leu Tyr
85 90 95

Arg Tyr Ala Lys Gly Ala Met Leu Arg Ala Glu Gln Asp Tyr Asp Gly
100 105 110

Ala Ile Glu Leu Tyr Gln Gln Ile Leu Gln Thr Gln Pro Gln Leu Ala
115 120 125

Tyr Pro Arg Phe Asp Leu Gly Val Met Leu Phe Glu Asn Lys Gln Tyr
130 135 140

Arg Glu Ala Lys Gln Gln Leu Asn Lys Ala Arg Lys Ser Leu Asp Pro
145 150 155 160

Gln Met Gln Pro Leu Val Glu Arg Tyr Leu Gln Ala Met Ala Glu Arg
165 170 175

Gln Asn Trp Gln Pro Asp Ala Glu Leu Gln Tyr Thr Gln Thr Asp Asn

180 185 190

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

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

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

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

<210> 55

<211> 1455

<212> DNA

<213> A. rudis SLAM 1

<400> 55

atggctctcc catcactgct ctttgcagcg gaggatagtg atacaagatt acgtttggat 60

cagggcctat tacagcaaaa tatagaaaag caaaaaccac taattgaaca acaaaaacaa 120

gatcaactac cgaccatggt cattgatgga gaaatgatta aagttgaaaa caacctcaat 180

gatcttggtc gagctttata tattgcagtg atgcaaaaac aatggtcagc tgccagcatt 240

tatttgcagc gttatgaaaa gttagaaggt tacgatgttt cattgctgaa atttgcacaa 300

ggggctttgg ctcgcgtgca aggtcatcag gacgaagctg agcaatattt taaagatgca 360

ctgctccttc aaccgaacaa cgccatgatt aaactcgaac tggcacgact actcacagag 420

cggcaaaaaa accaacaagc aaagtacttg ttcttagagg taaagcaaga gttacagcat 480

agcgatgatc cactgattca gagtattact aaaacaatag atgtctattt aaaaggttta 540

aataaacgtg atgagtggca agggagtctg agtttaggca cacgttatgc aacgaatatt 600

aatagtgcat cagatcacaa agctattact tcccactatg taatagatca ggacggtaac 660

aagattttag ttaaacagga gactagaggt acaccagatc caatcgatgc tcaggcattt 720

gattacgaag tcgctttaaa taaacgttgg tctttgcagg ataaccatgg gattgcattt 780

aaagcgtttg ggtatggtcg cgcttatgat gaccataaaa actttaatga aatgactcta 840

aatttaaatg caggttatag ctatcaagat cagcgcaatc aaattttaat cgcccctgtt 900

tttgagcatc gtcgatatca aaacaagagt ttatccaatg cgtggggagg gcgtgtggag 960

tggatgcgtt ttgtgggtaa agataaggca tttaagttgg aagctgagtt taaggatatt 1020

gataatgtct tgtattcaaa ccaaagcggt gtagaaagtt caggctttgc tacattttgg 1080

aaagttttac caaagcagtg gactttattt ggggggattg attttattga tcacaatagc 1140

gaggaggtgt atttcaccgc atatcaacag cagggtatac gtctaggttt gagtaaacag 1200

tttgcacagg attttaatgc gacactcttt agttcgttcc gttggcgcca gtacgataag 1260

ttcaacaaat ttttagaggc gaagcgcgat gattttgagc aaaaccatat gctcattgtg 1320

agtgctccaa agtgggagtt ttatgggatg attcctagtt tgatgtatca atacaataga 1380

aataaaagta acgtggattg gttctattcc tacgataaac ataatgcaag ttttaaattg 1440

gaatatcgtt tttag 1455

<210> 56

<211> 484

<212> PRT

<213> A. rudis SLAM 1

<400> 56

Met Ala Leu Pro Ser Leu Leu Phe Ala Ala Glu Asp Ser Asp Thr Arg
1 5 10 15

Leu Arg Leu Asp Gln Gly Leu Leu Gln Gln Asn Ile Glu Lys Gln Lys
20 25 30

Pro Leu Ile Glu Gln Gln Lys Gln Asp Gln Leu Pro Thr Met Val Ile
35 40 45

Asp Gly Glu Met Ile Lys Val Glu Asn Asn Leu Asn Asp Leu Gly Arg
50 55 60

Ala Leu Tyr Ile Ala Val Met Gln Lys Gln Trp Ser Ala Ala Ser Ile
65 70 75 80

Tyr Leu Gln Arg Tyr Glu Lys Leu Glu Gly Tyr Asp Val Ser Leu Leu
85 90 95

Lys Phe Ala Gln Gly Ala Leu Ala Arg Val Gln Gly His Gln Asp Glu
100 105 110

Ala Glu Gln Tyr Phe Lys Asp Ala Leu Leu Leu Gln Pro Asn Asn Ala
115 120 125

Met Ile Lys Leu Glu Leu Ala Arg Leu Leu Thr Glu Arg Gln Lys Asn
130 135 140

Gln Gln Ala Lys Tyr Leu Phe Leu Glu Val Lys Gln Glu Leu Gln His
145 150 155 160

Ser Asp Asp Pro Leu Ile Gln Ser Ile Thr Lys Thr Ile Asp Val Tyr
165 170 175

Leu Lys Gly Leu Asn Lys Arg Asp Glu Trp Gln Gly Ser Leu Ser Leu
180 185 190

Gly Thr Arg Tyr Ala Thr Asn Ile Asn Ser Ala Ser Asp His Lys Ala
195 200 205

Ile Thr Ser His Tyr Val Ile Asp Gln Asp Gly Asn Lys Ile Leu Val
210 215 220

Lys Gln Glu Thr Arg Gly Thr Pro Asp Pro Ile Asp Ala Gln Ala Phe

225 230 235 240

Asp Tyr Glu Val Ala Leu Asn Lys Arg Trp Ser Leu Gln Asp Asn His

245 250 255

Gly Ile Ala Phe Lys Ala Phe Gly Tyr Gly Arg Ala Tyr Asp Asp His

260 265 270

Lys Asn Phe Asn Glu Met Thr Leu Asn Leu Asn Ala Gly Tyr Ser Tyr

275 280 285

Gln Asp Gln Arg Asn Gln Ile Leu Ile Ala Pro Val Phe Glu His Arg

290 295 300

Arg Tyr Gln Asn Lys Ser Leu Ser Asn Ala Trp Gly Gly Arg Val Glu

305 310 315 320

Trp Met Arg Phe Val Gly Lys Asp Lys Ala Phe Lys Leu Glu Ala Glu

325 330 335

Phe Lys Asp Ile Asp Asn Val Leu Tyr Ser Asn Gln Ser Gly Val Glu

340 345 350

Ser Ser Gly Phe Ala Thr Phe Trp Lys Val Leu Pro Lys Gln Trp Thr

355 360 365

Leu Phe Gly Gly Ile Asp Phe Ile Asp His Asn Ser Glu Glu Val Tyr

370 375 380

Phe Thr Ala Tyr Gln Gln Gln Gly Ile Arg Leu Gly Leu Ser Lys Gln

385 390 395 400

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

405 410 415

Gln Tyr Asp Lys Phe Asn Lys Phe Leu Glu Ala Lys Arg Asp Asp Phe

420 425 430

Glu Gln Asn His Met Leu Ile Val Ser Ala Pro Lys Trp Glu Phe Tyr

435 440 445

Gly Met Ile Pro Ser Leu Met Tyr Gln Tyr Asn Arg Asn Lys Ser Asn

450 455 460

Val Asp Trp Phe Tyr Ser Tyr Asp Lys His Asn Ala Ser Phe Lys Leu

465 470 475 480

Glu Tyr Arg Phe

<210> 57

<211> 1440

<212> DNA

<213> A. segnis SLAM 1

<400> 57

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gcagaagttg ctacaccgaa gagcgcctca cccgaagaac gattaaagct tgctacccct 120

cgattgcctc aacatgaaac agtggaagaa tctacttcaa aagaaaatac gctttctatt 180

acgaaagaag aacttgctaa acgacctgat ttaattatcc gcggattgat ccctgcattg 240

ttgcaaaata atgtggacgt ggtggcattg ctgtttccgt tatatcagca gcaacaaccg 300

gcgcaacaag atccgttttt gctggcttgg ggggaagcta tgatggcaac gcatcaaggg 360

gattatgcat cggcggtgca acaataccgt gaattatttg cgaaacgtcc tgaaattttg 420

cagttgcgtt atcaattagc ccatgcgttg tttttgaata acgataatga agcggcgaaa 480

gatcagttcc aaaaactccg tgcggaggtg aatgatactt catcacagca gatgatcgac 540

cagtatttga ttgcgattaa ccaacgagat cagtggaaaa ttaacggtgg tatcagtttt 600

ttaaacgaat ccaatattaa taatgcgccc aaagcgggca cccgtattgg ggcgtggaaa 660

gcttgggaga gagaacaggc gcatgggttg tcttattatg ttggtgccga aaaaaaatgg 720

tcgttgcctc atcagttttt tgcaaaactg gtgttagatg ggcaaggcaa atattattgg 780

gataacaaaa aatataacga atttaatgct cgaatcggtg ccggtttggg ttatcacacg 840

gcaaataccg aactctcttt cctgtctttc actgagcgac gttggtattc cggcggttct 900

tccggcagtg atgccatgaa acaatattct aaaaattccg gtgtgcgtgt tgatgtgatt 960

cattggctca ataaatcatg gcaaatttcg accgcacttg aatatggtga gcaacgttat 1020

gcctcgcgta aacatttaaa tggcaataat tatttgtggt cgaatacgct cttatttttg 1080

ccttacagcg gacaatattg gtatattggt gcggattata atcgcgaaaa tacgcgtgat 1140

ctcgataacg cctatcaacg taaaaatgta cgtttaggtt gggtgcaaga atggccgttg 1200

ggcatttcca gtcgtctttc tgtcgcttat gcaagacggg cttataaagg tgaagattta 1260

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gtgtattttt ggggcattac gccgaaaatt acctggtctt accaaaaaaa tgacagcaat 1380

catccatttt atcgctatga taaaaatcgg atttatttag aaatgagtaa aacgttttaa 1440

<210> 58

<211> 479

<212> PRT

<213> A. segnis SLAM 1

<400> 58

Met Met Lys Leu Pro Leu Phe Phe Ser Val Ile Gly Ala Leu Val Ser
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Ile Ser Val Ala Ala Glu Val Ala Thr Pro Lys Ser Ala Ser Pro Glu
20 25 30

Glu Arg Leu Lys Leu Ala Thr Pro Arg Leu Pro Gln His Glu Thr Val
35 40 45

Glu Glu Ser Thr Ser Lys Glu Asn Thr Leu Ser Ile Thr Lys Glu Glu
50 55 60

Leu Ala Lys Arg Pro Asp Leu Ile Ile Arg Gly Leu Ile Pro Ala Leu
65 70 75 80

Leu Gln Asn Asn Val Asp Val Val Ala Leu Leu Phe Pro Leu Tyr Gln
85 90 95

Gln Gln Gln Pro Ala Gln Gln Asp Pro Phe Leu Leu Ala Trp Gly Glu
100 105 110

Ala Met Met Ala Thr His Gln Gly Asp Tyr Ala Ser Ala Val Gln Gln
115 120 125

Tyr Arg Glu Leu Phe Ala Lys Arg Pro Glu Ile Leu Gln Leu Arg Tyr
130 135 140

Gln Leu Ala His Ala Leu Phe Leu Asn Asn Asp Asn Glu Ala Ala Lys
145 150 155 160

Asp Gln Phe Gln Lys Leu Arg Ala Glu Val Asn Asp Thr Ser Ser Gln
165 170 175

Gln Met Ile Asp Gln Tyr Leu Ile Ala Ile Asn Gln Arg Asp Gln Trp
180 185 190

Lys Ile Asn Gly Gly Ile Ser Phe Leu Asn Glu Ser Asn Ile Asn Asn

195 200 205

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

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

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

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

Lys Ile Thr Trp Ser Tyr Gln Lys Asn Asp Ser Asn His Pro Phe Tyr
450 455 460

Arg Tyr Asp Lys Asn Arg Ile Tyr Leu Glu Met Ser Lys Thr Phe
465 470 475

<210> 59

<211> 1461

<212> DNA

<213> A. succinogenes SLAM 1

<400> 59

atgcccggtt tcaacttttt tattttattg tttttatttt ttcttcctat atccgcccac 60

gcgacagaaa ttgcagtcat aacagagcaa aacacgcctg aacgtaatgt aatggaagcc 120

aaacccaaat ctattgcaaa tgtagaaaaa ttacccgaaa catcgttagc tatcgacaaa 180

aaaacgggac gagggggggc acgaaatatt catacggata aaaatttagc cgagtatgcg 240

ttaaataaag cgattgaacg gggccatccg aatatgattg aaaaagcgtt aaaaatttac 300

cgcacttttc ctaatctaga tccaattttg gttaaatttg ccgaagccaa aatagcaaaa 360

gcgcgtcaag attattccgt ggcaatccgt ttattccgcg agattatcgc agagcgtgcg 420

gatctcaacc cggtacgcat cgaattagcg attgttttgt ttttagacaa acaggacagt 480

gccgctaagg cgcagtttga aaaagccttg agtgacgaaa gcactccgcc ggatattgtc 540

cggctgatta atctttatct ggaggcgctg aataaacgcg atacatggca attcaatgtg 600

aatgcaggat atatgcggga agaaaatgtc aataacgtgt ccgattccct ttatattgaa 660

aatacggcgt ttaaaaaagg cgactccatg ttgccgcaaa aagctcacgg cattcaattt 720

tacgtaggat tcgaacgcga tttcaattta atgtattccc attatctcca catcgaaaat 780

cttacctatg gtaaagccta ttgggacaat aacgattaca ccgatattac caaccgcaca 840

tatctcggct atcgtcataa atccgccaaa accgcctggt ccgttctgcc attttacgaa 900

cgtcaatggt atgccacgca ccgttataag aaagcgaccg gagtacgggg agaattaaat 960

cattggttga accgaaactg gcaaatatcc accgcgcttg aatacggcaa agaacaatat 1020

catcgaaacg ctttgctgga cggtaataac aaattagctt ccgctacttt ggtttggttg 1080

cgtacgccgc ggcaatattt ctatttcggc ggcgattaca gttttcaacg cgctcaggca 1140

cgtcactacg gctatgattt aaaaaccgca cgtatcggtt ggggacaaga atgggaacgg 1200

ggtatttcga cccgtctggg ctttgccgtt tcaaagcgtg agtataaagc cgaccatgtg 1260

ctgggcaacg tattttattt cagcaaaccg cgggaagacg atatttacaa catcaacgcc 1320

tccttatgga aacgcgattg gcatttatgg ggtattacgc ccaaacttcg tttcaactgg 1380

aaaaaacaac gcagcaactt tgacagcctt tattcgtaca tagatcgcag cataacagtt 1440

tcggttgaga aaacttttta a 1461

<210> 60

<211> 486

<212> PRT

<213> A. succinogenes SLAM 1

<400> 60

Met Pro Gly Phe Asn Phe Phe Ile Leu Leu Phe Leu Phe Phe Leu Pro
1 5 10 15

Ile Ser Ala His Ala Thr Glu Ile Ala Val Ile Thr Glu Gln Asn Thr
20 25 30

Pro Glu Arg Asn Val Met Glu Ala Lys Pro Lys Ser Ile Ala Asn Val
35 40 45

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

50 55 60

Gly Gly Ala Arg Asn Ile His Thr Asp Lys Asn Leu Ala Glu Tyr Ala
65 70 75 80

Leu Asn Lys Ala Ile Glu Arg Gly His Pro Asn Met Ile Glu Lys Ala
85 90 95

Leu Lys Ile Tyr Arg Thr Phe Pro Asn Leu Asp Pro Ile Leu Val Lys
100 105 110

Phe Ala Glu Ala Lys Ile Ala Lys Ala Arg Gln Asp Tyr Ser Val Ala

115 120 125

Ile Arg Leu Phe Arg Glu Ile Ile Ala Glu Arg Ala Asp Leu Asn Pro
130 135 140

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

Ala Ala Lys Ala Gln Phe Glu Lys Ala Leu Ser Asp Glu Ser Thr Pro
165 170 175

Pro Asp Ile Val Arg Leu Ile Asn Leu Tyr Leu Glu Ala Leu Asn Lys

180 185 190

Arg Asp Thr Trp Gln Phe Asn Val Asn Ala Gly Tyr Met Arg Glu Glu

195 200 205

Asn Val Asn Asn Val Ser Asp Ser Leu Tyr Ile Glu Asn Thr Ala Phe

210 215 220

Lys Lys Gly Asp Ser Met Leu Pro Gln Lys Ala His Gly Ile Gln Phe

225 230 235 240

Tyr Val Gly Phe Glu Arg Asp Phe Asn Leu Met Tyr Ser His Tyr Leu

245 250 255

His Ile Glu Asn Leu Thr Tyr Gly Lys Ala Tyr Trp Asp Asn Asn Asp

260 265 270

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

275 280 285

Ala Lys Thr Ala Trp Ser Val Leu Pro Phe Tyr Glu Arg Gln Trp Tyr

290 295 300

Ala Thr His Arg Tyr Lys Lys Ala Thr Gly Val Arg Gly Glu Leu Asn

305 310 315 320

His Trp Leu Asn Arg Asn Trp Gln Ile Ser Thr Ala Leu Glu Tyr Gly

325 330 335

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

340 345 350

Ala Ser Ala Thr Leu Val Trp Leu Arg Thr Pro Arg Gln Tyr Phe Tyr

355 360 365

Phe Gly Gly Asp Tyr Ser Phe Gln Arg Ala Gln Ala Arg His Tyr Gly

370 375 380

Tyr Asp Leu Lys Thr Ala Arg Ile Gly Trp Gly Gln Glu Trp Glu Arg

385 390 395 400

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

405 410 415

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

420 425 430

Asp Asp Ile Tyr Asn Ile Asn Ala Ser Leu Trp Lys Arg Asp Trp His

435 440 445

Leu Trp Gly Ile Thr Pro Lys Leu Arg Phe Asn Trp Lys Lys Gln Arg

450 455 460

Ser Asn Phe Asp Ser Leu Tyr Ser Tyr Ile Asp Arg Ser Ile Thr Val

465 470 475 480

Ser Val Glu Lys Thr Phe

485

<210> 61

<211> 1296

<212> DNA

<213> A. succinogenes SLAM 2

<400> 61

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tcaattgaat ataatttaaa gcaggcaatt tatcggcaga acggtcaaca gattcaaatt 120

ttattacggg attattttca agagaaaaat aaagatccga ttcttattgc ttatgctcaa 180

gcaaaattag cgtttataca aaaagattat gttacggcga ttaatattta tcggaaaatc 240

atcagttatc gtcccgattt aaattcgatg agaacggaac ttgcgatcgc tttgtttatg 300

gatcatcagg atgccgcagc tagagtacag ctggacaaag tgaggagtgc taagggctta 360

cctgattcgg cttataggtt gattgaacaa tacattgatg cgctcaatca acgtaatagt 420

tggcaaattg aaggcggttt ttcttatatt aaaacgaaca atgtagagaa tgtatctgat 480

aggattgata tagaaaatac cggatttata aaaagtgaaa atatgttgcc gaaaaaagct 540

aatggattag cctataactt aagtattggt aaagatttca atatctatca atcccattat 600

ttgtcattaa ataatgaaac gataggaaaa acgtattggg ataatcatca atatgatgat 660

ttgtctaatc gctttttttat ggggtatgca tacaagaaaa atgatcagac gattcgtatt 720

cgacctttct atgataagcg ttggtatggc ggcaattcgt accattggtc aaacggagtt 780

caattcgatt acggtttatg gctatcatca aattggcaaa gttaccatac acttgaatat 840

gagaaacgta atttctttaa aaataaggaa ttttcgggaa acattaaaac attttctacc 900

agcctgatct ggtatcgaaa ccccgaacat atatggtata tcgggacaac tttttcacga 960

gaaaatatgc aggaacgcca atatagttcg gatataaaaa atatcagaat cggttggttg 1020

caagaatatt cttggggaat ttctactaaa ttaagcatgg gggcaactat tcgtcagttc 1080

aaagcggaag cgattcttgg tgggattttg cccttgaaca aaactcgtca agatcatatt 1140

tataccgcta ttgcgcagct ttggaagaga gattggcatt tatggaatat cactccaaag 1200

ttgagtttaa attggaaaaa acaaaagagt aatttagatt cgctttattc ttatcaggaa 1260

aagaatgcta ccattgtgtt tgaaaaagta ttttag 1296

<210> 62

<211> 431

<212> PRT

<213> A. succinogenes SLAM 2

<400> 62

Met Arg Phe Tyr Leu Phe Leu Cys Leu Phe Phe Ser Ser Ala Val Leu
1 5 10 15

Ala Gln Asp Leu Ser Ile Glu Tyr Asn Leu Lys Gln Ala Ile Tyr Arg
20 25 30

Gln Asn Gly Gln Gln Ile Gln Ile Leu Leu Arg Asp Tyr Phe Gln Glu
35 40 45

Lys Asn Lys Asp Pro Ile Leu Ile Ala Tyr Ala Gln Ala Lys Leu Ala

50 55 60

Phe Ile Gln Lys Asp Tyr Val Thr Ala Ile Asn Ile Tyr Arg Lys Ile
65 70 75 80

Ile Ser Tyr Arg Pro Asp Leu Asn Ser Met Arg Thr Glu Leu Ala Ile
85 90 95

Ala Leu Phe Met Asp His Gln Asp Ala Ala Ala Arg Val Gln Leu Asp
100 105 110

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

115 120 125

Glu Gln Tyr Ile Asp Ala Leu Asn Gln Arg Asn Ser Trp Gln Ile Glu
130 135 140

Gly Gly Phe Ser Tyr Ile Lys Thr Asn Asn Val Glu Asn Val Ser Asp
145 150 155 160

Arg Ile Asp Ile Glu Asn Thr Gly Phe Ile Lys Ser Glu Asn Met Leu
165 170 175

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

180 185 190

Phe Asn Ile Tyr Gln Ser His Tyr Leu Ser Leu Asn Asn Glu Thr Ile

195 200 205

Gly Lys Thr Tyr Trp Asp Asn His Gln Tyr Asp Asp Leu Ser Asn Arg

210 215 220

Phe Phe Met Gly Tyr Ala Tyr Lys Lys Asn Asp Gln Thr Ile Arg Ile

225 230 235 240

Arg Pro Phe Tyr Asp Lys Arg Trp Tyr Gly Gly Asn Ser Tyr His Trp

245 250 255

Ser Asn Gly Val Gln Phe Asp Tyr Gly Leu Trp Leu Ser Ser Asn Trp

260 265 270

Gln Ser Tyr His Thr Leu Glu Tyr Glu Lys Arg Asn Phe Phe Lys Asn

275 280 285

Lys Glu Phe Ser Gly Asn Ile Lys Thr Phe Ser Thr Ser Leu Ile Trp

290 295 300

Tyr Arg Asn Pro Glu His Ile Trp Tyr Ile Gly Thr Thr Phe Ser Arg

305 310 315 320

Glu Asn Met Gln Glu Arg Gln Tyr Ser Ser Asp Ile Lys Asn Ile Arg

325 330 335

Ile Gly Trp Leu Gln Glu Tyr Ser Trp Gly Ile Ser Thr Lys Leu Ser

340 345 350

Met Gly Ala Thr Ile Arg Gln Phe Lys Ala Glu Ala Ile Leu Gly Gly

355 360 365

Ile Leu Pro Leu Asn Lys Thr Arg Gln Asp His Ile Tyr Thr Ala Ile

370 375 380

Ala Gln Leu Trp Lys Arg Asp Trp His Leu Trp Asn Ile Thr Pro Lys

385 390 395 400

Leu Ser Leu Asn Trp Lys Lys Gln Lys Ser Asn Leu Asp Ser Leu Tyr

405 410 415

Ser Tyr Gln Glu Lys Asn Ala Thr Ile Val Phe Glu Lys Val Phe

420 425 430

<210> 63

<211> 1464

<212> DNA

<213> A. suis SLAM 1

<400> 63

atgaaattaa atctactcat tcctacactt gccgtatcta cggcatattc agcatttgct 60

aatacgacag agcaacaaat ttctgaacat ttaaacgatt tacgcagcca aacggaagta 120

gcgattgaat ctcgtatcca aaaacctgcc agtcacccaa tgcctcaact tgcgattcag 180

caaaaaaagc gtctaagtat gagcaaagag gaattttcta agcgcccaga tttaatttca 240

aacgcgctta ttttggcatt acagcaatct aactctgatt cagtcagctt tctttatcca 300

ttttatagta agctgccaac acaataccaa gatccaatta tgcttaagtg gtctgaagct 360

attttagctc gctacagagg taactataat agtgcaatta caaaatatcg tgaaatatta 420

gccgaacatt ctggtttagg cttagtccgt ttacaacttg caatggcact ctttgagaat 480

aatgaattgg aagcggccga agatcaattt caaaaaatac gatccgaaaa tccaccttcc 540

caaatcaaag gtttgattga tcagtacatt accgcaattg caaataaaga tcgttggaca 600

ttctccggtg gcttcaccta tttaaacgat cctaacatta ataatgcacc gaaatccggc 660

acaacttacg gacaatggag cgcacctaaa tcagaatctg cacaagggat cggctttaat 720

ttctatgccg gtaaaaaatg gtcttgggga aataatttct ataatgaatt tcgtctaagc 780

agtaacggaa aatattattg gaataataaa aaatataatg aagtaagtgc aagaggaagc 840

cttggtttag gctatcaaac cgctcgcttt accatggcac tccttccttt tatggagcaa 900

acactttatg ccggtggctc aaacagcagt gaaagtttaa aacgcttttc taaagcaagt 960

ggtgcaacgt tagaaacaag ttattggatc tcacctaaat ggcaatggga atccagctat 1020

gaatatgccg aacaacgtta tatggatcgc aaacatttaa acggcaatta ccatttcgtc 1080

tctagcggct taacctacct tgcgaatgca aaacaatatt ggtttagcaa tatcaactat 1140

aatagaacag caactcgaga taaagacgat agttatgtcc gtcgcggaat tgtgcttggt 1200

tggggacaag aatggccact cggactatca acacgattaa gtgttaacta tgcacaaaaa 1260

aattacaaag cgccaatgcc aatctttggt attacacaac gtaataaaga atacggtgca 1320

tcattaagtc tatggcatcg tgccgtacat tattgggggа ttacgcctcg cctgacgtat 1380

agctttaata aagtaaaaag taatcacgta ttctatagct acgataaaca ccgtgctttt 1440

gtggagttta gcaaacgttt ctag 1464

<210> 64

<211> 487

<212> PRT

<213> A. suis SLAM 1

<400> 64

Met Lys Leu Asn Leu Leu Ile Pro Thr Leu Ala Val Ser Thr Ala Tyr
1 5 10 15

Ser Ala Phe Ala Asn Thr Thr Glu Gln Gln Ile Ser Glu His Leu Asn
20 25 30

Asp Leu Arg Ser Gln Thr Glu Val Ala Ile Glu Ser Arg Ile Gln Lys
35 40 45

Pro Ala Ser His Pro Met Pro Gln Leu Ala Ile Gln Gln Lys Lys Arg
50 55 60

Leu Ser Met Ser Lys Glu Glu Phe Ser Lys Arg Pro Asp Leu Ile Ser
65 70 75 80

Asn Ala Leu Ile Leu Ala Leu Gln Gln Ser Asn Ser Asp Ser Val Ser
85 90 95

Phe Leu Tyr Pro Phe Tyr Ser Lys Leu Pro Thr Gln Tyr Gln Asp Pro
100 105 110

Ile Met Leu Lys Trp Ser Glu Ala Ile Leu Ala Arg Tyr Arg Gly Asn
115 120 125

Tyr Asn Ser Ala Ile Thr Lys Tyr Arg Glu Ile Leu Ala Glu His Ser
130 135 140

Gly Leu Gly Leu Val Arg Leu Gln Leu Ala Met Ala Leu Phe Glu Asn
145 150 155 160

Asn Glu Leu Glu Ala Ala Glu Asp Gln Phe Gln Lys Ile Arg Ser Glu
165 170 175

Asn Pro Pro Ser Gln Ile Lys Gly Leu Ile Asp Gln Tyr Ile Thr Ala
180 185 190

Ile Ala Asn Lys Asp Arg Trp Thr Phe Ser Gly Gly Phe Thr Tyr Leu
195 200 205

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

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

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

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

450 455 460

Val Lys Ser Asn His Val Phe Tyr Ser Tyr Asp Lys His Arg Ala Phe
465 470 475 480
Val Glu Phe Ser Lys Arg Phe
485

<210> 65
<211> 1443
<212> DNA
<213> A. suis SLAM 2
<400> 65

atgtttaaaa aattagcgtt tttatgtgct ggcttattct atttgcttca atttaatatc 60
gcttatgcgg agcaacaaat taatacacct gaaaagaatg tggaaattgc taagttactt 120
aaggaaaccc caaaattacc tgaattaacc ataaattcga ttgaaaatat tcaacaatct 180
gaacaagatt tattaaataa taaattgttt gttgagcaat ttctgaataa tgcaatcgaa 240

acaggtcacc tttcttcaat taaatattta ttggcgattt atcgtcaatt ccagaattct 300
gatcctattt taattctttt tgcacaagct cagattgcta aaatccagca acaatatgcc 360
gaggcggcta aattatatcg tgaaatatta gcgattaaac caaggcttac tcctgtccgc 420
atacaacttg caattgtatt gttcctgtct caacaggata aggcagctaa agagcagttt 480
gaaaaatcat tgagtgaacc acagctccct gctgatattg aacaattaat tcatctttat 540
ttgcaggcat tggaacagcg caatgtatgg caagtttcgt tgagtgctaa ttatttacgt 600
gaagacaatg taaatcatgt ttcaagcgaa cgatatattg aaaataccgc ttttataaaa 660

ggcgaaagta tgttgccaca aaaagcacaa ggcatcagct attactttgg tttagagcgc 720
gatatcaatt tatggaatgc tcattattta cgtatcgata atagtttata cggtaaaaat 780
tactgggatc agcatgatta tgacgatatt accaatcgcc tatcgttagg ctatgtacat 840
aaaggctcac agcaacgctt tgcgattttg ccgttttatg aacagcaatg gtatggcggt 900
catcgataca agcgcagtaa tggtggcaga atagaattta atcgttggtt aaattcaaat 960
tggcaatttt caacggccgc agagtatgct cggaatttct attcaaatag cttaagttta 1020
aacggtaaga gtaagttagc ttcattaacg atgttatggc gtgctagtcc tcgtacttat 1080

ttttatttag gagcggatta cgctcaagaa cgcactaaag ttcgtcatta cagctatgac 1140
ttaaaaacag cccgtattgg ttgggggcaa gaatggtatg ggggaatttc ttctcgttta 1200
agtttttctg cttctaagcg agagtataag gataatcttt cgctcggttc ggcttttcat 1260

ttcgataaac agcgtgaaga ccgaatctat catatcaatg caaccgtttg gaaacgagat 1320

tggcacttat gggggattac tccaaagctt aattatcact ggaaaaaaca acgtagcaat 1380

tttgtaagcc tttattctta ctcggataaa agtatcaaca taatactgga aaaaactttt 1440

taa 1443

<210> 66

<211> 480

<212> PRT

<213> A. suis SLAM 2

<400> 66

Met Phe Lys Lys Leu Ala Phe Leu Cys Ala Gly Leu Phe Tyr Leu Leu
1 5 10 15

Gln Phe Asn Ile Ala Tyr Ala Glu Gln Gln Ile Asn Thr Pro Glu Lys
20 25 30

Asn Val Glu Ile Ala Lys Leu Leu Lys Glu Thr Pro Lys Leu Pro Glu
35 40 45

Leu Thr Ile Asn Ser Ile Glu Asn Ile Gln Gln Ser Glu Gln Asp Leu
50 55 60

Leu Asn Asn Lys Leu Phe Val Glu Gln Phe Leu Asn Asn Ala Ile Glu
65 70 75 80

Thr Gly His Leu Ser Ser Ile Lys Tyr Leu Leu Ala Ile Tyr Arg Gln
85 90 95

Phe Gln Asn Ser Asp Pro Ile Leu Ile Leu Phe Ala Gln Ala Gln Ile
100 105 110

Ala Lys Ile Gln Gln Gln Tyr Ala Glu Ala Ala Lys Leu Tyr Arg Glu
115 120 125

Ile Leu Ala Ile Lys Pro Arg Leu Thr Pro Val Arg Ile Gln Leu Ala
130 135 140

Ile Val Leu Phe Leu Ser Gln Gln Asp Lys Ala Ala Lys Glu Gln Phe
145 150 155 160

Glu Lys Ser Leu Ser Glu Pro Gln Leu Pro Ala Asp Ile Glu Gln Leu
165 170 175

Ile His Leu Tyr Leu Gln Ala Leu Glu Gln Arg Asn Val Trp Gln Val

180 185 190

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

195 200 205

Ser Glu Arg Tyr Ile Glu Asn Thr Ala Phe Ile Lys Gly Glu Ser Met

210 215 220

Leu Pro Gln Lys Ala Gln Gly Ile Ser Tyr Tyr Phe Gly Leu Glu Arg

225 230 235 240

Asp Ile Asn Leu Trp Asn Ala His Tyr Leu Arg Ile Asp Asn Ser Leu

245 250 255

Tyr Gly Lys Asn Tyr Trp Asp Gln His Asp Tyr Asp Asp Ile Thr Asn

260 265 270

Arg Leu Ser Leu Gly Tyr Val His Lys Gly Ser Gln Gln Arg Phe Ala

275 280 285

Ile Leu Pro Phe Tyr Glu Gln Gln Trp Tyr Gly Gly His Arg Tyr Lys

290 295 300

Arg Ser Asn Gly Gly Arg Ile Glu Phe Asn Arg Trp Leu Asn Ser Asn

305 310 315 320

Trp Gln Phe Ser Thr Ala Ala Glu Tyr Ala Arg Asn Phe Tyr Ser Asn

325 330 335

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

340 345 350

Trp Arg Ala Ser Pro Arg Thr Tyr Phe Tyr Leu Gly Ala Asp Tyr Ala

355 360 365

Gln Glu Arg Thr Lys Val Arg His Tyr Ser Tyr Asp Leu Lys Thr Ala

370 375 380

Arg Ile Gly Trp Gly Gln Glu Trp Tyr Gly Gly Ile Ser Ser Arg Leu

385 390 395 400

Ser Phe Ser Ala Ser Lys Arg Glu Tyr Lys Asp Asn Leu Ser Leu Gly

405 410 415

Ser Ala Phe His Phe Asp Lys Gln Arg Glu Asp Arg Ile Tyr His Ile

420 425 430

Asn Ala Thr Val Trp Lys Arg Asp Trp His Leu Trp Gly Ile Thr Pro

435 440 445

Lys Leu Asn Tyr His Trp Lys Lys Gln Arg Ser Asn Phe Val Ser Leu

450 455 460

Tyr Ser Tyr Ser Asp Lys Ser Ile Asn Ile Ile Leu Glu Lys Thr Phe

465 470 475 480

<210> 67

<211> 1416

<212> DNA

<213> A. suis SLAM 3

<400> 67

atgaagaaat ttccattact gttttttttt ccgacattac tctttgctca agatcccaat 60

agtacaccta gccaaataga acatatcgct aaaccaacat cggcaccctt acagcttgca 120

gtggaacaat cgtctcgcca cattttaac gaagctgaat tacgtgctaa tcaggcatta 180

accgaaaaat tactcagcca agctatctat actcgccagc tcactaatat ggaaaaactg 240

gtgataattt atcaagattt taaccaaatt gacccaattt tattgcgcta tgctcaaggt 300

aaaatcgcgc tacttaaagg aaattattca caagctattc gagagtttcg cactattctt 360

gctaaacaac ctgaactaaa taccgtacga attgaactgg caattgcatt actacatgat 420

caacaaacga atgcggcaag tgaacaattc gataaagcta aaagtgccaa aaacctacct 480

tataaagtgc agcaactgat tgaacagtat cagcaatatc tggagaaaaa acaagcttgg 540

aagttcaatt tctctgccca ctatgtacgg gatggtaata tcaataacac atccaaacaa 600

actgaaattg agcataccgg ctatgtgaaa cagcctaacc tgttaccaca aactgcgcac 660

ggaattcact attcttttgg actacaaaga gattttaacc tacttggctc gcattacctt 720

agtttcgata atcaaacgca gggggaactt tattgggata atcatgacta cgatgaaatc 780

accaatcgcg ctttgtttgg ctatgcttac aaaaagtcac accaaaccac ccgcgtattg 840

ccattttatg aaaaacgctg gaaacatcat caatcagaac gctggacaaa cggattaagg 900

ctagaacatg catattggct ttctattcac tggcaacttg ctactgcatt cgagtatggg 960

aaaaaacgct atttcgacca gcacatttac aatggcagct ataaacttgc ttcagctacc 1020

ctactctggc tacgtaatcc gcaacagttt ttctttattg gtaccgattt caaccgagat 1080

aaaaccgtat tgaaacaaca tagttctgat accaaaagct tacgtttcgg ctggcagcag 1140

gaatggcaaa cacttggatt atcaagccgc ctgacccttg cttacaccga cagacattat 1200

aaagacactg cggtgctggg tggcaaactt aatctaggta aaattcgcca tgaccgtgtg 1260

aacagcatta atcttaccct ttggaaacga gattggcatt ggttagggct tacacccaaa 1320

ctgcaacttg gctatgctaa acatcatagc aacttaccaa gcctatatgc ttacacggat 1380

aaaaatgcga atctgatcat cgaaagtcgt ttttaa 1416

<210> 68

<211> 471

<212> PRT

<213> A. suis SLAM 3

<400> 68

Met Lys Lys Phe Pro Leu Leu Phe Phe Phe Pro Thr Leu Leu Phe Ala
1 5 10 15

Gln Asp Pro Asn Ser Thr Pro Ser Gln Ile Glu His Ile Ala Lys Pro
20 25 30

Thr Ser Ala Pro Leu Gln Leu Ala Val Glu Gln Ser Ser Arg His Ile
35 40 45

Phe Asn Glu Ala Glu Leu Arg Ala Asn Gln Ala Leu Thr Glu Lys Leu
50 55 60

Leu Ser Gln Ala Ile Tyr Thr Arg Gln Leu Thr Asn Met Glu Lys Leu
65 70 75 80

Val Ile Ile Tyr Gln Asp Phe Asn Gln Ile Asp Pro Ile Leu Leu Arg
85 90 95

Tyr Ala Gln Gly Lys Ile Ala Leu Leu Lys Gly Asn Tyr Ser Gln Ala
100 105 110

Ile Arg Glu Phe Arg Thr Ile Leu Ala Lys Gln Pro Glu Leu Asn Thr
115 120 125

Val Arg Ile Glu Leu Ala Ile Ala Leu Leu His Asp Gln Gln Thr Asn
130 135 140

Ala Ala Ser Glu Gln Phe Asp Lys Ala Lys Ser Ala Lys Asn Leu Pro
145 150 155 160

Tyr Lys Val Gln Gln Leu Ile Glu Gln Tyr Gln Gln Tyr Leu Glu Lys

165 170 175

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

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

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

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

His Asp Arg Val Asn Ser Ile Asn Leu Thr Leu Trp Lys Arg Asp Trp
420 425 430

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

<210> 69
<211> 1644
<212> DNA
<213> A. xylosoxidans SLAM 1
<400> 69

gtgccgcccc gcccttcgcg ccgctccgag cgttccgccg cgctcatcct tgcgctgttc 60
gtcctgagcc tgccgcccgc gctccaggcc caaccggccg cgccgctccc cgccgccctg 120

cccgcccccg tccggccgct ggaaccggac accccgccgc tgccgccccc gcctcgtccc 180
acgccggcca tcacgcaccg ccaccccgcc caacccgcga acccgcgggt ttttttaat 240
gatacggcga ccaccgagat ctacactctt tccctccacg acgctcttcc gatctctcgt 300
cccacgccgg ccatcacgca ccgccacccc gcccaacccg cgaacccgcg ggtcgaactg 360
acggaccagg acctggcccg caacctcaag ctgaccgaac gcatcctcaa ccaggccatg 420
ctgcaggagg actggagcac cttgcggcgc gtgatgcgct tttatccctg gatgaccggc 480
gtcgatccga tcctgcgcga ctatgtgcat ggcgcgctgc tgcgccacga tggacgcctg 540

gccgaggcca tcgcgcttta ccgccagttg atcgcgcaac atcccgacct gggctacgtg 600
cggctggaac tggccgccat gctgatggag gaccgccaat tcgcgcagtc cgacgccgaa 660
ctggcggacc tgcgcctggg atcgctggaa ccggcggcgc agcgcagcgt gatgcagtac 720
cggcaggcgc tggcccagca gcgccgctgg aatttccgcc tgggcgcggg caccgtccac 780
agcaacaacg tcaattcggc caatcgcgac ccgatgctgt acctgccgat cgcgacgcgg 840
cgggggccgg tgtgggcgcc gttcgccaag agccgcgatg cgctgcccaa atcggattgg 900
ggtttgaagt acagcggcag cgccaatgtc gaacgcaatc tcggcgggca tcactactac 960

acgctgggcg cggatatcga cggcaccgcc taccgcgtgc agcgggacta cagcgaccgt 1020
accgtgaccc tgcgcggcgg ctacaagtgg caggatgcca cgcgctggtt cgccgcgacg 1080

ccgcaggcgg gccgaagctg gatgggtggc cggcgctaca gccacaacca cggcatgagc 1140

ctggaatacg gttggcggcc agcgcccgac tggcaattga tgggcgcctg gctatggctc 1200

aagcgcggct atgacgaccg cgcctatgcc gcctacgacg gccacctgga cgtgctgtcg 1260

ctgacggcta tccgcgtgtt ctcgccggcg ctgctggcct acggcagcgt cggcctgcag 1320

cgcgaagcgg tggcggcggg cgagtacacc tatcgcttcc cgtgggcgca attgggcgtg 1380

gtcaagacct tcggccgggt gctcggcgcg cgcctgagcg cgcgctacgg ccggcaggcg 1440

tatgagtcgc cctacgccct gttcctgaac cagcggcgcc gcgaccgcga attgcgcgtg 1500

gacgcctcgg tctggtcgcc ggacttcaag atcgccgggc tggaaccgaa gctgaacctc 1560

agttacctca agatcgccag caatttgccc atgtatgcgc gggaccggac cgaagtcagc 1620

ctgatgttgg agaagcggtt ctga 1644

<210> 70

<211> 547

<212> PRT

<213> A. xylosoxidans SLAM 1

<400> 70

Met Pro Pro Arg Pro Ser Arg Arg Ser Glu Arg Ser Ala Ala Leu Ile

1 5 10 15

Leu Ala Leu Phe Val Leu Ser Leu Pro Pro Ala Leu Gln Ala Gln Pro

20 25 30

Ala Ala Pro Leu Pro Ala Ala Leu Pro Ala Pro Val Arg Pro Leu Glu

35 40 45

Pro Asp Thr Pro Pro Leu Pro Pro Pro Pro Arg Pro Thr Pro Ala Ile

50 55 60

Thr His Arg His Pro Ala Gln Pro Ala Asn Pro Arg Val Phe Phe Asn

65 70 75 80

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

85 90 95

Pro Ile Ser Arg Pro Thr Pro Ala Ile Thr His Arg His Pro Ala Gln

100 105 110

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

115 120 125

Leu Lys Leu Thr Glu Arg Ile Leu Asn Gln Ala Met Leu Gln Glu Asp

130 135 140

Trp Ser Thr Leu Arg Arg Val Met Arg Phe Tyr Pro Trp Met Thr Gly
145 150 155 160
Val Asp Pro Ile Leu Arg Asp Tyr Val His Gly Ala Leu Leu Arg His
165 170 175
Asp Gly Arg Leu Ala Glu Ala Ile Ala Leu Tyr Arg Gln Leu Ile Ala
180 185 190
Gln His Pro Asp Leu Gly Tyr Val Arg Leu Glu Leu Ala Ala Met Leu

195 200 205

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

260 265 270

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

325 330 335

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

370 375 380

Trp Arg Pro Ala Pro Asp Trp Gln Leu Met Gly Ala Trp Leu Trp Leu

385 390 395 400

Lys Arg Gly Tyr Asp Asp Arg Ala Tyr Ala Ala Tyr Asp Gly His Leu

405 410 415

Asp Val Leu Ser Leu Thr Ala Ile Arg Val Phe Ser Pro Ala Leu Leu

420 425 430

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

435 440 445

Tyr Thr Tyr Arg Phe Pro Trp Ala Gln Leu Gly Val Val Lys Thr Phe

450 455 460

Gly Arg Val Leu Gly Ala Arg Leu Ser Ala Arg Tyr Gly Arg Gln Ala

465 470 475 480

Tyr Glu Ser Pro Tyr Ala Leu Phe Leu Asn Gln Arg Arg Arg Asp Arg

485 490 495

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

500 505 510

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

515 520 525

Leu Pro Met Tyr Ala Arg Asp Arg Thr Glu Val Ser Leu Met Leu Glu

530 535 540

Lys Arg Phe

545

<210> 71

<211> 1512

<212> DNA

<213> Acinetobacter sp. ADP1 SLAM 1

<400> 71

ttgcttcagg tttattgttt tatgaaacga acgcttttgt gctgtctgac attgttgagt 60

tgtccatttt tatatgccga cgaagacaca cagcttcgtc tcaatcaaag cttggaccaa 120

acgcttttac aagaacagcg ccagtttcac gagcagggaa ccattcgtag taccgagcaa 180

ttaccaaaac ttcaaattaa tggacaagaa tacagtattg aacaaaacca gaatgatctt 240

gccaaggcgt tatatttggc agtcatgcaa aaacagtggc tcaaagccac ggtttattta 300

gaacattata agaaatatgt tggctacgat cgggctttaa ccgactttgc cgaaggggca 360

gttgcacgtt ctcagggtca actgaaattg gctgaacaaa aatttcaaag cagcctaaaa 420

caacaacctc ataatttaat ttgtgaactt gagttagcgc gcgtgctgtt tgaacaacag 480

aaaaataagg aagcagcacg ccttttttatt tccattcaag atcaacttaa acaaagtgac 540

cctgcggtaa tcccgtctgg agttttaacc acagtgaata cttttgttca ggcattaaaa 600

gaacgagact cttggcaagg ctcggtttca gcgggttata cctatgtcag taatttaaat 660

agttcttctg aacagagtaa aacatggacg ctttatggca aagatagtaa cggtaatatt 720

atcccaattg agcaagttac ccgtgggacg cctaaagctg aatcggcaac gggtttagat 780

tacgaagcca gtcttataaa acgctatgcg attaaggggc atcatggcgt ggctttacgt 840

gcgctggcgt ttggacagtc ctataacgac cacgcggcat ttaatgaatc taccgttaac 900

attaatgctg gctacagcta ctttgactta aaaaatcaaa ttggggtgag tccgcttttt 960

gaacataaac gttatggcaa tgatggcctt tacaatgcgt ggggcgcgcg tgccgagtgg 1020

atgcatttta tctcagcaga taaagccttc aagcttgaag ctgagagtaa agatttaaat 1080

tatcagaaat ataaaaccct agatggggta gaaagttcag cttttgttac tttctggaaa 1140

atcctcccaa atcagtggac cgtttttagt ggtttagacg tagtcgacca ttcgacccaa 1200

gaaaaatata tggctgcata ccagcagcaa ggtgtgcggt tgggcttaag caaatcttgg 1260

agcacaggat ttaataccac tttgctgagt tcttatcgtt ggcgtatgtt tgataaatat 1320

gcagaaactt tcttagctcg tcgtcatgat tttgaacaga actatacctt tgtcgtgcaa 1380

atgccgcgct ttgagtttta tggcatgacg cctaatttaa cctatcgcta taaccataat 1440

aaaagcaatg tcgattggct ctattcctac gataaacaca acattagcct caagcttgag 1500

caccattttt ag 1512

<210> 72

<211> 503

<212> PRT

<213> Acinetobacter sp. ADP1 SLAM 1

<400> 72

Met Leu Gln Val Tyr Cys Phe Met Lys Arg Thr Leu Leu Cys Cys Leu

1 5 10 15

Thr Leu Leu Ser Cys Pro Phe Leu Tyr Ala Asp Glu Asp Thr Gln Leu

20 25 30

Arg Leu Asn Gln Ser Leu Asp Gln Thr Leu Leu Gln Glu Gln Arg Gln

35 40 45

Phe His Glu Gln Gly Thr Ile Arg Ser Thr Glu Gln Leu Pro Lys Leu

50 55 60

Gln Ile Asn Gly Gln Glu Tyr Ser Ile Glu Gln Asn Gln Asn Asp Leu

65 70 75 80

Ala Lys Ala Leu Tyr Leu Ala Val Met Gln Lys Gln Trp Leu Lys Ala

85 90 95

Thr Val Tyr Leu Glu His Tyr Lys Lys Tyr Val Gly Tyr Asp Arg Ala

100 105 110

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

115 120 125

Lys Leu Ala Glu Gln Lys Phe Gln Ser Ser Leu Lys Gln Gln Pro His

130 135 140

Asn Leu Ile Cys Glu Leu Glu Leu Ala Arg Val Leu Phe Glu Gln Gln

145 150 155 160

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

165 170 175

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

180 185 190

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

195 200 205

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

210 215 220

Gln Ser Lys Thr Trp Thr Leu Tyr Gly Lys Asp Ser Asn Gly Asn Ile

225 230 235 240

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

245 250 255

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

260 265 270

Gly His His Gly Val Ala Leu Arg Ala Leu Ala Phe Gly Gln Ser Tyr

275 280 285

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

290 295 300

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

305 310 315 320

Glu His Lys Arg Tyr Gly Asn Asp Gly Leu Tyr Asn Ala Trp Gly Ala

325 330 335

Arg Ala Glu Trp Met His Phe Ile Ser Ala Asp Lys Ala Phe Lys Leu

340 345 350

Glu Ala Glu Ser Lys Asp Leu Asn Tyr Gln Lys Tyr Lys Thr Leu Asp

355 360 365

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

370 375 380

Gln Trp Thr Val Phe Ser Gly Leu Asp Val Val Asp His Ser Thr Gln

385 390 395 400

Glu Lys Tyr Met Ala Ala Tyr Gln Gln Gln Gly Val Arg Leu Gly Leu

405 410 415

Ser Lys Ser Trp Ser Thr Gly Phe Asn Thr Thr Leu Leu Ser Ser Tyr

420 425 430

Arg Trp Arg Met Phe Asp Lys Tyr Ala Glu Thr Phe Leu Ala Arg Arg

435 440 445

His Asp Phe Glu Gln Asn Tyr Thr Phe Val Val Gln Met Pro Arg Phe

450 455 460

Glu Phe Tyr Gly Met Thr Pro Asn Leu Thr Tyr Arg Tyr Asn His Asn

465 470 475 480

Lys Ser Asn Val Asp Trp Leu Tyr Ser Tyr Asp Lys His Asn Ile Ser

485 490 495

Leu Lys Leu Glu His His Phe

500

<210> 73

<211> 1491

<212> DNA

<213> Acinetobacter sp. ANC 3929 SLAM 1

<400> 73

atgaaaagaa cattgctgtg ctgtctgact ctattggctg cttcatcact ctatgcagat 60

gatgatacta aacttcgcct gaatcaaagc ttagatcaaa atttattaca acaacagcac 120

caactacaac aacaaggcac aattcgtgat accgagaaac tacctagtat tcttatcaat 180

ggccaaattt ttgcggtaga gaaaaatgag gatgatttgg caaaagctct ttatttggct 240

gtcatgcaaa aacaatgggg caatgctgcg gtttatttaa agcattatca gcaatatcaa 300

gactatgatc aggctttaac tgattttgcc gaaggggcac tggcacgtgc tcaggggcag 360

ctcaaattag ccgagcaaaa atttcaaagc agtctcaata aacaacccaa taatctgatt 420

tgtgaactag agttagcgcg cgtgctgttt gaacagcaga agaacaaaga agcagcacgc 480

ctttttacat caattcaaaa caaactggga cagagtgatc gtacggtgat accgccagaa 540

gtagaacaaa cggttaatct gttcgtcaaa gcactcgatc agcgagattc atggcaaggc 600

agtgtcgcga ttggtccatc ctatgccaca aatctgaata gttcttctga acaaagtaaa 660

acatggacgt tatatggcat tgacgataag ggcaatgcga ctcccattca agaaattacc 720

cgtggcagcc ctaaagcagc atcagcaaca ggtatggact atgaagccag tttaatgaaa 780

cgcttttctc tctacggcaa tcatggggtt gccttacgtg gtttagcgta tggacagtct 840

tatgatgatc atgccgacta taacgaatcc accctaaata ttaatgcagg ctatagcttt 900

ttcgatttaa aaaatcagat cagcattgca ccattatttg aacataaacg ttatgcaaat 960

gacggtttat acaatgcatg gggtgcacgt gctgaatgga tgcgatttat tgcagcagac 1020

aaagcattca agctcgaagc tgaaatcaaa gatctggatt atcaaaaata taaaacacta 1080

gatggtaaag aaagctcagc gatgttcacg ttttggaaga ttctacctaa gcaatggaca 1140

ttatttagtg gactggatgt gcttgatcat gacacgcaag aaaaatatat ggcagcctat 1200

caacaacaag gcattcggtt cgggttgagc aagtcttgga atgttgggtt gaataccact 1260

ttattcagtt catatcgctg gcggcagttt gatcaatatg tagagacatt tgcggcccgc 1320

cgtcatgatt ttgaacaaaa ttataccgtt gttgtgcaga tgccccgatt taaattttac 1380

ggcatgacac caaatctgac ttatcgttat aaccacaaca gtagcaatgt ggattggtta 1440

tattcctacg ataaacacaa tgtcagctta aagcttgagc atcgttttta g 1491

<210> 74

<211> 496

<212> PRT

<213> Acinetobacter sp. ANC 3929 SLAM 1

<400> 74

Met Lys Arg Thr Leu Leu Cys Cys Leu Thr Leu Leu Ala Ala Ser Ser
1 5 10 15

Leu Tyr Ala Asp Asp Asp Thr Lys Leu Arg Leu Asn Gln Ser Leu Asp
20 25 30

Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Thr Ile
35 40 45

Arg Asp Thr Glu Lys Leu Pro Ser Ile Leu Ile Asn Gly Gln Ile Phe
50 55 60

Ala Val Glu Lys Asn Glu Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Gly Asn Ala Ala Val Tyr Leu Lys His Tyr
85 90 95

Gln Gln Tyr Gln Asp Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly
100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe
115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu
130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Glu Ala Ala Arg
145 150 155 160

Leu Phe Thr Ser Ile Gln Asn Lys Leu Gly Gln Ser Asp Arg Thr Val
165 170 175

Ile Pro Pro Glu Val Glu Gln Thr Val Asn Leu Phe Val Lys Ala Leu
180 185 190

Asp Gln Arg Asp Ser Trp Gln Gly Ser Val Ala Ile Gly Pro Ser Tyr
195 200 205

Ala Thr Asn Leu Asn Ser Ser Ser Glu Gln Ser Lys Thr Trp Thr Leu
210 215 220

Tyr Gly Ile Asp Asp Lys Gly Asn Ala Thr Pro Ile Gln Glu Ile Thr
225 230 235 240

Arg Gly Ser Pro Lys Ala Ala Ser Ala Thr Gly Met Asp Tyr Glu Ala

245 250 255

Ser Leu Met Lys Arg Phe Ser Leu Tyr Gly Asn His Gly Val Ala Leu

260 265 270

Arg Gly Leu Ala Tyr Gly Gln Ser Tyr Asp Asp His Ala Asp Tyr Asn

275 280 285

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

290 295 300

Asn Gln Ile Ser Ile Ala Pro Leu Phe Glu His Lys Arg Tyr Ala Asn

305 310 315 320

Asp Gly Leu Tyr Asn Ala Trp Gly Ala Arg Ala Glu Trp Met Arg Phe

325 330 335

Ile Ala Ala Asp Lys Ala Phe Lys Leu Glu Ala Glu Ile Lys Asp Leu

340 345 350

Asp Tyr Gln Lys Tyr Lys Thr Leu Asp Gly Lys Glu Ser Ser Ala Met

355 360 365

Phe Thr Phe Trp Lys Ile Leu Pro Lys Gln Trp Thr Leu Phe Ser Gly

370 375 380

Leu Asp Val Leu Asp His Asp Thr Gln Glu Lys Tyr Met Ala Ala Tyr

385 390 395 400

Gln Gln Gln Gly Ile Arg Phe Gly Leu Ser Lys Ser Trp Asn Val Gly

405 410 415

Leu Asn Thr Thr Leu Phe Ser Ser Tyr Arg Trp Arg Gln Phe Asp Gln

420 425 430

Tyr Val Glu Thr Phe Ala Ala Arg Arg His Asp Phe Glu Gln Asn Tyr

435 440 445

Thr Val Val Val Gln Met Pro Arg Phe Lys Phe Tyr Gly Met Thr Pro

450 455 460

Asn Leu Thr Tyr Arg Tyr Asn His Asn Ser Ser Asn Val Asp Trp Leu

465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 75

<211> 1491

<212> DNA

<213> Acinetobacter sp. ANC 4105 SLAM 1

<400> 75

atgaaaatag cattgctgtg ttgtctgatt ctattggctg gttcatcact ctatgcagat 60

gatgatactc aacttcgtct gaatcaaaac ttggatcaaa atttattaca acaacagcat 120

caactacaac aacaaggggc gattcggagc acggatgagc tgcccaatat tgtgattaat 180

ggacaagtat ttgaagttga aaagaaccaa gatgatctgg caaaagcttt atatttggcg 240

gttatgcaaa agcaatgggg caatgctacg gtttatttaa aacattatca gcaatatcaa 300

ggctatgatc aggctttaac ggattttgcc gaaggtgcgt tagcacgtgc tcagggacag 360

ctcaaattag cagagcaaaa atttcaaagc agtctcaata aacaaccgaa taatctaatt 420

tgtgaactcg agttagcgcg cgtgctgttt gaacagcaga agaacaaaga agcagcacgc 480

ctttttacat caattcagag caagctagga caaagcgatc gtgcggtgat accaccagaa 540

gtagaacaaa cggttaatct gttcgtcaaa gcactggatc agcgggattc atggcaaggc 600

agtgtcgcga taggtccatc ctatgccaca aatctgaata gttcttctga acaaagcaaa 660

acatggacct tgtatggcat tgatgacaag ggcaatgcga cccccattca agaaattaga 720

cgtggcagcc ccaaagcagc atcagcaacg ggtctggatt atgaagccag tttaatcaaa 780

cgcttttctc tctatggcaa ccatggcgtt tccttacgtg gtttagccta tgggcaatcc 840

tatgatgatc aggctgacta taacgaatcg accttgaata ttaatgcagg ctatagtttt 900

ttcgatttaa aaaatcagat cagtattgca ccactgtttg aacataaacg ttatgccaat 960

gatggtttat acaatgcatg gggggcacgt gctgaatgga tgcgatttat tgctgcagac 1020

aaagcattca agctggaagc tgaaatcaaa gatctggact atcaaaaata taaaacgcta 1080

gatggtaaag aaagctcagc gatgttcacg ttttggaaga ttctacctaa gcaatggaca 1140

ctatttagtg gactagatgt acttgatcat gacacgcaag aaaaatacat ggcggcctat 1200

caacaacaag gcatacgctt cgggttgagc aagtcttgga atgctgggtt gaatactacc 1260

ttgttcagtt catatcgctg gcggcagttt gatcggtatg ccgaaagtct agaagcccgt 1320

cgtcatgatt ttgaacaaaa ttatacattc gtggtgcaga tgccccgatt taaattttat 1380

ggtgtgacgc caaatctgac ttatcgttat aaccacaaca gtagtaatgt tgactggctg 1440

tattcctatg ataaacacaa tgtcagctta aagcttgaac atcgttttta g 1491

<210> 76

<211> 496

<212> PRT

<213> Acinetobacter sp. ANC 4105 SLAM 1

<400> 76

Met Lys Ile Ala Leu Leu Cys Cys Leu Ile Leu Leu Ala Gly Ser Ser
1 5 10 15

Leu Tyr Ala Asp Asp Asp Thr Gln Leu Arg Leu Asn Gln Asn Leu Asp
20 25 30

Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Ala Ile
35 40 45

Arg Ser Thr Asp Glu Leu Pro Asn Ile Val Ile Asn Gly Gln Val Phe
50 55 60

Glu Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Gly Asn Ala Thr Val Tyr Leu Lys His Tyr
85 90 95

Gln Gln Tyr Gln Gly Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly
100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe
115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu
130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Glu Ala Ala Arg
145 150 155 160

Leu Phe Thr Ser Ile Gln Ser Lys Leu Gly Gln Ser Asp Arg Ala Val
165 170 175

Ile Pro Pro Glu Val Glu Gln Thr Val Asn Leu Phe Val Lys Ala Leu
180 185 190

Asp Gln Arg Asp Ser Trp Gln Gly Ser Val Ala Ile Gly Pro Ser Tyr
195 200 205

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

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

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

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

450 455 460

Asn Leu Thr Tyr Arg Tyr Asn His Asn Ser Ser Asn Val Asp Trp Leu
465 470 475 480
Tyr Ser Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe
485 490 495

<210> 77

<211> 1464

<212> DNA

<213> Acinetobacter sp. ATCC 27244 SLAM 1

<400> 77

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cggagcactg aaaagttacc tgaactccaa atcaatggaa aagtctatgt cgtagagaag 180

aaccaagatg atctagccaa agcgctatat ctagcggtta tgcaaaaaca atgggttaat 240

gttcaaattt atttagtgca ttatcaaagc tatcctgagt atgatcaggc tttaactgat 300

ttcgctgaag gtgcattggc acgtgctcag ggacaactaa aactggctga acaaaaattc 360

caaagcagtt taaataaaca accgaacaat ctgatttgtg aactcgagtt agcgcgtgtg 420

ctgtttgaac aacagaagaa caaagaggca gcacaccttt ttataacgat tcaaaataaa 480

ttagaacaaa gtgatcacag tgtcattcca ccagaagtac aaaaaacggt tcagcttttc 540

gtcaaagcgc ttgctcaacg agatgcatgg caaggttcta ttgctatagg tccgacttat 600

gcgagcaatc taaacagttc atcagaacaa agcaaaactt ggacgctgta tggcatggat 660

aaagatggca acattatccc agctcaaatt acacgaggaa gtccaaaagc agtttcagca 720

aatggtatag attatgacgc aagcctgatc aaacgttttt ccatcaaaga aaatcatggt 780

gttgcactac gtgctctagc ttatggacag tcctacgata accaaagcaa ttataacgaa 840

tccaccctca acgtaaatgc aggttatagc tattacgatt taaaaaacca aattaatttc 900

agtccactat ttgaacacaa acgttatggc aacgagagtt tgtacgatgc ttggggcggg 960

cggattgaat ggatgcgatt tatttcagga gataaagcac tcaaacttga agcagaaatt 1020

aaagatttta attatcaaac ctataaaaca cttaatgggc aagagcgttc ggtgctggcg 1080

acttttgga aaattttacc agaacaatgg acattctttg gtggactcga cctccttgat 1140

cgttcgacac aagaacaata taccgcggct taccagcaac aaggaattcg tctaggtata 1200

agtaaaccat ggagtattgg aattcataca acattattaa gtacttatcg ttggcgacaa 1260

tttgataaat acgcaaaggt ttatgaagca aggcgacatg attttgaaca aaattatacg 1320

tttgttgtgc aaatgccacg cttcaaattt tatggcgtaa cgccgaattt aacttatcgc 1380

tataaccaca atgatagcaa tgtggactgg ttgtacactt atgacaagca caatgtcagc 1440

ctgaaactcg aacaccgttt ctag 1464

<210> 78

<211> 487

<212> PRT

<213> Acinetobacter sp. ATCC 27244 SLAM 1

<400> 78

Met Ala Leu Trp Gly Asn Thr Ser Leu Tyr Ala Asp Asp Glu Thr Gln
1 5 10 15

Leu Arg Leu Asn Gln Ser Leu Asp Gln Gln Leu Leu Gln Gln Gln Arg
20 25 30

Ser Leu Gln Ala Gln Gly Thr Ile Arg Ser Thr Glu Lys Leu Pro Glu
35 40 45

Leu Gln Ile Asn Gly Lys Val Tyr Val Val Glu Lys Asn Gln Asp Asp
50 55 60

Leu Ala Lys Ala Leu Tyr Leu Ala Val Met Gln Lys Gln Trp Val Asn
65 70 75 80

Val Gln Ile Tyr Leu Val His Tyr Gln Ser Tyr Pro Glu Tyr Asp Gln
85 90 95

Ala Leu Thr Asp Phe Ala Glu Gly Ala Leu Ala Arg Ala Gln Gly Gln
100 105 110

Leu Lys Leu Ala Glu Gln Lys Phe Gln Ser Ser Leu Asn Lys Gln Pro
115 120 125

Asn Asn Leu Ile Cys Glu Leu Glu Leu Ala Arg Val Leu Phe Glu Gln
130 135 140

Gln Lys Asn Lys Glu Ala Ala His Leu Phe Ile Thr Ile Gln Asn Lys
145 150 155 160

Leu Glu Gln Ser Asp His Ser Val Ile Pro Pro Glu Val Gln Lys Thr
165 170 175

Val Gln Leu Phe Val Lys Ala Leu Ala Gln Arg Asp Ala Trp Gln Gly
180 185 190

Ser Ile Ala Ile Gly Pro Thr Tyr Ala Ser Asn Leu Asn Ser Ser Ser
195 200 205

Glu Gln Ser Lys Thr Trp Thr Leu Tyr Gly Met Asp Lys Asp Gly Asn
210 215 220

Ile Ile Pro Ala Gln Ile Thr Arg Gly Ser Pro Lys Ala Val Ser Ala
225 230 235 240

Asn Gly Ile Asp Tyr Asp Ala Ser Leu Ile Lys Arg Phe Ser Ile Lys
245 250 255

Glu Asn His Gly Val Ala Leu Arg Ala Leu Ala Tyr Gly Gln Ser Tyr
260 265 270

Asp Asn Gln Ser Asn Tyr Asn Glu Ser Thr Leu Asn Val Asn Ala Gly
275 280 285

Tyr Ser Tyr Tyr Asp Leu Lys Asn Gln Ile Asn Phe Ser Pro Leu Phe
290 295 300

Glu His Lys Arg Tyr Gly Asn Glu Ser Leu Tyr Asp Ala Trp Gly Gly
305 310 315 320

Arg Ile Glu Trp Met Arg Phe Ile Ser Gly Asp Lys Ala Leu Lys Leu
325 330 335

Glu Ala Glu Ile Lys Asp Phe Asn Tyr Gln Thr Tyr Lys Thr Leu Asn
340 345 350

Gly Gln Glu Arg Ser Val Leu Ala Thr Phe Trp Lys Ile Leu Pro Glu
355 360 365

Gln Trp Thr Phe Phe Gly Gly Leu Asp Leu Leu Asp Arg Ser Thr Gln
370 375 380

Glu Gln Tyr Thr Ala Ala Tyr Gln Gln Gln Gly Ile Arg Leu Gly Ile
385 390 395 400

Ser Lys Pro Trp Ser Ile Gly Ile His Thr Thr Leu Leu Ser Thr Tyr
405 410 415

Arg Trp Arg Gln Phe Asp Lys Tyr Ala Lys Val Tyr Glu Ala Arg Arg

420 425 430

His Asp Phe Glu Gln Asn Tyr Thr Phe Val Val Gln Met Pro Arg Phe

435 440 445

Lys Phe Tyr Gly Val Thr Pro Asn Leu Thr Tyr Arg Tyr Asn His Asn

450 455 460

Asp Ser Asn Val Asp Trp Leu Tyr Thr Tyr Asp Lys His Asn Val Ser

465 470 475 480

Leu Lys Leu Glu His Arg Phe

485

<210> 79

<211> 1401

<212> DNA

<213> Acinetobacter sp. CIP 102136 SLAM 1

<400> 79

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ttacttaaaa aaacagtaga taaagattta aagctttcta cactacctcc aaactcaagt 180

ttagaagatt atattaatca agccattatt cataaagact ggaaagaact tgagaaacta 240

ctagataaat acagaaaaac tgataattac gatcacattt tatacgagta tggcttaggt 300

gctttatatc gttttcaagg aaagcaaaag aaagccatag aaatgtacca agagattatt 360

acaaagaatc caaatttata ttatccccgt tttgatctag ccatgatgtt atttgaaaat 420

aaacaatata ctgaagctaa aaatgaattt agagcagtaa gacctttct tcctactcag 480

atccaagcat taatagatca gctattgagt actatggaag agtctcaagg atggcaacca 540

aacgtaaatt ttaattttga aaaaacagat aatgttaatc aatcatcgag tataaaagag 600

atttctattg gaaaagcaac tttcatacgt gatcaggaat cactaccaca aaaggcagaa 660

ggtatcggtt atacgctgaa tgcatcacgt gaacaaaata tgatgagcaa tcattatgta 720

tattttaatg caacattaaa cggtattcat tattgggata atacagaatt tagtgagcaa 780

accttacgta tcgatactgg ttacaagtat aaagatctta agcaatcctt aggcataatt 840

ccatttattg ggcaaaatat actaggtgat agtcgttaca gtcataacta tggtgcagga 900

ttagaatata accgattatt atcagatcgc tggcaagttt ctgctaatac atctcatatc 960

caaaaacgat atcaggattc agatcttgca caatattata atggtcatgc taatagtcag 1020

gctgcattga tgctgtatca accgaaatcg aaattactca tatatagtgg cttagactgg 1080

atgcaagatc gcttagcgga cgaagcagaa tcatctaata aaaaaggtat acgaagtggt 1140

ttttatact ttggggactc attgggtatt agtagcaaca tacgttattc taagcgtaat 1200

tttttagcag ataatatttg gtatggtatt caacgcaaag acagtgaata tgaatttggt 1260

atagctactt ggcgtaagca atggcagtgg aaaggtttta ctcccaagtt aaattataga 1320

tatcaaaaaa ttgacagcaa tttaccactt tatgagcgta ataacggcac atggtttatc 1380

acaatagata aaaaaattta a 1401

<210> 80

<211> 466

<212> PRT

<213> Acinetobacter sp. CIP 102136 SLAM 1

<400> 80

Met Asn Ile Lys Tyr Leu Val Ile Leu Ser Val Thr Phe Ser Ser Thr

1 5 10 15

Ala Phe Ser Gln Glu Leu Pro Pro Ala Gln Thr Val Phe Phe Glu Gln

20 25 30

Asp Ser Phe Ile Gln Pro Glu Leu Leu Leu Lys Lys Thr Val Asp Lys

35 40 45

Asp Leu Lys Leu Ser Thr Leu Pro Pro Asn Ser Ser Leu Glu Asp Tyr

50 55 60

Ile Asn Gln Ala Ile Ile His Lys Asp Trp Lys Glu Leu Glu Lys Leu

65 70 75 80

Leu Asp Lys Tyr Arg Lys Thr Asp Asn Tyr Asp His Ile Leu Tyr Glu

85 90 95

Tyr Gly Leu Gly Ala Leu Tyr Arg Phe Gln Gly Lys Gln Lys Lys Ala

100 105 110

Ile Glu Met Tyr Gln Glu Ile Ile Thr Lys Asn Pro Asn Leu Tyr Tyr

115 120 125

Pro Arg Phe Asp Leu Ala Met Met Leu Phe Glu Asn Lys Gln Tyr Thr

130 135 140

Glu Ala Lys Asn Glu Phe Arg Ala Val Arg Pro Phe Leu Pro Thr Gln

145 150 155 160

Ile Gln Ala Leu Ile Asp Gln Leu Leu Ser Thr Met Glu Glu Ser Gln
165 170 175
Gly Trp Gln Pro Asn Val Asn Phe Asn Phe Glu Lys Thr Asp Asn Val
180 185 190
Asn Gln Ser Ser Ser Ile Lys Glu Ile Ser Ile Gly Lys Ala Thr Phe

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

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

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

385 390 395 400
Phe Leu Ala Asp Asn Ile Trp Tyr Gly Ile Gln Arg Lys Asp Ser Glu

405 410 415

Tyr Glu Phe Gly Ile Ala Thr Trp Arg Lys Gln Trp Gln Trp Lys Gly

420 425 430

Phe Thr Pro Lys Leu Asn Tyr Arg Tyr Gln Lys Ile Asp Ser Asn Leu

435 440 445

Pro Leu Tyr Glu Arg Asn Asn Gly Thr Trp Phe Ile Thr Ile Asp Lys

450 455 460

Lys Ile

465

<210> 81

<211> 1401

<212> DNA

<213> Acinetobacter sp. CIP 102637 SLAM 1

<400> 81

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ttacttaaaa aaacagtaga taaagattta aatctttcta cactacctcc aaactcaagt 180

ttagaagatt atattaatca agcaattatt cataaagact ggaaagaact tgagaaacta 240

ctagataaat acagaaaaac tgataattac gatcacattt tatacgaata tggcttaggt 300

gctttatatc gttttcaagg aaagcaaaag aaagccatag aaatgtacca agagattatt 360

acaaagaatc caaatttata ttatccccgt tttgatctag ccatgatgtt atttgaaaat 420

aaacaatata ctgaagctaa aaatgaattt agagcagtaa gacctttct tcctactcag 480

atccaagcat taatagatca gctattgagt actatggaag agtctcaagg atggcaacca 540

aacgtaaatt ttaattttga aaaaacagat aatgttaatc aaacatcgag tataaaagag 600

atttctattg gagaagcaac tttcatacgt gatcaggaat cactaccaca aaaggcagaa 660

ggtatcggtt atacgctgaa tgcatcacgt gaacaaaata tgatgagcaa tcattatgta 720

tattttaatg caacattaaa cggtatttat tattgggata atacagaatt tagtgagcaa 780

accttacgta tcgatactgg ttacaagtat aaagatctta agcaatcctt aggcataatt 840

ccatttattg ggcaaaatat actaggtgat agtcgttaca gtcataacta tggtgcagga 900

ttagaatata accgattatt atcagatcgt tggcaagtct ctgctaatac atctcatatc 960

caaaaacgat atcaggattc agatcttgca caatattata atggtcatgc taatagtcag 1020

gctgcattga tgctgtatca accgaaatca aaattactca tatatagtgg cttagactgg 1080

atgcaagatc gcttagcgga cgaagcagaa tcatccaata agaaaggtat acgaagtggt 1140

ttttatact ttggggactc attgggtatt agtagcaaca tacgttattc taagcgtaat 1200

tttttagcag ataatatttg gtatggtatt caacgcaaag acagtgaata tgaatttggt 1260

atagctactt ggcgtaagca atggcagtgg aaaggtttta ctcccaagtt aaattataga 1320

tatcaaaaaa ttgacagcaa tttaccactt tatgagcgta ataacggcac atggtttatc 1380

acaatagata aaaaaattta a 1401

<210> 82

<211> 466

<212> PRT

<213> Acinetobacter sp. CIP 102637 SLAM 1

<400> 82

Met Asn Ile Lys Tyr Leu Val Ile Leu Ser Val Thr Phe Ser Ser Thr

1 5 10 15

Ala Phe Ser Gln Glu Leu Leu Pro Ala Gln Thr Val Phe Phe Glu Gln

20 25 30

Asp Ser Phe Ile Gln Pro Glu Leu Leu Leu Lys Lys Thr Val Asp Lys

35 40 45

Asp Leu Asn Leu Ser Thr Leu Pro Pro Asn Ser Ser Leu Glu Asp Tyr

50 55 60

Ile Asn Gln Ala Ile Ile His Lys Asp Trp Lys Glu Leu Glu Lys Leu

65 70 75 80

Leu Asp Lys Tyr Arg Lys Thr Asp Asn Tyr Asp His Ile Leu Tyr Glu

85 90 95

Tyr Gly Leu Gly Ala Leu Tyr Arg Phe Gln Gly Lys Gln Lys Lys Ala

100 105 110

Ile Glu Met Tyr Gln Glu Ile Ile Thr Lys Asn Pro Asn Leu Tyr Tyr

115 120 125

Pro Arg Phe Asp Leu Ala Met Met Leu Phe Glu Asn Lys Gln Tyr Thr

130 135 140

Glu Ala Lys Asn Glu Phe Arg Ala Val Arg Pro Phe Leu Pro Thr Gln

145 150 155 160

Ile Gln Ala Leu Ile Asp Gln Leu Leu Ser Thr Met Glu Glu Ser Gln
165 170 175
Gly Trp Gln Pro Asn Val Asn Phe Asn Phe Glu Lys Thr Asp Asn Val
180 185 190
Asn Gln Thr Ser Ser Ile Lys Glu Ile Ser Ile Gly Glu Ala Thr Phe

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

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

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

385 390 395 400
Phe Leu Ala Asp Asn Ile Trp Tyr Gly Ile Gln Arg Lys Asp Ser Glu

405 410 415

Tyr Glu Phe Gly Ile Ala Thr Trp Arg Lys Gln Trp Gln Trp Lys Gly

420 425 430

Phe Thr Pro Lys Leu Asn Tyr Arg Tyr Gln Lys Ile Asp Ser Asn Leu

435 440 445

Pro Leu Tyr Glu Arg Asn Asn Gly Thr Trp Phe Ile Thr Ile Asp Lys

450 455 460

Lys Ile

465

<210> 83

<211> 1491

<212> DNA

<213> Acinetobacter sp. CIP 64.2 SLAM 1

<400> 83

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gatgagacac aacttcgcct gaatcaaagc cttgatcaga atttattaca acaacagcac 120

caactacaac aacaaggtgc aattcgaagc accgatgaac taccgaatat tgtgattaac 180

ggtcaagtat tcgaagttgc aaaaaatcaa gatgacctcg caaaagcttt atatttggct 240

gttatgcaaa agcaatgggg taatgctgct gtttatctaa agcattatca acaatatgat 300

ggctatgacc aagcattaac cgattttgcc gagggagcat tggctcgtgc gcaaggccag 360

ctcaaattag ccgaacaaaa atttcaaagc agtctcaata aacaaccgaa taaccttatt 420

tgtgaacttg agttagcgcg cgtgctgttt gaacagcaga agaacaaaca agcagcacgc 480

ctttttacat cgattcaaaa caaattgggg cagagtgatc gtggtgtgat tccaccagag 540

gttgaacaaa cggttaattt gtttgttaaa gcacttgatc agcgtgatgc atggcaaggc 600

agtgttgcga ttggcccaac ctacgccacg aatctaaata gttcttctga acaaagtaaa 660

acttggatgt tgtatggcat tgaccaaaag ggcaatgtga tccccattca ggagattacc 720

cgtggaagtc ctaaagctga gtcggcaacg ggtgtggact acgaagccag tttaatgaaa 780

cgcttttctc tgtatggcaa tcatggggtt tccttacgtg gtttggctta tggacagtct 840

tatgacgatc atgccgactt taatgaatcc accctcaata tcaatgcagg ctatagtttt 900

tttgatttaa aaaatcaaat caccattgca ccgttatttg agcacaaacg ttatgccaat 960

gatggtttgt acaatgcttg gggcgcgcgt gcagaatgga tgcgctttat ctccgccgat 1020

aaagcactca agcttgaagc tgaaatcaaa gatttaaatt atcaaacata taaaacttta 1080

gatggtaaag aaagttccgc catgctgacc ttttggaaaa tcctacctga acaatggact 1140

ctgtttggtg gtgtggatgt cttagatcac gatactcaag aaaaatatat ggcagcctat 1200

cagcaacaag gtgttcgttt gggtctgagc aaaccgtgga atattggatt aaacacgacc 1260

ttgttcagtt cctatcgttg gcgtcagttt gatcgttatg tggcagcatt tgagacacgt 1320

cgtcaagatt ttgagcaaaa ctacaccttt gtattgcaaa tgcctcgttt caaattctat 1380

ggcatgacgc cgaacctgac ctatcgctat aaccgtaata acagcaatgt ggattggttg 1440

tattcctacg acaaacataa tatcagctta aagcttgagc accgtttcta g 1491

<210> 84

<211> 496

<212> PRT

<213> Acinetobacter sp. CIP 64.2 SLAM 1

<400> 84

Met Lys Arg Thr Leu Leu Cys Cys Leu Ile Leu Leu Ala Asn Ser Ser
1 5 10 15

Leu His Ala Asp Asp Glu Thr Gln Leu Arg Leu Asn Gln Ser Leu Asp
20 25 30

Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Ala Ile
35 40 45

Arg Ser Thr Asp Glu Leu Pro Asn Ile Val Ile Asn Gly Gln Val Phe
50 55 60

Glu Val Ala Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Gly Asn Ala Ala Val Tyr Leu Lys His Tyr
85 90 95

Gln Gln Tyr Asp Gly Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly
100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe
115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu
130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Gln Ala Ala Arg

145 150 155 160

Leu Phe Thr Ser Ile Gln Asn Lys Leu Gly Gln Ser Asp Arg Gly Val

165 170 175

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

180 185 190

Asp Gln Arg Asp Ala Trp Gln Gly Ser Val Ala Ile Gly Pro Thr Tyr

195 200 205

Ala Thr Asn Leu Asn Ser Ser Ser Glu Gln Ser Lys Thr Trp Met Leu

210 215 220

Tyr Gly Ile Asp Gln Lys Gly Asn Val Ile Pro Ile Gln Glu Ile Thr

225 230 235 240

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

245 250 255

Ser Leu Met Lys Arg Phe Ser Leu Tyr Gly Asn His Gly Val Ser Leu

260 265 270

Arg Gly Leu Ala Tyr Gly Gln Ser Tyr Asp Asp His Ala Asp Phe Asn

275 280 285

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

290 295 300

Asn Gln Ile Thr Ile Ala Pro Leu Phe Glu His Lys Arg Tyr Ala Asn

305 310 315 320

Asp Gly Leu Tyr Asn Ala Trp Gly Ala Arg Ala Glu Trp Met Arg Phe

325 330 335

Ile Ser Ala Asp Lys Ala Leu Lys Leu Glu Ala Glu Ile Lys Asp Leu

340 345 350

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

355 360 365

Leu Thr Phe Trp Lys Ile Leu Pro Glu Gln Trp Thr Leu Phe Gly Gly

370 375 380

Val Asp Val Leu Asp His Asp Thr Gln Glu Lys Tyr Met Ala Ala Tyr

385 390 395 400

Gln Gln Gln Gly Val Arg Leu Gly Leu Ser Lys Pro Trp Asn Ile Gly
405 410 415

Leu Asn Thr Thr Leu Phe Ser Ser Tyr Arg Trp Arg Gln Phe Asp Arg
420 425 430

Tyr Val Ala Ala Phe Glu Thr Arg Arg Gln Asp Phe Glu Gln Asn Tyr
435 440 445

Thr Phe Val Leu Gln Met Pro Arg Phe Lys Phe Tyr Gly Met Thr Pro
450 455 460

Asn Leu Thr Tyr Arg Tyr Asn Arg Asn Asn Ser Asn Val Asp Trp Leu
465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Ile Ser Leu Lys Leu Glu His Arg Phe
485 490 495

<210> 85

<211> 1491

<212> DNA

<213> Acinetobacter sp. CIP 70.18 SLAM 1

<400> 85

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caattacagc aacaaggggc aattcggagc acggatgaac tacccaatat tgtgattaat 180

ggacaagtat ttgaagttga aaagaaccaa gatgatctgg caaaagcttt atatttggcg 240

gttatgcaaa agcaatgggg caatgcggca gtctatctaa agcattatca acaatatgat 300

ggctatgacc aagctttaac agactttgcc gagggtgcat tggctcgcgc tcaaggccag 360

ctcaagatag cagagcaaaa attccaaagt agtttaaata aacaacccaa taatctgatt 420

tgcgaactcg agttagcgcg cgtgctgttt gaacagcaga agaacaaaca agcagcacgc 480

ctttttacat ccattcaaag caaattgggg cagagtgatc gtggtgtgat tccacctgag 540

gtcgagcaaa cagttaatct gtttgttaag gcccttgatc aacgtgacgc atggcaaggc 600

agtgtcgcga taggtccatc ctatgccacg aatctaaata gttcttctga acaaagtaaa 660

acttggatgt tgtatggcct tgaccaaaaa ggcaatgtga tccccattca ggaaattacc 720

cgtggaagtc ctaaagctga gtcggcaacg ggtatggact atgaagccag tttaatgaaa 780

cgcttttcgt tctatggcaa tcatggggtt tccttacgtg gtttagcgta tggacagtct 840

tatgatgatc atgctgactt taatgaatcc acactgaata tcaatgcagg ctatagtttt 900

tttgatttaa aaaatcaaat cacaattgca ccgctatttg agcataaacg ttatgccaat 960
gatggtttgt acaatgcttg gggggcacgt gcggaatgga tgcgatttat ctccaccgat 1020
aaagcactca agcttgaagc tgaaatcaaa gatttaaatt atcaaacata taaaacttta 1080
gatggtaaag aaagttcagc catgctgacc ttttggaaaa ttctacctga acaatggaca 1140
ttgtttgggg gcgtggatgt cttagatcat gatactcaag aaaaatacat ggcagcctat 1200
cagcaacaag gtgttcgttt aggtctgagt aaaccgtgga gtgttggctt taataccacc 1260
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cgtcaagatt ttgagcaaaa ctacaccttt gtgttgcaaa tgcctctttt caagttctat 1380
ggcatgacgc cgaatctgac ttatcgctat aaccgtaata acagtaatgt ggattggtta 1440
tattcctatg acaaacacaa tgtcagccta aaacttgagc accgttttta g 1491

<210> 86
<211> 496
<212> PRT
<213> Acinetobacter sp. CIP 70.18 SLAM 1
<400> 86

Met Lys Arg Thr Leu Leu Cys Cys Leu Ile Leu Leu Ala Ser Ser Ser
1 5 10 15
Leu Tyr Ala Asp Asp Glu Thr Gln Leu Arg Leu Asn Gln Asn Leu Asp

20 25 30
Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Ala Ile
35 40 45
Arg Ser Thr Asp Glu Leu Pro Asn Ile Val Ile Asn Gly Gln Val Phe
50 55 60
Glu Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80
Val Met Gln Lys Gln Trp Gly Asn Ala Ala Val Tyr Leu Lys His Tyr

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

115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu

130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Gln Ala Ala Arg

145 150 155 160

Leu Phe Thr Ser Ile Gln Ser Lys Leu Gly Gln Ser Asp Arg Gly Val

165 170 175

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

180 185 190

Asp Gln Arg Asp Ala Trp Gln Gly Ser Val Ala Ile Gly Pro Ser Tyr

195 200 205

Ala Thr Asn Leu Asn Ser Ser Ser Glu Gln Ser Lys Thr Trp Met Leu

210 215 220

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

225 230 235 240

Arg Gly Ser Pro Lys Ala Glu Ser Ala Thr Gly Met Asp Tyr Glu Ala

245 250 255

Ser Leu Met Lys Arg Phe Ser Phe Tyr Gly Asn His Gly Val Ser Leu

260 265 270

Arg Gly Leu Ala Tyr Gly Gln Ser Tyr Asp Asp His Ala Asp Phe Asn

275 280 285

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

290 295 300

Asn Gln Ile Thr Ile Ala Pro Leu Phe Glu His Lys Arg Tyr Ala Asn

305 310 315 320

Asp Gly Leu Tyr Asn Ala Trp Gly Ala Arg Ala Glu Trp Met Arg Phe

325 330 335

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

340 345 350

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

355 360 365

Leu Thr Phe Trp Lys Ile Leu Pro Glu Gln Trp Thr Leu Phe Gly Gly
370 375 380
Val Asp Val Leu Asp His Asp Thr Gln Glu Lys Tyr Met Ala Ala Tyr
385 390 395 400
Gln Gln Gln Gly Val Arg Leu Gly Leu Ser Lys Pro Trp Ser Val Gly

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

465 470 475 480
Tyr Ser Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe
485 490 495

<210> 87
<211> 1488
<212> DNA
<213> Acinetobacter sp. CIP-A165 SLAM 1
<400> 87

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tcacttcaag cacaaggtac gattcggagc actgaaaagt tacctgaact ccaaatcaat 180

ggaaaagtct atgtcgtaga gaagaaccaa gatgatctag ccaaagcgct atatctagcg 240
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tgtgaactcg agttagcgcg tgtgctgttt gaacaacaga agaacaaaga ggcagcacac 480
ctttttataa cgattcaaaa taaattagaa caaagtgatc acagtgtcat tccaccagaa 540
gtacaaaaaa cggttcagct tttcgtcaaa gcgcttgctc aacgagatgc atggcaaggt 600

tctattgcta taggtccgac ttatgcgagc aatctaaaca gttcatcaga acaaagcaaa 660

acttggacgc tgtatggcat ggataaagat ggcaacatta tcccagctca aattacacga 720

ggaagtccaa aagcagtttc agcaaatggt ctagattatg acgcaagcct gatcaaacgt 780

ttttccatca aagaaaatca tggtgttgca ctacgtgctc tagcttatgg acagtcctac 840

gataaccaaa gcaattataa cgaatccacc ctcaacgtaa atgcaggtta tagctattac 900

gatttaaaaa accaaattaa tttcagtcca ctatttgaac acaaacctta tggcaacgag 960

agtttatacg atgcttgggg cgggcggatt gaatggatgc gatttatttc aggcgataaa 1020

gcactcaaac ttgaagcaga aattaaagat tttgattatc acacctataa aacacttaat 1080

gggcaagagc gttcggtact ggcgactttt tggaaaattt taccagaaca atggacatta 1140

tttggtggac tcgacctcct tgatcgttcg acacaagaac aatataccgc ggcttaccag 1200

caacaaggaa ttcgtctagg tataagtaaa ccatggaata ttggaattaa tacaacatta 1260

ttaagctctt atcgttggcg acaatttgat aaatacgcaa aggtttatga agcaagacga 1320

catgattttg aacaaaatta tacttttgtt gtgcaaatgc cacgcttcaa attttatggt 1380

gtaacaccga atttaacata tcgctataac cacaatgata gcaatgtgga ttggttgtac 1440

acctatgaca agcacaatgt cagcctgaaa ctcgaacacc gtttctag 1488

<210> 88

<211> 495

<212> PRT

<213> Acinetobacter sp. CIP-A165 SLAM 1

<400> 88

Met Lys Arg Thr Leu Leu Cys Cys Leu Ala Leu Trp Gly Asn Thr Ser
1 5 10 15

Leu Tyr Ala Asp Asp Glu Thr Gln Leu Arg Leu Asn Gln Ser Leu Asp
20 25 30

Gln Gln Leu Leu Gln Gln Gln Arg Ser Leu Gln Ala Gln Gly Thr Ile
35 40 45

Arg Ser Thr Glu Lys Leu Pro Glu Leu Gln Ile Asn Gly Lys Val Tyr
50 55 60

Val Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Val Asn Val Gln Ile Tyr Leu Val His Tyr
85 90 95

Gln Ser Tyr Pro Glu Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly
100 105 110

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

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

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

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

340 345 350

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

355 360 365

Thr Phe Trp Lys Ile Leu Pro Glu Gln Trp Thr Leu Phe Gly Gly Leu

370 375 380

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

385 390 395 400

Gln Gln Gly Ile Arg Leu Gly Ile Ser Lys Pro Trp Asn Ile Gly Ile

405 410 415

Asn Thr Thr Leu Leu Ser Ser Tyr Arg Trp Arg Gln Phe Asp Lys Tyr

420 425 430

Ala Lys Val Tyr Glu Ala Arg Arg His Asp Phe Glu Gln Asn Tyr Thr

435 440 445

Phe Val Val Gln Met Pro Arg Phe Lys Phe Tyr Gly Val Thr Pro Asn

450 455 460

Leu Thr Tyr Arg Tyr Asn His Asn Asp Ser Asn Val Asp Trp Leu Tyr

465 470 475 480

Thr Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 89

<211> 1491

<212> DNA

<213> Acinetobacter sp. ETR1 SLAM 1

<400> 89

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aaactactca aatcagaaga ccctaaaaac acacaagcat taccgaatct gatcatacaa 180

ggtcaagaat atgtggttaa ggatgaaccc gcagaagtcg catatgcact ttacttggca 240

gtgatgcaaa aacaatggca agtggcttta agctatcttc gaaaatataa aaaatttcca 300

aattatgacc aggctttgac tgagttcgct gagggcgtca tggcacgaac acaggggat 360

ttaagtttag ctgagagtaa acttaaacat agcctagaga ttcaatccaa taatttaatg 420

acccaacttg agctggctcg tgtctacacc gaacaacaaa aaaatcagca aggtcaacag 480

ttatttcagc agattcaatc tcaactggtt ctgtctacag atcctgctgc ccaaggtata 540

ggtcaaaccg tagagatgta tctcaaaggg cttaaacaac gagatgaatg gcatggttca 600

ttggcttttg gttcacgtta tgccagtaat gttaataatg cttccgataa atacgacatc 660

attactcgct atggtataga tccagataca gacgaagtgg tgcctataga acggatcaga 720

cgtggcacac ctgatgcgat cagtgcacaa ggtttggatt atgaagcgac cttaactaaa 780

cgatggtcgc tttctggaca acatggcatt gcattgcgcg gattattcta tggtcaagtt 840

tatccagagc agacagatta taatgaatta acttttaact ttaatgcggg ttatagttat 900

tacaacgaac gtaatcaagt cttgattgca cccgtatttg aacataaata ctatgcccac 960

gacccactgt atagtgccta tgggctaagg ggtgagtgga tgcgttttat ctctaacgac 1020

aaagctgtca agttagaagc cgaattgaaa gatataaatt attcccaata taaaggccaa 1080

gatggcgtgg aatattcagt ctattcaacc ttttggaaaa ttttaccgaa aaactggacg 1140

ctatttggcg gactggattt tgtcgaccat aatacccaag aacaatattt tacggcttat 1200

caacaacaag gcgtgcgttt aggcctttcc aaaaactttg actcaggttt taacgcaaat 1260

ttatttagtt ctttccgttg gcgtcaattt gataaattta ctccagtgtt ggagtctaga 1320

cgacaggatt ttgaacaaaa ttatactttg attctaagtg caccacgctg ggctttttat 1380

ggtttaacac ctaatctcac ttatcaatat aatcaaaata acagcaatgt agagtggcta 1440

tattcttatg ataaacacaa tgtcagttta aagctggagc atcggtttta a 1491

<210> 90

<211> 496

<212> PRT

<213> Acinetobacter sp. ETR1 SLAM 1

<400> 90

Met Lys Lys Ile Val Leu Leu Gly Ala Val Leu Gln Cys Gly Gln Cys

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Val Tyr Ala Ala Asp Asp Thr Ser Ile Arg Leu Asn Gln Glu Ile Ser

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Gln Gln Gln Tyr Gln Asn Asp Lys Lys Leu Leu Lys Ser Glu Asp Pro

35 40 45

Lys Asn Thr Gln Ala Leu Pro Asn Leu Ile Ile Gln Gly Gln Glu Tyr

50 55 60

Val Val Lys Asp Glu Pro Ala Glu Val Ala Tyr Ala Leu Tyr Leu Ala

65 70 75 80

Val Met Gln Lys Gln Trp Gln Val Ala Leu Ser Tyr Leu Arg Lys Tyr

85 90 95

Lys Lys Phe Pro Asn Tyr Asp Gln Ala Leu Thr Glu Phe Ala Glu Gly

100 105 110

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

115 120 125

Lys His Ser Leu Glu Ile Gln Ser Asn Asn Leu Met Thr Gln Leu Glu

130 135 140

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

145 150 155 160

Leu Phe Gln Gln Ile Gln Ser Gln Leu Val Leu Ser Thr Asp Pro Ala

165 170 175

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

180 185 190

Gln Arg Asp Glu Trp His Gly Ser Leu Ala Phe Gly Ser Arg Tyr Ala

195 200 205

Ser Asn Val Asn Asn Ala Ser Asp Lys Tyr Asp Ile Ile Thr Arg Tyr

210 215 220

Gly Ile Asp Pro Asp Thr Asp Glu Val Val Pro Ile Glu Arg Ile Arg

225 230 235 240

Arg Gly Thr Pro Asp Ala Ile Ser Ala Gln Gly Leu Asp Tyr Glu Ala

245 250 255

Thr Leu Thr Lys Arg Trp Ser Leu Ser Gly Gln His Gly Ile Ala Leu

260 265 270

Arg Gly Leu Phe Tyr Gly Gln Val Tyr Pro Glu Gln Thr Asp Tyr Asn

275 280 285

Glu Leu Thr Phe Asn Phe Asn Ala Gly Tyr Ser Tyr Tyr Asn Glu Arg

290 295 300

Asn Gln Val Leu Ile Ala Pro Val Phe Glu His Lys Tyr Tyr Ala His

305 310 315 320

Asp Pro Leu Tyr Ser Ala Tyr Gly Leu Arg Gly Glu Trp Met Arg Phe

325 330 335

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

340 345 350

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

355 360 365

Ser Thr Phe Trp Lys Ile Leu Pro Lys Asn Trp Thr Leu Phe Gly Gly

370 375 380

Leu Asp Phe Val Asp His Asn Thr Gln Glu Gln Tyr Phe Thr Ala Tyr

385 390 395 400

Gln Gln Gln Gly Val Arg Leu Gly Leu Ser Lys Asn Phe Asp Ser Gly

405 410 415

Phe Asn Ala Asn Leu Phe Ser Ser Phe Arg Trp Arg Gln Phe Asp Lys

420 425 430

Phe Thr Pro Val Leu Glu Ser Arg Arg Gln Asp Phe Glu Gln Asn Tyr

435 440 445

Thr Leu Ile Leu Ser Ala Pro Arg Trp Ala Phe Tyr Gly Leu Thr Pro

450 455 460

Asn Leu Thr Tyr Gln Tyr Asn Gln Asn Asn Ser Asn Val Glu Trp Leu

465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 91

<211> 1491

<212> DNA

<213> Acinetobacter sp. MN12 SLAM 1

<400> 91

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caattacagc gacaaggggt gattcggagc acggatgaac tacctaatat tgtgattaat 180

gggcaagtat ttgaagttga aaagaaccaa gatgatctgg caaaagcttt atatttggcg 240

gttatgcaaa agcaatgggg caatgcggca gtctatctaa agcattatca acaatatgat 300

ggttatgacc aagctttaac tgactttgcc gagggtgcat tggctcgtgc tcaaggccag 360

ctcaagatag cagagcaaaa attccaaagt agtttaaata aacaatcgaa taatctgatt 420

tgtgaactcg agttagcgcg cgtgctgttt gaacagcaga agaacaaaca agcagcacgc 480

ctttttacat ccattcagag caaattgggg cagagtgatc gtggtgtgat tccacctgag 540

gtcgagcaaa cagttaatct gtttgttaag gcccttgatc aacgtgacgc atggcaaggc 600

agtgtggcga ttggaccaac ctatgccacg aatctaaata gttcttctga acaaagtaaa 660

acttggatgt tgtatggcct tgaccaaaaa ggcaatgtga tccccattca ggaaattacc 720

cgtggaagtc ctaaagctga gtcggcaacg ggtatggact atgaagccag tttaatgaaa 780

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tttgatttaa aaaatcaaat cacaattgca ccgctatttg agcataaacg ttatgccaat 960

gatggtttgt acaatgcttg gggggcacgt gcggaatgga tgcgatttat ctccaccgat 1020

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gatggtaaag aaagttcagc catgctgacc ttttggaaaa ttctacctga acaatggaca 1140

ttgtttgggg gcgtggatgt cttagatcat gatacccaag aaaaatacat ggcagcctat 1200

cagcaacaag gtgttcgttt aggtctgagt aaaccgtgga gtgttggctt taataccacc 1260

ttgttcagtt cctatcgttg gcgtcagttt gatcgttacg tggcagcatt tgagacacgt 1320

cgtcaagatt ttgagcaaaa ctacaccttt gtgttgcaaa tgcctctttt caagttctat 1380

ggcatgacgc cgaatctgac ttatcgctat aaccgtaata acagtaatgt ggattggtta 1440

tattcctatg acaaacacaa tgtcagccta aaacttgagc accgtttta g 1491

<210> 92

<211> 496

<212> PRT

<213> Acinetobacter sp. MN12 SLAM 1

<400> 92

Met Lys Arg Thr Leu Leu Cys Cys Leu Ile Leu Leu Ala Ser Ser Ser

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Leu Tyr Ala Asp Asp Glu Thr Gln Leu Arg Leu Asn Gln Asn Leu Asp

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Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Arg Gln Gly Val Ile

35 40 45

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

50 55 60

Glu Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala

65 70 75 80

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

85 90 95

Gln Gln Tyr Asp Gly Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly

100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Ile Ala Glu Gln Lys Phe

115 120 125

Gln Ser Ser Leu Asn Lys Gln Ser Asn Asn Leu Ile Cys Glu Leu Glu

130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Gln Ala Ala Arg

145 150 155 160

Leu Phe Thr Ser Ile Gln Ser Lys Leu Gly Gln Ser Asp Arg Gly Val

165 170 175

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

180 185 190

Asp Gln Arg Asp Ala Trp Gln Gly Ser Val Ala Ile Gly Pro Thr Tyr

195 200 205

Ala Thr Asn Leu Asn Ser Ser Ser Glu Gln Ser Lys Thr Trp Met Leu

210 215 220

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

225 230 235 240

Arg Gly Ser Pro Lys Ala Glu Ser Ala Thr Gly Met Asp Tyr Glu Ala

245 250 255

Ser Leu Met Lys Arg Phe Ser Phe Tyr Gly Asn His Gly Val Ser Leu

260 265 270

Arg Gly Leu Ala Tyr Gly Gln Ser Tyr Asp Asp His Ala Asp Phe Asn

275 280 285

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

290 295 300

Asn Gln Ile Thr Ile Ala Pro Leu Phe Glu His Lys Arg Tyr Ala Asn

305 310 315 320

Asp Gly Leu Tyr Asn Ala Trp Gly Ala Arg Ala Glu Trp Met Arg Phe

325 330 335

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

340 345 350

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

355 360 365

Leu Thr Phe Trp Lys Ile Leu Pro Glu Gln Trp Thr Leu Phe Gly Gly

370 375 380

Val Asp Val Leu Asp His Asp Thr Gln Glu Lys Tyr Met Ala Ala Tyr

385 390 395 400

Gln Gln Gln Gly Val Arg Leu Gly Leu Ser Lys Pro Trp Ser Val Gly

405 410 415

Phe Asn Thr Thr Leu Phe Ser Ser Tyr Arg Trp Arg Gln Phe Asp Arg

420 425 430

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

435 440 445

Thr Phe Val Leu Gln Met Pro Leu Phe Lys Phe Tyr Gly Met Thr Pro

450 455 460

Asn Leu Thr Tyr Arg Tyr Asn Arg Asn Asn Ser Asn Val Asp Trp Leu

465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 93

<211> 1491

<212> DNA

<213> Acinetobacter sp. NIPH 1847 SLAM 1

<400> 93

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caattacaac aacaaggcac cattcgtgac accgagaaac tacccagcat ccgtattaat 180

ggccaaattt acgcggtaga gcagaatccg gatgatctgg ccaaagcgct atatctggcg 240

gttatgcaaa agcaatgggg caatgctgcg atttacttaa aacactatca gcagtatcaa 300

ggctatgatc aggctttaac cgattttgcc gaagcggctt tggcgcgcgc tcagggaaag 360

ctcaaattag ccgaacaaaa atttcaaagt agtcttaatc aacaaccgaa taatctgatt 420

tgtgaactcg agttagcgcg cgtgctgttt gaacagcaga agaataaaca agcagcacgc 480

ctttttacat cgattcagga caagctaggg cagagcaatg gggcaatgat cccaccagaa 540

gtgcaacaaa cggttgatct gttcgtcaaa gcacttgatc agcgggattc gtggcaaggc 600

agtgtcgcaa ttggcccatc ctatgccacc aatctgaata gctcttctga acaaagcaaa 660

acatggacct tgtatggcat tgatgacaag tgcaaggcga ctccaattca ggaaattacc 720

cgtggcagtc ccaaagcagc atcagcaaca ggggttgact atgaggccag tctaatcaag 780

cgcttttcgc tttcgggcaa tcatggcatt tccttacgcg gtttagcatt tgggcaatcc 840

tatgctgatc atgcgctcta taacgaatcc accctgaata tcaatgcagg ctatagtttt 900

tttgatttaa aaaatcaaat caccattgca ccgctatttg aacataaacg ttatgccaat 960

gatggtttat acaatgcatg gggggcacgt actgaatgga tgcgatttct agcaccagac 1020

aaagccttca agcttgaagc tgaaatcaaa gatctgggct atcaaaagta taaaaaccta 1080

gatggtaaag aaagctcggc aatgtttaca ttctggaaaa ttctaccgca gcaatggaca 1140

ctttttagcg gactggatgt actggatcat gacacccagg aaaaatatat ggcggcttat 1200

cagcaacaag gcatccgtct aggactgagc aaatcctgga aagcaggttt aaataccacg 1260

ctattaacct cataccgctg gcggcagttt gaccgctacg tcgagacctt tgctgcacgt 1320

cgccatgatt ttgaacagaa ctataccctg gttgtacaaa tgccacggtt taagttttat 1380

ggtatgacgc cgaatttgac ctatcgctac aaccataatg acagtaatgt cgactggctc 1440

tattcctacg ataaacacaa tatcagctta aagctggaac atcgttttta g 1491

<210> 94

<211> 496

<212> PRT

<213> Acinetobacter sp. NIPH 1847 SLAM 1

<400> 94

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

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

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

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

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

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

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

Thr Leu Val Val Gln Met Pro Arg Phe Lys Phe Tyr Gly Met Thr Pro
450 455 460
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Tyr Ser Tyr Asp Lys His Asn Ile Ser Leu Lys Leu Glu His Arg Phe
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<210> 95

<211> 1491

<212> DNA

<213> Acinetobacter sp. NIPH 1859 SLAM 1

<400> 95

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caactacaac aacaaggtgc aattcgaagc accgatgaac taccgaatat tgtgattaac 180

ggtcaagtat tcgaagttgc aaaaaatcaa gatgacctcg caaaagcttt atatttggct 240

gttatgcaaa agcaatgggg taatgctgct gtttatctaa agcattatca acaatatgat 300

ggctatgacc aagcattaac cgattttgcc gagggagcat tggctcgtgc gcaaggccag 360

ctcaaattag ccgaacaaaa atttcaaagc agtctcaata aacaaccgaa taaccttatt 420

tgtgaacttg agttagcgcg cgtgctgttt gaacagcaga agaacaaaca agcagcacgc 480

ctttttacat cgattcaaaa caaattgggg cagagtgatc gtggtgtgat tccaccagag 540

gttgaacaaa cggttaattt gtttgttaaa gcacttgatc agcgtgatgc atggcaaggc 600

agtgttgcga ttggcccaac ctacgccacg aatctaaata gttcttctga acaaagtaaa 660

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cgtggaagtc ctaaagctga gtcggcaacg ggtgtggact acgaagccag tttaatgaaa 780

cgcttttctc tgtatggcaa tcatggggtt tccttacgtg gtttggctta tggacagtct 840

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gatggtaaag aaagttccgc catgctgacc ttttggaaaa tcctacctga acaatggact 1140

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cagcaacaag gtgttcgttt gggtctgagc aaaccgtgga atattggatt aaacaccacc 1260

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cgtcaagatt ttgagcaaaa ctatactttt gtgttgcaaa tgcctcgttt caaattctat 1380

ggcatgacgc cgaacctgac ctatcgctat aaccgtaata acagcaatgt ggattggttg 1440

tattcctacg acaaacataa tatcagctta aagcttgagc accgtttcta g 1491

<210> 96

<211> 496

<212> PRT

<213> Acinetobacter sp. NIPH 1859 SLAM 1

<400> 96

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Leu Tyr Ala Asp Asp Glu Thr Gln Leu Arg Leu Asn Gln Ser Leu Asp

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Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Ala Ile
35 40 45

Arg Ser Thr Asp Glu Leu Pro Asn Ile Val Ile Asn Gly Gln Val Phe
50 55 60

Glu Val Ala Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

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

85 90 95

Gln Gln Tyr Asp Gly Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly
100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe
115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu
130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Gln Ala Ala Arg

145 150 155 160

Leu Phe Thr Ser Ile Gln Asn Lys Leu Gly Gln Ser Asp Arg Gly Val
165 170 175

Ile Pro Pro Glu Val Glu Gln Thr Val Asn Leu Phe Val Lys Ala Leu
180 185 190

Asp Gln Arg Asp Ala Trp Gln Gly Ser Val Ala Ile Gly Pro Thr Tyr
195 200 205

Ala Thr Asn Leu Asn Ser Ser Ser Glu Gln Ser Lys Thr Trp Met Leu

210 215 220

Tyr Gly Ile Asp Gln Lys Gly Asn Val Ile Pro Ile Gln Glu Ile Thr

225 230 235 240

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

245 250 255

Ser Leu Met Lys Arg Phe Ser Leu Tyr Gly Asn His Gly Val Ser Leu

260 265 270

Arg Gly Leu Ala Tyr Gly Gln Ser Tyr Asp Asp His Ala Asp Phe Asn

275 280 285

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

290 295 300

Asn Gln Ile Thr Ile Ala Pro Leu Phe Glu His Lys Arg Tyr Ala Asn

305 310 315 320

Asp Gly Leu Tyr Asn Ala Trp Gly Ala Arg Ala Glu Trp Met Arg Phe

325 330 335

Ile Ser Ala Asp Lys Ala Leu Lys Leu Glu Ala Glu Ile Lys Asp Leu

340 345 350

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

355 360 365

Leu Thr Phe Trp Lys Ile Leu Pro Glu Gln Trp Thr Leu Phe Gly Gly

370 375 380

Val Asp Val Leu Asp His Asp Thr Gln Glu Lys Tyr Met Ala Ala Tyr

385 390 395 400

Gln Gln Gln Gly Val Arg Leu Gly Leu Ser Lys Pro Trp Asn Ile Gly

405 410 415

Leu Asn Thr Thr Leu Phe Ser Ser Tyr Arg Trp Arg Gln Phe Asp Arg

420 425 430

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

435 440 445

Thr Phe Val Leu Gln Met Pro Arg Phe Lys Phe Tyr Gly Met Thr Pro

450 455 460

Asn Leu Thr Tyr Arg Tyr Asn Arg Asn Asn Ser Asn Val Asp Trp Leu

465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Ile Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 97

<211> 1491

<212> DNA

<213> Acinetobacter sp. NIPH 1867 SLAM 1

<400> 97

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gttatgcaaa aacaatgggg caatgctgcg gtttatttaa aacattatca gcaatatcaa 300

ggctacgatc aggctttaac ggattttgcc gaaggtgcgt tagcacgtgc tcagggacag 360

ctcaaattag cagagcaaaa atttcaaagc agtctcaata aacaaccgaa taatctgatt 420

tgtgaactag agttagcgcg cgtgctgttt gaacagcaga agaacaaaca agcagcacgc 480

ctttttatat caattcagaa caagctagga caaagcgatc gtgcggtgat accgccagaa 540

gtagaaaaaa cagttaatct gttcgtcaaa gcactggatc agcgggactc atggcaaggc 600

agtgtcgcga taggtccatc ctatgccaca aatctgaata gttcttctga acaaagcaaa 660

acatggacct tgtatggcat tgatgacaag ggcaatgcga cccccattca agaaattaga 720

cgtggcagcc caaaagcagc atcagcaacg ggtatggatt atgaagccag tttaatcaaa 780

cgcttttcgc tctatggcaa ccatggcgtt tccttacgtg gtttagccta tgggcaatcc 840

tatgatgatt atgctgacta taatgaatcc accctaaata ttaatgcagg ctatagtttt 900

ttcgatttaa aaaatcagat cagtattgca ccactgtttg aacataaacg ttatgccaat 960

gatggtttat acaatgcatg gggtgcacgt gctgaatgga tgcgatttat tgctgcagac 1020

aaagcattca agctggaagc tgaaatcaaa gatctagact atcaaaaata taaaacgcta 1080

gatggtaaag aaagctcggc gatgttcacc ttttggaaga ttctacccaa acaatggaca 1140

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caacaacaag gtgtccgttt aggattgagc aagtcttgga atgtcggatt gaatacaacg 1260

ttattcagtt catatcgctg gcgccagttt gatcggtatg ccgaaagtct agaagcccgt 1320

cgtcatgatt ttgaacaaaa ttatacattc gtggtgcaaa tgcctcgatt taaattttat 1380

ggtgtgacgc caaatctgac ttatcgttat aaccacaaca gtagcaatgt tgactggctg 1440

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<210> 98

<211> 496

<212> PRT

<213> Acinetobacter sp. NIPH 1867 SLAM 1

<400> 98

Met Lys Arg Thr Leu Leu Cys Cys Leu Ile Leu Leu Ala Gly Ser Ser
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Leu Tyr Ala Asp Asp Asp Thr Gln Leu Arg Leu Asn Gln Asn Leu Asp
20 25 30

Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Ala Ile
35 40 45

Arg Ser Thr Asp Glu Leu Pro Asn Ile Val Ile Asn Gly Gln Val Phe
50 55 60

Glu Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Gly Asn Ala Ala Val Tyr Leu Lys His Tyr
85 90 95

Gln Gln Tyr Gln Gly Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly
100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe
115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu
130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Gln Ala Ala Arg
145 150 155 160

Leu Phe Ile Ser Ile Gln Asn Lys Leu Gly Gln Ser Asp Arg Ala Val
165 170 175

Ile Pro Pro Glu Val Glu Lys Thr Val Asn Leu Phe Val Lys Ala Leu

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Asp Gln Arg Asp Ser Trp Gln Gly Ser Val Ala Ile Gly Pro Ser Tyr
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Ala Thr Asn Leu Asn Ser Ser Ser Glu Gln Ser Lys Thr Trp Thr Leu
    210                 215                 220
Tyr Gly Ile Asp Asp Lys Gly Asn Ala Thr Pro Ile Gln Glu Ile Arg
225                 230                 235                 240

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

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

Phe Thr Phe Trp Lys Ile Leu Pro Lys Gln Trp Thr Leu Phe Ser Gly
    370                 375                 380
Leu Asp Val Leu Asp His Asp Thr Gln Glu Lys Tyr Met Ala Ala Tyr
385                 390                 395                 400
Gln Gln Gln Gly Val Arg Leu Gly Leu Ser Lys Ser Trp Asn Val Gly
                405                 410                 415
Leu Asn Thr Thr Leu Phe Ser Ser Tyr Arg Trp Arg Gln Phe Asp Arg
            420                 425                 430
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Tyr Ala Glu Ser Leu Glu Ala Arg Arg His Asp Phe Glu Gln Asn Tyr
435 440 445

Thr Phe Val Val Gln Met Pro Arg Phe Lys Phe Tyr Gly Val Thr Pro
450 455 460

Asn Leu Thr Tyr Arg Tyr Asn His Asn Ser Ser Asn Val Asp Trp Leu
465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe
485 490 495

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<211> 1491

<212> DNA

<213> Acinetobacter sp. NIPH 2100 SLAM 1

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ggccaaattt ttgcggtaga gaaaaatcaa gatgatttgg caaaagccct ctatttggct 240

gtcatgcaaa aacaatgggg caatgctgcg gtttatttaa agcattatca gcaatatcaa 300

gactatgatc aggctttaac tgattttgcc gaaggggcat tggcacgtgc tcagggtcag 360

ctcaaattag ccgagcaaaa atttcaaagc agtctcaata aacaaccgaa taatcttatt 420

tgtgaactag agttagcgcg cgtgctgttt gaacagcaga agaacaaaga agcagcacgc 480

ctttttacat caattcaaaa caaactggga cagagtgatc gtgcggtgat accgccagaa 540

gtagaacaaa cggttaatct gttcgtcaaa gcactcgatc agcgggattc atggcaaggc 600

agtgtcgcga ttggtccatc ctatgccaca aatctgaata gttcttctga acaaagtaaa 660

acatggacgt tatatggcat tgacgataag ggcaatgcga ctcccattca agaaattacc 720

cgtggcagcc ctaaagcagc atcagcaaca ggtatggact atgaagccag tttaatgaaa 780

cgcttttctc tctacggcaa tcatggggtt tccttacgtg ggctagctta tggacagtcc 840

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ctcgatttaa aaaatcagat cagcattgca ccattgtttg aacataaacg ttatgcaaat 960

gacggtttat acaatgcatg gggtgcacgt gctgaatgga tgcgatttat tgccgcagac 1020

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gatggtaaag aaagctcagc gatgttcacg ttttggaaga ttctacctaa gcaatggaca 1140

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cagcagcaag gcattcgttt aggcttaagt aagtcttgga atgtcgggtt gaataccacc 1260

ttattcagtt catatcgctg gcggcagttt gatcaatatg tcgagacatt tgcggcccgc 1320

cgtcatgatt ttgaacaaaa ttataccttt gttgtgcaga tgccccgatt taaattttac 1380

ggcatgacac caaatctgac ttatcgttat aaccacaaca gtagcaatgt ggattggtta 1440

tattcctacg ataaacacaa tgtcagcttg aagcttgagc atcgttttta a 1491

<210> 100

<211> 496

<212> PRT

<213> Acinetobacter sp. NIPH 2100 SLAM 1

<400> 100

Met Lys Arg Thr Leu Leu Cys Cys Leu Thr Leu Leu Ala Thr Ser Ser

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Leu Tyr Ala Asp Asp Asp Thr Gln Leu Arg Leu Asn Gln Ser Leu Asp

20 25 30

Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Thr Ile

35 40 45

Arg Asp Thr Glu Lys Leu Pro Ser Ile Leu Ile Asn Gly Gln Ile Phe

50 55 60

Ala Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala

65 70 75 80

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

85 90 95

Gln Gln Tyr Gln Asp Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly

100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe

115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu

130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Glu Ala Ala Arg

145 150 155 160

Leu Phe Thr Ser Ile Gln Asn Lys Leu Gly Gln Ser Asp Arg Ala Val
165 170 175
Ile Pro Pro Glu Val Glu Gln Thr Val Asn Leu Phe Val Lys Ala Leu
180 185 190
Asp Gln Arg Asp Ser Trp Gln Gly Ser Val Ala Ile Gly Pro Ser Tyr
195 200 205
Ala Thr Asn Leu Asn Ser Ser Ser Glu Gln Ser Lys Thr Trp Thr Leu
210 215 220
Tyr Gly Ile Asp Asp Lys Gly Asn Ala Thr Pro Ile Gln Glu Ile Thr
225 230 235 240
Arg Gly Ser Pro Lys Ala Ala Ser Ala Thr Gly Met Asp Tyr Glu Ala
245 250 255
Ser Leu Met Lys Arg Phe Ser Leu Tyr Gly Asn His Gly Val Ser Leu
260 265 270
Arg Gly Leu Ala Tyr Gly Gln Ser Tyr Asp Asp His Ala Asp Tyr Asn
275 280 285
Glu Ser Thr Leu Asn Ile Asn Ala Gly Tyr Ser Phe Leu Asp Leu Lys
290 295 300
Asn Gln Ile Ser Ile Ala Pro Leu Phe Glu His Lys Arg Tyr Ala Asn
305 310 315 320
Asp Gly Leu Tyr Asn Ala Trp Gly Ala Arg Ala Glu Trp Met Arg Phe
325 330 335
Ile Ala Ala Asp Lys Ala Phe Lys Leu Glu Ala Glu Ile Lys Asp Leu
340 345 350
Asp Tyr Gln Lys Tyr Lys Thr Leu Asp Gly Lys Glu Ser Ser Ala Met
355 360 365
Phe Thr Phe Trp Lys Ile Leu Pro Lys Gln Trp Thr Leu Phe Ser Gly
370 375 380
Leu Asp Val Leu Asp His Asp Thr Gln Glu Lys Tyr Met Ala Ala Tyr
385 390 395 400
Gln Gln Gln Gly Ile Arg Leu Gly Leu Ser Lys Ser Trp Asn Val Gly

405 410 415

Leu Asn Thr Thr Leu Phe Ser Ser Tyr Arg Trp Arg Gln Phe Asp Gln

420 425 430

Tyr Val Glu Thr Phe Ala Ala Arg Arg His Asp Phe Glu Gln Asn Tyr

435 440 445

Thr Phe Val Val Gln Met Pro Arg Phe Lys Phe Tyr Gly Met Thr Pro

450 455 460

Asn Leu Thr Tyr Arg Tyr Asn His Asn Ser Ser Asn Val Asp Trp Leu

465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Val Ser Leu Lys Leu Glu His Arg Phe

485 490 495

<210> 101

<211> 1491

<212> DNA

<213> Acinetobacter sp. NIPH 2168 SLAM 1

<400> 101

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caactacaac aacaaggcac aattcgtgat accgagaaac tccccagtat ccgtatcaat 180

ggtcaaattt atgcagtaga aaaaaatcag gatgatttgg ccaaagccct ctatctggct 240

gtcatgcaaa aacagtgggg caatgctacg gtttatttaa agcattatca gcaatatgaa 300

ggctatgatc aggctttaac tgattttgct gaaggggcat tggcacgtgc ccaagggcag 360

ctcaaattag ccgagcaaaa atttcaaagc agtctcaata aacaacccaa taatcttatt 420

tgtgaactag agttagcgcg cgtgctgttt gaacagcaaa agaacaaaga agcagcacgc 480

ctttttacat caattcaaaa caaattggga cagagtgatc gggcggtgat accgcctgaa 540

gtagaacaaa cggttaatct gttcgtcaaa gcgctcgatc agcgtgattc atggcaaggc 600

agtgtcgcga ttggtccatc ctatgccaca aatctgaata gttcttctga acaaagtaaa 660

acttggacgt tgtatggtat tgacgataag ggcaatgcga ctcccatcca agaaattacc 720

cgtggcagtc ccaaagcagc atcagcaacg ggtatggact atgaagccag tttaatgaaa 780

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<210> 102

<211> 496

<212> PRT

<213> Acinetobacter sp. NIPH 2168 SLAM 1

<400> 102

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Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Thr Ile
35 40 45

Arg Asp Thr Glu Lys Leu Pro Ser Ile Arg Ile Asn Gly Gln Ile Tyr
50 55 60

Ala Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Gly Asn Ala Thr Val Tyr Leu Lys His Tyr
85 90 95

Gln Gln Tyr Glu Gly Tyr Asp Gln Ala Leu Thr Asp Phe Ala Glu Gly
100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Leu Ala Glu Gln Lys Phe
115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu
130 135 140
Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Glu Ala Ala Arg
145 150 155 160

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

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

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

Asp Tyr Gln Lys Tyr Lys Thr Leu Asp Gly Lys Glu Ser Ser Ala Met
355 360 365
Phe Thr Phe Trp Lys Ile Leu Pro Lys Gln Trp Thr Leu Phe Ser Gly

370 375 380

Leu Asp Val Leu Asp His Asp Thr Gln Glu Lys Tyr Met Ala Ala Tyr

385 390 395 400

Gln Gln Gln Gly Val Arg Leu Gly Leu Ser Lys Ser Trp Asn Val Gly

405 410 415

Leu Asn Thr Thr Leu Phe Ser Ser Tyr Arg Trp Arg Gln Phe Asp Arg

420 425 430

Tyr Ala Glu Ser Leu Gln Ala Arg Arg His Asp Phe Glu Gln Asn Tyr

435 440 445

Thr Phe Val Leu Gln Met Pro Arg Phe Lys Phe Tyr Gly Met Thr Pro

450 455 460

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485 490 495

<210> 103

<211> 1401

<212> DNA

<213> Acinetobacter sp. NIPH 713 SLAM 1

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ttagaagatt atattaatca agccattatt gataaagact ggaaagaact tgagaaacta 240

ctagataaat acagaaaaac tgataattac gatcacattt tatacgagta tggcttaggt 300

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aaacaatata ctgaagctaa aaatgaattt agagcaataa gacctttct tcctactcag 480

atccaagcat taatagatca gctattgagt actatggaag agtctcaagg atggcaacca 540

aacgtaaatt ttaattttga aaaaacagat aatgttaatc aatcatcgag tataaaagag 600

atttctattg gagaagcaac tttcatacgt gatcaggaat cactaccaca aaaggcagaa 660

ggtatcggtt atacgctgaa tgcatcacgt gaacaaaata tgatgagcaa tcattatgta 720

tattttaatg cagcattaaa cggtattcat tattgggata atacagaatt tagtgagcaa 780

accttacgta tcgatactgg ttacaagtat aaagatctta agcaatcctt aggcataatt 840

ccatttattg ggcaaaatat actaggtgat agtcgttaca gtcataacta tggtgcagga 900

ttagaatata accgattatt atcagatcgt tggcaagttt ctgctaatac atctcttatc 960

caaaaacgat atcaggattc agatcttgca caatattata atggtcatgc taatagtcag 1020

gctgcattga tgctgtatca accgaaatca aaattactca tatatagtgg cttagactgg 1080

atgcaagatc gcttagcgga cgaagcagaa tcatccaata agaaaggtat acgaagtggt 1140

tttttatact ttggggactc attgggtatt agtagcaaca tacgttattc taagcgtaat 1200

tttttagcag ataatatttg gtatggtatt caacgcaaag acagtgaata tgaatttggt 1260

atagctactt ggcgtaagca atggcagtgg aaaggtttta ctcccaagtt aaattataga 1320

tatcaaaaaa ttgacagcaa tttaccactt tatgagcgta ataacggcac atggtttatc 1380

acaatagata aaaaaattta a 1401

<210> 104

<211> 466

<212> PRT

<213> Acinetobacter sp. NIPH 713 SLAM 1

<400> 104

Met Asn Ile Lys Tyr Val Val Ile Leu Ser Val Thr Phe Ser Ser Thr
1 5 10 15

Ala Phe Ser Gln Glu Leu Pro Pro Ala Gln Thr Val Phe Phe Glu Gln
20 25 30

Asp Ser Phe Ile Gln Pro Glu Leu Leu Leu Lys Lys Thr Val Asp Lys
35 40 45

Asp Leu Lys Leu Ser Thr Leu Pro Pro Asn Ser Ser Leu Glu Asp Tyr
50 55 60

Ile Asn Gln Ala Ile Ile Asp Lys Asp Trp Lys Glu Leu Glu Lys Leu
65 70 75 80

Leu Asp Lys Tyr Arg Lys Thr Asp Asn Tyr Asp His Ile Leu Tyr Glu
85 90 95

Tyr Gly Leu Gly Ala Leu Tyr Arg Phe Gln Gly Lys Gln Lys Lys Ala
100 105 110

Ile Glu Met Tyr Lys Ala Ile Ile Thr Lys Asn Pro Asn Leu Tyr Tyr
115 120 125

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

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

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

Gln Lys Arg Tyr Gln Asp Ser Asp Leu Ala Gln Tyr Tyr Asn Gly His
325 330 335
Ala Asn Ser Gln Ala Ala Leu Met Leu Tyr Gln Pro Lys Ser Lys Leu
340 345 350
Leu Ile Tyr Ser Gly Leu Asp Trp Met Gln Asp Arg Leu Ala Asp Glu

355 360 365

Ala Glu Ser Ser Asn Lys Lys Gly Ile Arg Ser Gly Phe Leu Tyr Phe

370 375 380

Gly Asp Ser Leu Gly Ile Ser Ser Asn Ile Arg Tyr Ser Lys Arg Asn

385 390 395 400

Phe Leu Ala Asp Asn Ile Trp Tyr Gly Ile Gln Arg Lys Asp Ser Glu

405 410 415

Tyr Glu Phe Gly Ile Ala Thr Trp Arg Lys Gln Trp Gln Trp Lys Gly

420 425 430

Phe Thr Pro Lys Leu Asn Tyr Arg Tyr Gln Lys Ile Asp Ser Asn Leu

435 440 445

Pro Leu Tyr Glu Arg Asn Asn Gly Thr Trp Phe Ile Thr Ile Asp Lys

450 455 460

Lys Ile

465

<210> 105

<211> 1491

<212> DNA

<213> Acinetobacter sp. NIPH 809 SLAM 1

<400> 105

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gatgagacac aacttcgcct gaatcaaaac ttggatcaga atttattaca acaacagcat 120

caattacaac aacaaggggc aattcggagc acagacgaat tacccaatat tgtaattaat 180

gggcaagtat ttgaagttga aaagaaccaa gatgatctgg caaaagcttt atatttggca 240

gtcatgcaaa agcaatgggg caatgcggca gtctatctaa agcattatca acaatatgat 300

ggctatgaca aagctttaac agactttgcc gagggtgcat tggctcgtgc tcaaggccag 360

ctcaagatag cagagcataa attccaaagt agtttaaata aacaacccaa taatctgatt 420

tgtgaactcg agttagcgcg cgtgctgttt gaacagcaga agaacaaaca agcagcacgc 480

ctttttacat ccattcagag caaattgggg caaagtgatc gtggggtaat tccgcctgag 540

gtcgaacaaa cggttaagct gttcgttaag gcactggagc agcgggattc atggcaaggc 600

agtgttgcga ttggaccaac ctatgccacg aatctaaata gttcttctga acaaagtaaa 660

acttggatgt tgtatggcct tgaccaaaaa ggcaatgtga tccccattca ggagattacc 720

cgtggaagtc ctaaagctga gtcggcaacg ggtatggact atgaagccag tttaatgaaa 780

cgcttttcgc tctatggcaa tcatggggtt tccttacgtg gtttagcgta tggacaatct 840

tatgatgatc atgctgactt taatgaatcc acactgaata tcaatgcagg ttatagtttt 900

tttgatttaa aaaatcaaat cacaattgca ccgctatttg agcataaacg ttatgccaat 960

gatggtttgt acaatgcctg gggggcacgt gcggaatgga tgcgatttat ctccgccgat 1020

aaagcactca agcttgaagc tgaaatcaaa gatttaaatt atcaaacata taaaacttta 1080

gatggcaaag aaagttcagc catgctgacc ttttggaaaa tcttacctga acaatggacc 1140

ttgtttggtg gtgcggatgt cttagatcat gatacccaag aaaaatacat ggcagcctat 1200

cagcagcaag gtgttcgttt gggtctgagt aaaccgtgga gtgctggctt taataccact 1260

ttattcagtt tgtatcgctg gcgccagttt gatcgttacg tggcggcatt tcaaacacgt 1320

cgtcaagatt ttgagcaaaa ctacaccttt gtgttgcaaa tgcctcgttt caaattctat 1380

ggaatgacgc cgaatttgac ctatcgctat aaccgtaata atagcaatgt ggattggtta 1440

tattcctatg acaaacacaa tgtcagccta aaacttgagc accgttttta g 1491

<210> 106

<211> 496

<212> PRT

<213> Acinetobacter sp. NIPH 809 SLAM 1

<400> 106

Met Lys Arg Thr Leu Leu Cys Cys Leu Ile Leu Leu Ala Ser Ser Ser

1 5 10 15

Leu Tyr Ala Asp Asp Glu Thr Gln Leu Arg Leu Asn Gln Asn Leu Asp

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Gln Asn Leu Leu Gln Gln Gln His Gln Leu Gln Gln Gln Gly Ala Ile

35 40 45

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

50 55 60

Glu Val Glu Lys Asn Gln Asp Asp Leu Ala Lys Ala Leu Tyr Leu Ala

65 70 75 80

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

85 90 95

Gln Gln Tyr Asp Gly Tyr Asp Lys Ala Leu Thr Asp Phe Ala Glu Gly

100 105 110

Ala Leu Ala Arg Ala Gln Gly Gln Leu Lys Ile Ala Glu His Lys Phe

115 120 125

Gln Ser Ser Leu Asn Lys Gln Pro Asn Asn Leu Ile Cys Glu Leu Glu

130 135 140

Leu Ala Arg Val Leu Phe Glu Gln Gln Lys Asn Lys Gln Ala Ala Arg

145 150 155 160

Leu Phe Thr Ser Ile Gln Ser Lys Leu Gly Gln Ser Asp Arg Gly Val

165 170 175

Ile Pro Pro Glu Val Glu Gln Thr Val Lys Leu Phe Val Lys Ala Leu

180 185 190

Glu Gln Arg Asp Ser Trp Gln Gly Ser Val Ala Ile Gly Pro Thr Tyr

195 200 205

Ala Thr Asn Leu Asn Ser Ser Ser Glu Gln Ser Lys Thr Trp Met Leu

210 215 220

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

225 230 235 240

Arg Gly Ser Pro Lys Ala Glu Ser Ala Thr Gly Met Asp Tyr Glu Ala

245 250 255

Ser Leu Met Lys Arg Phe Ser Leu Tyr Gly Asn His Gly Val Ser Leu

260 265 270

Arg Gly Leu Ala Tyr Gly Gln Ser Tyr Asp Asp His Ala Asp Phe Asn

275 280 285

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

290 295 300

Asn Gln Ile Thr Ile Ala Pro Leu Phe Glu His Lys Arg Tyr Ala Asn

305 310 315 320

Asp Gly Leu Tyr Asn Ala Trp Gly Ala Arg Ala Glu Trp Met Arg Phe

325 330 335

Ile Ser Ala Asp Lys Ala Leu Lys Leu Glu Ala Glu Ile Lys Asp Leu

340 345 350

Asn Tyr Gln Thr Tyr Lys Thr Leu Asp Gly Lys Glu Ser Ser Ala Met
355 360 365
Leu Thr Phe Trp Lys Ile Leu Pro Glu Gln Trp Thr Leu Phe Gly Gly

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

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

<210> 107
<211> 1491
<212> DNA
<213> Acinetobacter sp. WC-323 SLAM 1

<400> 107
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caattacaac aacaaggcac cattcgtgac accgagaaac tacccagcat ccgtattaat 180
ggccaaattt acgcggtaga gcagaatccg gatgatctgg ccaaagcgct atatctggcg 240
gttatgcaaa agcaatgggg caatgctgcg atttacttaa aacactatca gcagtatcaa 300
ggctatgatc aggctttaac cgattttgcc gaagcggctt tggcgcgcgc tcagggaaag 360
ctcaaattag ccgaacaaaa atttcaaagt agtcttaatc aacaaccgaa taatctgatt 420

tgtgaactcg agttagcgcg cgtgctgttt gaacagcaga agaataaaca agcagcacgc 480

cttttttacat cgattcagga caagctaggg cagagcaatg gggcaatgat cccaccagaa 540

gtgcaacaaa cggttgatct gttcgtcaaa gcacttgatc agcgggattc gtggcaaggc 600

agtgtcgcaa ttggcccatc ctatgccaca aatctgaata gctcttctga acaaagcaaa 660

acatggacct tgtatggcat tgatgacaag ggcaaggcga ctccaattca ggaaattacc 720

cgtggcagcc ccaaagcagc atcagcaaca ggggttgact atgaggccag tctaatcaag 780

cgcttttcgc tttcgggcaa tcatggcatt tccttacgcg gtttagcatt tgggcaatcc 840

tatgctgatc atgcgctcta taacgaatcc accctgaata tcaatgcagg ctatagtttt 900

tttgatttaa aaaatcaaat caccattgca ccgctatttg aacataaacg ttatgccaat 960

gatggtttat acaatgcatg gggggcacgt actgaatgga tgcgatttct agcaccagac 1020

aaagccttca agcttgaagc tgaaatcaaa gatctgggct atcaaaaata taaaaaccta 1080

gatggtaaag aaagctcggc catgtttaca ttctggaaaa ttctaccgca gcaatggaca 1140

ctttttagcg gactggatgt actggaccat gacacccagg aaaaatatat ggcggcttat 1200

cagcaacaag gcatccgtct aggactgagc aaatcctgga aagcaggttt gaataccacg 1260

ctattaacct cataccgctg gcggcagttt gaccgctacg tcgagacctt tgctgcacgt 1320

cgccatgatt ttgaacagaa ctataccctg gttgtacaaa tgccacggtt taagttttat 1380

ggtatgacgc cgaatttgac ctatcgctac aaccataatg acagtaatgt cgactggctc 1440

tattcctacg ataaacacaa tatcagctta aagctggaac atcgttttta g 1491

<210> 108

<211> 496

<212> PRT

<213> Acinetobacter sp. WC-323 SLAM 1

<400> 108

Met Asn Lys Thr Leu Leu Cys Cys Val Ile Leu Leu Ala Ala Ser Ser

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Leu Tyr Ala Asp Asp Glu Thr Gln Leu Arg Leu Asn Gln Ser Leu Asp

20 25 30

Gln Asn Leu Phe Gln Gln Gln His Gln Leu Gln Gln Gln Gly Thr Ile

35 40 45

Arg Asp Thr Glu Lys Leu Pro Ser Ile Arg Ile Asn Gly Gln Ile Tyr

50 55 60

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

65 70 75 80

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

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

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

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

Asp Gly Leu Tyr Asn Ala Trp Gly Ala Arg Thr Glu Trp Met Arg Phe
325 330 335

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

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

Asn Leu Thr Tyr Arg Tyr Asn His Asn Asp Ser Asn Val Asp Trp Leu
465 470 475 480
Tyr Ser Tyr Asp Lys His Asn Ile Ser Leu Lys Leu Glu His Arg Phe
485 490 495

<210> 109
<211> 1491
<212> DNA
<213> Acinetobacter sp. WC-743 SLAM 1
<400> 109
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aaactactca aatcagatga tcccaaaaaa gaccaagcat taccgaatct gatcatacaa 180
ggtcaggaat atatggtgaa ggatgaaccc gcagaagttg cttatgcgct ttatttggca 240

gtgatgcaaa aacaatggca agtcgcttta cgttatttag aaaaatataa aaattttcca 300

aattatgatc aggctttgac tgaattcgct gaaggcgtca tggcacgaac acagggaaat 360

ttaagcttag ctgaaagtaa actacaacac agtctaaaga ttcaatccaa taatttaatg 420

acacagcttg agctggcacg tgtctacacc gaacaacaga aaaatcagca aggactacag 480

ttatttcagc agattcaatc tcaattgagc atgtctaccg atcctgctgc tcaaggtatt 540

cttcaaactg tagagatgta tcttaaagga cttaaacaac gtgatgcatg gcaaggttcc 600

ttagcttttg gttcacgtta tgccagtaat atcaataacg cttcaaataa atacgacatt 660

gtgacctatt acggtattga cccagagacg aaggaagtcg tgcctgtcga acaattaaag 720

cgaggtacac cagatgcgat cagtgcgcaa ggtctggatt atgaagccac tttaaccaag 780

cgttggtcac tttctggaca gcatggtatt gctttacgtg gattattcta tggtcaagtt 840

tacccagaac agacagatta taatgaatta acttttaatt taaatgcggg ttatagtttt 900

tataatgaac gtaatcaagt cttggttgct cctgtatttg aacataaata ctatgcacat 960

gatccactct acagtgctta tgggttaaga ggcgagtgga tgcgttttat ttccaacgat 1020

aaagccgtca agttagaagc tgaaatgaaa gatatgaact attctcagta taaggggcag 1080

aatggcacgg aatattcagt ctattcaact ttttggaaaa ttttaccaaa aaactggacc 1140

ttatttggtg gactggattt cgttgaccat aatacccaag agcaatattt cacagcatat 1200

caacaacaag gcatacgttt agggctgtcc aaaaatttta ccgcaggctt taacaccaat 1260

ttatttagtt cttttcgttg gcgtcaattt gataaattta cgcctgcatt ggaggctagg 1320

cgacatgatt ttgaacaaaa ctataccttg attttaagtg cgccacgttg ggctttttac 1380

ggtttaacac cgaatcttac ttatcaatat aatcaaaata acagtaatgt agagtggttg 1440

tattcctatg ataaacataa tatcagctta aagttagaac atcgttttta a 1491

<210> 110

<211> 496

<212> PRT

<213> Acinetobacter sp. WC-743 SLAM 1

<400> 110

Met Lys Lys Ile Val Leu Leu Gly Val Val Leu Leu Cys Gly Glu Thr

1 5 10 15

Val Tyr Ala Ala Asp Asp Thr Ser Ile Arg Leu Asn Gln Glu Ile Ser

20 25 30

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

35 40 45

Lys Lys Asp Gln Ala Leu Pro Asn Leu Ile Ile Gln Gly Gln Glu Tyr
50 55 60

Met Val Lys Asp Glu Pro Ala Glu Val Ala Tyr Ala Leu Tyr Leu Ala
65 70 75 80

Val Met Gln Lys Gln Trp Gln Val Ala Leu Arg Tyr Leu Glu Lys Tyr
85 90 95

Lys Asn Phe Pro Asn Tyr Asp Gln Ala Leu Thr Glu Phe Ala Glu Gly
100 105 110

Val Met Ala Arg Thr Gln Gly Asn Leu Ser Leu Ala Glu Ser Lys Leu
115 120 125

Gln His Ser Leu Lys Ile Gln Ser Asn Asn Leu Met Thr Gln Leu Glu
130 135 140

Leu Ala Arg Val Tyr Thr Glu Gln Gln Lys Asn Gln Gln Gly Leu Gln
145 150 155 160

Leu Phe Gln Gln Ile Gln Ser Gln Leu Ser Met Ser Thr Asp Pro Ala
165 170 175

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

Gln Arg Asp Ala Trp Gln Gly Ser Leu Ala Phe Gly Ser Arg Tyr Ala
195 200 205

Ser Asn Ile Asn Asn Ala Ser Asn Lys Tyr Asp Ile Val Thr Tyr Tyr
210 215 220

Gly Ile Asp Pro Glu Thr Lys Glu Val Val Pro Val Glu Gln Leu Lys
225 230 235 240

Arg Gly Thr Pro Asp Ala Ile Ser Ala Gln Gly Leu Asp Tyr Glu Ala
245 250 255

Thr Leu Thr Lys Arg Trp Ser Leu Ser Gly Gln His Gly Ile Ala Leu
260 265 270

Arg Gly Leu Phe Tyr Gly Gln Val Tyr Pro Glu Gln Thr Asp Tyr Asn
275 280 285

Glu Leu Thr Phe Asn Leu Asn Ala Gly Tyr Ser Phe Tyr Asn Glu Arg
290 295 300

Asn Gln Val Leu Val Ala Pro Val Phe Glu His Lys Tyr Tyr Ala His
305 310 315 320

Asp Pro Leu Tyr Ser Ala Tyr Gly Leu Arg Gly Glu Trp Met Arg Phe
325 330 335

Ile Ser Asn Asp Lys Ala Val Lys Leu Glu Ala Glu Met Lys Asp Met
340 345 350

Asn Tyr Ser Gln Tyr Lys Gly Gln Asn Gly Thr Glu Tyr Ser Val Tyr
355 360 365

Ser Thr Phe Trp Lys Ile Leu Pro Lys Asn Trp Thr Leu Phe Gly Gly
370 375 380

Leu Asp Phe Val Asp His Asn Thr Gln Glu Gln Tyr Phe Thr Ala Tyr
385 390 395 400

Gln Gln Gln Gly Ile Arg Leu Gly Leu Ser Lys Asn Phe Thr Ala Gly
405 410 415

Phe Asn Thr Asn Leu Phe Ser Ser Phe Arg Trp Arg Gln Phe Asp Lys
420 425 430

Phe Thr Pro Ala Leu Glu Ala Arg Arg His Asp Phe Glu Gln Asn Tyr
435 440 445

Thr Leu Ile Leu Ser Ala Pro Arg Trp Ala Phe Tyr Gly Leu Thr Pro
450 455 460

Asn Leu Thr Tyr Gln Tyr Asn Gln Asn Asn Ser Asn Val Glu Trp Leu
465 470 475 480

Tyr Ser Tyr Asp Lys His Asn Ile Ser Leu Lys Leu Glu His Arg Phe
485 490 495

<210> 111

<211> 1437

<212> DNA

<213> Aggregatibacter sp. oral taxon 458 SLAM 1

<400> 111

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cctcaattgc ctcaaaatga cgttgtagag acctccactt caaaagaaca taccctatct 180

attacaaaag aagaacttgc caaacgaccg gatttgatta tccgtggcct gattccggca 240

ttgctacaaa gccatgtgga ggcagtggca ttgttgttgc ccttatacaa aaatttgcca 300

caacaagatc ctttttggt ggcttggggc gaggctatga tggcgacgca tcaagggaat 360

tatgcctcag cggtgcagca atatcgtgaa ttatttgcaa aacatcctga agttttacca 420

ttgcgttatc aattagccca tgcgttattt ttgaataacg ataatgaagc ggcgaaagat 480

caattccaaa aacttcgtgc ggaagtgaat gatgcctcat cgcagcaaat gatcgatcag 540

tatttaaccg caattaacca acgagatcag tggaaaatca acggtggtat cagtttttta 600

aacgaatcca atattaataa tgcgccaaaa gccggcaccc gtattggtgc gtggaaagct 660

tgggagcgag aacaggcgca tgggctgtct tattatgcgg gggctgaaaa gaaatggtcg 720

ttgcctcatc agctttttgc aaaattggtg ttagatgggc aaggcaaata ttattgggat 780

aataaaaaat ataacgaatt taatgctcga atcggtgccg gtttggggta tcaaacggca 840

aatactgaac ttgctttagt gcctttcact gaacgacgtt ggtattccgg cggatcgtcc 900

ggcagtgatg ccatgaaaca atattctaaa aattccggtg tgcgtgttga tgtgactcat 960

tggctcaata aatcatggca aatttcgacc gcacttgaat atggcgagca gcgttatgcc 1020

acacgtaaac atttaaatgg caataattat ttgtggtcga atacgctctt atttttacct 1080

tacagcggac aatattggta tatcggtgcg gattataatc gtgaaaatac gcgcgatctt 1140

gataatgcct atcagcgtaa aaacgtgcgt ttaggttggg tgcaagaatg gccgttgggc 1200

atttccagtc gtctttctgt cgcctatgca agacgggctt ataaagggga agatttactt 1260

ggtattcgtc aaaaaaacaa ggaatatcaa accaatgtca ctttatggca tcgtaacgtg 1320

tatttttggg gcattacgcc gaaaatcacg tggtcatacc aaaaaaatga cagcaatcat 1380

ccgttttatc gctatgataa aaatcggatt tatttagaaa tgagcaaaac gttctaa 1437

<210> 112

<211> 478

<212> PRT

<213> Aggregatibacter sp. oral taxon 458 SLAM 1

<400> 112

Met Met Lys Leu Pro Leu Ser Phe Gly Ile Ala Ile Gly Val Phe Val

1 5 10 15

Ser Ala Ser Ala Ala Ala Glu Ile Thr Ala Pro Lys Asn Ala Ser Pro

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            20                  25                  30
Glu Glu His Leu Lys Leu Ala Ser Pro Gln Leu Pro Gln Asn Asp Val
        35                  40                  45
Val Glu Thr Ser Thr Ser Lys Glu His Thr Leu Ser Ile Thr Lys Glu
    50                  55                  60

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

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

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

Tyr Tyr Trp Asp Asn Lys Lys Tyr Asn Glu Phe Asn Ala Arg Ile Gly
            260                 265                 270
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Ala Gly Leu Gly Tyr Gln Thr Ala Asn Thr Glu Leu Ala Leu Val Pro
275 280 285

Phe Thr Glu Arg Arg Trp Tyr Ser Gly Gly Ser Ser Gly Ser Asp Ala
290 295 300

Met Lys Gln Tyr Ser Lys Asn Ser Gly Val Arg Val Asp Val Thr His
305 310 315 320

Trp Leu Asn Lys Ser Trp Gln Ile Ser Thr Ala Leu Glu Tyr Gly Glu
325 330 335

Gln Arg Tyr Ala Thr Arg Lys His Leu Asn Gly Asn Asn Tyr Leu Trp
340 345 350

Ser Asn Thr Leu Leu Phe Leu Pro Tyr Ser Gly Gln Tyr Trp Tyr Ile
355 360 365

Gly Ala Asp Tyr Asn Arg Glu Asn Thr Arg Asp Leu Asp Asn Ala Tyr
370 375 380

Gln Arg Lys Asn Val Arg Leu Gly Trp Val Gln Glu Trp Pro Leu Gly
385 390 395 400

Ile Ser Ser Arg Leu Ser Val Ala Tyr Ala Arg Arg Ala Tyr Lys Gly
405 410 415

Glu Asp Leu Leu Gly Ile Arg Gln Lys Asn Lys Glu Tyr Gln Thr Asn
420 425 430

Val Thr Leu Trp His Arg Asn Val Tyr Phe Trp Gly Ile Thr Pro Lys
435 440 445

Ile Thr Trp Ser Tyr Gln Lys Asn Asp Ser Asn His Pro Phe Tyr Arg
450 455 460

Tyr Asp Lys Asn Arg Ile Tyr Leu Glu Met Ser Lys Thr Phe
465 470 475

<210> 113

<211> 1296

<212> DNA

<213> Aggregatibacter sp. oral taxon 458 SLAM 2

<400> 113

atggccgaac atagtgattt acaccactta caagaaaacc ctcaacttat tgaatcgttt 60

ttgtcagaaa atatatatca attaacggcg gaacaattac tgacattaat aaaaatctac 120

caaaccgtgc ctcaatataa tgaaaggctt tttctttttg ctcaaggacg aatcgctttt 180

ttacaacaaa attatgcaga agcaactcgg ttatatcgcc ttgtattatc tgaaaatccg 240

acattaaatc cggtgagaat tgaattggca cttgcgttgt tttatcaaaa gcaagatcgt 300

gcagcacaaa tgcaatttga aaaagcaaaa tcggaagcga atcttccgga acctacacta 360

caattcattg atgaatatct caatgcgctg aaaacacggc aagactggaa aattgatctt 420

tcttttcatt atttaagaga taaaaatgtc aataatgcag cggatgccaa gcagattgcg 480

ttgtcaaatc gtgccatatt aaccaaatcg gaaaaaatgc gtcctcagtc ggcacatggg 540

ctggcgtatc atttgggcat ttcgcgtgat tttaatcttg ttgattccca ttatttgtcc 600

gtcagtaata aattatgggg aaaaaattat tgggataatc atgaatatga tgatatttcc 660

aaccgcactt tgattggcta tgcctacaaa acggcaatac aaacactaaa aatcggacct 720

ttttatgaac gccgttggta tggcaatcat cgttatcgtt ggaataatgg cgcgcttttg 780

gaatataccc attggttaac ccctaatttg cagttatctc atacgttaga aatggctaag 840

caacattatt ttgccgagcg ggtattagac ggtaatctaa aacttttttc atctaccctt 900

atttggcagc ctaatgcaaa acaatttttc tatttaggtg gtgatttcat ttctgaacgg 960

actcaggtga aacaatatgc ctctgatagt caagggattc gtttaggttg ggggcaagaa 1020

tggggaggag gaatttcatc tcaacttggg ttatctgtag tgaaacgcca atataaagat 1080

accgcaaaac tgggaaacct ggatattttc tcttttaaaa aatcacgttc agatcatatt 1140

tattccgcca atatgacatt ttggaaacga gattggcatt ttgggggaat aacgcctaag 1200

ctacaattga attggaagaa acaggagagc aatattcccc aaatgtactc ttaccaacag 1260

aaaaatatca tgctcatttt tgaaagtacg ttttga 1296

<210> 114

<211> 431

<212> PRT

<213> Aggregatibacter sp. oral taxon 458 SLAM 2

<400> 114

Met Ala Glu His Ser Asp Leu His His Leu Gln Glu Asn Pro Gln Leu

1 5 10 15

Ile Glu Ser Phe Leu Ser Glu Asn Ile Tyr Gln Leu Thr Ala Glu Gln

20 25 30

Leu Leu Thr Leu Ile Lys Ile Tyr Gln Thr Val Pro Gln Tyr Asn Glu

35 40 45

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

50 55 60

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

65 70 75 80

Thr Leu Asn Pro Val Arg Ile Glu Leu Ala Leu Ala Leu Phe Tyr Gln

85 90 95

Lys Gln Asp Arg Ala Ala Gln Met Gln Phe Glu Lys Ala Lys Ser Glu

100 105 110

Ala Asn Leu Pro Glu Pro Thr Leu Gln Phe Ile Asp Glu Tyr Leu Asn

115 120 125

Ala Leu Lys Thr Arg Gln Asp Trp Lys Ile Asp Leu Ser Phe His Tyr

130 135 140

Leu Arg Asp Lys Asn Val Asn Asn Ala Ala Asp Ala Lys Gln Ile Ala

145 150 155 160

Leu Ser Asn Arg Ala Ile Leu Thr Lys Ser Glu Lys Met Arg Pro Gln

165 170 175

Ser Ala His Gly Leu Ala Tyr His Leu Gly Ile Ser Arg Asp Phe Asn

180 185 190

Leu Val Asp Ser His Tyr Leu Ser Val Ser Asn Lys Leu Trp Gly Lys

195 200 205

Asn Tyr Trp Asp Asn His Glu Tyr Asp Asp Ile Ser Asn Arg Thr Leu

210 215 220

Ile Gly Tyr Ala Tyr Lys Thr Ala Ile Gln Thr Leu Lys Ile Gly Pro

225 230 235 240

Phe Tyr Glu Arg Arg Trp Tyr Gly Asn His Arg Tyr Arg Trp Asn Asn

245 250 255

Gly Ala Leu Leu Glu Tyr Thr His Trp Leu Thr Pro Asn Leu Gln Leu

260 265 270

Ser His Thr Leu Glu Met Ala Lys Gln His Tyr Phe Ala Glu Arg Val

275 280 285

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

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

385 390 395 400
Leu Gln Leu Asn Trp Lys Lys Gln Glu Ser Asn Ile Pro Gln Met Tyr
405 410 415
Ser Tyr Gln Gln Lys Asn Ile Met Leu Ile Phe Glu Ser Thr Phe
420 425 430

<210> 115

<211> 1422

<212> DNA

<213> Aggregatibacter sp. oral taxon 458 SLAM 3

<400> 115

atgaaaaaac ttccctattt tatcattcta cttcccttag ttactcaagc cgaaaccttc 60

caagcaccac agcctgtttt ctttgaaaag aatattgtgc cgaaaacgga agaaccacag 120

ataaaaacgc cggagaaatc caccgcactt tcagcaccga tgacatttga atccaatgac 180

aatacccaaa ctaaactgga aaaactgatc aactatagtg tggtaaaaca acaatggggc 240

atattgaaac aaacgttgcc gctttatcaa tcgcaacctc agcacgatgt cacgctatat 300

cgttatgccc taggggcaat gttgcgggca gaacgcaacc ataagcaagc gattcgtctt 360

tatcagcaga ttgttgatga aaagccagaa ctggcttatc cacgttttga tttgggcgta 420

atgttgtttg aaaataaaca atatcgccaa gccaaggcag aacttgagcg tgctaaaccg 480

gcattatccc cagccatgca acaatttact cagcgttact tggaggcaat gaaagaacgc 540

caaggctgga aagcggatgt agaatggcaa tatacccaaa ccgacaatgt gaataacgcc 600
tcatctcaac aagatatttt attaggtaaa ttgcgcttta aaaaagacaa agaatctttg 660
ccacaaaaag cacacggttt tcgttatggg ctgggcttaa gtcgtaaaat caatgtcgcc 720
ggcaatcatt ttgtgacctt aaacagccgt tttggcggcg tgcattattg ggacaatcaa 780
gactacagtg aaaaatctct ctatacagcc ataggctata aacatcgtac aatattacag 840
acatggggaa ttacgccgtt ttttgagcaa aattggttag gcgcaccacg ctatagccaa 900
aattatggca ttaccgtaga tttacgccgt gaattaaccg cactttggtc gttctccagc 960

acgctttccc atacgcaaaa acgctatgcg gatgctaacg ttgcacgccg tcataacggc 1020
tatatcaatg gcacaacgct ctcattaagt tatcaggcaa agccgaattg gttacttttc 1080
ggcggtgtgg aaggcagcct agatcgcagt aaagacaaag cagaatcctc gcttcgtcgt 1140
ggtgttaatc tcggcaccgt ctggcaaatc aaggatttcg cgacacgctt aagcattcgg 1200
tatgtcaaac gcgattttcg ggcaaaaaac ttctatttcc caatgaaaaa acgacaagat 1260
aaagaatatg gttttaacgc ctcactgtgg cataacaaaa tgcaatggaa aggctttatt 1320
cctaagttaa attatcgtta ccgtaaaatt gacagtaata ttcctgaatt ttattcccgc 1380

accagcggag agtggtttgt gtctgtcgaa cgtaatttct aa 1422

<210> 116
<211> 473
<212> PRT
<213> Aggregatibacter sp. oral taxon 458 SLAM 3
<400> 116

Met Lys Lys Leu Pro Tyr Phe Ile Ile Leu Leu Pro Leu Val Thr Gln
1 5 10 15
Ala Glu Thr Phe Gln Ala Pro Gln Pro Val Phe Phe Glu Lys Asn Ile
20 25 30
Val Pro Lys Thr Glu Glu Pro Gln Ile Lys Thr Pro Glu Lys Ser Thr
35 40 45

Ala Leu Ser Ala Pro Met Thr Phe Glu Ser Asn Asp Asn Thr Gln Thr
50 55 60
Lys Leu Glu Lys Leu Ile Asn Tyr Ser Val Val Lys Gln Gln Trp Gly
65 70 75 80

Ile Leu Lys Gln Thr Leu Pro Leu Tyr Gln Ser Gln Pro Gln His Asp
85 90 95
Val Thr Leu Tyr Arg Tyr Ala Leu Gly Ala Met Leu Arg Ala Glu Arg
100 105 110

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

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

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

Thr Val Asp Leu Arg Arg Glu Leu Thr Ala Leu Trp Ser Phe Ser Ser
305 310 315 320
Thr Leu Ser His Thr Gln Lys Arg Tyr Ala Asp Ala Asn Val Ala Arg

325 330 335

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

340 345 350

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

355 360 365

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

370 375 380

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

385 390 395 400

Tyr Val Lys Arg Asp Phe Arg Ala Lys Asn Phe Tyr Phe Pro Met Lys

405 410 415

Lys Arg Gln Asp Lys Glu Tyr Gly Phe Asn Ala Ser Leu Trp His Asn

420 425 430

Lys Met Gln Trp Lys Gly Phe Ile Pro Lys Leu Asn Tyr Arg Tyr Arg

435 440 445

Lys Ile Asp Ser Asn Ile Pro Glu Phe Tyr Ser Arg Thr Ser Gly Glu

450 455 460

Trp Phe Val Ser Val Glu Arg Asn Phe

465 470

<210> 117

<211> 1464

<212> DNA

<213> Alcaligenes sp. EGD-AK7 SLAM 1

<400> 117

ttgtgcctgt tgctggccat ggcatccagc gcggtgcaag ccaacgacga cgatacgcgc 60

cgacttctga atcaaatcga ccgcaatctg aacgaacgcg aacgctccca tttagtggaa 120

gaaaccccgc ctgatgtgga cccatcggcc ctgatcacca tcaacggcac aacttatagc 180

gtcgatgcca cactgaccga tctggaaccg gccatttatg tcgccatcaa tctgcaacag 240

tgggccaagg tggatcagtt tgtagaaaaa tatcaggagc tgcccggcca caaccctgcc 300

ctggtgctga tggctcaagg agtggtggcc cgtagcaagg acaatcacag cctggcgatc 360

agcaagctgc gccaggctca ggaaagcgat cccactatga tgcgcgccaa gctggagctg 420

gcccgcgtac tgttcgagga ctatcaatcc agcgaagcga aagaactgtt cagccagatt 480

tcctctgccg gtattcctga tgaagtacgg cccgtaattg aaggcttcca gggtgccttg 540
caggaccgca atgcctggca cggttccgcc tcgattggct tgggctacaa cagcaatatc 600
aacaaagaaa acggccagca agacaccttc tttacctgct atttctttgg gtgctttccg 660
tcagtgcgca agatgccgga cccggtcaaa tccaccgcca tggtctacga cctgaccttg 720
aaccggcgtt tccagctaag cggcaaccac aacctactac tgcgcggcct gagctacggc 780
aatctttacg acaagcataa ggaagccgag cccaaggaca tttattacag cgacaacacc 840
agcattattt acgcgggcta caactatcag gacgctaaaa acgatctgtc gattacgccc 900

ttgttcgaga acaattacac caaccgtcgc accagctatc agtcctgggg cgggcgcgtg 960
gactggaagc acaatcttag cgacaggctg caagtaggcg tgaatgccca gcacaagagc 1020
ctgtcctaca aaggcgattt acggcagtac tttgaagaag tcaaagagaa ccagataggc 1080
ttgtacggct cgtatctgat tgatgccaaa accgtggtct acgggggcct gaattacacc 1140
cgtaatctgc agtctcagca aaccgcgcaa agccgcagct atatggcaaa cttgggaatt 1200
tacagggcct ttgatgcggg tttcaatatc aacgccacgg cactataccg gcagacccga 1260
cacgatgccg aggacttgtt cctgggcggg ctgcgcaagg accgtcagca gatttatatc 1320

ctgaacgtag gcatgccgcg ctttgcgttc caaggcatta cgcccaattt gtatgtgaaa 1380
cacactttca acaacagcaa tatcgactgg gctttcaaat acaagcaaac cgaagtcgcg 1440
ctgaagctgg aaaagcgttt ttaa 1464

<210> 118
<211> 487
<212> PRT
<213> Alcaligenes sp. EGD-AK7 SLAM 1
<400> 118

Met Cys Leu Leu Leu Ala Met Ala Ser Ser Ala Val Gln Ala Asn Asp
1 5 10 15
Asp Asp Thr Arg Arg Leu Leu Asn Gln Ile Asp Arg Asn Leu Asn Glu

20 25 30
Arg Glu Arg Ser His Leu Val Glu Glu Thr Pro Pro Asp Val Asp Pro
35 40 45
Ser Ala Leu Ile Thr Ile Asn Gly Thr Thr Tyr Ser Val Asp Ala Thr
50 55 60

Leu Thr Asp Leu Glu Pro Ala Ile Tyr Val Ala Ile Asn Leu Gln Gln
65 70 75 80
Trp Ala Lys Val Asp Gln Phe Val Glu Lys Tyr Gln Glu Leu Pro Gly

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

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

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

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

305 310 315 320

Asp Trp Lys His Asn Leu Ser Asp Arg Leu Gln Val Gly Val Asn Ala

325 330 335

Gln His Lys Ser Leu Ser Tyr Lys Gly Asp Leu Arg Gln Tyr Phe Glu

340 345 350

Glu Val Lys Glu Asn Gln Ile Gly Leu Tyr Gly Ser Tyr Leu Ile Asp

355 360 365

Ala Lys Thr Val Val Tyr Gly Gly Leu Asn Tyr Thr Arg Asn Leu Gln

370 375 380

Ser Gln Gln Thr Ala Gln Ser Arg Ser Tyr Met Ala Asn Leu Gly Ile

385 390 395 400

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

405 410 415

Arg Gln Thr Arg His Asp Ala Glu Asp Leu Phe Leu Gly Gly Leu Arg

420 425 430

Lys Asp Arg Gln Gln Ile Tyr Ile Leu Asn Val Gly Met Pro Arg Phe

435 440 445

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

450 455 460

Asn Ser Asn Ile Asp Trp Ala Phe Lys Tyr Lys Gln Thr Glu Val Ala

465 470 475 480

Leu Lys Leu Glu Lys Arg Phe

485

<210> 119

<211> 1386

<212> DNA

<213> B. psittacipulmonis SLAM 1

<400> 119

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ccgattcatt ttcagtcgat cgactatcaa cgtgaaaaat gggtagaggc gaacatgagc 120

ttatccaacg ataccctacc tctagctgaa tatcagcttt cgtctgtcga ggcacagatt 180

acaaaattca ttcgatccaa acaatgggac gcattgatag cagtattgta ccaatatgca 240

cagcatccga ataaagatat agccttgtac tattatgcat taggtgcttt gcaacgagcg 300

gaaggactgc aatcacaagc gattcataca tatcaggttt tgacgaaata tcgttctgac 360

ttaatttatt ctcaatatga tttagcctta atgttaatgg aggattatca atatcaagaa 420

gccaaaaagt tgctgacagt attaataaaa cgatcagatg aagccttgtc agaaagggtt 480

tatgcacgtt tacggcatat tgaaaaacaa caatcatggc aaccgttttt tgatattcaa 540

tacgtaaaaa cggataatgt gaataatgca gcgacttccc ctgtgattgt gattaatggt 600

aaaacgtttg tcagagatga agaaagcaga ccgaaatcag ctcatggcgt atcttataca 660

atcggtgcga cacgtcgtta tcagataata ggtcatcacc atttttacac ttctttgggg 720

gcgaatggca cttattattg ggatgccaaa gactatcgcg aagagagttt gcagacggta 780

ttgggctatg tgtacaaaaa tataaagcaa gaatggcgag tattgccttt ttgggaccat 840

aatcgcttag gtgggcacgc atacagccgt tattatggtg tgagaatggg gtggtttcaa 900

aaattaggac ctaagtggtg ggtatcaggt agctatcaat atcgaaaaac agcttatttt 960

gatgaagtga ttgccgatcg ttataatgct cgtcagcatt ggatcttgat gaatcaacgc 1020

tggttgataa atccttactg gatgctatcg gcaggggtgg actatactcg agaatatgca 1080

tttgatccgt cgctatcttc ccgtaaaaag ggagtttcag caggggtata ttacgaaaaa 1140

gattggggag ctcatctcag cgcttattat ggttggcgac attttgatcg ggaacacgtg 1200

atctttgatc tcaaacgcaa agacaaagaa cgtcatgtta gcgtatcttt atggcataaa 1260

agcgctaaat ggaaaggcat acagcctacc attaattaca cctatcgtcg cataaaaagc 1320

aatctcagcg atttatatga tcgttctgaa tcgaccgtat tgattagctt ttcaaaaacg 1380

ttttaa 1386

<210> 120

<211> 461

<212> PRT

<213> B. psittacipulmonis SLAM 1

<400> 120

Met Gly Leu Cys Val Ser Leu Cys Leu Gly Val Val Arg Ala Glu Val
1 5 10 15

Leu Thr Val Glu Pro Ile His Phe Gln Ser Ile Asp Tyr Gln Arg Glu
20 25 30

Lys Trp Val Glu Ala Asn Met Ser Leu Ser Asn Asp Thr Leu Pro Leu

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        35                  40                  45
Ala Glu Tyr Gln Leu Ser Ser Val Glu Ala Gln Ile Thr Lys Phe Ile
    50                  55                  60

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

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

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

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

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

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

Ser Glu Ser Thr Val Leu Ile Ser Phe Ser Lys Thr Phe
450 455 460

<210> 121
<211> 1440
<212> DNA
<213> B. psittacipulmonis SLAM 2
<400> 121

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aacattcttt atacgcccaa tattgctcag gaagtcaaag atcattttga tgcgtatcaa 120
caaaatgaac agtggctcaa acaacgttca tctggcccta ccgctattgg tcccactatt 180
tctgattcac aaaccctatc gcttagtagc caagagctgt tacagcattc tgaattatta 240

gagaaagctt ttattattgc tttgaacacc tttcaaatag ggggaattga aaaactgctt 300

ccttgtacc gacaacttcc acaagctaat tctcatctaa ttcattatgc acaaggtctc 360

cttgcattca agaatcaaga ggcttctagc agtgcccaat attttaagaa aattctcgat 420

gaacatccca acgctgtcgt agcagattat ttttatgcct tatctagctt taaaaataaa 480

cattatgatg aggcaaacac acgttttaaa gcactcttaa acactaatat tcccgaaacc 540

aaaaaacaag acatcatacc gtttcatcag tttattcaga actaccaaaa atgggatgtt 600

tcattgatgg tcagtccttt ttatgaccaa aacatcaaca atgcccccga tcaacgtcat 660

tggaacggct ttacttttgc ggaaaaaata gcggactatg gcatgcgtta ttatttatct 720

gtcagtaaaa aaatattatt gcccaaagga tgggtggtcg caccaagcgt agccagctat 780

ggaaaaatat ttaaaaatga aaaaaccttt aacgatgtca atctcaaaac ttttgtaaat 840

atcattcaac agtcgcaata tcaggacttt ctcattcaac cttatttcca taaacgctgg 900

tttggtaatc aagcttactc acaaagcaaa ggcctgactc ttggctgggg acaagactgg 960

tcgtccatat tgagcactca agtcaatgtc gcttatgaac gagaaaagtt tcacggtcgt 1020

acttttttaa ataattacaa acaaatggct gatggtgtca tcttttatc ccccagtgac 1080

acacatacct ttatttttca acaaggcttt gttcatcaat atgccactcg cgaccaagat 1140

gatcgttaca tttccctacg ttcatccatc gcatggattc acacctttc acatggccta 1200

aacacgcgaa tcggtgtatt ttatgaaagc acgcgttata aaggccccac tctattaacg 1260

ggccaagaaa accgaaaaga caaagcatac ggctggtcat tagatgtaaa acacgcgtcc 1320

atccaataca aaggaattca acctagtcta ggttttcgtt acagcaaaca ccgcagtaat 1380

agtgccttac atcgttacac caaaaaggat gttgtattca gcattcaaaa aagtttttga 1440

<210> 122

<211> 479

<212> PRT

<213> B. psittacipulmonis SLAM 2

<400> 122

Met Thr Asn Lys Ile Leu Phe Thr Cys Phe Ser Ile Phe Ala Phe Gln

1 5 10 15

Ser Thr Val Ala Asn Ile Leu Tyr Thr Pro Asn Ile Ala Gln Glu Val

20 25 30

Lys Asp His Phe Asp Ala Tyr Gln Gln Asn Glu Gln Trp Leu Lys Gln

35 40 45

Arg Ser Ser Gly Pro Thr Ala Ile Gly Pro Thr Ile Ser Asp Ser Gln

50 55 60

Thr Leu Ser Leu Ser Ser Gln Glu Leu Leu Gln His Ser Glu Leu Leu

65 70 75 80

Glu Lys Ala Phe Ile Ile Ala Leu Asn Thr Phe Gln Ile Gly Gly Ile

85 90 95

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

100 105 110

Leu Ile His Tyr Ala Gln Gly Leu Leu Ala Phe Lys Asn Gln Glu Ala

115 120 125

Ser Ser Ser Ala Gln Tyr Phe Lys Lys Ile Leu Asp Glu His Pro Asn

130 135 140

Ala Val Val Ala Asp Tyr Phe Tyr Ala Leu Ser Ser Phe Lys Asn Lys

145 150 155 160

His Tyr Asp Glu Ala Asn Thr Arg Phe Lys Ala Leu Leu Asn Thr Asn

165 170 175

Ile Pro Glu Thr Lys Lys Gln Asp Ile Ile Pro Phe His Gln Phe Ile

180 185 190

Gln Asn Tyr Gln Lys Trp Asp Val Ser Leu Met Val Ser Pro Phe Tyr

195 200 205

Asp Gln Asn Ile Asn Asn Ala Pro Asp Gln Arg His Trp Asn Gly Phe

210 215 220

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

225 230 235 240

Val Ser Lys Lys Ile Leu Leu Pro Lys Gly Trp Val Val Ala Pro Ser

245 250 255

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

260 265 270

Val Asn Leu Lys Thr Phe Val Asn Ile Ile Gln Gln Ser Gln Tyr Gln

275 280 285

Asp Phe Leu Ile Gln Pro Tyr Phe His Lys Arg Trp Phe Gly Asn Gln

290 295 300

Ala Tyr Ser Gln Ser Lys Gly Leu Thr Leu Gly Trp Gly Gln Asp Trp

305 310 315 320

Ser Ser Ile Leu Ser Thr Gln Val Asn Val Ala Tyr Glu Arg Glu Lys

325 330 335

Phe His Gly Arg Thr Phe Leu Asn Asn Tyr Lys Gln Met Ala Asp Gly

340 345 350

Val Ile Phe Leu Ser Pro Ser Asp Thr His Thr Phe Ile Phe Gln Gln

355 360 365

Gly Phe Val His Gln Tyr Ala Thr Arg Asp Gln Asp Asp Arg Tyr Ile

370 375 380

Ser Leu Arg Ser Ser Ile Ala Trp Ile His Thr Phe Ser His Gly Leu

385 390 395 400

Asn Thr Arg Ile Gly Val Phe Tyr Glu Ser Thr Arg Tyr Lys Gly Pro

405 410 415

Thr Leu Leu Thr Gly Gln Glu Asn Arg Lys Asp Lys Ala Tyr Gly Trp

420 425 430

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

435 440 445

Ser Leu Gly Phe Arg Tyr Ser Lys His Arg Ser Asn Ser Ala Leu His

450 455 460

Arg Tyr Thr Lys Lys Asp Val Val Phe Ser Ile Gln Lys Ser Phe

465 470 475

<210> 123

<211> 1452

<212> DNA

<213> B. trehalosi SLAM 1

<400> 123

atgcaaaaat tattcatttc atcactttcc ttaactcttg catgtacagt tttagcaaat 60

gagcagcaga aaattaacga tcgactagag gattctcgca ttcaaactga gcaaaaaatg 120

ccagatttcc caacagtaaa gaaaacagca gcaccgcagc aaagtacggc taatcatagt 180

attagtatga ccaaagaaca gctcgcccaa catcctgatt tagtcatacg ggctttagag 240

ccggctttac tttctggtaa tgccgatacc ttatcgctga tttttcctat ctatcaacaa 300
ttgccagagc aatatcgcca ccctttagcg actaaatggg caatggcgat cttagcgcga 360
gaacaagaga attataggca atctattcga ctttaccgtg aaatcttggc agaagatgcg 420
aataatgagg tagtacgctt gcaattagcc acggtacttt tttcaaataa cgaattagag 480
gcagcggaag atcaatttaa aaagctacgt gctgagccat tgccacaaac aattcaagta 540
ttaattgata attatcttga agcgatcact cgtaaagatc gttggacatt aagcggcggg 600
ttgacttatc taaatgatcc aaatattaat aatgcgccga aatcagggac gacttatggt 660

aactggagcg caccaaagcg tgaaagtgca gaaggtatag gctttaatct tgcgctaggt 720
aagaaatggt cttggggcaa tggtttttac aatgaattgc gcttaaatgg cagtggaaaa 780
tattattggg ataaccgtaa atataacgaa gtgactggac gttcaagttt agggttaggt 840
tttcaaaatg ccaaaacaaa cttggtgatt ttacctttta tggagcaaac gctatatgct 900
ggtggtagcc gccaaagtga aacgttaaaa cgtttttcta aagcagcagg tggaacgctt 960
gaactacaac attggttaaa ttcaaaatgg cagtttaata gttcttatga atatgctgaa 1020
caacgttata ccagccgtaa acatcttaat ggcaattatc attatgtttc catgggaggg 1080

gtatatttag tgaatgctaa acagtattgg tttagcaatg tgaattatac ccgaatgtcc 1140
actcgagatg cggatgacag ttacttccgc cgtggagtta atcttggctg gcaacaagaa 1200
tggaattggg gactttccac ccgttttagt gttagcctag cagaaaaacg ttataaagca 1260
ccaatgccaa tcttccaaat tacgcagcga aataaagaat atgggttgca aggttcaatc 1320
tggcatcgcg ctatacacta ttggggaatt acaccaagat tgacttatag ttttactcga 1380
acaaggagca atcacgcatt ttatagctat gataagcacc gtgtatttat tgattttagt 1440
cgctcatttt aa 1452

<210> 124
<211> 483
<212> PRT
<213> B. trehalosi SLAM 1
<400> 124

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

Arg Ile Gln Thr Glu Gln Lys Met Pro Asp Phe Pro Thr Val Lys Lys

35 40 45

Thr Ala Ala Pro Gln Gln Ser Thr Ala Asn His Ser Ile Ser Met Thr

50 55 60

Lys Glu Gln Leu Ala Gln His Pro Asp Leu Val Ile Arg Ala Leu Glu

65 70 75 80

Pro Ala Leu Leu Ser Gly Asn Ala Asp Thr Leu Ser Leu Ile Phe Pro

85 90 95

Ile Tyr Gln Gln Leu Pro Glu Gln Tyr Arg His Pro Leu Ala Thr Lys

100 105 110

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

115 120 125

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

130 135 140

Val Arg Leu Gln Leu Ala Thr Val Leu Phe Ser Asn Asn Glu Leu Glu

145 150 155 160

Ala Ala Glu Asp Gln Phe Lys Lys Leu Arg Ala Glu Pro Leu Pro Gln

165 170 175

Thr Ile Gln Val Leu Ile Asp Asn Tyr Leu Glu Ala Ile Thr Arg Lys

180 185 190

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

195 200 205

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

210 215 220

Pro Lys Arg Glu Ser Ala Glu Gly Ile Gly Phe Asn Leu Ala Leu Gly

225 230 235 240

Lys Lys Trp Ser Trp Gly Asn Gly Phe Tyr Asn Glu Leu Arg Leu Asn

245 250 255

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

260 265 270

Gly Arg Ser Ser Leu Gly Leu Gly Phe Gln Asn Ala Lys Thr Asn Leu

275 280 285

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

290 295 300

Gln Ser Glu Thr Leu Lys Arg Phe Ser Lys Ala Ala Gly Gly Thr Leu

305 310 315 320

Glu Leu Gln His Trp Leu Asn Ser Lys Trp Gln Phe Asn Ser Ser Tyr

325 330 335

Glu Tyr Ala Glu Gln Arg Tyr Thr Ser Arg Lys His Leu Asn Gly Asn

340 345 350

Tyr His Tyr Val Ser Met Gly Gly Val Tyr Leu Val Asn Ala Lys Gln

355 360 365

Tyr Trp Phe Ser Asn Val Asn Tyr Thr Arg Met Ser Thr Arg Asp Ala

370 375 380

Asp Asp Ser Tyr Phe Arg Arg Gly Val Asn Leu Gly Trp Gln Gln Glu

385 390 395 400

Trp Asn Trp Gly Leu Ser Thr Arg Phe Ser Val Ser Leu Ala Glu Lys

405 410 415

Arg Tyr Lys Ala Pro Met Pro Ile Phe Gln Ile Thr Gln Arg Asn Lys

420 425 430

Glu Tyr Gly Leu Gln Gly Ser Ile Trp His Arg Ala Ile His Tyr Trp

435 440 445

Gly Ile Thr Pro Arg Leu Thr Tyr Ser Phe Thr Arg Thr Arg Ser Asn

450 455 460

His Ala Phe Tyr Ser Tyr Asp Lys His Arg Val Phe Ile Asp Phe Ser

465 470 475 480

Arg Ser Phe

<210> 125

<211> 1416

<212> DNA

<213> B. trehalosi SLAM 2

<400> 125

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agtacaccta gccaaataga acatattgct aaaccaacat cggcaccctt acagcttgca 120

gtggaacaat cgtctcgcca cattttaac gaagctgaat tacgtgctaa tcaggcatta 180

accgaaaaat tactcagcca agctatctat actcgccagc tcactaatat ggaaaaactg 240

gtcacaattt atcaagattt tgcccatatt gacccaattt tattgcgcta tgctcaaggt 300

aaaatcgcgc tacttaaagg aaattattca caagctattc gagagtttcg cactattctt 360

gctaaacaac ctgaactaaa taccgtacga attgaactgg caattgcatt actacatgat 420

caacaaacga atgcggcaag tgaacaattc gataaagcta aaagtgccga aaatctacct 480

tataaagtgc agcaactgat tgaacagtat cagcaatatc tggagaaaaa acaagcttgg 540

aagttcaatt tctctgccca ctatgtacgg gatggtaata tcaataacac atccaaacaa 600

actgaaattg agcataccgg ctatgtgaaa cagcctaacc tgttaccaca aactgcgcac 660

ggaattcact attcttttgg actacaaaga gattttaacc tacttggctc gcattacctt 720

agtttcgata atcaaacgca gggggaactt tattgggata atcatgacta cgatgaaatt 780

accaatcgcg ctttgtttgg ctatgcttac aaaaagtcac accaagccac ccgcgtattg 840

ccattttatg aaaaacgctg gaaacatcat caatcagaac gctggacaaa cggattaagg 900

ctagaacatg cgcattggct ttcttctcgc tggcaacttg ctactgcatt cgagtatggt 960

aaaaaacgct atttcgacca acacatttac aatggcaact ataaacttgc ttcagccacc 1020

ctactctggc tacgtaatcc gcaacaattt ttctttattg gcacggattt caaccgagat 1080

aaaaccgtat tgaaacaaca tagttctgat accaaaagct tacgtttcgg ctggcagcag 1140

gaatggcaaa cacttggatt atcaagccgc ctgacccttg cttacaccga cagacattat 1200

aaagacactg cggtgctggg tggcaaactt aatctgggta aaattcgcca tgatcgtgtg 1260

aacagcatta atcttaccct ttggaaacga gattggcatt ggttcgggtt tacacccaaa 1320

ctgcaacttg gctatgctaa acatcatagc aacttaccaa gcctatatgc ttacacggat 1380

aaaaatgcga atctgatcat cgaaagtcgc ttttaa 1416

<210> 126

<211> 471

<212> PRT

<213> B. trehalosi SLAM 2

<400> 126

Met Lys Lys Phe Pro Leu Leu Phe Phe Phe Pro Thr Leu Leu Phe Ala

1 5 10 15

Gln Asp Pro Asn Ser Thr Pro Ser Gln Ile Glu His Ile Ala Lys Pro

20 25 30

Thr Ser Ala Pro Leu Gln Leu Ala Val Glu Gln Ser Ser Arg His Ile

35 40 45

Phe Asn Glu Ala Glu Leu Arg Ala Asn Gln Ala Leu Thr Glu Lys Leu

50 55 60

Leu Ser Gln Ala Ile Tyr Thr Arg Gln Leu Thr Asn Met Glu Lys Leu

65 70 75 80

Val Thr Ile Tyr Gln Asp Phe Ala His Ile Asp Pro Ile Leu Leu Arg

85 90 95

Tyr Ala Gln Gly Lys Ile Ala Leu Leu Lys Gly Asn Tyr Ser Gln Ala

100 105 110

Ile Arg Glu Phe Arg Thr Ile Leu Ala Lys Gln Pro Glu Leu Asn Thr

115 120 125

Val Arg Ile Glu Leu Ala Ile Ala Leu Leu His Asp Gln Gln Thr Asn

130 135 140

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

145 150 155 160

Tyr Lys Val Gln Gln Leu Ile Glu Gln Tyr Gln Gln Tyr Leu Glu Lys

165 170 175

Lys Gln Ala Trp Lys Phe Asn Phe Ser Ala His Tyr Val Arg Asp Gly

180 185 190

Asn Ile Asn Asn Thr Ser Lys Gln Thr Glu Ile Glu His Thr Gly Tyr

195 200 205

Val Lys Gln Pro Asn Leu Leu Pro Gln Thr Ala His Gly Ile His Tyr

210 215 220

Ser Phe Gly Leu Gln Arg Asp Phe Asn Leu Leu Gly Ser His Tyr Leu

225 230 235 240

Ser Phe Asp Asn Gln Thr Gln Gly Glu Leu Tyr Trp Asp Asn His Asp

245 250 255

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

260 265 270

Ser His Gln Ala Thr Arg Val Leu Pro Phe Tyr Glu Lys Arg Trp Lys

275 280 285

His His Gln Ser Glu Arg Trp Thr Asn Gly Leu Arg Leu Glu His Ala

290 295 300

His Trp Leu Ser Ser Arg Trp Gln Leu Ala Thr Ala Phe Glu Tyr Gly

305 310 315 320

Lys Lys Arg Tyr Phe Asp Gln His Ile Tyr Asn Gly Asn Tyr Lys Leu

325 330 335

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

340 345 350

Ile Gly Thr Asp Phe Asn Arg Asp Lys Thr Val Leu Lys Gln His Ser

355 360 365

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

370 375 380

Leu Gly Leu Ser Ser Arg Leu Thr Leu Ala Tyr Thr Asp Arg His Tyr

385 390 395 400

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

405 410 415

His Asp Arg Val Asn Ser Ile Asn Leu Thr Leu Trp Lys Arg Asp Trp

420 425 430

His Trp Phe Gly Phe Thr Pro Lys Leu Gln Leu Gly Tyr Ala Lys His

435 440 445

His Ser Asn Leu Pro Ser Leu Tyr Ala Tyr Thr Asp Lys Asn Ala Asn

450 455 460

Leu Ile Ile Glu Ser Arg Phe

465 470

<210> 127

<211> 1461

<212> DNA

<213> B. trehalosi SLAM 3

<400> 127

atggcttttc ataagaacta ttttttttct gtactatttt ttatcccttt tcctatcgct 60

gcggaaagtt tttctgcctc tttttctgtt cctgaaacaa atcctgtttt gtctgatatt 120

aaattgcctg aaactgtttt aattgaaaga cgttcagtgg aaccggcgca aaatattgaa 180

ttggatgcgc atttgcaaaa attaaagcaa gatcaagcat tgacagaaaa ggttttaaat 240

tacctattac ctaaagggag cgctcaaaca attcaattgg tattagatgt gtaccgctcc 300

tttgcacatc ccgatcagtt attgatcgca cgagcagaaa caagaattgc agaaagaaat 360

ggcgatcatc aacaggcaat gtctcgttat cagcaaattc ttgccaaata tcctgatttt 420

acgcctattc gaattcaata cgcccaaggt ttaatgtcta ctcttcgaca taaagaggca 480

caaactgaat ttcagaaaat tttgtcaagt cctgatttac caccagattt agccgcttta 540

attcgacatt atcagcaggc agttaagtat cgagatcgtt ggaaattctc agcggcagca 600

aattatgtgc gtgaacgtaa tgtaaacaat gcgtcaagtg caagccaaat tgagaataca 660

gggtttgtga aaaatagctc aatgctgccg caaacggcac acggtataaa ttactatgtt 720

gcagcagaga aagattttaa tttctataaa gcgcattatc tccactttca aagttacttg 780

agtggagtga gttattggga taatcacgac tacgatgaaa tgacatctcg tacttatttt 840

gggtatatcc ataaatgggc aacaaagcgt ttgagttttt tgcctttcta tgaacgtcac 900

tggtatgcca atcatcgtta taaaaatatc actggagcaa gaatcagctt taatcagtgg 960

ctgacgccta aattgcaatt agcactatct acagaatatg gaaaatctcg ttactatgat 1020

catcgtgatt taaacgggaa cggtaaattt gtctctcttg ctttacattg gtttcctacg 1080

caactacgtc atttttcagt aggaagtgat ttctatcgag aaaatactgc gttacgcaat 1140

tatagctacg atttaaaaac agttcgtcta ggttggacag aagaatgggg aaaacagatt 1200

gtcagccgac ttaactacag ttttagcgaa cgtcattata aagataatct gattttagga 1260

cgaggtttcc gtttttctcg tccccgtatc gaccgtattt atcaagtcaa tgctacggta 1320

tggaaaaaag attgggcatt gcctgttttt gagattgtgc cgaaattgca atttcgctgg 1380

aaaaaacaac gtagcacatt tccaagttta tacaattata ccgaccgtag tttaaatcta 1440

ttaatcgaaa aaagttttta a 1461

<210> 128

<211> 486

<212> PRT

<213> B. trehalosi SLAM 3

<400> 128

Met Ala Phe His Lys Asn Tyr Phe Phe Ser Val Leu Phe Phe Ile Pro

1 5 10 15

Phe Pro Ile Ala Ala Glu Ser Phe Ser Ala Ser Phe Ser Val Pro Glu

20 25 30

Thr Asn Pro Val Leu Ser Asp Ile Lys Leu Pro Glu Thr Val Leu Ile

35 40 45

Glu Arg Arg Ser Val Glu Pro Ala Gln Asn Ile Glu Leu Asp Ala His

50 55 60

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

65 70 75 80

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

85 90 95

Val Tyr Arg Ser Phe Ala His Pro Asp Gln Leu Leu Ile Ala Arg Ala

100 105 110

Glu Thr Arg Ile Ala Glu Arg Asn Gly Asp His Gln Gln Ala Met Ser

115 120 125

Arg Tyr Gln Gln Ile Leu Ala Lys Tyr Pro Asp Phe Thr Pro Ile Arg

130 135 140

Ile Gln Tyr Ala Gln Gly Leu Met Ser Thr Leu Arg His Lys Glu Ala

145 150 155 160

Gln Thr Glu Phe Gln Lys Ile Leu Ser Ser Pro Asp Leu Pro Pro Asp

165 170 175

Leu Ala Ala Leu Ile Arg His Tyr Gln Gln Ala Val Lys Tyr Arg Asp

180 185 190

Arg Trp Lys Phe Ser Ala Ala Ala Asn Tyr Val Arg Glu Arg Asn Val

195 200 205

Asn Asn Ala Ser Ser Ala Ser Gln Ile Glu Asn Thr Gly Phe Val Lys

210 215 220

Asn Ser Ser Met Leu Pro Gln Thr Ala His Gly Ile Asn Tyr Tyr Val

225 230 235 240

Ala Ala Glu Lys Asp Phe Asn Phe Tyr Lys Ala His Tyr Leu His Phe

245 250 255

Gln Ser Tyr Leu Ser Gly Val Ser Tyr Trp Asp Asn His Asp Tyr Asp
260 265 270
Glu Met Thr Ser Arg Thr Tyr Phe Gly Tyr Ile His Lys Trp Ala Thr
275 280 285

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

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

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

Leu Ile Glu Lys Ser Phe
485

<210> 129

<211> 1248

<212> DNA

<213> B. trehalosi SLAM 4

<400> 129

atgatgaaaa aagcacttct ttccattttt cttatcccct ctctgctttt ggcacaagaa 60

acggagagca gttatcgtgt cgcggaatta aagcaagatc ctgcgacaac agaacgtttg 120

ttaatctttg ctttgcaaac agaacaatgg ttttcagtaa aacgtttatt agctatttat 180

tcgacgtttt cccaaacaga tcagcgactt gtcagttacg ccaacattcg ccttgcccag 240

cggtcatttt ttaattaccg aaatcgtgaa gctcgcaaag catttcaagc ggtgcaaaat 300

caggcaaatt tagccaatga agaacgagaa attgttgagc agtatttgag tgtgattgat 360

aaacgagaaa gctggcaatt ttcggggcgc atgaattatg tttatgataa aaacgtgaat 420

aaaacctcat cagatcatca tattgaagat acaggattta ttaaaggcga gggaatgtta 480

cctcaaaaag ctcacggttt tgcttattcg gcagaagtgg agaaaaattg gaatttaaac 540

ggttcacaca atctccattt tgccaatgaa atcagtggca aaagctattg ggataaccat 600

gattatgatg aattaaataa tcgtacttat ttgggatatg cgttccaaaa tgcccaatat 660

cgttgggcaa taaggccatt ttatgaacgc caatggttta gcaatcatcg ctatcattgg 720

gcaaatggcg tgagaatgga atatcgccaa atatttgcaa aaaattggca aatttctacc 780

gcttgggagt ttagccagcc acgttatttt aaacagcaag agcgtaatgg caccattaaa 840

ttagcctctg ctacacttgt ttatgcgttt agcgaaaaag gttatctcta tttaagcacg 900

gattttatcc gtgaacaaac aagggaaaaa cagtacagca atgatttaaa atcattgcgt 960

gcagggtgga aacagacatg gggtgatgac attagcacac aattaaacgg ttcaatttca 1020

ctacgacaat ataaagattt tgcctctttg ggtgggattt tgccattaaa tgcgattcgc 1080

cgagataaaa tctacatagc aaatttaacg ctttggaaaa ataattggca ttggtatgga 1140

ttcaccccga aggttcaatg gcgatggaaa cggcaaagta gcaacattcc gtctatgttc 1200

tcttattcgg atagctatgt gcagatgcta atagagaaag cgttttaa 1248

<210> 130

<211> 415

<212> PRT

<213> B. trehalosi SLAM 1

<400> 130

Met Met Lys Lys Ala Leu Leu Ser Ile Phe Leu Ile Pro Ser Leu Leu

1 5 10 15

Leu Ala Gln Glu Thr Glu Ser Ser Tyr Arg Val Ala Glu Leu Lys Gln

20 25 30

Asp Pro Ala Thr Thr Glu Arg Leu Leu Ile Phe Ala Leu Gln Thr Glu

35 40 45

Gln Trp Phe Ser Val Lys Arg Leu Leu Ala Ile Tyr Ser Thr Phe Ser

50 55 60

Gln Thr Asp Gln Arg Leu Val Ser Tyr Ala Asn Ile Arg Leu Ala Gln

65 70 75 80

Arg Ser Phe Phe Asn Tyr Arg Asn Arg Glu Ala Arg Lys Ala Phe Gln

85 90 95

Ala Val Gln Asn Gln Ala Asn Leu Ala Asn Glu Glu Arg Glu Ile Val

100 105 110

Glu Gln Tyr Leu Ser Val Ile Asp Lys Arg Glu Ser Trp Gln Phe Ser

115 120 125

Gly Arg Met Asn Tyr Val Tyr Asp Lys Asn Val Asn Lys Thr Ser Ser

130 135 140

Asp His His Ile Glu Asp Thr Gly Phe Ile Lys Gly Glu Gly Met Leu

145 150 155 160

Pro Gln Lys Ala His Gly Phe Ala Tyr Ser Ala Glu Val Glu Lys Asn

165 170 175

Trp Asn Leu Asn Gly Ser His Asn Leu His Phe Ala Asn Glu Ile Ser

180 185 190

Gly Lys Ser Tyr Trp Asp Asn His Asp Tyr Asp Glu Leu Asn Asn Arg

195 200 205

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

210 215 220

Arg Pro Phe Tyr Glu Arg Gln Trp Phe Ser Asn His Arg Tyr His Trp

225 230 235 240

Ala Asn Gly Val Arg Met Glu Tyr Arg Gln Ile Phe Ala Lys Asn Trp

245 250 255

Gln Ile Ser Thr Ala Trp Glu Phe Ser Gln Pro Arg Tyr Phe Lys Gln

260 265 270

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

275 280 285

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

290 295 300

Glu Gln Thr Arg Glu Lys Gln Tyr Ser Asn Asp Leu Lys Ser Leu Arg

305 310 315 320

Ala Gly Trp Lys Gln Thr Trp Gly Asp Asp Ile Ser Thr Gln Leu Asn

325 330 335

Gly Ser Ile Ser Leu Arg Gln Tyr Lys Asp Phe Ala Ser Leu Gly Gly

340 345 350

Ile Leu Pro Leu Asn Ala Ile Arg Arg Asp Lys Ile Tyr Ile Ala Asn

355 360 365

Leu Thr Leu Trp Lys Asn Asn Trp His Trp Tyr Gly Phe Thr Pro Lys

370 375 380

Val Gln Trp Arg Trp Lys Arg Gln Ser Ser Asn Ile Pro Ser Met Phe

385 390 395 400

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

405 410 415

<210> 131

<211> 374

<212> PRT

<213> B. trehalosi SLAM 5

<400> 131

Met Trp His Tyr Ala His Ala Ala Leu Ala Tyr Ala Lys Lys Asp His

1 5 10 15

Gln Met Ala Val Phe His Tyr Arg Gln Leu Leu Ala Lys Asn Pro Ser

20 25 30

Leu Val Tyr Pro Arg Phe Asp Leu Ala Leu Ile Leu Ala Glu Asp Gln

35 40 45

Gln Phe Arg Ala Ala Glu Trp Glu Phe Gln Gln Leu Gln Ala His Leu

50 55 60

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

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

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

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

Lys Arg Tyr Phe Ala Asp Lys His Tyr Leu Phe Gly Tyr Lys Arg Leu
305 310 315 320

Asp Thr Glu Tyr Gln Ala Asn Val Ala Val Trp Asn Arg Thr Trp His
325 330 335

Trp Arg Gly Ile Val Pro Lys Leu Asn Phe Arg Tyr Gln Lys Ile Asp
340 345 350

Ser Asn Ile Pro Asp Phe Tyr Thr Arg Gln Asn Gln Glu Trp Phe Ile
355 360 365

Thr Leu Glu Lys Leu Phe
370

<210> 132

<211> 1125

<212> DNA

<213> B. trehalosi SLAM 5

<400> 132

ttgtggcact acgcccacgc cgcacttgcc tatgcgaaaa aagatcatca aatggcagtt 60

tttcactatc gccaactgtt agccaagaac ccgagtttgg tttatcctcg ttttgatttg 120

gcgttgattt tggcagaaga tcagcaattt cgtgcggcag aatgggaatt tcagcaactt 180

caagcccatt taccgccaga actcgctaaa attgcccgca atacccaagc ccaaattgct 240

gaaaatgagg cgtggcagtc cgatttttat ctgcaatata cccaaaccga taacgtgaat 300

aatgcctcat cttcaccgat tgtgaatgtg aatgggcgga ttttccataa aaatgaagag 360

agtttgccac aatcggcaaa aggcgtgcgt tatggtttag ggttgagtaa attacacaac 420

gtgaaaggca atcattttgc cggtttaacg ctcaattata gcgggattta ctattgggat 480

aaccgagatt accgtgagca atcgctttct atttcgccaa gttatagtta ccgcaaggct 540

ctctatcgct ttagtttttc gccgtttatc gaacagaatt ggctggggag tagtcgttat 600

aattaccagt ttggagcaac tgtaagtggc ttgcgttatc tcaattcaca atggttggtg 660

tcgggtcgtt ttacccattt gcaaaaacgt tattttgagg aacttaccgc aagccgttat 720

aacagctatc agcaccaact cggtggcggt gtgcagtggc aagcggttaa aaatgggcgg 780

ttttttgcaa atttagatgg cgtgcgtgaa attgcacggg aaacagcaca aagttcgaat 840

aaatggttgg ctcgagtggg agcggttttt cagggcgaac gctgggcaat gcaggcaagt 900

atcggctttg gcaagcgata ttttgcggat aagcactatt tgtttggcta taagcggtta 960

gacacggaat atcaggctaa tgtggcagtc tggaaccgca cttggcattg gcgaggcatt 1020

gtgcctaagc tcaatttccg ttatcagaaa attgatagta acatacccga tttctatact 1080

cgtcaaaatc aagaatggtt tatcacatta gaaaaactat tttag 1125

<210> 133

<211> 1575

<212> DNA

<213> Brenneria sp. EniD312 SLAM 1

<400> 133

atgtcgtatc agccggattt gttcgccgta atccaatcag aacaatggcg cagaaagtgt 60

ttttccccgt gggcgacgcc gggtcgattt gccgtgactg cctttatccg cgttttcatc 120

ttttttctct gcctgccgct gacgggcgtc gttgtggcgc aggaacgcga cgatacgcgc 180

cgcctgctgg agcagagcat cgagagccgg gcgtttgagc gcgagcgcga actgctgcgc 240

gacgagcggg aacaacccgc cgcaagccgg ccgaccctta cccttgacgg ccgcacctat 300

accgtcgaac gtaccgccgc cgcgttgggg caggctctct atctgtcatt gcagcaccga 360

cagtggggcg cggcgcggcg ttttctggat gaatacctaa ccttgccgga ccacgatccc 420

ctgctggtgc actatgccag gggaatgttg gcccgcgcgg ccggactgct ggcgcaggcg 480

gaggcggaat tccgcgcgct gctggcgctg cggcccgcct ttctgcccgc ccggctcgaa 540

ctggcgcgcg tactgttcga ggacggtcag gagcgcgagg cagaactggc gttcgtggat 600

attctggcgt ccatcaatgc tgcggatccc aagacagccg gggtgcgcaa gacgattgcg 660

gcctaccgca atgcgctacg acagcgcagc gattggcacg gttccttttc cttcggcccg 720

acctggtccg ataatgtcaa ccgcacctcg gcgagccaga cctgtctctg gctgttggca 780

aacggtctct gtctggtgga acgcaagctg ccggacgcca tctccgccgg cggcctggcc 840

ttcgacgcca gcgcgcagcg gcgcataccg ctacgcggcc gccacggcct ctatctccga 900

tcgtccctgt atggcgcgca ataccgtcat cacggcgact acaacgaaac cacgttcacg 960

gcgcagggcg gctacagcta tcgcggcggg cggcatcagt tacagttggc cccctccttc 1020

gaatattacc aatggggcag ggaagcgctt tacggcgcct ggggagcgca tgccgactgg 1080

agctacatac cgtggcgcaa cgcgctgcta aagctggaag gggagtataa ggatatgagc 1140

tatcggcggc gggcgtacgc caataatttc gacggcgcaa cgcgccaact gtacgccacc 1200

tattatcatg aagtgggcgc cggctggacg ctgttcggcg gcgtcgattg ggtggacagc 1260

gatgcgcggc tggaggccaa cggctaccgg cagacggggc tacgccttgg cgctgccgtg 1320

acctattccg gtttttccgc cacgctgttc ggcgcctacc gggtacggga ctacgacgca 1380

tacaaccccc tgctggcggc ccgcagggaa gatgacgaac agaattatac cttgatcctc 1440

aaagcgccgc gctggcaggc ggccggcttc gttccggtcc tgaccctgcg tcataataaa 1500

gtgaaaagca acgtggactg gctctactcc tacgatcgca acgatatcag cctgaagctg 1560

gagcgcactt tctaa 1575

<210> 134

<211> 524

<212> PRT

<213> Brenneria sp. EniD312 SLAM 1

<400> 134

Met Ser Tyr Gln Pro Asp Leu Phe Ala Val Ile Gln Ser Glu Gln Trp

1 5 10 15

Arg Arg Lys Cys Phe Ser Pro Trp Ala Thr Pro Gly Arg Phe Ala Val

20 25 30

Thr Ala Phe Ile Arg Val Phe Ile Phe Phe Leu Cys Leu Pro Leu Thr

35 40 45

Gly Val Val Val Ala Gln Glu Arg Asp Asp Thr Arg Arg Leu Leu Glu

50 55 60

Gln Ser Ile Glu Ser Arg Ala Phe Glu Arg Glu Arg Glu Leu Leu Arg

65 70 75 80

Asp Glu Arg Glu Gln Pro Ala Ala Ser Arg Pro Thr Leu Thr Leu Asp

85 90 95

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

100 105 110

Leu Tyr Leu Ser Leu Gln His Arg Gln Trp Gly Ala Ala Arg Arg Phe

115 120 125

Leu Asp Glu Tyr Leu Thr Leu Pro Asp His Asp Pro Leu Leu Val His

130 135 140

Tyr Ala Arg Gly Met Leu Ala Arg Ala Ala Gly Leu Leu Ala Gln Ala

145 150 155 160

Glu Ala Glu Phe Arg Ala Leu Leu Ala Leu Arg Pro Ala Phe Leu Pro

165 170 175

Ala Arg Leu Glu Leu Ala Arg Val Leu Phe Glu Asp Gly Gln Glu Arg

180 185 190

Glu Ala Glu Leu Ala Phe Val Asp Ile Leu Ala Ser Ile Asn Ala Ala

195 200 205

Asp Pro Lys Thr Ala Gly Val Arg Lys Thr Ile Ala Ala Tyr Arg Asn

210 215 220

Ala Leu Arg Gln Arg Ser Asp Trp His Gly Ser Phe Ser Phe Gly Pro

225 230 235 240

Thr Trp Ser Asp Asn Val Asn Arg Thr Ser Ala Ser Gln Thr Cys Leu

245 250 255

Trp Leu Leu Ala Asn Gly Leu Cys Leu Val Glu Arg Lys Leu Pro Asp

260 265 270

Ala Ile Ser Ala Gly Gly Leu Ala Phe Asp Ala Ser Ala Gln Arg Arg

275 280 285

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

290 295 300

Gly Ala Gln Tyr Arg His His Gly Asp Tyr Asn Glu Thr Thr Phe Thr

305 310 315 320

Ala Gln Gly Gly Tyr Ser Tyr Arg Gly Gly Arg His Gln Leu Gln Leu

325 330 335

Ala Pro Ser Phe Glu Tyr Tyr Gln Trp Gly Arg Glu Ala Leu Tyr Gly

340 345 350

Ala Trp Gly Ala His Ala Asp Trp Ser Tyr Ile Pro Trp Arg Asn Ala

355 360 365

Leu Leu Lys Leu Glu Gly Glu Tyr Lys Asp Met Ser Tyr Arg Arg Arg

370 375 380

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

385 390 395 400

Tyr Tyr His Glu Val Gly Ala Gly Trp Thr Leu Phe Gly Gly Val Asp

405 410 415

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

420 425 430

Gly Leu Arg Leu Gly Ala Ala Val Thr Tyr Ser Gly Phe Ser Ala Thr

435 440 445

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

450 455 460

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

465 470 475 480

Lys Ala Pro Arg Trp Gln Ala Ala Gly Phe Val Pro Val Leu Thr Leu

485 490 495

Arg His Asn Lys Val Lys Ser Asn Val Asp Trp Leu Tyr Ser Tyr Asp

500 505 510

Arg Asn Asp Ile Ser Leu Lys Leu Glu Arg Thr Phe

515 520

<210> 135

<211> 1485

<212> DNA

<213> Brenneria sp. EniD312 SLAM 2

<400> 135

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gccgccatcg gcgccgcccg tgggcagatg cccgtcattc ccggcgaaca gcgcagcttt 120

cccgcgcccg atatcgaccg ccagtggcaa aaagaacaga acgaggcgct ggagcgcgcg 180

cgtcgtcgtc gggcgccgcg cggcgaaagc ccggccgcgc cggtattgaa cgacgccgcg 240

gtggcggcca atagcgcggt ggcggagctg attctggaga cggcgctgca acatcaggac 300

tgggacacta tcgagcgggt gctgccgctg tacgccggcc atccgcgcca cgaccggcag 360

ctttatcgct tcgtcaaagg ggcgatgctc cgggcgcgct ggcggctcgg gccggccatc 420

gacctgtatc gccaaatgct cgacgccgac ccgacgctga acaatgtgcg cttcgacctg 480

gcggtgatgc agttcgagaa caaatcctat agccaggcga aacggcaatt tttgctgctg 540

gccgataacc cgcgggagcc gctgttccgc gagctgtcgc taaactacct gaaacggatt 600

gccgaacgcg ccaggccgtc gctcaacctt accgccgatc tgctgcacac cgacaactac 660

aatcagggca gcgacgtgga atacatctat ctgtggggcc tgccgttcag gaacaacaac 720

cgccggcaga gcagttccgg ccagtccctg ttcgtgacgc tggagcagga cgtcaacctt 780

gccggcaacc attttctggg ctattcggcc tatttcaacg cgcttaatta cgccagagac 840

aaccattacg acgaaagaac ggcgttgctg gggctggact accagtacca gagcctgcgc 900

gataccttt ccgtcgggcc ggtttacacc taccggcggc tgggggggcga gagttatgcc 960

agggacgtcg ggctgagcgc cagttacggc cgctggctga cgccccgctg gcaggccgcg 1020

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ggcaagatcg ccatccacag cctgaatctg atgcgcgccg tttcgaaccg ttttctgctc 1140

tacggcgggg tattccacga gcgcgagaag ctgggcgccg ccgatgtctc ttcccggcag 1200

agcggcgtca acggcggctt tacctatatc gcgcagggcg gcctggacgt cagaatgcag 1260

ctaagattcg ggcgcaagcg ctttgacgag gagaacgcct ttttcggcgt ccggcgccgc 1320

gacgccgtca cccgccttgc gctgcggttg cagtaccggc cctggacttt tcagggcatt 1380

acgccgcggc tggtttatca gcgtgaaaaa accaccagca atattccggc gttctatggc 1440

aaatcctcca atcagctgat gctctccttc agcaaggagt tttga 1485

<210> 136

<211> 494

<212> PRT

<213> Brenneria sp. EniD312 SLAM 2

<400> 136

Met Pro Tyr Ala Pro Ser Ile Leu Lys Ile Val Ile Thr Thr Leu Leu
1 5 10 15

Phe Pro Leu Pro Ala Ala Ile Gly Ala Ala Arg Gly Gln Met Pro Val
20 25 30

Ile Pro Gly Glu Gln Arg Ser Phe Pro Ala Pro Asp Ile Asp Arg Gln
35 40 45

Trp Gln Lys Glu Gln Asn Glu Ala Leu Glu Arg Ala Arg Arg Arg Arg
50 55 60

Ala Pro Arg Gly Glu Ser Pro Ala Ala Pro Val Leu Asn Asp Ala Ala
65 70 75 80

Val Ala Ala Asn Ser Ala Val Ala Glu Leu Ile Leu Glu Thr Ala Leu
85 90 95

Gln His Gln Asp Trp Asp Thr Ile Glu Arg Val Leu Pro Leu Tyr Ala
100 105 110

Gly His Pro Arg His Asp Arg Gln Leu Tyr Arg Phe Val Lys Gly Ala

115 120 125

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

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

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

Arg Asp Val Gly Leu Ser Ala Ser Tyr Gly Arg Trp Leu Thr Pro Arg
325 330 335
Trp Gln Ala Ala Leu Gly Tyr Arg Leu Leu Asp Arg Arg Tyr Tyr Arg
340 345 350
Gln Pro Ile Gly Glu Leu Tyr Asp Gly Lys Ile Ala Ile His Ser Leu
355 360 365

Asn Leu Met Arg Ala Val Ser Asn Arg Phe Leu Leu Tyr Gly Gly Val
370 375 380

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

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

<210> 137
<211> 1425
<212> DNA
<213> C. hominis SLAM 1
<400> 137
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gtcccgcccg cgccagtacg tgacaccgcc acgccggacg aaaaactgcc cgacaccgcc 120
gaacgcgccg ccgccgacaa aaaccaggcg cgccaacaaa acgcccaagt cctgcaagtc 180
accgaagccg aactgctcgc cgacccgccg ctgctcgcca acgccctcga cagcgccatc 240
atcaacggcg acgccgacgc cgtcgccatg ctattgccca tctaccgcaa actgcccgcc 300
gacaaacaag acaaaatgct gctgcgcttt ggcgaagcca tgaaagcgcg cgccgacggc 360
gacctcagcc gcgccatcgc ccgcctgcgc gaaatgattg ccgaagaccc cagcctgcaa 420
cccgtgcgcc tgcaccttgc catggcacta ctcgccgacc atcaggacga agccgcgcgc 480

acccagctcg aaaaactgcg ctcggacgaa ctgccggaag acatccgcaa catcgtcagc 540
caagcgctgg ataccctgcg cgaacgccaa agctggacct tcaacgccag cggctactac 600

cgccacgaca aaaacatcaa cgacgcgccg cgccaacgcg aacgccaagt cggcaacggc 660

aaatggacct tccccgaacg caaaagcgcg cacggcgtac acttcgacgt ctccgccgaa 720

cgccgcatcc ccatccacaa cggcttctac ggccaagtag aagcgggcat caatggcgac 780

tggttctggg acgcgcacaa cttcgacgac ttccgcctgc gcaccggcgc tggcgtaggc 840

tggcaaaact cgcgctggga catcagcctc acccccttca tccagcgccg catctactcc 900

aacaaaggct actccaccaa cttcggcacc gacgccaaca tctcctactg gctcaccccg 960

cgctggcgcc tgagcagctc gatgcaggcc atgcacaaaa accacgacac ccgccgctgg 1020

ctgaacggca accaatacta cggcagcctg aacgtcctct ttgcgccgaa cgcgcgccaa 1080

tactggttcg ccggagcgaa cgccatgcgc agccaggcaa gagacagctc ggacgccttc 1140

aaacgctacg gcatcagcgc cggctgggga caagaatggg gctggggcat gtccagccgc 1200

ctgagcggca actttgccta ccgtccgtat gacagcaaag acttcttcgg catcgtgcgc 1260

aaagaccacg aatacggcgc caccctcagc ctctggaacc gcaacctcta cttctggggc 1320

atcaccccgc gcctgacctt ctcctgggac aaaaccaaga gcaaccactt ctattacgac 1380

aaccacaata tggatgtcta tctggagttt agtaagtcat tttga 1425

<210> 138

<211> 474

<212> PRT

<213> C. hominis SLAM 1

<400> 138

Met Arg Leu Ile Pro Leu Ile Thr Leu Thr Leu Phe Ser Ser Ile Ala

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

20 25 30

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

35 40 45

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

50 55 60

Leu Leu Ala Asp Pro Pro Leu Leu Ala Asn Ala Leu Asp Ser Ala Ile

65 70 75 80

Ile Asn Gly Asp Ala Asp Ala Val Ala Met Leu Leu Pro Ile Tyr Arg

85 90 95

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

100 105 110

Ala Met Lys Ala Arg Ala Asp Gly Asp Leu Ser Arg Ala Ile Ala Arg

115 120 125

Leu Arg Glu Met Ile Ala Glu Asp Pro Ser Leu Gln Pro Val Arg Leu

130 135 140

His Leu Ala Met Ala Leu Leu Ala Asp His Gln Asp Glu Ala Ala Arg

145 150 155 160

Thr Gln Leu Glu Lys Leu Arg Ser Asp Glu Leu Pro Glu Asp Ile Arg

165 170 175

Asn Ile Val Ser Gln Ala Leu Asp Thr Leu Arg Glu Arg Gln Ser Trp

180 185 190

Thr Phe Asn Ala Ser Gly Tyr Tyr Arg His Asp Lys Asn Ile Asn Asp

195 200 205

Ala Pro Arg Gln Arg Glu Arg Gln Val Gly Asn Gly Lys Trp Thr Phe

210 215 220

Pro Glu Arg Lys Ser Ala His Gly Val His Phe Asp Val Ser Ala Glu

225 230 235 240

Arg Arg Ile Pro Ile His Asn Gly Phe Tyr Gly Gln Val Glu Ala Gly

245 250 255

Ile Asn Gly Asp Trp Phe Trp Asp Ala His Asn Phe Asp Asp Phe Arg

260 265 270

Leu Arg Thr Gly Ala Gly Val Gly Trp Gln Asn Ser Arg Trp Asp Ile

275 280 285

Ser Leu Thr Pro Phe Ile Gln Arg Arg Ile Tyr Ser Asn Lys Gly Tyr

290 295 300

Ser Thr Asn Phe Gly Thr Asp Ala Asn Ile Ser Tyr Trp Leu Thr Pro

305 310 315 320

Arg Trp Arg Leu Ser Ser Ser Met Gln Ala Met His Lys Asn His Asp

325 330 335

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

340 345 350

Leu Phe Ala Pro Asn Ala Arg Gln Tyr Trp Phe Ala Gly Ala Asn Ala

355 360 365

Met Arg Ser Gln Ala Arg Asp Ser Ser Asp Ala Phe Lys Arg Tyr Gly

370 375 380

Ile Ser Ala Gly Trp Gly Gln Glu Trp Gly Trp Gly Met Ser Ser Arg

385 390 395 400

Leu Ser Gly Asn Phe Ala Tyr Arg Pro Tyr Asp Ser Lys Asp Phe Phe

405 410 415

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

420 425 430

Asn Arg Asn Leu Tyr Phe Trp Gly Ile Thr Pro Arg Leu Thr Phe Ser

435 440 445

Trp Asp Lys Thr Lys Ser Asn His Phe Tyr Tyr Asp Asn His Asn Met

450 455 460

Asp Val Tyr Leu Glu Phe Ser Lys Ser Phe

465 470

<210> 139

<211> 1560

<212> DNA

<213> C. hominis SLAM 2

<400> 139

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accctcgccg taactaccgg cctgctgctc accgctactg ctgtcgccca acccgcaccg 120

cctgccggac gtgacattcc cgtccccctt gaccgcggta acgaacgcct ttcagaagac 180

aacatcggca aggctgccgt agaaaacgcg ccgaaacagc ccacggtgcg ccccgccaac 240

accctgccga gcgacgcggc cagtagcaag gaagacatcg tctatacccc cgaatacctg 300

atggaacacc cggacgagct ggaaaaactc ctggtcgaac ttatccgccg caacgaaacc 360

gacggtctca aactgctgtt gccgatttat gccaaagtac cgaatcgcga tgactcgctc 420

attgactggg gcaatgccat catcgccatg aacgagaacc gtacggatga cgccgtccgt 480

ctctatcgca aactcgtcgc cgccctgccg gacaaccgca tgctgcgctt ccagacggca 540

ctggcgctct accgcaacaa cgaaatgatc gccgccaaag aacagctgca aaaactgcgc 600

agctcggatg tctccgaagc agaccgcaaa gcgctggacg aatacatcgc tgccattgat 660

cgccgcgacc aatggtcatt caacggcagt ctgagctacg ttcacgacaa taacgtcaac 720

ggcgttgcca aaaaaggcac acgcctggaa ctgggcaacg gccgcacctt caccgccagc 780

cgtgagcaag aaaaagccaa cggcatcagc tacagcatcg gtgcggacaa aaaatggtcg 840

ctcagcgaca acctctacag ctcgctgcac ggcgacatca gcggtgtgta ctactacaac 900

aacaaaaact acaacgacat cactgcccgc ctcgccgccg gtggtggcta ccgcaacgcg 960

cgcattgacg tagaagtcac cccgttcgta caaaaacgct tctacggcca gggcagcagc 1020

ggcgacggca acctgcacag ctactccgaa tccgccgggc tgcacgtgga cacctcctac 1080

tggctgaccc cgcgctggcg ctggcaaaac agcctcgatt acagctacga caaacacatc 1140

aaaacctaca actacctcga cggcaaccgc gtcagcatcg gtaacaccgt catgttctcg 1200

ccgaaccaaa aacaatactg gttcgccgga ctggatctca gccacaaaag cgcacgcagc 1260

gcgagcgatg cctacaaccg cttctccacc cgccttggct gggggcaaga atggggcaaa 1320

ggcatctcga cccgcctgat cggcagcttc ggcaaacgct acgccaaagg cgaagacttc 1380

ttcaacatca agcgtcgcga caacgaatac aacgccaacc tggcgctgtg gcaccgcaac 1440

atccacttct tcggcatcac cccgcgcatc gtcttctcct acagcaagat cgacagcaac 1500

aacaagttct acagctacga caccagcaaa gtctatctgg acttcagccg ctccttctaa 1560

<210> 140

<211> 519

<212> PRT

<213> C. hominis SLAM 2

<400> 140

Met Arg Arg Phe Ala Leu Pro Ile Thr Thr Asn Glu Asn Leu Met Asn
1 5 10 15

Ile Thr Arg Met Thr Leu Ala Val Thr Thr Gly Leu Leu Leu Thr Ala
20 25 30

Thr Ala Val Ala Gln Pro Ala Pro Pro Ala Gly Arg Asp Ile Pro Val
35 40 45

Pro Leu Asp Arg Gly Asn Glu Arg Leu Ser Glu Asp Asn Ile Gly Lys
50 55 60

Ala Ala Val Glu Asn Ala Pro Lys Gln Pro Thr Val Arg Pro Ala Asn

65 70 75 80

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

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

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

Ile Gly Ala Asp Lys Lys Trp Ser Leu Ser Asp Asn Leu Tyr Ser Ser
275 280 285
Leu His Gly Asp Ile Ser Gly Val Tyr Tyr Tyr Asn Asn Lys Asn Tyr
290 295 300
Asn Asp Ile Thr Ala Arg Leu Ala Ala Gly Gly Gly Tyr Arg Asn Ala
305 310 315 320

Arg Ile Asp Val Glu Val Thr Pro Phe Val Gln Lys Arg Phe Tyr Gly
325 330 335

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

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

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

<210> 141
<211> 1452
<212> DNA
<213> C. kuhniae SLAM 1

<400> 141

gtgggcgtgt tgctgttgtt gtcggcacag gtgcttgcca acggtacggt gtcggacgag 60

caaatccgcg aacggctgaa cgacagccgc attcaggacg agagccgtcc cgaagccgcg 120

ccgcccgccg ccgcgcccga aaaaccgtcc gccgcccccg ccgctgatga gggcaaaacg 180

ctggaattga gcaaagaaca gttgttggaa caccccgatt tgctggtgcg ggcgctgatg 240

gcggcgctgc tgcaaaacaa tcccgaacat gtggcgatgc tgtatccgat ttaccgccgc 300

ctgcccgaca atgcgcgcga gcaggtgctg gaagattggg gcgcggcggt gtcggcacgg 360

catcaggggc gttacggcga agcggtgcgc cgctaccgtg cggtgttgtc ggcgcagccc 420

gatttgctgc tggcgcgttt gcagttggca acggcattgt ttgaagacaa gcagtttgaa 480

gcggcagaag accagttccg ccgtttgcgc agcgaaacgt ctttgcccga ccatctgcac 540

gcgcacatcg accaatattt ggcagcgttg cggcgcggca gcccgtggcg tttcggcggc 600

ggcatgacct accaaagcga caaaaacatc aacaatgccc ccaaaaaccc cgatttgggc 660

aacggcttcc gcagcgaccc gcccgaagcc gccaacggca tcgccctgtc gctgaacgcg 720

ggcaaaaaat ttgtgcgcgg caacgggctg tttggcgaag tgcgcgccga tgccaacggc 780

aaatattatt ggaacaacaa aaaatacaat gatttttccg tgcgtacggc ggcgggggcg 840

ggctatcaga acgcccgcag cagcgtggca ttgctgccgt ttttcgagca cacttggtat 900

gcgggcgcga ccaagcagag caacaagctg caacgctttt cgcgcagcgc gggcatcacc 960

ttggaagcat cgcaccgctt cagccccaaa tggcagagca attttgtggt cgaatacggg 1020

cgtcagcgtt accgcacccg tccgcacctg aacgggcgca gcctgtttgg ttccgccacc 1080

gtgtcctatc tgcccaatgc ccgccaatat tggtttgccg gcatcgacca caaccgcagc 1140

cgcgcccgcg accttgacga ttccagcaac cgcaccggcg tgcgcgtggg ctgggggcag 1200

gaatggggtc agggcttctc cagccgcttg accttgagcc acgcccgcaa aaaccacttg 1260

ggcatcaact ttttcggcag ccgccagcaa aaccgcgaat ggggcgtaaa cacttccctg 1320

tggcaccgca aattgcactg gaaaggcgtt accccgcgtt tgacgtggca ctaccaccgc 1380

cagcgcagca atcaggtgtt ttacagctac agcaaacacc gtgtctttgt cgaactgggc 1440

aaacagtttt aa 1452

<210> 142

<211> 484

<212> PRT

<213> C. kuhniae SLAM 1

<400> 142

Met Val Gly Val Leu Leu Leu Leu Ser Ala Gln Val Leu Ala Asn Gly

1 5 10 15

Thr Val Ser Asp Glu Gln Ile Arg Glu Arg Leu Asn Asp Ser Arg Ile
20 25 30
Gln Asp Glu Ser Arg Pro Glu Ala Ala Pro Pro Ala Ala Ala Pro Glu
35 40 45
Lys Pro Ser Ala Ala Pro Ala Ala Asp Glu Gly Lys Thr Leu Glu Leu
50 55 60
Ser Lys Glu Gln Leu Leu Glu His Pro Asp Leu Leu Val Arg Ala Leu
65 70 75 80

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

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

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

Ala Asp Ala Asn Gly Lys Tyr Tyr Trp Asn Asn Lys Lys Tyr Asn Asp
260 265 270

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

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

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

Asn Gln Val Phe Tyr Ser Tyr Ser Lys His Arg Val Phe Val Glu Leu
465 470 475 480
Gly Lys Gln Phe

<210> 143

<211> 1404

<212> DNA

<213> C. kuhniae SLAM 2

<400> 143

atgttgctgc tgcccgttgc cgcttgggca gaacacagcc cgacaccccc cgcccgtccc 60

gaacctttgc ccgaccccgc gcctgaaatc cgtgccgaac cgcccgcaac ggcaaccccg 120

cccgcaccgc cccaagccca caccataaag ctttccgcag acgaattggc acggcagccc 180

cgtttgctgc accgcgccct caccgccgcc gtcttgcgcc aacaccccga caacatcaaa 240

ctgctgctgc ccctgtatct gcgtttgccc gaagcccaac gcggcgacaa agtgctgatt 300

gaattggcac aagcggcgtt ggcagaacag gcgcaacatc ccggccgcgc cgccgcccac 360

taccgcaatg cactcgcaca cgaacccgat atgcctgtgg tgcgcctgaa tttggctgcc 420

gcactcaccc gcgaccacca aaaccgcgat gccgatgccc tgcttgccga catcgccgcc 480

gaccccgccc tgcccgaacg caccgccgca tcggtggcaa acgcccgcgc cgccatcgcc 540

gaacgccgcc gttggcacat tcacgcgggc ggacactacg tccgcgatgc caacatcaac 600

aacacaccca aacaacgggt catcaaacgc ggaagcggca ccatcgaatt gcccaagccc 660

gaagccgtgc aaggcttcgc ctaccgcgcc gaagccgaaa aagactggat gctgcccaaa 720

aaccaccgca tccgcaccgc cctatcgctc aacggcagag actattggga acactccaaa 780

tacgatgaac tgaacgtccg cgcccaagcc ggccccgcct accgcagcgc ccgcagccaa 840

agcgccctga tgccctatta cgaacggcgt tggtacagtg gcagccgcta cgccgccgaa 900

aaagggctgc gcatcgaaca cagccgccac ttgggcaaac gcgcccactt gtcctttgcg 960

ggcgaagccg cacgcctgcg ccacgaccgc cgccgctttc tggacggcgc atcgttcaac 1020

gcttcggcag atttgacgtg ggttgttacc ccgcgcagcc gcttgggcat cggcaccgat 1080

tttgcccgca aacgcgccca agaccccagc gacgcctacc gccgccgcaa ccttcgcgcc 1140

acttgggggc aaacatgggg caaagggctg aacacctccg tacacgctgc cgccgccctg 1200

cgccgctacg atgccgccga ctttttcaac atcacccgcc gcgacaccga atacagcctt 1260

tccttcagcg tgtggcacaa caacatcaaa ttttggggca tcaccccgcg cttggtgggc 1320

gtgtaccaaa aaaaccgcag caaccatttc atgtacgact accaaaaagc ctacggtttc 1380

atacgcttgg caaaatcgat ttaa 1404

<210> 144

<211> 476

<212> PRT

<213> C. kuhniae SLAM 2

<400> 144

Met Ala Met Lys Thr Thr Pro Cys Leu Met Leu Leu Leu Pro Val Ala
1 5 10 15
Ala Trp Ala Glu His Ser Pro Thr Pro Pro Ala Arg Pro Glu Pro Leu
20 25 30
Pro Asp Pro Ala Pro Glu Ile Arg Ala Glu Pro Pro Ala Thr Ala Thr
35 40 45
Pro Pro Ala Pro Pro Gln Ala His Thr Ile Lys Leu Ser Ala Asp Glu
50 55 60

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

His Tyr Arg Asn Ala Leu Ala His Glu Pro Asp Met Pro Val Val Arg
130 135 140
Leu Asn Leu Ala Ala Ala Leu Thr Arg Asp His Gln Asn Arg Asp Ala
145 150 155 160
Asp Ala Leu Leu Ala Asp Ile Ala Ala Asp Pro Ala Leu Pro Glu Arg
165 170 175
Thr Ala Ala Ser Val Ala Asn Ala Arg Ala Ala Ile Ala Glu Arg Arg
180 185 190

Arg Trp His Ile His Ala Gly Gly His Tyr Val Arg Asp Ala Asn Ile
195 200 205
Asn Asn Thr Pro Lys Gln Arg Val Ile Lys Arg Gly Ser Gly Thr Ile
210 215 220
Glu Leu Pro Lys Pro Glu Ala Val Gln Gly Phe Ala Tyr Arg Ala Glu

225 230 235 240

Ala Glu Lys Asp Trp Met Leu Pro Lys Asn His Arg Ile Arg Thr Ala

245 250 255

Leu Ser Leu Asn Gly Arg Asp Tyr Trp Glu His Ser Lys Tyr Asp Glu

260 265 270

Leu Asn Val Arg Ala Gln Ala Gly Pro Ala Tyr Arg Ser Ala Arg Ser

275 280 285

Gln Ser Ala Leu Met Pro Tyr Tyr Glu Arg Arg Trp Tyr Ser Gly Ser

290 295 300

Arg Tyr Ala Ala Glu Lys Gly Leu Arg Ile Glu His Ser Arg His Leu

305 310 315 320

Gly Lys Arg Ala His Leu Ser Phe Ala Gly Glu Ala Ala Arg Leu Arg

325 330 335

His Asp Arg Arg Arg Phe Leu Asp Gly Ala Ser Phe Asn Ala Ser Ala

340 345 350

Asp Leu Thr Trp Val Val Thr Pro Arg Ser Arg Leu Gly Ile Gly Thr

355 360 365

Asp Phe Ala Arg Lys Arg Ala Gln Asp Pro Ser Asp Ala Tyr Arg Arg

370 375 380

Arg Asn Leu Arg Ala Thr Trp Gly Gln Thr Trp Gly Lys Gly Leu Asn

385 390 395 400

Thr Ser Val His Ala Ala Ala Ala Leu Arg Arg Tyr Asp Ala Ala Asp

405 410 415

Phe Phe Asn Ile Thr Arg Arg Asp Thr Glu Tyr Ser Leu Ser Phe Ser

420 425 430

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

435 440 445

Gly Val Tyr Gln Lys Asn Arg Ser Asn His Phe Met Tyr Asp Tyr Gln

450 455 460

Lys Ala Tyr Gly Phe Ile Arg Leu Ala Lys Ser Ile

465 470 475

<210> 145

<211> 1404

<212> DNA

<213> C. kuhniae SLAM 2

<400> 145

atgccccatc tgatgttgag aaccgcttgg caaaccatcg tatttttcgg ctgctgtgcc 60

gccgccgccg cttcaccgcc gccgcaaggc gtgtgggacg atgcggcact gatgcaacaa 120

cctgcgctgt tggaaaacct gctgtaccgt gcattggacg gcggcgatgc ccgactgctg 180

gcatcgcttg ccgactccta ccgccgcacc gcttcgcccg accccgtctt gctgctgcgg 240

gcagatgccg tgcaactgcg cctgaacaaa cgtttggacg aagccgaaca ggcataccgc 300

cgtttgcccg ccgcttatcc cgatgccgtg cgcgaccgtt tggacttggc ggcggtgctg 360

tttgaaaacg gcaaaatccg cgaagcggac gccgaatttg ccgccgtatc ggcacaaagc 420

ggcttgcccg ccgccgtgcg cgacaacatc aacgtgttcc gccgcgccat cgaccgccaa 480

aaacaatggc gttttgccgc gacattccgc cccgtgtacg accacaacgt caatcaagcc 540

ccgccgccgc actgcatcaa agatgcgtac tgcacccgca cccgcgccca acgcgcttac 600

ggcgccgcct atgcgctggg cgcggaaaaa cgcctgcccc tgcgcggcaa acacggcgtg 660

ctgctgcggc tgcatcaggg cgggacgttt tatttcggac acaaggacca caacgaagcc 720

gccgcccgtg ccgatttggg ctggcaatac cgcgatgcgc ggcgcgaatg ggcatggctg 780

ccgttttacc aagcacattt ggcgggcaac gcgtcttttg atgcgccgcg cccgcagcgt 840

accctgccct atgcctaccg ccacgatgcg ggcatggcag tgcattggca cgaacggctg 900

acaccaagca gcagcgcgcg cctgacggtg gaacgccgtt tcagccgtta ccgcgaagcg 960

gcgcacgccc gccgtctgaa cggcacgcaa gatgcggcaa cgctggtgtt gggcaaacac 1020

ttcggcacgc ataccgccgt gttcggcagc taccgcgccg tgcgcttcca accggcgcgg 1080

gaacgcatcg gcacggcgca aaacaatgcg gcatttgtgt ttcacggcat cggtgcgggc 1140

tggacgcaat cttggcgcaa cggcttgcac acgcagttgt cgctggatta cggtgtgcgg 1200

cgttatcgcg gcattgccgc attcgacacg cagccgcaac gcaaccgcga atacgctttc 1260

ggcgcgggca tcgcccaccg caagctgcaa tggcggggct ggcaaccgat gctgcactac 1320

cgctacagcc gcacccgcag cccgcagcct tgggcagaac gccgccgcca tgatgcgggc 1380

atcggcgtgg cggcggattt ttag 1404

<210> 146

<211> 467

<212> PRT

<213> C. kuhniae SLAM 3

<400> 146

Met Pro His Leu Met Leu Arg Thr Ala Trp Gln Thr Ile Val Phe Phe
1 5 10 15

Gly Cys Cys Ala Ala Ala Ala Ala Ser Pro Pro Pro Gln Gly Val Trp
20 25 30

Asp Asp Ala Ala Leu Met Gln Gln Pro Ala Leu Leu Glu Asn Leu Leu
35 40 45

Tyr Arg Ala Leu Asp Gly Gly Asp Ala Arg Leu Leu Ala Ser Leu Ala

50 55 60

Asp Ser Tyr Arg Arg Thr Ala Ser Pro Asp Pro Val Leu Leu Leu Arg
65 70 75 80

Ala Asp Ala Val Gln Leu Arg Leu Asn Lys Arg Leu Asp Glu Ala Glu
85 90 95

Gln Ala Tyr Arg Arg Leu Pro Ala Ala Tyr Pro Asp Ala Val Arg Asp
100 105 110

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

115 120 125

Ala Asp Ala Glu Phe Ala Ala Val Ser Ala Gln Ser Gly Leu Pro Ala
130 135 140

Ala Val Arg Asp Asn Ile Asn Val Phe Arg Arg Ala Ile Asp Arg Gln
145 150 155 160

Lys Gln Trp Arg Phe Ala Ala Thr Phe Arg Pro Val Tyr Asp His Asn
165 170 175

Val Asn Gln Ala Pro Pro Pro His Cys Ile Lys Asp Ala Tyr Cys Thr

180 185 190

Arg Thr Arg Ala Gln Arg Ala Tyr Gly Ala Ala Tyr Ala Leu Gly Ala
195 200 205

Glu Lys Arg Leu Pro Leu Arg Gly Lys His Gly Val Leu Leu Arg Leu
210 215 220

His Gln Gly Gly Thr Phe Tyr Phe Gly His Lys Asp His Asn Glu Ala

225 230 235 240

Ala Ala Arg Ala Asp Leu Gly Trp Gln Tyr Arg Asp Ala Arg Arg Glu

245 250 255

Trp Ala Trp Leu Pro Phe Tyr Gln Ala His Leu Ala Gly Asn Ala Ser

260 265 270

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

275 280 285

Asp Ala Gly Met Ala Val His Trp His Glu Arg Leu Thr Pro Ser Ser

290 295 300

Ser Ala Arg Leu Thr Val Glu Arg Arg Phe Ser Arg Tyr Arg Glu Ala

305 310 315 320

Ala His Ala Arg Arg Leu Asn Gly Thr Gln Asp Ala Ala Thr Leu Val

325 330 335

Leu Gly Lys His Phe Gly Thr His Thr Ala Val Phe Gly Ser Tyr Arg

340 345 350

Ala Val Arg Phe Gln Pro Ala Arg Glu Arg Ile Gly Thr Ala Gln Asn

355 360 365

Asn Ala Ala Phe Val Phe His Gly Ile Gly Ala Gly Trp Thr Gln Ser

370 375 380

Trp Arg Asn Gly Leu His Thr Gln Leu Ser Leu Asp Tyr Gly Val Arg

385 390 395 400

Arg Tyr Arg Gly Ile Ala Ala Phe Asp Thr Gln Pro Gln Arg Asn Arg

405 410 415

Glu Tyr Ala Phe Gly Ala Gly Ile Ala His Arg Lys Leu Gln Trp Arg

420 425 430

Gly Trp Gln Pro Met Leu His Tyr Arg Tyr Ser Arg Thr Arg Ser Pro

435 440 445

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

450 455 460

Ala Asp Phe

465

<210> 147

<211> 1434

<212> DNA

<213> C. kuhniae SLAM 4

<400> 147

atgataaaaa acattgttcg gacaagcatg gcagcatggc tgctggcatg ggcatctgta 60

ttgcccgccg ccgacaacac caccctgccg ggcaaaccgt tgggcaaaac cgcacaagcg 120

ccgtccatgc tttccgaaag cgaacagcag caattggaac gcgcactggt ggtatcggta 180

aacccctacg acattgcccg cgccaatcaa aatgccgtgc gctttcttgc caacgaatac 240

cgcacccgcg tgtctgccga caagcgcgat gattcgctgc tggattgggc agacattatt 300

ctaaacatcg gcagcgactg gcagcgcacc gtgcagcaat accgcaaatt gctggacaaa 360

tttccgcagc agtccctatt gcgttttcaa ttggcacagg cattgttcca caatggcgag 420

cctgatgcgg cgcagcgcga atttgaaaaa ttccgtgcca cgccgaacct cacctaaac 480

catgaaaaag aagccgaccg ttggattatg caaatccagc agcgtcaaaa atggcagttt 540

gatttgcagt ttcagttgct caacaacagc aatgtgaatc aggcgccccg ccataccgtg 600

tattaccgtt tgcccggcgg cgcaacgttt tccaatgccg aaaccgcaca gcgcggctac 660

ggctaccgtc tcgggctgaa cgcgcaaaaa cgttggcatc tgcctttgcg ttatcatgct 720

ttgcgcttga atacgggctt ggatttcgac cattatttga atctgaaaaa atacagccgc 780

atcgatacca atgtgggttt gggctggctc tacgaaacgc cgcgccatca ggcggaagtc 840

cagccgtttt ggcgcaaggc gtggaatgcg cggggcgaag gaaggcgcaa agaaggacgg 900

atgttgccct attcagacga atacggtgtt cgttttcggg tgtggcattg gctcaatacc 960

cgttttcaat acgatttgat gtatcagcct tcttatgtca aatacgataa tcccattgtg 1020

gcgcgaactt ccgatgcttc acgccatttt gtccatgcat cgctgagtta tcagcccaac 1080

agcaagcaaa attggcaatt gggcgcacat tggagcttgc tcaatgccaa agacaaaacc 1140

aatgccaata aaactgtggg ggtgaatttg ggctggcgtc aggagtggcc gaaaagtttc 1200

tacaccgatt taacagtcgg ggcatctcgg gtacgcaatc aggcgcctta ttggtttggc 1260

ttgcggcgca ccaatcacat ttattcggta aacgcgcaag tattcaatcc gacttggcag 1320

tttaaaggct ttatgccgcg cttggtggtg aattatcaga aaaacaaaag caatctgacc 1380

acccagtcgt atgatacgcg tgatgcttat atttttattc agaaaacttt ttaa 1434

<210> 148

<211> 477

<212> PRT

<213> C. kuhniae SLAM 4

<400> 148

Met Ile Lys Asn Ile Val Arg Thr Ser Met Ala Ala Trp Leu Leu Ala
1 5 10 15

Trp Ala Ser Val Leu Pro Ala Ala Asp Asn Thr Thr Leu Pro Gly Lys
20 25 30

Pro Leu Gly Lys Thr Ala Gln Ala Pro Ser Met Leu Ser Glu Ser Glu
35 40 45

Gln Gln Gln Leu Glu Arg Ala Leu Val Val Ser Val Asn Pro Tyr Asp
50 55 60

Ile Ala Arg Ala Asn Gln Asn Ala Val Arg Phe Leu Ala Asn Glu Tyr
65 70 75 80

Arg Thr Arg Val Ser Ala Asp Lys Arg Asp Asp Ser Leu Leu Asp Trp
85 90 95

Ala Asp Ile Ile Leu Asn Ile Gly Ser Asp Trp Gln Arg Thr Val Gln
100 105 110

Gln Tyr Arg Lys Leu Leu Asp Lys Phe Pro Gln Gln Ser Leu Leu Arg
115 120 125

Phe Gln Leu Ala Gln Ala Leu Phe His Asn Gly Glu Pro Asp Ala Ala
130 135 140

Gln Arg Glu Phe Glu Lys Phe Arg Ala Thr Pro Asn Leu Thr Leu Asn
145 150 155 160

His Glu Lys Glu Ala Asp Arg Trp Ile Met Gln Ile Gln Gln Arg Gln
165 170 175

Lys Trp Gln Phe Asp Leu Gln Phe Gln Leu Leu Asn Asn Ser Asn Val
180 185 190

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

Thr Phe Ser Asn Ala Glu Thr Ala Gln Arg Gly Tyr Gly Tyr Arg Leu
210 215 220

Gly Leu Asn Ala Gln Lys Arg Trp His Leu Pro Leu Arg Tyr His Ala

225 230 235 240

Leu Arg Leu Asn Thr Gly Leu Asp Phe Asp His Tyr Leu Asn Leu Lys

245 250 255

Lys Tyr Ser Arg Ile Asp Thr Asn Val Gly Leu Gly Trp Leu Tyr Glu

260 265 270

Thr Pro Arg His Gln Ala Glu Val Gln Pro Phe Trp Arg Lys Ala Trp

275 280 285

Asn Ala Arg Gly Glu Gly Arg Arg Lys Glu Gly Arg Met Leu Pro Tyr

290 295 300

Ser Asp Glu Tyr Gly Val Arg Phe Arg Val Trp His Trp Leu Asn Thr

305 310 315 320

Arg Phe Gln Tyr Asp Leu Met Tyr Gln Pro Ser Tyr Val Lys Tyr Asp

325 330 335

Asn Pro Ile Val Ala Arg Thr Ser Asp Ala Ser Arg His Phe Val His

340 345 350

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

355 360 365

Ala His Trp Ser Leu Leu Asn Ala Lys Asp Lys Thr Asn Ala Asn Lys

370 375 380

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

385 390 395 400

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

405 410 415

Tyr Trp Phe Gly Leu Arg Arg Thr Asn His Ile Tyr Ser Val Asn Ala

420 425 430

Gln Val Phe Asn Pro Thr Trp Gln Phe Lys Gly Phe Met Pro Arg Leu

435 440 445

Val Val Asn Tyr Gln Lys Asn Lys Ser Asn Leu Thr Thr Gln Ser Tyr

450 455 460

Asp Thr Arg Asp Ala Tyr Ile Phe Ile Gln Lys Thr Phe

465 470 475

<210> 149

<211> 1446

<212> DNA

<213> C. steedae SLAM 1

<400> 149

atggcgttgt gctgtgctgt gtggctgttg cccttggcag cggctgccga tgcgcccgaa 60

gcggtacaaa aacagctcaa cgaccgccgt gtgcaggacg aacaccgtcc agaggttgcg 120

cctgtggtga tgccgaatgc caatacgcct gcggcggcgg caggcgatac cactttggaa 180

atcagccccg atgatctgtt aaaacgccct gatttgttgg tgcgggcgat gatggcggcg 240

ttgttgcaca accgtggcga acacattgat attttgctgc cgatttaccg ccgtttgccc 300

gattcggtgc gtgaaaccgt tttggaacat tgggcggcgg cggtttcggc gcgttataac 360

gggcagtacc gtcaggcggt gcgccactac cgcgcagtat tgtcggagca gcccgaattg 420

ctgatggtgc gtttgcaatt ggcagcggca ttgtttgaag acaagcagtt tgaagcagca 480

gaagaccaat tccgccgttt acgcagcgaa agtgctttgc ccgatgccct gcacgcgcaa 540

attgaccaat atttagatgc catccgccgt ggcagtccgt ggcagtttgg tggtggcatt 600

acctatttaa acgacaaaaa catcaacaac gccccccaaaa atcccgattt gggcaacggc 660

ttccgcaccg acccacccga atcaggcaac ggcattgccc tgtctgccaa tgctgctaaa 720

aaatggattg gcggtaaggg cgcgtttggc gaagtgcgtt ttgacaccaa tggcaaatat 780

ttttggaata acaaaaaata caatgaactg actgcgcgtg ccagcgtggg tggcggtttt 840

cagaatgccc gcagcagcat tgccctgttg ccgtttttttg agcatacttg gtatgcgggc 900

ggcaacaaaa aaaatgaaaa actgaaacgt ttttcacaca gcagcggcgt gggtgtggaa 960

gcctcgcacc gcttgtcccc gcactggcag ggcagtgtgg cagccgaata cagccgtcag 1020

cactaccgca accgcccgca tttaaacgga cgcaccctgt ttgcctccac caccatgtct 1080

tacctaccag gggcgcgaca atactggttt ggcgggctgg accacacccg tgtgcgtacc 1140

cgcgaccgtg acgattccta caaccgcagc ggcattcgcg caggttgggg tcaggaatgg 1200

ggcaaaggct tgtccacccg cattaccgtt aattacgcgc acaaacgtta tctcgccccc 1260

aatttttttca acagcgcaca aaaaaaccgc gaatacggcg tacaaaccgc cttgtggcac 1320

cgcaaaattc actggttggg cattaccccg cgcctgattt ggagccacca gcgcaaccgc 1380

agcaaccaag ccttgtacaa ctaccaaaaa aaccgcctgt ttattgaagc agcaaaacag 1440

ttttga 1446

<210> 150

<211> 481

<212> PRT

<213> C. steedae SLAM 1

<400> 150

Met Ala Leu Cys Cys Ala Val Trp Leu Leu Pro Leu Ala Ala Ala Ala
1 5 10 15
Asp Ala Pro Glu Ala Val Gln Lys Gln Leu Asn Asp Arg Arg Val Gln
20 25 30
Asp Glu His Arg Pro Glu Val Ala Pro Val Val Met Pro Asn Ala Asn

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

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

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

Pro Pro Glu Ser Gly Asn Gly Ile Ala Leu Ser Ala Asn Ala Ala Lys

225 230 235 240

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

245 250 255

Asn Gly Lys Tyr Phe Trp Asn Asn Lys Lys Tyr Asn Glu Leu Thr Ala

260 265 270

Arg Ala Ser Val Gly Gly Gly Phe Gln Asn Ala Arg Ser Ser Ile Ala

275 280 285

Leu Leu Pro Phe Phe Glu His Thr Trp Tyr Ala Gly Gly Asn Lys Lys

290 295 300

Asn Glu Lys Leu Lys Arg Phe Ser His Ser Ser Gly Val Gly Val Glu

305 310 315 320

Ala Ser His Arg Leu Ser Pro His Trp Gln Gly Ser Val Ala Ala Glu

325 330 335

Tyr Ser Arg Gln His Tyr Arg Asn Arg Pro His Leu Asn Gly Arg Thr

340 345 350

Leu Phe Ala Ser Thr Thr Met Ser Tyr Leu Pro Gly Ala Arg Gln Tyr

355 360 365

Trp Phe Gly Gly Leu Asp His Thr Arg Val Arg Thr Arg Asp Arg Asp

370 375 380

Asp Ser Tyr Asn Arg Ser Gly Ile Arg Ala Gly Trp Gly Gln Glu Trp

385 390 395 400

Gly Lys Gly Leu Ser Thr Arg Ile Thr Val Asn Tyr Ala His Lys Arg

405 410 415

Tyr Leu Ala Pro Asn Phe Phe Asn Ser Ala Gln Lys Asn Arg Glu Tyr

420 425 430

Gly Val Gln Thr Ala Leu Trp His Arg Lys Ile His Trp Leu Gly Ile

435 440 445

Thr Pro Arg Leu Ile Trp Ser His Gln Arg Asn Arg Ser Asn Gln Ala

450 455 460

Leu Tyr Asn Tyr Gln Lys Asn Arg Leu Phe Ile Glu Ala Ala Lys Gln

465 470 475 480

Phe

<210> 151

<211> 1437

<212> DNA

<213> C. steedae SLAM 2

<400> 151

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ccctatccgc ttaacccacc cagcgaaccc gaaccgcgtt ttgacgttgc ccccgaaccg 120

cgccgcgaca gcgagcctat tccccccgca acacctgcac ccaccgagcc aaaaaaactg 180

aaagtgtcgc ccgaagagct gctgcaacag cccgaattgc tgcatcgcgc ccttacttcc 240

gccgttttgc tgaaaaatat tgaaggcatc aaagttctgc tgccgctgta tcagcaattg 300

cccgaagccc aacgccgcga caccatttta attgagctgg cgcaagccgc gcttgccgaa 360

gccgaacagc gtcccgaccg cgctgttcgc cattaccgcg aagcactcaa acacgaagcc 420

gatatgccct cggtgcgcct gaatctggcg ggtgcattgg tgcgcgacca gcaaaaccgc 480

gaagcccaag ccctgttgga cgacatcgct caagacccac aactgcccga acccgccgcc 540

gctgcggtaa acgcctaccg tcgggtgctg aaacagcgca gccgttggca attgagcgcg 600

ggcgcacact atatccgcga ccccaatatc aacaacaccc caaaacaacg cattattaaa 660

cgaggcagag gcacgtttga actgcccccg cccgaaaccg cgcacggttt gtcctaccgc 720

gccagtgctg aaaaagattg gatgttgccc caatactacc gcatccgcac aggcatcgat 780

ttaaacggca aagactattg ggaccattcc aaatacgacg atttaagcgt ccgcgcccaa 840

gcaggtgtgg cacgacagag cgcccgcagc gaaagtgcct tactgcccta ttacgaacgg 900

cgttggtaca gcggcagccg ctattctgcc gaaaaaggca ttcgtgccga acacagccgt 960

cccgtcagcc actcactgcg tgtgtcgctg gcaggcgaag ccgcccgtgt gcgccacgac 1020

cgccgccgtt ttttagacgg cgccagcttc aacgcttccg ccaccgtatt gtggacaccc 1080

aacgcccgca gttattttac cctcggcacc gatttttccc gcaaacgcgc ccttgacccg 1140

tctgatgcct atcaccgccg cggtatgcgc ggcagttggg gacaggcttg gggcaaaggt 1200

ttccaaaccg tgctgcacgc aggcatcggc agacgcagct acgatgcggc ggatttttc 1260

cgcatcaccc gccgcgacac cgaatacaac ctttccttaa gcgtgtggaa caacaaactc 1320

aaactttggg gtgttacccc gcgcttggtg ggcgtgtatc aaaaaacccg cagcaaccat 1380

tttgtttaca actaccgcaa agcctatgcc tttatccaat tgagcaaatc catttaa 1437

<210> 152

<211> 479

<212> PRT

<213> C. steedae SLAM 2

<400> 152

Met Met Lys Lys Ile Pro Tyr Ile Cys Leu Leu Leu Pro Ala Ala Ala
1 5 10 15

Trp Ala Asp Gly Asn Pro Tyr Pro Leu Asn Pro Pro Ser Glu Pro Glu
20 25 30

Pro Arg Phe Asp Val Ala Pro Glu Pro Arg Arg Asp Ser Glu Pro Ile
35 40 45

Pro Pro Ala Thr Pro Ala Pro Thr Glu Pro Lys Lys Leu Lys Val Ser
50 55 60

Pro Glu Glu Leu Leu Gln Gln Pro Glu Leu Leu His Arg Ala Leu Thr
65 70 75 80

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

Leu Tyr Gln Gln Leu Pro Glu Ala Gln Arg Arg Asp Thr Ile Leu Ile
100 105 110

Glu Leu Ala Gln Ala Ala Leu Ala Glu Ala Glu Gln Arg Pro Asp Arg
115 120 125

Ala Val Arg His Tyr Arg Glu Ala Leu Lys His Glu Ala Asp Met Pro
130 135 140

Ser Val Arg Leu Asn Leu Ala Gly Ala Leu Val Arg Asp Gln Gln Asn
145 150 155 160

Arg Glu Ala Gln Ala Leu Leu Asp Asp Ile Ala Gln Asp Pro Gln Leu
165 170 175

Pro Glu Pro Ala Ala Ala Ala Val Asn Ala Tyr Arg Arg Val Leu Lys
180 185 190

Gln Arg Ser Arg Trp Gln Leu Ser Ala Gly Ala His Tyr Ile Arg Asp
195 200 205

Pro Asn Ile Asn Asn Thr Pro Lys Gln Arg Ile Ile Lys Arg Gly Arg
210 215 220

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

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

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

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

450 455 460

Asn Tyr Arg Lys Ala Tyr Ala Phe Ile Gln Leu Ser Lys Ser Ile

465 470 475

<210> 153

<211> 1392

<212> DNA

<213> C. steedae SLAM 3

<400> 153

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caaatcccgt ccgacactgt ttgggacaat cagcgtttgc agcagcaacc cgaattattg 120

gaacggctgc ttattgatgc catggacggc agcgatgcca agctgttggc atctttaaac 180

gaagcctatg cccaactgcc acaagccgat gagttgttaa aaatgcgggc gcaagccgta 240

ttgctgcgtt taaatggacg tttggacgaa gccgaagacc tgtatcgccg tttgccgcac 300

gaccactcca accatttgcg cgaccgtttg gacgaagccg ctgttttatt tgaaaacggc 360

aaaacccgtg aagccgatgc tgcattcgcc gcactcgccg aagaaaccct gcctgccgcc 420

gttcacgcca atatcgcccg tttccgtcac gccatcgccc gccgccaaca atggcagtgg 480

ggttttgcgc tgcaacccgt ttataacgac aacatcaaca acgccccgcc gccgcattgt 540

ttaaacggcg tgtactgcac ccgcaccacc gcgcaaagcg catacggtgg cagttacgcc 600

atacagcttg ccaaaacaca gcccctgcat ggcaaacaca atctggcagt acagcttcaa 660

catgatggca cattttattt tgggcaaaac ggttacaatg aagcatcggc gcgtgctgct 720

ttgggctggc aataccgcga tgcccgacat gaatggtcgc tgctgccgtt ttaccaaatc 780

cgtttagaag gggcagaatc gtttagtggc aaccgtgcgg cgcgtgcttt gccttacgca 840

caccgacaca ctttgggaac gcgcttggct tgggcatacc gccccgacag atacagcttg 900

ttccgcattc aattggaagc gcaacgccac cgctaccgcg acgctgccta cgcacaacgt 960

caagacggta atcaatggtc gtcagccata tcgtttgcca aacaaatcac gccgcaagct 1020

tcgctgtctg ctgcttaccg ttatgaatta ttccgcccca aacaccagca tatcggcgca 1080

tttgaaaaca atgctgcgtt tcagtttcat ggattatcgg gcgtgtggtc gcaacattgg 1140

caaggcacag gtacagacac gcgcttgtcg gcgcattacg gcatcagaca atatcgcggc 1200

atcgcggcat tcggcacgca ggcacagcgc aaccgcgaat acggcgcggg tattgccgtc 1260

agtcagcggc aactgcaatg gcgcggctgg caacccgttt tgttttacca acacagtcgc 1320

atccgcagca atatgccgtg ggcgcaacgg cgcaagcgtt cgttcggtat cggcttggaa 1380

gcgggatttt ga 1392

<210> 154

<211> 463

<212> PRT

<213> C. steedae SLAM 3

<400> 154

Met Leu Arg Ser Asn Trp Leu His Ile Ile Phe Leu Cys Ala Cys Trp
1 5 10 15

Gln Ala His Ala Gln Ile Pro Ser Asp Thr Val Trp Asp Asn Gln Arg
20 25 30

Leu Gln Gln Gln Pro Glu Leu Leu Glu Arg Leu Leu Ile Asp Ala Met
35 40 45

Asp Gly Ser Asp Ala Lys Leu Leu Ala Ser Leu Asn Glu Ala Tyr Ala
50 55 60

Gln Leu Pro Gln Ala Asp Glu Leu Leu Lys Met Arg Ala Gln Ala Val
65 70 75 80

Leu Leu Arg Leu Asn Gly Arg Leu Asp Glu Ala Glu Asp Leu Tyr Arg
85 90 95

Arg Leu Pro His Asp His Ser Asn His Leu Arg Asp Arg Leu Asp Glu
100 105 110

Ala Ala Val Leu Phe Glu Asn Gly Lys Thr Arg Glu Ala Asp Ala Ala
115 120 125

Phe Ala Ala Leu Ala Glu Glu Thr Leu Pro Ala Ala Val His Ala Asn
130 135 140

Ile Ala Arg Phe Arg His Ala Ile Ala Arg Arg Gln Gln Trp Gln Trp
145 150 155 160

Gly Phe Ala Leu Gln Pro Val Tyr Asn Asp Asn Ile Asn Asn Ala Pro
165 170 175

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

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

195 200 205

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

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

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

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

Gln Arg Arg Lys Arg Ser Phe Gly Ile Gly Leu Glu Ala Gly Phe
450 455 460

<210> 155

<211> 1428

<212> DNA

<213> C. steedae SLAM 4

<400> 155

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accttatccg caaacgaaca acaacaattg gaacaagcat tagctgttgc cattaatcct 180

tacgacatca cccaagccaa ccgcaatgcc gtgcgctccc tcagctatgc ctaccgcacc 240

cgcgttcctg ccgaaaaacg cgatgattcc ctgctggatt gggcagatat cattatggat 300

gcaggagaag actggcaaaa aaccgtacag caataccgca aactgctggc aaaattcccc 360

aaacaggaac tgctgcgctt tcaattggca caagccctgt tgtacaacgg cgaacccgat 420

gccgcacaaa acgaatttga aaaattccgc gccacgcccg atttaaccgt aaactatgaa 480

aaagctgccg accgttggat tatgcaaatc cagcaacggc aaaaatggca gtttggtttt 540

acctttcaat ttctgaacaa cagcaatgtc aatcaggcac cccgccacac cgtttattat 600

cagcttcccg gtggtgctac tttttccaac tccgaaaccg ccaaacgcgg ctacggcttc 660

cgcgtgggct ttaatgcgca aaaacgttgg catttaccgt ggcgacgtaa tgccttgcgc 720

ctcaatacag gcatagattg ggaccactat tttaatgcca agaaatacag ccaaatcaac 780

accaatatcg gtttgggctg gctgtatgaa accccgcgct atcatgccga attccaaccg 840

tttttacgca gcaattggaa tgcgcgcggc gaaggcagac gggaagaagg acacttggca 900

cgttattcag acgaatatgg cgcacgtttc cgcgtttggc gttggttaaa cagccgtttt 960

caatacgatt taatgtacca gccctcttat atcaaataca ataatccctt ggtggcacgt 1020

acatcagacg gcgtacgcca ttttgttcat tcatcgcttt cttatcagca aaacgacaaa 1080

caaagctggc aattgggcat gtattggagc cgtttaaata ccaaagacaa aaccaatgcc 1140

aataaaacgg taggggttaa tttgggttgg cggcaagaat ggcccaagaa tttttatacc 1200

gattttactg tgggtgcttc ccgcacacgc aatcaaaagc cctactggtt tggtttacaa 1260

agaaaaaacc acagctattc ggtaaatgcc caagtattta accccacatg gcagtttaaa 1320

ggatttatgc caagattggt ttttaactat caaaaaacca aaagcaattt aaccacgcaa 1380

tcatacgata cgcgggacgc ttatattttt attcaaaaaa ccttttaa 1428

<210> 156

<211> 475

<212> PRT

<213> C. steedae SLAM 4

<400> 156

Met Lys Arg Ile Ile Leu Ser Leu Ile Gly Thr Phe Ile Leu Cys Thr
1 5 10 15

Thr Ala Phe Ala Glu Asn Thr Thr Val Pro Gly Lys Pro Leu Gly Ser
20 25 30

Ala Val Ser Thr Pro Asp Thr Gln Thr Leu Ser Ala Asn Glu Gln Gln
35 40 45

Gln Leu Glu Gln Ala Leu Ala Val Ala Ile Asn Pro Tyr Asp Ile Thr
50 55 60

Gln Ala Asn Arg Asn Ala Val Arg Ser Leu Ser Tyr Ala Tyr Arg Thr
65 70 75 80

Arg Val Pro Ala Glu Lys Arg Asp Asp Ser Leu Leu Asp Trp Ala Asp
85 90 95

Ile Ile Met Asp Ala Gly Glu Asp Trp Gln Lys Thr Val Gln Gln Tyr
100 105 110

Arg Lys Leu Leu Ala Lys Phe Pro Lys Gln Glu Leu Leu Arg Phe Gln
115 120 125

Leu Ala Gln Ala Leu Leu Tyr Asn Gly Glu Pro Asp Ala Ala Gln Asn
130 135 140

Glu Phe Glu Lys Phe Arg Ala Thr Pro Asp Leu Thr Val Asn Tyr Glu
145 150 155 160

Lys Ala Ala Asp Arg Trp Ile Met Gln Ile Gln Gln Arg Gln Lys Trp
165 170 175

Gln Phe Gly Phe Thr Phe Gln Phe Leu Asn Asn Ser Asn Val Asn Gln
180 185 190

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

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

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

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

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

450 455 460

Arg Asp Ala Tyr Ile Phe Ile Gln Lys Thr Phe

465 470 475

<210> 157

<211> 1425

<212> DNA

<213> C. valvarum SLAM 1

<400> 157

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aatccggtgg taaccacccc cgacctgcac acccccgatg aaaaactgcc tgcttcggcg 120

gaaaaagcgg cggcagatac gcaaaagaac cggcaggtaa aaggaaacgt catggaagtg 180

accgaagagc aactgttggc cgatccacct ctgctcgcca atgcgcttga cagcgccatc 240

atcaacggtg atgccgatgc cgtcgccata ctgctgccca tctaccgcaa actgcccgcc 300

gacaaacagg acaaaatgct gctgcgcttc ggcgaagcga tgcaggcgcg cagcaccggt 360

aatctttcgc tggccattgc ccgttaccgg gaaatgattg ccgaagaccc cagcctgcaa 420

ccggtgcgtc tgcatttggc gatggcgctt atggccgatc atcaggatga agcggcgcgt 480

ggtcagctgg aaaaactgcg ctccgacaaa ctgccggacg acatccgcaa aattgtggac 540

gatgcccttg ccaccctgcg cgagcaacgc agctggacct tcaacgtcgg cggctactac 600

cgctacgaga acaacatcaa cggcgcgcca cgtgaacgtg agcgtcgggg cggtcgcggt 660

acctggacct tcccggcacc gaaaaaagcg cacggcattc accttgatct ctccgccgag 720

cggcggatgc ccactgcaaa cggctggtat gcgcaggtcg aaggcagcgt gaatagcgac 780

tggtactggg acgcccacga ttacgacgac ttccgtttcc gcctcggcat gggcggtggc 840

tggcagaatg cccgctggga cgccagcctc attcccttcg tgcagcgccg tatctacgcc 900

gggcaggggt attcgaccaa cctcggcgcc gatgccaacg tctcctactg gctcaccccg 960

aaatggcgct tgggcacctc cgtccagatt atgcacaaac agcacgaccg ccgcgaatgg 1020

ctggacggca accagtacta cggcggcctg agcactctct acacaccgaa cgcgcgccaa 1080

tactggttcg gtggcgtcaa tgccatgcgc agcaaggcac aggaccgctc ggatgccttc 1140

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ctggttggta cctacgcgcg gcgcaactac gacggactcg acttttttcgg catcaaacgc 1260

aaggataagg aatacggggt ttccctcagc ctttggaacc gtaacctcta cttctgggga 1320

attaccccgc gcctgacctt cagctggaac cgcaccgcca gcaaccactt ctactacgat 1380

gaccacgatc aggatgtgta cctcgaactg agtaaatcgt tctga 1425

<210> 158

<211> 474

<212> PRT

<213> C. valvarum SLAM 1

<400> 158

Met Arg Ile Leu Pro Ala Leu Phe Pro Ala Leu Leu Ala Ser Ser Leu

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Tyr Ala Ala Pro Asn Pro Val Val Thr Thr Pro Asp Leu His Thr Pro

20 25 30

Asp Glu Lys Leu Pro Ala Ser Ala Glu Lys Ala Ala Ala Asp Thr Gln

35 40 45

Lys Asn Arg Gln Val Lys Gly Asn Val Met Glu Val Thr Glu Glu Gln

50 55 60

Leu Leu Ala Asp Pro Pro Leu Leu Ala Asn Ala Leu Asp Ser Ala Ile

65 70 75 80

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

85 90 95

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

100 105 110

Ala Met Gln Ala Arg Ser Thr Gly Asn Leu Ser Leu Ala Ile Ala Arg

115 120 125

Tyr Arg Glu Met Ile Ala Glu Asp Pro Ser Leu Gln Pro Val Arg Leu

130 135 140

His Leu Ala Met Ala Leu Met Ala Asp His Gln Asp Glu Ala Ala Arg

145 150 155 160

Gly Gln Leu Glu Lys Leu Arg Ser Asp Lys Leu Pro Asp Asp Ile Arg

165 170 175

Lys Ile Val Asp Asp Ala Leu Ala Thr Leu Arg Glu Gln Arg Ser Trp

180 185 190

Thr Phe Asn Val Gly Gly Tyr Tyr Arg Tyr Glu Asn Asn Ile Asn Gly

195 200 205

Ala Pro Arg Glu Arg Glu Arg Arg Gly Gly Arg Gly Thr Trp Thr Phe

210 215 220

Pro Ala Pro Lys Lys Ala His Gly Ile His Leu Asp Leu Ser Ala Glu

225 230 235 240

Arg Arg Met Pro Thr Ala Asn Gly Trp Tyr Ala Gln Val Glu Gly Ser

245 250 255

Val Asn Ser Asp Trp Tyr Trp Asp Ala His Asp Tyr Asp Asp Phe Arg

260 265 270

Phe Arg Leu Gly Met Gly Gly Gly Trp Gln Asn Ala Arg Trp Asp Ala

275 280 285

Ser Leu Ile Pro Phe Val Gln Arg Arg Ile Tyr Ala Gly Gln Gly Tyr

290 295 300

Ser Thr Asn Leu Gly Ala Asp Ala Asn Val Ser Tyr Trp Leu Thr Pro

305 310 315 320

Lys Trp Arg Leu Gly Thr Ser Val Gln Ile Met His Lys Gln His Asp

325 330 335

Arg Arg Glu Trp Leu Asp Gly Asn Gln Tyr Tyr Gly Gly Leu Ser Thr

340 345 350

Leu Tyr Thr Pro Asn Ala Arg Gln Tyr Trp Phe Gly Gly Val Asn Ala

355 360 365

Met Arg Ser Lys Ala Gln Asp Arg Ser Asp Ala Phe Lys Arg Phe Gly

370 375 380

Val Asn Leu Gly Trp Gly Gln Glu Trp Gly Trp Gly Met Ser Ser Arg

385 390 395 400

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

405 410 415

Gly Ile Lys Arg Lys Asp Lys Glu Tyr Gly Val Ser Leu Ser Leu Trp

420 425 430

Asn Arg Asn Leu Tyr Phe Trp Gly Ile Thr Pro Arg Leu Thr Phe Ser

435 440 445

Trp Asn Arg Thr Ala Ser Asn His Phe Tyr Tyr Asp Asp His Asp Gln

450 455 460

Asp Val Tyr Leu Glu Leu Ser Lys Ser Phe

465 470

<210> 159

<211> 1572

<212> DNA

<213> C. valvarum SLAM 2

<400> 159

atgccgcgct ttcatcgcca acacaggaat ctcaagatga ccacaaaaac cactataacc 60

ctgcaactca cactcgcttc cggcatcctt ttcgccgcca tgcctgctgt tgcccaaaac 120

gcgccccccgc catcacgcgc cctcccggta gatattgacc ggggcaatga gcgcctgtcc 180

gaggatgatg tcggcaagaa tgtacggctg ccacaagtgc ctgctgtcaa acccgccgcc 240

cccaccaccc tgccgagtga tgcccaggct gccaaagaag atgtcgttta cactcccgaa 300

gaactcgcca acaaccccga acaactggaa aaactcctgg tcgaggctat ccgtcttaac 360

gaagtcgaag gcctgaaggt actactgccg ctgtacgcta aagtagatgc cagccgccgt 420

gatgattccc tcattgactg gggtaatgcc attatcgcca tgaacgaggg ccgcaccgcc 480

gaagccgtta ccctttaccg caaacttatc gccaacctgc cggataaccg catgttgcgc 540

ttccaaacgg cccttgcgct ctaccgcaac aacgaactcc tcgccgccaa agagcaactg 600

caaaaactgc gcagtggcga tgtttccgaa gccgaccgca aaaccctgga tgaattcatc 660

gccgccattg accgccgtga ttcctggtcg ttcagcggca gcctgagcta cattcacgac 720

aacaacgtca acaacgtcgc cccgaaaggc acccgcttcc gcctcagtaa tggccgttcc 780

ctcgagagca atcgcgatca ggaaaaggcc aacggtatca gctataacct ggatgcagac 840

aaaaaatggt ccattaccga caactactac gcctcattgc acggctcgct gagcggctcc 900

tactacttcc acaaaagaaa ctataacgat gtgaccacac gcgtggcagc cggcggcggc 960

ttccgcaaca acaaaattga cctcgaaatc accccgttcg tgcaaaaacg cctctacgga 1020

cgcggcagca acggcgacaa caaactgcat gcgtattcca acagcgccgg cttgagcgcc 1080

tccaactcct actggataaa ccccaaatgg cgcctgaaca ccaacgccga attcagctat 1140

gacaaatacg tcagaaccta tgactacctg gacggcaagc gcatcagcct gagtaacacc 1200

ctgacgtaca cacccaacca aaaacaatac tggttcgccg ggcttgacct cagccacaaa 1260

ggcgcacgca gcgccagcga tggctatgac cgcttcaaca cccgtcttgg ctggggacag 1320

gaatggggca aaggcatctc cacccgcctg atgggcagct acggcaagcg ctacgccaaa 1380

ggcgtggatt tcttcaacat tgaccgcgaa gacaaagaat acaacgccaa cctgtccgtc 1440

tggcaccgtg gcatccactt cttcggcatc accccgcgcc tcgtcttctc gtacagcaaa 1500

attgacagca ataaccgctt ctatagctac gacgccagca aaatctatat ggacttcacc 1560

aagaccttct ag 1572

<210> 160

<211> 523

<212> PRT

<213> C. valvarum SLAM 2

<400> 160

Met Pro Arg Phe His Arg Gln His Arg Asn Leu Lys Met Thr Thr Lys
1 5 10 15

Thr Thr Ile Thr Leu Gln Leu Thr Leu Ala Ser Gly Ile Leu Phe Ala
20 25 30

Ala Met Pro Ala Val Ala Gln Asn Ala Pro Pro Pro Ser Arg Ala Leu
35 40 45

Pro Val Asp Ile Asp Arg Gly Asn Glu Arg Leu Ser Glu Asp Asp Val
50 55 60

Gly Lys Asn Val Arg Leu Pro Gln Val Pro Ala Val Lys Pro Ala Ala
65 70 75 80

Pro Thr Thr Leu Pro Ser Asp Ala Gln Ala Ala Lys Glu Asp Val Val
85 90 95

Tyr Thr Pro Glu Glu Leu Ala Asn Asn Pro Glu Gln Leu Glu Lys Leu
100 105 110

Leu Val Glu Ala Ile Arg Leu Asn Glu Val Glu Gly Leu Lys Val Leu
115 120 125

Leu Pro Leu Tyr Ala Lys Val Asp Ala Ser Arg Arg Asp Asp Ser Leu
130 135 140

Ile Asp Trp Gly Asn Ala Ile Ile Ala Met Asn Glu Gly Arg Thr Ala
145 150 155 160

Glu Ala Val Thr Leu Tyr Arg Lys Leu Ile Ala Asn Leu Pro Asp Asn

165 170 175

Arg Met Leu Arg Phe Gln Thr Ala Leu Ala Leu Tyr Arg Asn Asn Glu

180 185 190

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

195 200 205

Ser Glu Ala Asp Arg Lys Thr Leu Asp Glu Phe Ile Ala Ala Ile Asp

210 215 220

Arg Arg Asp Ser Trp Ser Phe Ser Gly Ser Leu Ser Tyr Ile His Asp

225 230 235 240

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

245 250 255

Asn Gly Arg Ser Leu Glu Ser Asn Arg Asp Gln Glu Lys Ala Asn Gly

260 265 270

Ile Ser Tyr Asn Leu Asp Ala Asp Lys Lys Trp Ser Ile Thr Asp Asn

275 280 285

Tyr Tyr Ala Ser Leu His Gly Ser Leu Ser Gly Ser Tyr Tyr Phe His

290 295 300

Lys Arg Asn Tyr Asn Asp Val Thr Thr Arg Val Ala Ala Gly Gly Gly

305 310 315 320

Phe Arg Asn Asn Lys Ile Asp Leu Glu Ile Thr Pro Phe Val Gln Lys

325 330 335

Arg Leu Tyr Gly Arg Gly Ser Asn Gly Asp Asn Lys Leu His Ala Tyr

340 345 350

Ser Asn Ser Ala Gly Leu Ser Ala Ser Asn Ser Tyr Trp Ile Asn Pro

355 360 365

Lys Trp Arg Leu Asn Thr Asn Ala Glu Phe Ser Tyr Asp Lys Tyr Val

370 375 380

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

385 390 395 400

Leu Thr Tyr Thr Pro Asn Gln Lys Gln Tyr Trp Phe Ala Gly Leu Asp

405 410 415

Leu Ser His Lys Gly Ala Arg Ser Ala Ser Asp Gly Tyr Asp Arg Phe

420 425 430

Asn Thr Arg Leu Gly Trp Gly Gln Glu Trp Gly Lys Gly Ile Ser Thr

435 440 445

Arg Leu Met Gly Ser Tyr Gly Lys Arg Tyr Ala Lys Gly Val Asp Phe

450 455 460

Phe Asn Ile Asp Arg Glu Asp Lys Glu Tyr Asn Ala Asn Leu Ser Val

465 470 475 480

Trp His Arg Gly Ile His Phe Phe Gly Ile Thr Pro Arg Leu Val Phe

485 490 495

Ser Tyr Ser Lys Ile Asp Ser Asn Asn Arg Phe Tyr Ser Tyr Asp Ala

500 505 510

Ser Lys Ile Tyr Met Asp Phe Thr Lys Thr Phe

515 520

<210> 161

<211> 1347

<212> DNA

<213> Caulobacter sp. AP07 SLAM 1

<400> 161

ttgagactcg gcggtcgggc ggccttcgcc gccctggccg ccgcgatcgt cctggcgccc 60

ggcccagccc gggcccaatc cgaagaggcg cgggaggccg gcgcgggcgt cgtgacgctc 120

tccggcgacc aggccttcgc gacggcgctg caactgttca tccgggccgg cgattatcgc 180

caggcgctcg acctgatcga cacccgcccc gacctggctg accgggccga tgtcgtgcgc 240

ctgcgggccc agttgatggc gctgaccggt cgcgagcccg aggccctggc ccttctggaa 300

gggcatctga cccgcgacgc ggccgacgcc ctggcccgct tccaggtcgc cgaactgcac 360

ttcgccgccg ggcgcgacgt ctcggccgcc ttggcctatc gcctgtccct ggccggcgcc 420

ctggacccgg gacgggcccg catcgccaat cttcgcctgg agcagatcca gcagcgtcgg 480

cgctggcgct tctgggcggg ggcgtcggtc gcccccgaca gcaacgtcaa cggcgcgacc 540

aacgcctcgc ggatcgagct gttcggtctg ccgttcgagc tggacgacaa ggcccgccgc 600

cgcagcggcg tcacggtctc ggcccagggc ggggtggagc ggcgctttcg gctggacggg 660

cggagggcgg tgcgcgcggc cctggtcgga gcggtgaccg acgctcccgg cggcgacttc 720

gacgacgcct tcctgtcgtt gcgcgccggg cccgaatgga cgctgtcacc ccgcgcccag 780

gtcaccctgc aggcggcggt caacggccgc tggtacggcg gcgcgctgct ggagaccagc 840

cggggcctga gggtcgaggg cgagctgtcg acccgcgaca acatccgctg ggtgggtgcg 900

gcgcgcttcg acctggtcga tgcgcggatc aacgacggtc gcgacggcga actctacggg 960

ctggagctgg cgcggacccg gtatctgggg ccaacctcgc tgtggcgggc cagcggttcg 1020

ctgacggcgc gcgaggctcg gtcgtcgacc gaggcctatg accaggtcca gctggcggcg 1080

gggcgcctgt atcccctgcc gttcaccacc ctggcctatg tcgagcccta tgtgatgcat 1140

cgacggttcg acggcctggc gccggcgttc ggaaagcggc ggatcgacag cgagtatggc 1200

gtggtcaccc ggctttccaa gcgcgactgg acgctgaagg gcgctttccc gtttgtcgcg 1260

ctgtcgatgg cccgcaacga ctcgacgatc gtcctcaaca gcttcacccg gcgtcgggtc 1320

gaggtcggct tgacgcgcga gttctag 1347

<210> 162

<211> 448

<212> PRT

<213> Caulobacter sp. AP07 SLAM 1

<400> 162

Met Arg Leu Gly Gly Arg Ala Ala Phe Ala Ala Leu Ala Ala Ala Ile

1 5 10 15

Val Leu Ala Pro Gly Pro Ala Arg Ala Gln Ser Glu Glu Ala Arg Glu

20 25 30

Ala Gly Ala Gly Val Val Thr Leu Ser Gly Asp Gln Ala Phe Ala Thr

35 40 45

Ala Leu Gln Leu Phe Ile Arg Ala Gly Asp Tyr Arg Gln Ala Leu Asp

50 55 60

Leu Ile Asp Thr Arg Pro Asp Leu Ala Asp Arg Ala Asp Val Val Arg

65 70 75 80

Leu Arg Ala Gln Leu Met Ala Leu Thr Gly Arg Glu Pro Glu Ala Leu

85 90 95

Ala Leu Leu Glu Gly His Leu Thr Arg Asp Ala Ala Asp Ala Leu Ala

100 105 110

Arg Phe Gln Val Ala Glu Leu His Phe Ala Ala Gly Arg Asp Val Ser

115 120 125

Ala Ala Leu Ala Tyr Arg Leu Ser Leu Ala Gly Ala Leu Asp Pro Gly

130 135 140

Arg Ala Arg Ile Ala Asn Leu Arg Leu Glu Gln Ile Gln Gln Arg Arg

145 150 155 160

Arg Trp Arg Phe Trp Ala Gly Ala Ser Val Ala Pro Asp Ser Asn Val

165 170 175

Asn Gly Ala Thr Asn Ala Ser Arg Ile Glu Leu Phe Gly Leu Pro Phe

180 185 190

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

195 200 205

Gln Gly Gly Val Glu Arg Arg Phe Arg Leu Asp Gly Arg Arg Ala Val

210 215 220

Arg Ala Ala Leu Val Gly Ala Val Thr Asp Ala Pro Gly Gly Asp Phe

225 230 235 240

Asp Asp Ala Phe Leu Ser Leu Arg Ala Gly Pro Glu Trp Thr Leu Ser

245 250 255

Pro Arg Ala Gln Val Thr Leu Gln Ala Ala Val Asn Gly Arg Trp Tyr

260 265 270

Gly Gly Ala Leu Leu Glu Thr Ser Arg Gly Leu Arg Val Glu Gly Glu

275 280 285

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

290 295 300

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

305 310 315 320

Leu Glu Leu Ala Arg Thr Arg Tyr Leu Gly Pro Thr Ser Leu Trp Arg

325 330 335

Ala Ser Gly Ser Leu Thr Ala Arg Glu Ala Arg Ser Ser Thr Glu Ala

340 345 350

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

355 360 365

Thr Thr Leu Ala Tyr Val Glu Pro Tyr Val Met His Arg Arg Phe Asp

370 375 380

Gly Leu Ala Pro Ala Phe Gly Lys Arg Arg Ile Asp Ser Glu Tyr Gly

385 390 395 400

Val Val Thr Arg Leu Ser Lys Arg Asp Trp Thr Leu Lys Gly Ala Phe

405 410 415

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

420 425 430

Asn Ser Phe Thr Arg Arg Arg Val Glu Val Gly Leu Thr Arg Glu Phe

435 440 445

<210> 163

<211> 1485

<212> DNA

<213> Caulobacter sp. AP07 SLAM 2

<400> 163

atgacccgcc ccaaatgttt cccgatccgc atcgccgccg gctgcgcggc cttggccctg 60

ctggccctgg ccggagcggc gcgggcccaa agcgacgacg acacccgtct gcgcctgaac 120

caggatctgt cgcgcaaggc ggcggagcgt gaggccaaga ctctggaaga ggcctcgccc 180

gccgtgctgg tgatcgacgg tcaggcctac gccgtgggtc ccggcgccga cgatgtgggc 240

aaggcgctgt atctgtcgct ggcgcgtcgc cagtggccag acgctcgccg gttcctgaaa 300

gcctatctcg cccttcccga gcgcgacccc atgctggtgc gctacgccca gggcctgctg 360

gcccgccagg acggcgacct gcgcgccgcc gaacgggcgt tgcgcgagtt gctgacgctg 420

aaaccggact tcatgccggg ccggatcgaa ctggcccggg tgttgttcga gaaccagcac 480

gaccgcgagg ccctgtccgc cttccaggcg atcctggccg atctgccgac cagcgagccg 540

agtggggcgg gcgtgcgccg cagcgtggag ggctttgtcg ccgcgttgcg ccagcgtggc 600

gcctggcgcg gttcgctggc ccttggaccg ggctacaaca gcaacatcaa ccaggcctcc 660

ggcagctatg cctgcctgct gcccggtccc gacgggctct gcttcttcga ccgcaagacc 720

cccgatcccc tcggggcggc gagcgtcagt ttcgaagccg ccctcaatcg ccgcatgccg 780

ctgcggggat ccagcgggct gagcttgcgg gccttggcct atggcgagct ctatcccgaa 840

gagggcgcct acagccaggc gaccctgatc gcccaggcgg gctttgacta tcgcaccgcg 900

ggcttggccc taggggtggc tccgtcgctc gatatcggga ccctgggggc ccaacgactc 960

tacgatgcgc ccggcgtcca tatcgagctc agccgcgcct tcggcccatc gaccctgatc 1020

aagttggagg gcgactataa agtcctgcgc tatcgtcagg ccgccttcgc cccgctcgac 1080

ggggcgcagg cctcgctgtt cctgaccgcc ttgcgcggcc tcaagcacgg ctggacggtg 1140

ttcggcggct tcgacctcgc ggacaaggac gccgaccagc cggtcaacgc ctatcgacag 1200

gcaggcttgc ggctgggcgc tgtcacgccg acgttcgcgg gcctcaacgc caacgtcttc 1260

gcctcggtgc gccgcaagcg ttgggatgcc gtcaacgaga ccttggaggc ccgccgccgc 1320

gacgacgagc aagctgtcac cgcgatcgtc cgcgcgccgc gcctgaagat ggtcggcctg 1380

acgcccagcc tgacggtgca atacgccaag gtcgccagca gcatcgactg gctgttctcc 1440

tacgagaagg tggcggcgag cctgaaactt gagcgggtgt tttga 1485

<210> 164

<211> 494

<212> PRT

<213> Caulobacter sp. AP07 SLAM 2

<400> 164

Met Thr Arg Pro Lys Cys Phe Pro Ile Arg Ile Ala Ala Gly Cys Ala
1 5 10 15

Ala Leu Ala Leu Leu Ala Leu Ala Gly Ala Ala Arg Ala Gln Ser Asp
20 25 30

Asp Asp Thr Arg Leu Arg Leu Asn Gln Asp Leu Ser Arg Lys Ala Ala
35 40 45

Glu Arg Glu Ala Lys Thr Leu Glu Glu Ala Ser Pro Ala Val Leu Val
50 55 60

Ile Asp Gly Gln Ala Tyr Ala Val Gly Pro Gly Ala Asp Asp Val Gly
65 70 75 80

Lys Ala Leu Tyr Leu Ser Leu Ala Arg Arg Gln Trp Pro Asp Ala Arg
85 90 95

Arg Phe Leu Lys Ala Tyr Leu Ala Leu Pro Glu Arg Asp Pro Met Leu
100 105 110

Val Arg Tyr Ala Gln Gly Leu Leu Ala Arg Gln Asp Gly Asp Leu Arg
115 120 125

Ala Ala Glu Arg Ala Leu Arg Glu Leu Leu Thr Leu Lys Pro Asp Phe

130 135 140

Met Pro Gly Arg Ile Glu Leu Ala Arg Val Leu Phe Glu Asn Gln His
145 150 155 160
Asp Arg Glu Ala Leu Ser Ala Phe Gln Ala Ile Leu Ala Asp Leu Pro
165 170 175
Thr Ser Glu Pro Ser Gly Ala Gly Val Arg Arg Ser Val Glu Gly Phe
180 185 190

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

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

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

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

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

<210> 165
<211> 1383
<212> DNA
<213> D. alkaliphilus SLAM 1
<400> 165
atgtttagac gattccccag gcgcaagacc caaaggcaag ctcaggtggg cggttttatg 60

atgaaaaggc aacaagttgg tccctgttcg gcagccgcga ttttgctggc cctggtgctc 120
ttcttcggtt ctttgccggc ggcggcagac ccggtgctct ccgggcgcca gatgctggcc 180
gagcagcgct atgacgaggc ctacgagtta ctgctgacgg ccttccgggc cgaccccggc 240
catcccgaaa tcaattttct tttgggccgc gccgcctttg agtcgggccg caccgaagag 300
gcggtgatgg cctacgaacg ggtgctgctg cataatccgg aggccaaccg ggccaagctg 360
gagttggccc gctcctacct gcgcctgggc tcccgggagc tggcccgcca gtattttcac 420
gaggtgctgg ccaccaaccc gccggagccg gtctggcaaa acatccagcg ttttctggcg 480

gccatggatg cggcggaaaa aaagcatttc atcaacggcc tggtcaccct gggggtgggg 540
tatgacgaca acgtcaacac cttcccggcc aacgatacgg tgcgcttcaa cggttggcag 600
gtggacttga aaggggagga aaagagcaac tggctgctca acaccaacct ggtcctcaac 660
catatctacc gcgcccgcta taacagcccc tggaactgga aaaccacctt caccaactac 720
aacgccttcc acgaaagcgt caacgacatg gacctcaacc tctttgcctt gagcaccggc 780

cccacctggc gccgcgaccg tttgctgctg caggcggcgg tgggttacac ccatgtcgac 840

ctgggttttg atcgctacct gggcatgctc ggcttatctg ccggcggcac ctggctgctc 900

tcgcccaact gggcgctcaa cggtggcctg gagtggcggg accgggactt tcataaaaac 960

gacgaccggg actccaccaa cctgctggtt accctggggc cggtattcag ccacggcgac 1020

aaccgggtcg gcctgacctt gggctatgaa accaacgacg ccgacaccga ccattattcc 1080

tacgaccgct ggcggctggg cctgcgttac gatcgccagt tgcccaacga ttttgccgcc 1140

tttgccgcgg tgcgctacca ggaaaccgac tacgatgacg acgagccgtt gttcaataag 1200

gcccgcgaag atgaaacgat cttttatcaa ctcgggctct ccagagtgtt ctggcgggcg 1260

gcagacagcc ggcgcagcct caccggccag atcagctaca gctataccga cgccgactcc 1320

aatatcgagt tgtacgaata caccaaaagc gtggccaatt tggccctgac ctatacctttt 1380

tag 1383

<210> 166

<211> 460

<212> PRT

<213> D. alkaliphilus SLAM 1

<400> 166

Met Phe Arg Arg Phe Pro Arg Arg Lys Thr Gln Arg Gln Ala Gln Val
1 5 10 15

Gly Gly Phe Met Met Lys Arg Gln Gln Val Gly Pro Cys Ser Ala Ala
20 25 30

Ala Ile Leu Leu Ala Leu Val Leu Phe Phe Gly Ser Leu Pro Ala Ala
35 40 45

Ala Asp Pro Val Leu Ser Gly Arg Gln Met Leu Ala Glu Gln Arg Tyr
50 55 60

Asp Glu Ala Tyr Glu Leu Leu Leu Thr Ala Phe Arg Ala Asp Pro Gly
65 70 75 80

His Pro Glu Ile Asn Phe Leu Leu Gly Arg Ala Ala Phe Glu Ser Gly
85 90 95

Arg Thr Glu Glu Ala Val Met Ala Tyr Glu Arg Val Leu Leu His Asn
100 105 110

Pro Glu Ala Asn Arg Ala Lys Leu Glu Leu Ala Arg Ser Tyr Leu Arg

115 120 125

Leu Gly Ser Arg Glu Leu Ala Arg Gln Tyr Phe His Glu Val Leu Ala

130 135 140

Thr Asn Pro Pro Glu Pro Val Trp Gln Asn Ile Gln Arg Phe Leu Ala

145 150 155 160

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

165 170 175

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

180 185 190

Thr Val Arg Phe Asn Gly Trp Gln Val Asp Leu Lys Gly Glu Glu Lys

195 200 205

Ser Asn Trp Leu Leu Asn Thr Asn Leu Val Leu Asn His Ile Tyr Arg

210 215 220

Ala Arg Tyr Asn Ser Pro Trp Asn Trp Lys Thr Thr Phe Thr Asn Tyr

225 230 235 240

Asn Ala Phe His Glu Ser Val Asn Asp Met Asp Leu Asn Leu Phe Ala

245 250 255

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

260 265 270

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

275 280 285

Met Leu Gly Leu Ser Ala Gly Gly Thr Trp Leu Leu Ser Pro Asn Trp

290 295 300

Ala Leu Asn Gly Gly Leu Glu Trp Arg Asp Arg Asp Phe His Lys Asn

305 310 315 320

Asp Asp Arg Asp Ser Thr Asn Leu Leu Val Thr Leu Gly Pro Val Phe

325 330 335

Ser His Gly Asp Asn Arg Val Gly Leu Thr Leu Gly Tyr Glu Thr Asn

340 345 350

Asp Ala Asp Thr Asp His Tyr Ser Tyr Asp Arg Trp Arg Leu Gly Leu

355 360 365

Arg Tyr Asp Arg Gln Leu Pro Asn Asp Phe Ala Ala Phe Ala Ala Val
370 375 380

Arg Tyr Gln Glu Thr Asp Tyr Asp Asp Asp Glu Pro Leu Phe Asn Lys
385 390 395 400

Ala Arg Glu Asp Glu Thr Ile Phe Tyr Gln Leu Gly Leu Ser Arg Val
405 410 415

Phe Trp Arg Ala Ala Asp Ser Arg Arg Ser Leu Thr Gly Gln Ile Ser

420 425 430

Tyr Ser Tyr Thr Asp Ala Asp Ser Asn Ile Glu Leu Tyr Glu Tyr Thr
435 440 445

Lys Ser Val Ala Asn Leu Ala Leu Thr Tyr Thr Phe
450 455 460

<210> 167

<211> 1329

<212> DNA

<213> D. inopinatus SLAM 1

<400> 167

gtgatcgtcc tcgtactgtt aggctgtatc tgtatgttgc cttgcaacaa cgcgcaagcg 60

cagacaactg cggagaatat gcatatcaag gcagacaata caaaagccgc ggcattgatg 120

cgggaaggga atttgggcga agcgcgtgac atcttgttct cacgatatga agacgactct 180

tttgacaatc agtcgctttt cttgctcggt atggtgtccg gcaaaatggg gaatctcgat 240

cagagcgaaa agtactatcg cgaattgctc gagcgcgacc ccaaagcaca acgtgttcgc 300

cttgaactgg ccagtgtgct ttatgccatg gggcagtatg agaaagcgca agctgaactc 360

ctccgggtca aagaagccaa ccctccggag aatgttgggc tgaatatcga caagtttttg 420

gaagccattg ataagtccaa gccaaaggca tggcgggttc gtccgtcaat tggttttatg 480

tatgattcca atgtgacccg ctcgacgttc gatgacacgg ttcaactcat ggaccaacaa 540

tttcatttgt ccgaccgggc gcgcgcgcag gcagactggg ccatggtgta tggtctggaa 600

gcagattact ttcatttttt taccccgcaa agtgcattgc aatttcaatt tcgcgggtcg 660

tacaccgatt attcctatgt ggattggttt gatacggcgg acttgagcgc ttctcttggt 720

cccacgttcc aagttggacg ttggatcgtt tcactccctg ctgtgggaac gtatctcaaa 780

tatggatcgg aagatggaga ttttgcaaaa tactatacgg taagtgtcgg gttcgctcca 840

caggtccggt atcagttgac ggactcctgg gaagtcggga tgaatctcgc gtatttttc 900

aagaattatt atgatgacga tcgatactct aatttgttta ttgtgaatcc ctatcttcgc 960

ttttatccga acgctgtgtc gtatgctcag ctcggcgggt acttcatgcg tgaggatcaa 1020
aattgggata tttacagtaa cgatgcatac ggcattcagg cgacgtactt tcgcagcttt 1080
tttaatgatt ttaatatatt ttgtacggga atattggggc agacctttta cagcggatat 1140
cgtactctct atggtgaaac acagcaggat accttgctta tggggcgcgc gtcattgagt 1200
tataatatcg acgcattgtg ggggcttact ccggaactga gttatatcta tacaaagaac 1260
tggagcaaca tcgatatgtt ttcctacgac cgtcatcaag tcatgtttag cctgtcaaaa 1320
acgttctga 1329

<210> 168
<211> 452
<212> PRT
<213> D. inopinatus SLAM 1
<400> 168

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

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

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

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

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

370 375 380
Thr Phe Tyr Ser Gly Tyr Arg Thr Leu Tyr Gly Glu Thr Gln Gln Asp

385 390 395 400

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

405 410 415

Trp Gly Leu Thr Pro Glu Leu Ser Tyr Ile Tyr Thr Lys Asn Trp Ser

420 425 430

Asn Ile Asp Met Phe Ser Tyr Asp Arg His Gln Val Met Phe Ser Leu

435 440 445

Ser Lys Thr Phe

450

<210> 169

<211> 1452

<212> DNA

<213> D. nodosus SLAM 1

<400> 169

atgaatttat tgtcaaaaat ggtgatcagt ccggcattat tgatcgcgtt tcatgcattt 60

tcagcggata tgacgattaa accgcccgtt agcgataaac ataacgtcgt cgttcccgat 120

caacaagtaa aattgcctac ggctgctcct ttatccgatg ccgaattgga aaaattgcct 180

gccgcttatt ggcgggaaaa tccgagcgca ttggaaagcg ttttgtcgaa atacgtggtt 240

atgggagatg ccgaaggttt aaagaaatat ttgccgtatt accgcgatgt gcccaatcgc 300

gatccttctt tgattgaatg gggcgatgcc attattgccg cgcgcgccgg cgattttaaa 360

actgctattc gtttataccg caaaatcaat tcattattgc caaacgtcac gctggtgcgt 420

tttcaattag caatggcgtt atatgccgat aaacaatacg ttgccgccga acacgaattg 480

gaaaaattgc gcgccgaaca attgcccgag caatacgcgc aagctgttga tcatgtttta 540

aaaatgattc accggcagga acaatgggat ttttatgcat cagcgactta ttcttatgat 600

aaaaacgtca acgaagcgcc gccggtcggc acaaaaatgg tttttcctaa cggcagctcc 660

attaccagtc aacaagaacc gcgcagcgcc aacggcgttg aatttgattt ttctgccgat 720

aaacgctgga atttgcgcgg taattatttt gcggcattgc atttgagcac ttttggcaaa 780

ttgtattggg acgaaaaaac ctctaacgat ttaagcagcc gcatcggaat cggcggcggt 840

tatagcaacg cggtaaccga aattgaatta tcgccgtttt tctcgcatcg ttggtacgtc 900

aaccgcgacg ataacaacag caattttgat cactacaata cgggttacgg cttgcgtttg 960

agcggctcgc aatggttatc aacaaaattt aaatatcaag gcgcgttgga atggactcaa 1020

aatcgttacc gcagcgatta tcgtcattta aacggcaatg attatttgat gtcgcacacg 1080

ttaatgtatt tgcccgctgc gcgctattat tggttcggcg gcatcgatta cagcattcgc 1140

gatgtcgaat caaaaaccaa ctcttatgac cgctggggcg cacgtttggg ctggggacaa 1200
gaatggggca aaggttttgc aacgcgcacc acaatcggct acggcagaaa aacctttgat 1260
gacgtggatt tctttaatat caaacaaaaa aataacgaat acagcgcctc tgttagcctg 1320
tggaatcgta atttttattt cggcggtatc acgccgcgct tgacgtggtc ttatcgcaaa 1380
gttgacggca atcacccgtt ttataattac gataaacaaa acgtggttgt ggaattttct 1440
aaaacgtttt aa 1452

<210> 170
<211> 483
<212> PRT
<213> D. nodosus SLAM 1

<400> 170

Met Asn Leu Leu Ser Lys Met Val Ile Ser Pro Ala Leu Leu Ile Ala
1 5 10 15
Phe His Ala Phe Ser Ala Asp Met Thr Ile Lys Pro Pro Val Ser Asp
20 25 30
Lys His Asn Val Val Val Pro Asp Gln Gln Val Lys Leu Pro Thr Ala
35 40 45
Ala Pro Leu Ser Asp Ala Glu Leu Glu Lys Leu Pro Ala Ala Tyr Trp
50 55 60

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

Ile Asn Ser Leu Leu Pro Asn Val Thr Leu Val Arg Phe Gln Leu Ala
130 135 140
Met Ala Leu Tyr Ala Asp Lys Gln Tyr Val Ala Ala Glu His Glu Leu

145 150 155 160

Glu Lys Leu Arg Ala Glu Gln Leu Pro Glu Gln Tyr Ala Gln Ala Val

165 170 175

Asp His Val Leu Lys Met Ile His Arg Gln Glu Gln Trp Asp Phe Tyr

180 185 190

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

195 200 205

Val Gly Thr Lys Met Val Phe Pro Asn Gly Ser Ser Ile Thr Ser Gln

210 215 220

Gln Glu Pro Arg Ser Ala Asn Gly Val Glu Phe Asp Phe Ser Ala Asp

225 230 235 240

Lys Arg Trp Asn Leu Arg Gly Asn Tyr Phe Ala Ala Leu His Leu Ser

245 250 255

Thr Phe Gly Lys Leu Tyr Trp Asp Glu Lys Thr Ser Asn Asp Leu Ser

260 265 270

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

275 280 285

Glu Leu Ser Pro Phe Phe Ser His Arg Trp Tyr Val Asn Arg Asp Asp

290 295 300

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

305 310 315 320

Ser Gly Ser Gln Trp Leu Ser Thr Lys Phe Lys Tyr Gln Gly Ala Leu

325 330 335

Glu Trp Thr Gln Asn Arg Tyr Arg Ser Asp Tyr Arg His Leu Asn Gly

340 345 350

Asn Asp Tyr Leu Met Ser His Thr Leu Met Tyr Leu Pro Ala Ala Arg

355 360 365

Tyr Tyr Trp Phe Gly Gly Ile Asp Tyr Ser Ile Arg Asp Val Glu Ser

370 375 380

Lys Thr Asn Ser Tyr Asp Arg Trp Gly Ala Arg Leu Gly Trp Gly Gln

385 390 395 400

Glu Trp Gly Lys Gly Phe Ala Thr Arg Thr Thr Ile Gly Tyr Gly Arg
405 410 415

Lys Thr Phe Asp Asp Val Asp Phe Phe Asn Ile Lys Gln Lys Asn Asn
420 425 430

Glu Tyr Ser Ala Ser Val Ser Leu Trp Asn Arg Asn Phe Tyr Phe Gly
435 440 445

Gly Ile Thr Pro Arg Leu Thr Trp Ser Tyr Arg Lys Val Asp Gly Asn
450 455 460

His Pro Phe Tyr Asn Tyr Asp Lys Gln Asn Val Val Val Glu Phe Ser
465 470 475 480

Lys Thr Phe

<210> 171

<211> 1437

<212> DNA

<213> D. nodosus SLAM 2

<400> 171

atgaagcaat atagtgggtt attactgggt tttttgactt tatcggtgtg cgcacaagaa 60

gcttatcaag tgcaagttgc caaagaagtc aatccaacat tacgtctgcc cgaagttaaa 120

attccgtggg agatgttgtc atcattattg tcggaagaac aagatgcacc gttggattta 180

tcggaggatc ctcaagcggt ggcgcgctct ttggacaatg ccgttgcgca cggtcgttta 240

gagcaaataa aagttttatt gccgcattat aaaaagttcc ccgaacacga acgcaacgag 300

caattaattc gttttgcgga agcggcattg gcgcaatctg taggaaatgt gaaacaaacc 360

attgagttat atcgcgaaat gattgctaat gatcccaatt tgccgcccgt acgattgcag 420

ctcgcattgg cattgatgcg cgatcggcaa gatgcggctg caaaagatca attggaacgt 480

ttgcgtagcg aagatttgcc ggaagagatt gctgccgtgg tcgattcagc tttagcggct 540

cttagagaac ggcaggcgtg gtcgtttggc gtcagcggat attatgtgca cgattctaat 600

atcaatcagg cgccggatat tcgttctcgc gaaacggatc agtgcccttt tgctgaaaaa 660

tgtacgatta cttttccgga aaaagaaaat gccgatggac tttatttgcg gcttaatgcg 720

gatcggcgtt tgcccattaa aaataattgg tacgccaatt ttgaaggcag cgcacacgct 780

aattggtatt ggaatacgga tcaatatgat gatattcaag tgcgtttggg atcgggcgtg 840

ggttatgaaa atgcgcgctt tgatgcgagc gtattgccgt ttgttagtca acgtttttat 900

gctggaaaaa aatatgcgca cgccgctggc gccacggtca gcatgaatta ttggatgaca 960

ccaaaatggc ggttatcggg tatttatgaa ggcgaatatg cacaacacga tcatcattca 1020

tggttagacg gtcaacggca ttatcaagcg cttaatctct tatatttggc gcattctgga 1080

cgctattttt tcggcggcgt taatcattat tatcaagacg cccaagatga tgcggatcgc 1140

ttttttcggt acggcgtcaa cgctggttgg atagaggatt ggtcgggtgg actttctacg 1200

cggttaagcg cttccgttgg gaaacgtctt tatcaaggtg ctgatttaat ggcaaatatt 1260

aagcgtaacg atacggaata taataccggc gtgcaacttt ggtaccgcga ttggcatttt 1320

tggggcatta cgccaaaatt gtcactagaa tggaataaaa ccaatagtaa tcatttctat 1380

tacgatcgaa aaaatggcac gggtcgcgct tatattgaat tgagcaaaac attttaa 1437

<210> 172

<211> 478

<212> PRT

<213> D. nodosus SLAM 2

<400> 172

Met Lys Gln Tyr Ser Gly Leu Leu Leu Gly Phe Leu Thr Leu Ser Val
1 5 10 15

Cys Ala Gln Glu Ala Tyr Gln Val Gln Val Ala Lys Glu Val Asn Pro
20 25 30

Thr Leu Arg Leu Pro Glu Val Lys Ile Pro Trp Glu Met Leu Ser Ser
35 40 45

Leu Leu Ser Glu Glu Gln Asp Ala Pro Leu Asp Leu Ser Glu Asp Pro
50 55 60

Gln Ala Val Ala Arg Ser Leu Asp Asn Ala Val Ala His Gly Arg Leu
65 70 75 80

Glu Gln Ile Lys Val Leu Leu Pro His Tyr Lys Lys Phe Pro Glu His
85 90 95

Glu Arg Asn Glu Gln Leu Ile Arg Phe Ala Glu Ala Ala Leu Ala Gln
100 105 110

Ser Val Gly Asn Val Lys Gln Thr Ile Glu Leu Tyr Arg Glu Met Ile
115 120 125

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

130 135 140

Leu Met Arg Asp Arg Gln Asp Ala Ala Ala Lys Asp Gln Leu Glu Arg
145 150 155 160

Leu Arg Ser Glu Asp Leu Pro Glu Glu Ile Ala Ala Val Val Asp Ser
165 170 175

Ala Leu Ala Ala Leu Arg Glu Arg Gln Ala Trp Ser Phe Gly Val Ser
180 185 190

Gly Tyr Tyr Val His Asp Ser Asn Ile Asn Gln Ala Pro Asp Ile Arg
195 200 205

Ser Arg Glu Thr Asp Gln Cys Pro Phe Ala Glu Lys Cys Thr Ile Thr
210 215 220

Phe Pro Glu Lys Glu Asn Ala Asp Gly Leu Tyr Leu Arg Leu Asn Ala
225 230 235 240

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

Ser Ala His Ala Asn Trp Tyr Trp Asn Thr Asp Gln Tyr Asp Asp Ile
260 265 270

Gln Val Arg Leu Gly Ser Gly Val Gly Tyr Glu Asn Ala Arg Phe Asp
275 280 285

Ala Ser Val Leu Pro Phe Val Ser Gln Arg Phe Tyr Ala Gly Lys Lys
290 295 300

Tyr Ala His Ala Ala Gly Ala Thr Val Ser Met Asn Tyr Trp Met Thr
305 310 315 320

Pro Lys Trp Arg Leu Ser Gly Ile Tyr Glu Gly Glu Tyr Ala Gln His
325 330 335

Asp His His Ser Trp Leu Asp Gly Gln Arg His Tyr Gln Ala Leu Asn
340 345 350

Leu Leu Tyr Leu Ala His Ser Gly Arg Tyr Phe Phe Gly Gly Val Asn
355 360 365

His Tyr Tyr Gln Asp Ala Gln Asp Asp Ala Asp Arg Phe Phe Arg Tyr
370 375 380

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

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

<210> 173
<211> 1305
<212> DNA
<213> D. shibae SLAM 1
<400> 173

atgcgggccc gtccggggcg gcgaccggcg acctggtggc ggtgcggccc gcggatcctg 60

tgcagggtcg cggggctgtg cgcttgcctg gcagtcgcgg cacccgtggc ggcgcaaccc 120
gccctgcccg gcgccgcgcg cagcaccctg cccgtcgatg gcgcggcgat cgaggcgcgg 180
ttcctgcgcg ggcttgccct gctgaacggc ggtcaggcgg cggcggcgat cccgctcttt 240
ctcgacattc tggcgggaga cccgaccctg gtgcgggtcc ggctggaact ggcgcgggcc 300
tatttcgccg ccgaacagtg gagccgggcg cgggaggagt tcttcgccgt cctctccacc 360
gacctgccgg agccggcgcg gctgcgggtg ctgggcttca tccgggcgat cgacgcgcgg 420
cgggggttcg actgggacct gtccatcggc ctggtcaccc tgggcgaacg gcggcgctat 480

gacagcgaca cggtggatct ggagatcgcg ggcacggtgc tgcccttcac cctggagcgg 540
gacaccgaca ccgagccggg gctgcgggtg acgggggcgg cgcgctggcg gcaggggctg 600
acgcgggtcg gggcgacgga gcttgtgggg ttcgcggggg tcgatctcga tgcgctggag 660
gggccagggg cgcggtacga cgacatcaca atcggcgcgc ggacgggggt gcggtttctg 720
ggcgcgcgga gctcggtggt ggccgcggcc ttcgggcgga gccgccacgt ggcgggagac 780
gggttcgagg accgcttcgg cctggatctg tccttcgagc ggcgcagtgc gggcggcgtg 840

tcggtctttg gcgcggcgtc ctgggcggtg ctggacagcg caatttcgga cgaccgggac 900

gggcacgcgg tggcggccca gcttggcctg cggcgctccg tgggcgggcg cgcgacgctc 960
ggcgcggcgc tgcgggtgga agagaaccgg gtggcgttcg acctggagga ttaccgcgac 1020
accgagctgc gggtcttcgg cagctatgac gcggtccggg ggatcacgtt gcggcccgag 1080
ctgtccctgc ggtaccggga tttccgcgac cccagccccc tgttcaccgc cagcccgaac 1140
gagcgcgcgg tgcaggtcgc gctgacggtg cagaaatccg acctgttcct gggtgacggg 1200
ttctcgccct ttgcacgggt cagccatacc cgcagccggt cggacatcga cgcctacagc 1260
tataccgaga gcgaagttca gatcgggctg gagcggcggt tctga 1305

<210> 174
<211> 434
<212> PRT
<213> D. shibae SLAM 1
<400> 174

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

Trp Asp Leu Ser Ile Gly Leu Val Thr Leu Gly Glu Arg Arg Arg Tyr
145 150 155 160
Asp Ser Asp Thr Val Asp Leu Glu Ile Ala Gly Thr Val Leu Pro Phe
165 170 175
Thr Leu Glu Arg Asp Thr Asp Thr Glu Pro Gly Leu Arg Val Thr Gly

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

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

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

370 375 380
Gln Val Ala Leu Thr Val Gln Lys Ser Asp Leu Phe Leu Gly Asp Gly

385 390 395 400

Phe Ser Pro Phe Ala Arg Val Ser His Thr Arg Ser Arg Ser Asp Ile

405 410 415

Asp Ala Tyr Ser Tyr Thr Glu Ser Glu Val Gln Ile Gly Leu Glu Arg

420 425 430

Arg Phe

<210> 175

<211> 1458

<212> DNA

<213> Escherichia coli SLAM 1

<400> 175

atgaaattac tctgctcact gctgctgacc tgcctgtgcg ctggctcgct tacgccggcg 60

tttgccgcta ctaacgatga cgaccgcggg cttcgcctgt ggatgaagga tcggctggcc 120

tatcaggaaa caagcgacac cgcaccggat aaagaccagc cgctgctgca ggacccgctg 180

tcgctcagcc tggaggggaa aacctacagc ctgaacaaca atgcgcagga cctgggcctg 240

gccatctacc tcgccatcag ccatcgccag tttcgcgatg ccctgcgcct gttgccggcc 300

tatgaacggc tggcggatca cgatccgctg ctggtgctgt tcgcccgggc ggaatacgcc 360

cgcgatcgcg gccactacgc cgaggccatt gatgactacc ggcagatcct ccatcgctca 420

ccggatttcc tgcgcgtgcg gctggagctg gcgcgcaccc tgtttgaaga taatcagaac 480

cgcgaagcgc tggcgatgtt taaccgcatt ctcgccgacc gcggggcaga gttgcccgcg 540

gggacgatcg ccaccatcag gcagtttacc ggcgccattg aaacgcgtac ggcctggacc 600

ggcagtctct cgctgggcta cgtctggaac tccaatatta atcagacccc ggatcgcgac 660

gctccgtggc tttccggcgg cggactgtgg cgccgtgagg atcctaaaag cagcggcggc 720

gtgtcttacg acgccagtct gagcaaaatt tttccgctgg ccgggcacca cgctctgcag 780

ctgaagggca ccacctacgg tgaccgctac ccgcatcagg cacagttcag tgagaacacc 840

tccaccctgg cgctgctctg gcagtacagc aacgccacca cccgcgcggc catcgggccg 900

gtggtggaga tgaagctatc cgacgaacag aggctctata ccggacgcgg gctgcggctg 960

gatggcgact accgttttac cccacgcctg atgctgagcc tgaatgccga ctaccagaag 1020

ctgacctaca aaaaagagta tgaaacctcc gacggcgagc gcggcaacct ctatctgacc 1080

gggatttatg gcctgacgcc ggcgacctca ctgttcattg gcgcagacgg tacccgcgtc 1140

accacccagg tgcgcagcga tgactactac cagaccggcc tgcgcgcggg tgtgttcagc 1200

gccattaccc cggatatcaa cctgatggtg atggcgacgc gccgcaacag ccgctttgcc 1260
gcgtttaaca ccttcgtcgg cgatgaacgc cgcgatcgcg aacagctgta tatggcgcgg 1320
gtgagcctgc ccggctacca gatgctgacg ctgacgccct ttgccagcta ccgcttccgt 1380
aaaaaccaca gctctgccga cgggctttat tcgtaccgcc agcatgaagt ggtgatggga 1440
tttgaaacta acttttga 1458

<210> 176
<211> 485
<212> PRT
<213> Escherichia coli SLAM 1
<400> 176

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

Arg Glu Ala Leu Ala Met Phe Asn Arg Ile Leu Ala Asp Arg Gly Ala
165 170 175
Glu Leu Pro Ala Gly Thr Ile Ala Thr Ile Arg Gln Phe Thr Gly Ala
180 185 190
Ile Glu Thr Arg Thr Ala Trp Thr Gly Ser Leu Ser Leu Gly Tyr Val

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

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

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

385 390 395 400
Ala Ile Thr Pro Asp Ile Asn Leu Met Val Met Ala Thr Arg Arg Asn

405 410 415

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

420 425 430

Arg Glu Gln Leu Tyr Met Ala Arg Val Ser Leu Pro Gly Tyr Gln Met

435 440 445

Leu Thr Leu Thr Pro Phe Ala Ser Tyr Arg Phe Arg Lys Asn His Ser

450 455 460

Ser Ala Asp Gly Leu Tyr Ser Tyr Arg Gln His Glu Val Val Met Gly

465 470 475 480

Phe Glu Thr Asn Phe

485

<210> 177

<211> 1440

<212> DNA

<213> E. corrodens SLAM 1

<400> 177

atgagaatac agaacaagcc gcggctggcc gcctgcctgc tgctgttgcc ttttcaggta 60

gccttggccg atctgccggc agacaggctg gaaaccgagc cggataccgg cttcgacatc 120

acgccagcgg ccgcgccgca ggtggaggct gcgcccgctc ctgccaacac tcagcccgac 180

aaacgcctgc aaatgagccg cgaagaattg ctccagcgcc ccgagctgct gcaacaggcg 240

ctcagctatg ccgtgctcac ccacaatgcc gacggcgcgg cactgctgct gccgatttat 300

ctcgaattgc ccgggccgca cgatgcgctg ctggtggctt tggcacaggc gctgattgcc 360

cgtgccaagg gcgactacca gcgcgccatc ggcctctacc gcgccgtgct ggccgccgat 420

cccgatatcc cgccggtgcg cctttcgctg gcgcaaagtc tgtttgaaaa tcgtgccgac 480

aaagatgcgc ggcaagagtt cgaacatttc cgccaaactc ccaatctcgc gcccgagctg 540

caacagcttg ccgggcaata cctggaagcc ctgcgcaaac gcgaccgctg gagcttcggc 600

ggcagcgtaa acttcatcag cgacagcaat gtaaacaacg ccggacgcga gcgcgaaatc 660

cgcacctcgc gcggcgtatg gacactgccc gagcccgagt ccgcccaagg cttcgcctac 720

cgcctcaacg ccgatcgcga ctggaacgta cacggcaacc tctactggcg gctcagcctc 780

gacgactacg gcaaattcta ttggaataac cacaaatacg acgaccaaat cgcccgcctc 840

agcagcggcc ccgcctacaa aaccgcccgt gccgaagccg ccgttacccc ttattacgag 900

cgccgctggt atggcacaca caaatactcg cgcgaagtcg gcgtgcgcgc cgaatggcaa 960

tattggctca ccccgcgcca taaaatattg agcgcgcttg aaatcggcga gcagcgccac 1020

gaccgccgcc gctggctcga cggcgacagc tacaccgctt ccggcacttg gctcttcgtg 1080
cgcagcccca cccaatattt cagcttcggc ctcgactggc tgcgcaaaac cgccgaagac 1140
aacagcgaat cctacacccg caaaggcctg cgcttgggct ggacgcagca atggggctgg 1200
gggctcacca cctccgccca aatcagcgcc ggccaccgca gctacgacgc ccccgacctg 1260
ttccgcatca cccgccgcga ccacgagctt gccgccagcc tggtgctctc ccaccgcaaa 1320
ctgcaattcg ccggcatcac cccgcagctg gtgggcacct ggcagcgggt aaacagcaac 1380
cacttcttct atccctaccg caaaggcaac gtgtttatcc agtttgggcg ttcgttctaa 1440

<210> 178
<211> 479
<212> PRT
<213> E. corrodens SLAM 1
<400> 178

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

Pro Val Arg Leu Ser Leu Ala Gln Ser Leu Phe Glu Asn Arg Ala Asp
145 150 155 160
Lys Asp Ala Arg Gln Glu Phe Glu His Phe Arg Gln Thr Pro Asn Leu
165 170 175
Ala Pro Glu Leu Gln Gln Leu Ala Gly Gln Tyr Leu Glu Ala Leu Arg

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

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

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

370 375 380
Tyr Thr Arg Lys Gly Leu Arg Leu Gly Trp Thr Gln Gln Trp Gly Trp

385 390 395 400

Gly Leu Thr Thr Ser Ala Gln Ile Ser Ala Gly His Arg Ser Tyr Asp

405 410 415

Ala Pro Asp Leu Phe Arg Ile Thr Arg Arg Asp His Glu Leu Ala Ala

420 425 430

Ser Leu Val Leu Ser His Arg Lys Leu Gln Phe Ala Gly Ile Thr Pro

435 440 445

Gln Leu Val Gly Thr Trp Gln Arg Val Asn Ser Asn His Phe Phe Tyr

450 455 460

Pro Tyr Arg Lys Gly Asn Val Phe Ile Gln Phe Gly Arg Ser Phe

465 470 475

<210> 179

<211> 1539

<212> DNA

<213> E. corrodens SLAM 2

<400> 179

atgcagatga aaacgagtgc gcttctgatt atttttacgt tgtgtacagc acaacacagt 60

tggggcaata caacgccgga acaggatcag aagcgttttt tgcaaacggg gcagcagcag 120

tggctgcgac agttggaaaa caacgcgcaa atgcctgcag ccaaagatgg gcagcaggcc 180

gcgccggtgc ttacacagca ggatttgctg gcacggccac agctcttggc gcggatgctg 240

gtgcaggtgt taaacggccc gccgcagccg gaattgttgg cggatttgac ttcactgtat 300

gcgcaaacgc cgcagccaga catggtgttg ctgcggcgtg cacaaggcat gcaggctaga 360

tatgcgggcg actatgcgcg cgcagtgcaa atttatcggg aactggtggc agaagagccg 420

caggatgtgc gcatccgcct ggatttggcg gccatgctgg cagaagataa gcaatggcgc 480

gaatcggcac agctatttga aactgtgcgg agcgagccgg aagtgccggc ggaagtgcag 540

aataatgtgc agcattatct gaaccatatt gccaaacagc agcagtggca gtggagcggc 600

gggctttcgc cctcgtttga taacaatgtg aacaacgcac cgccgccgca ttgcagcccg 660

ttcggttgca gccgcgaacg cgcagaagat gctgtgggcg tggcttacag cctgggtgtg 720

gcgaaaaacc agccgctggc cgggcatcat aacttgcacg tgcagctgga tgtgagcggc 780

accaattatt attggagcaa caaatcggcc tacgacagcg cctacggccg tttgggtgcg 840

ggctggctct ggcaggatgc gcggcagcgg ctgttggtga tgccgtttta ccaattccag 900

ctcagcggca ccgacaactg ggatggccgc aaaccgcaaa acaaccacac gctgaaaatg 960

cacatgtggg cgcacgcccc cgggctgcgc acggaataca gccgcctgct cacccgcgc 1020
tggcagctgc acaccgcact ggatgcctac cgccagcact atcggatgga taccaaagca 1080
gaaatgtata acggctggta tttgggcgaa agcatttccc tggcttggcg tgccacagcg 1140
cgcaacacgc tgtatgccgg gctgaatttc aaccagatgc tgccggaaca atccaccctg 1200
agcggcaagc cgaacaatgc cgcctaccgc cgccacggca tcggcgccgg ttggattcat 1260
gattgggacg cactgggcgg cctctccacc cggctcaacg tatccttcgc cgaacggcgt 1320
ttccgcggca ccgcactaaa catcacaccg caaggcttcc cgcgcgaaca acgccgcgac 1380

cacgaaatcc aatactccgc ttcgctgtgg cacagaaact ggaccatcct cggcctcacc 1440
ccgaagctga atttctcctg gcaacacacc cgcagcagcc atgtgtgggc agaacgcaaa 1500
agccggcaag tgtttgtgga attggaaaag cagttttaa 1539

<210> 180
<211> 512
<212> PRT
<213> E. corrodens SLAM 2
<400> 180

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

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

Thr Ser Leu Tyr Ala Gln Thr Pro Gln Pro Asp Met Val Leu Leu Arg
100 105 110
Arg Ala Gln Gly Met Gln Ala Arg Tyr Ala Gly Asp Tyr Ala Arg Ala

115 120 125

Val Gln Ile Tyr Arg Glu Leu Val Ala Glu Glu Pro Gln Asp Val Arg

130 135 140

Ile Arg Leu Asp Leu Ala Ala Met Leu Ala Glu Asp Lys Gln Trp Arg

145 150 155 160

Glu Ser Ala Gln Leu Phe Glu Thr Val Arg Ser Glu Pro Glu Val Pro

165 170 175

Ala Glu Val Gln Asn Asn Val Gln His Tyr Leu Asn His Ile Ala Lys

180 185 190

Gln Gln Gln Trp Gln Trp Ser Gly Gly Leu Ser Pro Ser Phe Asp Asn

195 200 205

Asn Val Asn Asn Ala Pro Pro Pro His Cys Ser Pro Phe Gly Cys Ser

210 215 220

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

225 230 235 240

Ala Lys Asn Gln Pro Leu Ala Gly His His Asn Leu His Val Gln Leu

245 250 255

Asp Val Ser Gly Thr Asn Tyr Tyr Trp Ser Asn Lys Ser Ala Tyr Asp

260 265 270

Ser Ala Tyr Gly Arg Leu Gly Ala Gly Trp Leu Trp Gln Asp Ala Arg

275 280 285

Gln Arg Leu Leu Val Met Pro Phe Tyr Gln Phe Gln Leu Ser Gly Thr

290 295 300

Asp Asn Trp Asp Gly Arg Lys Pro Gln Asn Asn His Thr Leu Lys Met

305 310 315 320

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

325 330 335

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

340 345 350

His Tyr Arg Met Asp Thr Lys Ala Glu Met Tyr Asn Gly Trp Tyr Leu

355 360 365

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

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

Pro Lys Leu Asn Phe Ser Trp Gln His Thr Arg Ser Ser His Val Trp
485 490 495
Ala Glu Arg Lys Ser Arg Gln Val Phe Val Glu Leu Glu Lys Gln Phe
500 505 510

<210> 181
<211> 1371
<212> DNA
<213> E. hoshinae SLAM 1
<400> 181

atgctgatta aaatagaatc ccccctttca cagctaggct cagctattat tttaagcgta 60
ttaatgataa gcacagcgga tgccgctagc acttctcaat cggtaaaaaa tactgtcatc 120
ctttctccag cagaattaac agcacaccct cagattattt tccaaggtat gatccaggcg 180

gtgatgaaat cagacgccgc cgctgtcaag atcttgctgc cgctttatca ggcgcaggca 240
gggtacgatc caaccctggc cacctggggt aaggctattt tagccaaaga ggacggtaac 300
tatcgcgatg ccattcgtta ttaccgccgc gtcatcgcca aagagccaca gctaaatatt 360
gcccgactac agctggctat cgcactgttt caaaataaag accgcgcctc tgcgctactg 420
caattcaata aactgcgggc caatagcaac ggcgaaagag tcaatgagat agtggatagc 480
tatatcaagg cgatacagca gaaagacagt tggtcattca acgtaggggt taactatatt 540

aatgaaagta acattaataa tgcgccggga gataaggtaa aaattggtca gtggcaggcg 600

gaaaaacggc aaagcggaca gggtttctct tactatctta gcggcagtaa gacctggtca 660
ttaccggagg gggtgttcag cgagatccgt acgctgacct acgggaagta tttcaccaac 720
aatcatcgct acgatcaggc gacggcccgc ctgagcctag gtttgggcct acgcgacatc 780
gacgcctccc tgctgctgct gccctttata gagcgcgaat gggcatcgga taatcaggcg 840
ccctcccttg ctagcgaggg aacctcgccg gggctacgaa ttgaatcaaa ataccgtcta 900
agcccacgct ggaaaatcga cgttgaggct gagaaaagtc acactacaaa taaacgccgc 960
acccagcgtg acagtaaaaa ccatctactg tcagcgacgc tctattattt ccccagcccc 1020

gaacaatttt ggtttttggg cggtgactac caacgtgaaa acgttgcacg caagagttta 1080
gcttttcaga aaataaagtg gcggggcggc tggggaaatg agtggccggg cggcatatcc 1140
agcatcatgc agataaacta cgccaataag ttttacgata gcgctgactt cttcggaatt 1200
cagcaaagaa ataaagagta cggcgccctg ataacgctct ggcaccgtga catttattac 1260
tttggtatca cgccaaagat caacctgtca tattttaaaa gtgacagcaa tcatccattt 1320
tacgaatacg ataaaaaaat ggtctttcta acctttagta agttttttta a 1371

<210> 182
<211> 456
<212> PRT
<213> E. hoshinae SLAM 1

<400> 182

Met Leu Ile Lys Ile Glu Ser Pro Leu Ser Gln Leu Gly Ser Ala Ile
1 5 10 15
Ile Leu Ser Val Leu Met Ile Ser Thr Ala Asp Ala Ala Ser Thr Ser
20 25 30
Gln Ser Val Lys Asn Thr Val Ile Leu Ser Pro Ala Glu Leu Thr Ala
35 40 45
His Pro Gln Ile Ile Phe Gln Gly Met Ile Gln Ala Val Met Lys Ser
50 55 60

Asp Ala Ala Ala Val Lys Ile Leu Leu Pro Leu Tyr Gln Ala Gln Ala
65 70 75 80
Gly Tyr Asp Pro Thr Leu Ala Thr Trp Gly Lys Ala Ile Leu Ala Lys
85 90 95

Glu Asp Gly Asn Tyr Arg Asp Ala Ile Arg Tyr Tyr Arg Arg Val Ile
100 105 110
Ala Lys Glu Pro Gln Leu Asn Ile Ala Arg Leu Gln Leu Ala Ile Ala
115 120 125

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

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

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

Thr Gln Arg Asp Ser Lys Asn His Leu Leu Ser Ala Thr Leu Tyr Tyr
325 330 335
Phe Pro Ser Pro Glu Gln Phe Trp Phe Leu Gly Gly Asp Tyr Gln Arg

340 345 350

Glu Asn Val Ala Arg Lys Ser Leu Ala Phe Gln Lys Ile Lys Trp Arg

355 360 365

Gly Gly Trp Gly Asn Glu Trp Pro Gly Gly Ile Ser Ser Ile Met Gln

370 375 380

Ile Asn Tyr Ala Asn Lys Phe Tyr Asp Ser Ala Asp Phe Phe Gly Ile

385 390 395 400

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

405 410 415

Asp Ile Tyr Tyr Phe Gly Ile Thr Pro Lys Ile Asn Leu Ser Tyr Phe

420 425 430

Lys Ser Asp Ser Asn His Pro Phe Tyr Glu Tyr Asp Lys Lys Met Val

435 440 445

Phe Leu Thr Phe Ser Lys Phe Phe

450 455

<210> 183

<211> 1371

<212> DNA

<213> E. piscicida SLAM 1

<400> 183

atgttgatta aaatagaacc gccactttta cagataggct ctgctattct gttaagcata 60

ttaacgctga ccgcagcgga tgctgccggt gcacctcaat cggtaaaaga cacttttatc 120

ctctctcaag atgaattaaa aacacacccc cggattattt ttcagggaat gatccaggcg 180

gtaatcaaat cagacgtcgc cgctgtcaag atcttgctgc cgctttatca ggagcagcta 240

ggacacgatc caaatctggt cgcatgggga aaggctattt tagcaaaaga ggacggtaac 300

tatcgccagg cgattcgcta ttatcgccgc gttatcgccg aggaaccaca gctaaatatt 360

gcccgactgc agctggctat cgcgctgttt cagaataaag accgcgcctc tgcgctactg 420

cagttcaata agctgcgggc caatagcaac ggcgaaagaa tcaatgagat attggacagc 480

tatatcagag caatacaggg gaaagacagc tggtcattca atgtaggcgt taactatatt 540

aatgagagca atattaataa tgcgccaggc gataacgtga aaattggtca gtggcaggct 600

gaaaaacggc aaagtggaca gggcttctcc tactacctta gcggcagcaa aacctggtca 660

ttgccagagg gactgtttag cgagatccgc acgctggcct acgggaaata cttcaccaac 720

aatcatcgct acgatcaggc gacggcccgt ctgagcgcag gcctgggcct acgcaacatc 780
gatgcctccc tgctgctatt gccctttatc gagcgcgaat gggcatcgga taatcaggcg 840
ccctcccttt ctagcgaggg aacatcgccg gggctgcgta ttgagacaga ataccgtctg 900
aacccacgct ggaaaatcga cgttgacggt gagaaaagcc acactaaaaa taaacaccac 960
gcacagcgtg acagtaaaaa tcatctgctg tcagcaacgc tctattattt ttccagcccc 1020
gagcaatttt ggttttgggg cagtgactac caccgtgaaa acgttgaacg taagagctta 1080
gcctttcaga aaataaaatg gcgggcgggc tgggggaatg agtggccggg cggcgtatcc 1140

agcatcattc agataaatta cgccaacaag ttttacgata gcagcgactt cttcgggatt 1200
cagcaacgga ataaagagta cggcgcactg ataaccctct ggcatcgtga tatttattac 1260
tttggtatca cgccaaaaat caacctgtca tattttaaaa gtgacagcaa tcatccattt 1320
tacgaatacg ataagaaaat gatcttcctg acctttagta agctttttta a 1371

<210> 184
<211> 456
<212> PRT
<213> E. piscicida SLAM 1
<400> 184

Met Leu Ile Lys Ile Glu Pro Pro Leu Leu Gln Ile Gly Ser Ala Ile
1 5 10 15

Leu Leu Ser Ile Leu Thr Leu Thr Ala Ala Asp Ala Ala Gly Ala Pro
20 25 30
Gln Ser Val Lys Asp Thr Phe Ile Leu Ser Gln Asp Glu Leu Lys Thr
35 40 45
His Pro Arg Ile Ile Phe Gln Gly Met Ile Gln Ala Val Ile Lys Ser
50 55 60
Asp Val Ala Ala Val Lys Ile Leu Leu Pro Leu Tyr Gln Glu Gln Leu
65 70 75 80

Gly His Asp Pro Asn Leu Val Ala Trp Gly Lys Ala Ile Leu Ala Lys
85 90 95
Glu Asp Gly Asn Tyr Arg Gln Ala Ile Arg Tyr Tyr Arg Arg Val Ile
100 105 110

Ala Glu Glu Pro Gln Leu Asn Ile Ala Arg Leu Gln Leu Ala Ile Ala
115 120 125
Leu Phe Gln Asn Lys Asp Arg Ala Ser Ala Leu Leu Gln Phe Asn Lys
130 135 140

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

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

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

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

355 360 365

Ala Gly Trp Gly Asn Glu Trp Pro Gly Gly Val Ser Ser Ile Ile Gln

370 375 380

Ile Asn Tyr Ala Asn Lys Phe Tyr Asp Ser Ser Asp Phe Phe Gly Ile

385 390 395 400

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

405 410 415

Asp Ile Tyr Tyr Phe Gly Ile Thr Pro Lys Ile Asn Leu Ser Tyr Phe

420 425 430

Lys Ser Asp Ser Asn His Pro Phe Tyr Glu Tyr Asp Lys Lys Met Ile

435 440 445

Phe Leu Thr Phe Ser Lys Leu Phe

450 455

<210> 185

<211> 1371

<212> DNA

<213>

E. tarda SLAM 1

<400> 185

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ttaaccatga gcgcagcaga tgctgctagc gcgcctcaag cggtaaaaaa tacccttgtc 120

ctttctcaag aagcattaaa aacgcaccct cagattattt tccaaggcat gatccaggcg 180

gtgataaaat cagacgccgc cgccgtcaag atcttgctgc ctctttatca ggcgcaggca 240

ggatacgatc cgaccctggc cgcatggggc aaggctattt tagccaaaga ggacggtaac 300

tatcgcgacg ccattcgtta ttaccgccgc gtcatcgcca aggaaccaca gctaaatatt 360

gcccgactgc agctggctat cgcgctgttt cagaataaag accgcgcctc tgcgctactg 420

caattcaata agctgcgggc taatagcaac ggcgaaagag tcaatgagat agtggatggc 480

tatatcaggg caatacagcg gaaagacagc tggtcattca acgtaggcgt taactatatt 540

aatgagagta acattaataa tgcgccagac gctaacgtaa aaattggtca gtggcaggct 600

gagaaacggc aaagcggaca gggcttttcc tactatctta gtggtagcaa aacctggtca 660

ttgccggagg ggctgttcag cgaggtccgt acgctggcct acgggaagta cttcaccaac 720

aatcatcgct acgatcaggc aacggcccgt ctgagcgcag gtctgggcct acgcgatatc 780

aacgcctccc tgctgctctt gccctttata gagcgcgaat gggcatcgga taatcaggcg 840

ccctcccttt ctagcgaagg agcatcgccg gggctgcgta ttgagacaga ataccgtctg 900

agccctcgct ggaaaatcga tgttgacgct gagaaaagtc acactacgaa taaacatcac 960

gcccaacgcg acagcaaaaa tcatctgctg tctgcgacac tctattattt tcccagcccc 1020

gagcaatttt ggttttgggg tagtgactac cagcgtgaaa acgttgagcg taagagcata 1080

gcctttcaga aaataaagtg gcgaggcggc tggggaaatg agtggccggg cggcatatcc 1140

agcatcatgc agataaacta cgccaataag ttttacgata gcgctgactt cttcggaatt 1200

cagcaaagaa ataaagagta cggcgccctg ataacgctct ggcaccgtga catttattac 1260

tttggtatca cgccaaaaat caacctgtca tattttaaaa gtgacagcaa tcatccattt 1320

tatgaatacg ataaaaaaaat ggtcttcctg acctttagca agctttttta a 1371

<210> 186

<211> 456

<212> PRT

<213> F. aurantia SLAM 1

<400> 186

Met Leu Ile Lys Ile Glu Pro Pro Leu Leu Gln Ile Gly Ser Ala Ile
1 5 10 15

Leu Leu Ser Val Leu Thr Met Ser Ala Ala Asp Ala Ala Ser Ala Pro
20 25 30

Gln Ala Val Lys Asn Thr Leu Val Leu Ser Gln Glu Ala Leu Lys Thr

35 40 45

His Pro Gln Ile Ile Phe Gln Gly Met Ile Gln Ala Val Ile Lys Ser
50 55 60

Asp Ala Ala Ala Val Lys Ile Leu Leu Pro Leu Tyr Gln Ala Gln Ala
65 70 75 80

Gly Tyr Asp Pro Thr Leu Ala Ala Trp Gly Lys Ala Ile Leu Ala Lys
85 90 95

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

100 105 110

Ala Lys Glu Pro Gln Leu Asn Ile Ala Arg Leu Gln Leu Ala Ile Ala
115 120 125

Leu Phe Gln Asn Lys Asp Arg Ala Ser Ala Leu Leu Gln Phe Asn Lys

130 135 140

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

145 150 155 160

Tyr Ile Arg Ala Ile Gln Arg Lys Asp Ser Trp Ser Phe Asn Val Gly

165 170 175

Val Asn Tyr Ile Asn Glu Ser Asn Ile Asn Asn Ala Pro Asp Ala Asn

180 185 190

Val Lys Ile Gly Gln Trp Gln Ala Glu Lys Arg Gln Ser Gly Gln Gly

195 200 205

Phe Ser Tyr Tyr Leu Ser Gly Ser Lys Thr Trp Ser Leu Pro Glu Gly

210 215 220

Leu Phe Ser Glu Val Arg Thr Leu Ala Tyr Gly Lys Tyr Phe Thr Asn

225 230 235 240

Asn His Arg Tyr Asp Gln Ala Thr Ala Arg Leu Ser Ala Gly Leu Gly

245 250 255

Leu Arg Asp Ile Asn Ala Ser Leu Leu Leu Leu Pro Phe Ile Glu Arg

260 265 270

Glu Trp Ala Ser Asp Asn Gln Ala Pro Ser Leu Ser Ser Glu Gly Ala

275 280 285

Ser Pro Gly Leu Arg Ile Glu Thr Glu Tyr Arg Leu Ser Pro Arg Trp

290 295 300

Lys Ile Asp Val Asp Ala Glu Lys Ser His Thr Thr Asn Lys His His

305 310 315 320

Ala Gln Arg Asp Ser Lys Asn His Leu Leu Ser Ala Thr Leu Tyr Tyr

325 330 335

Phe Pro Ser Pro Glu Gln Phe Trp Phe Trp Gly Ser Asp Tyr Gln Arg

340 345 350

Glu Asn Val Glu Arg Lys Ser Ile Ala Phe Gln Lys Ile Lys Trp Arg

355 360 365

Gly Gly Trp Gly Asn Glu Trp Pro Gly Gly Ile Ser Ser Ile Met Gln

370 375 380

Ile Asn Tyr Ala Asn Lys Phe Tyr Asp Ser Ala Asp Phe Phe Gly Ile

385 390 395 400

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

405 410 415

Asp Ile Tyr Tyr Phe Gly Ile Thr Pro Lys Ile Asn Leu Ser Tyr Phe

420 425 430

Lys Ser Asp Ser Asn His Pro Phe Tyr Glu Tyr Asp Lys Lys Met Val

435 440 445

Phe Leu Thr Phe Ser Lys Leu Phe

450 455

<210> 187

<211> 1500

<212> DNA

<213> F. aurantia SLAM 1

<400> 187

atgcgcaaac gtgcaagatc tgcaggaccg ggacaggaag cggctcgccg cctcctgtcc 60

cttatcgtgt ggctgacgat gctgatggtt atcccggaac tgggccaggc ccagaccgtc 120

gaggacaacc agctgcggct gaaccagtcc ggccagcgcc ggtccgccag ccgagatcgt 180

gccttgctgg aggatacgga taccctgacc gtggatggtc gtgactacag cgtggcacat 240

accgtcagcg agataggcca ggccatctat atcgcactgg gccggcagca atggcctgac 300

gtgcagcgct ttctgcggcg ctatgccagc atgcccggcg ctgacccgat gctgctgcat 360

tatgctcgcg gcgggctggc ccgccacaag ggacatctgc gtcaggcaga gcgcgaatac 420

cgcgccctgc tggccttgca gccggatttt ctgcccggcc agctggaatt ggcccgggtc 480

ctgttcgaga accagcggga tcaggcagcc gcaacccagt tccggcagat tgccgccgcg 540

ctgccctcaa cggccaaggc cgacggcatc cgccataccg tacagctgtt tctgcaggcc 600

ttgcgacgac gacacagctg gcaaggcagc ttcgctctag gccccggcta caatgacaat 660

atcaaccagg cccaggccag ccagacctgc ctgtggatcg acggcgcggg caactgcatc 720

atccatcggc gcatgcccgc cgccatcgca gccaccggtc tggatatcga ggccagcctg 780

tttcgccagc aaccgttgtc gggtccgcac aatatctact tgcgcagcct gctgatgggc 840

agcctgtatc ccggccatac ccgctaccat cagctgaaca gcctcaacca gatcggctac 900

cagtaccgca acggccacga cacctggatg ctggcccccg gcttcgatgc cggcagctat 960

ggcagcggtc tgctctatcg ggcctggggc ctgcatggcg aatggagcca cggctttgct 1020

tcgtcctggc tgctgaagct ggaagccgat cacaagcgtt tccgttatcc catgttcggc 1080
taccgtgatt tcgacggcca tctggaggac ggctttgtca ccgtgtcgcg cgctgtcggc 1140
cagcactggc tgctgctggg tgggctggac ctggtcgaca agcaggcacg cgacccggct 1200
cagggtttca tgcagcgtgg cgcacgactg ggtgccgtct acagtctgga gaaccagttc 1260
agcctgtatc tgatggcttc cgtccgcgag cgcgactacg ccgccttcaa tcccatgctg 1320
gcacaacgac gccatgatct ggaacggaat ctgatcctga tcgccagcct gcctcgctgg 1380
tcgctgttcg ggatctatcc cagcctggtc gcccagatca gcgagatacg cagcaatgtg 1440

gactggctgt acagctatca acgacgccag atcagtctgc gtctgcaacg accgttttga 1500

<210> 188
<211> 499
<212> PRT
<213> F. aurantia SLAM 1
<400> 188

Met Arg Lys Arg Ala Arg Ser Ala Gly Pro Gly Gln Glu Ala Ala Arg
1 5 10 15
Arg Leu Leu Ser Leu Ile Val Trp Leu Thr Met Leu Met Val Ile Pro
20 25 30
Glu Leu Gly Gln Ala Gln Thr Val Glu Asp Asn Gln Leu Arg Leu Asn
35 40 45

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

Gly Ala Asp Pro Met Leu Leu His Tyr Ala Arg Gly Gly Leu Ala Arg
115 120 125
His Lys Gly His Leu Arg Gln Ala Glu Arg Glu Tyr Arg Ala Leu Leu

130 135 140

Ala Leu Gln Pro Asp Phe Leu Pro Gly Gln Leu Glu Leu Ala Arg Val
145 150 155 160
Leu Phe Glu Asn Gln Arg Asp Gln Ala Ala Ala Thr Gln Phe Arg Gln
165 170 175

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

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

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

Glu Asp Gly Phe Val Thr Val Ser Arg Ala Val Gly Gln His Trp Leu
370 375 380

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

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

Arg Pro Phe

<210> 189
<211> 1494
<212> DNA
<213> G. anatis SLAM 1
<400> 189
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tttccgtttg tttttataac aaatagttta gctgctcctg ttacttcccc gacaaccgtt 120
attgatgtta agactgagcc aaaagaatat attaatgtgg cacaaccgga tttacgttct 180
acgccaaaag tgcaaccaaa agagacagct acgaaacaag atgacagccg tgaaattacg 240
gatgaagaat tgcaacaacg ccctgaactt gcacgtaggt tattaaatta tgttattgat 300
acacaacgtt ggcatttatt gcctgatctt ttagagattt ataagaaaac tcgtgatcct 360

gatcctattc tcattgatta tgctcaagcg acactttatc gtgtacaagg taatttaaca 420
ggagcaatta gcttatatcg ccatattttg gcagacaatc caaactttgg acctgttcgt 480
ttcgcattag cacaagcctt attcgaggat taccaaacag aagcagcaga agatcaattt 540
aataaattac gagcaagctc aaaccttccg ccagagatta tggctgtttc tgagcaatat 600
ttaatggcaa ttaagcaaca atcagcatgg tcgtttagtg gctctttatc ttatttacaa 660

gatgataatg tgaataatgc agcaaaagat aaagtggttt atattggtaa tgtacctttc 720

caaaaaagtg aagaatcttt gccacaatca gcccatggtt tgcaatatag tatcaatttg 780

agcaaaaaat ttaatttaat tggtcgccat tcgctttatt tagaaaataa tttgtatgga 840

aaaagttttt gggataacca cgaatatgac gatattctga accgtactac agtgggttat 900

caatatcagg atataaagaa tcgttttgct attcttcctt tctatgctta tcgctggttc 960

ggtggtgaga aatatagccg taattatggt actcgttttg agtatgaacg ttggttatca 1020

ccaaaatggc aaaccagttc agccattgaa ttaagtaaaa cgaaatataa agaaaatagt 1080

gatgcggata gtaatagtca actttattct acaaccttac ttcacttatt taatgcgaaa 1140

acctattttt atgggggagt agattatcaa cgtgaaaaag ctcaaaatcg aatgttttct 1200

tccgatcgaa tgggatttcg tttggggtgg ggacaagaat ggaaatgggg actttctacc 1260

cgtttacaat ttggcataga acatcgtaac tttaaagaaa agaacctatt ttttaataag 1320

gttcgtaaag ataaagaata taatagtgtc tttactatat ggaatcgtga atggcattta 1380

tggggaatta ctccaaaact taattttagt tggatgagag tagatagtaa tattccagca 1440

ctgtatagtt atgataaaaa tagagttttt ttaaattttg agaaaacatt ctaa 1494

<210> 190

<211> 497

<212> PRT

<213> G. anatis SLAM 1

<400> 190

Met Pro Asn Leu Val Lys Lys Thr Ala Lys Phe Ala Phe Ser Pro Met

1 5 10 15

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

20 25 30

Pro Val Thr Ser Pro Thr Thr Val Ile Asp Val Lys Thr Glu Pro Lys

35 40 45

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

50 55 60

Gln Pro Lys Glu Thr Ala Thr Lys Gln Asp Asp Ser Arg Glu Ile Thr

65 70 75 80

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

85 90 95

Tyr Val Ile Asp Thr Gln Arg Trp His Leu Leu Pro Asp Leu Leu Glu
100 105 110
Ile Tyr Lys Lys Thr Arg Asp Pro Asp Pro Ile Leu Ile Asp Tyr Ala
115 120 125
Gln Ala Thr Leu Tyr Arg Val Gln Gly Asn Leu Thr Gly Ala Ile Ser

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

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

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

325 330 335
Arg Trp Leu Ser Pro Lys Trp Gln Thr Ser Ser Ala Ile Glu Leu Ser

340 345 350

Lys Thr Lys Tyr Lys Glu Asn Ser Asp Ala Asp Ser Asn Ser Gln Leu

355 360 365

Tyr Ser Thr Thr Leu Leu His Leu Phe Asn Ala Lys Thr Tyr Phe Tyr

370 375 380

Gly Gly Val Asp Tyr Gln Arg Glu Lys Ala Gln Asn Arg Met Phe Ser

385 390 395 400

Ser Asp Arg Met Gly Phe Arg Leu Gly Trp Gly Gln Glu Trp Lys Trp

405 410 415

Gly Leu Ser Thr Arg Leu Gln Phe Gly Ile Glu His Arg Asn Phe Lys

420 425 430

Glu Lys Asn Leu Phe Phe Asn Lys Val Arg Lys Asp Lys Glu Tyr Asn

435 440 445

Ser Val Phe Thr Ile Trp Asn Arg Glu Trp His Leu Trp Gly Ile Thr

450 455 460

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

465 470 475 480

Leu Tyr Ser Tyr Asp Lys Asn Arg Val Phe Leu Asn Phe Glu Lys Thr

485 490 495

Phe

<210> 191

<211> 1419

<212> DNA

<213> G. anatis SLAM 2

<400> 191

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gccgcacaag aattatcaca acccttgcca atcagcaata ttgctcaacc tgaacaacca 120

ccacaacaaa tacaaaatac gccaacagaa aacggaaatt ggcaacaggt tgatttctct 180

actaatatac aaaatcagct gaatctcgca ttgcgtaaac gtaatgcagc agaaatcgcc 240

tattggctca aacactatca agcaaacacg ccacagcaac aatttctgcg cgattatgct 300

cagggcgtat tagcacagct caacggggat tatacgcagg cagttactta ctatcgccaa 360

ttattagctc aatcaccaga tctaaacccg atccgccttg agcttgcacg ctcactgttt 420

gccttaaaac aagacgataa tgcgcgcact caatttgaaa aattactttc cgcaccggat 480

ttaccttccc cattacaacg agaaatcggt gcttatctca ataccttgca acaacgcaat 540

caatgggaaa ttcaattgag cggatattat gtacgtgata caaatgtgaa taacgccaat 600

gatacaaaac aaattgaagg tatcgctcag ctctataaaa aagatgattg gttaccacaa 660

actgcgcacg gcattgctta cagcttacaa gcaagacgag atttcaacct ttggcaagcc 720

tattatctac atttaaacgc ggaattattt ggcaaaacct attgggataa tcacgattat 780

gatgatctct acatccgtac ttatgtagga ataaagcaca aaagccaacg ccaaacttgg 840

gcgcttttgc ctttttacga acggcgcttt tacggcaatc atcgctatca agaaggtaca 900

ggattacgct tagaatatca acgttggcta tcgccaaatt ggcaaatcag ctcagcattg 960

gaatacactc gcacgcgtta tgatgaaatt gcgagcctaa atgggaataa tcgtttgtgg 1020

tcaaacaccc taatttggct tactagccca cgacaatttt ttattttagg ggctgattat 1080

caacaagaac gcacgcaagt aaaacgctac caaaaccata cacaaacctt acgcttaggc 1140

tggggacgag aatggcagct gggcatttca agccgaattc aatttagcat agccaaacga 1200

cattataaag acaaagcaaa aattgcgatt ttctcactag gtaaaattcg ccaagatcac 1260

atttatcgtg cggagatttt actatggaaa cgagattggc actggcttgg catcacccct 1320

aaattacaat tccaatggag aaaacagcac agcaacttac catcacttta taattatcag 1380

aacagaagta ttaatgtgat ttttgagaaa agcttttaa 1419

<210> 192

<211> 472

<212> PRT

<213> G. anatis SLAM 2

<400> 192

Met Arg Phe Ser Ile Pro Val Phe Thr Leu Ser Leu Leu Phe Val Ser
1 5 10 15

Asn Thr Leu Phe Ala Ala Gln Glu Leu Ser Gln Pro Leu Pro Ile Ser
20 25 30

Asn Ile Ala Gln Pro Glu Gln Pro Pro Gln Gln Ile Gln Asn Thr Pro
35 40 45

Thr Glu Asn Gly Asn Trp Gln Gln Val Asp Phe Ser Thr Asn Ile Gln
50 55 60

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

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

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

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

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

305 310 315 320

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

325 330 335

Asn Arg Leu Trp Ser Asn Thr Leu Ile Trp Leu Thr Ser Pro Arg Gln

340 345 350

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

355 360 365

Arg Tyr Gln Asn His Thr Gln Thr Leu Arg Leu Gly Trp Gly Arg Glu

370 375 380

Trp Gln Leu Gly Ile Ser Ser Arg Ile Gln Phe Ser Ile Ala Lys Arg

385 390 395 400

His Tyr Lys Asp Lys Ala Lys Ile Ala Ile Phe Ser Leu Gly Lys Ile

405 410 415

Arg Gln Asp His Ile Tyr Arg Ala Glu Ile Leu Leu Trp Lys Arg Asp

420 425 430

Trp His Trp Leu Gly Ile Thr Pro Lys Leu Gln Phe Gln Trp Arg Lys

435 440 445

Gln His Ser Asn Leu Pro Ser Leu Tyr Asn Tyr Gln Asn Arg Ser Ile

450 455 460

Asn Val Ile Phe Glu Lys Ser Phe

465 470

<210> 193

<211> 1398

<212> DNA

<213> G. anatis SLAM 3

<400> 193

atgaaaaaat tattgatcac cagttttgtc atttttgcat attcattaaa tgctgaatct 60

ttattacggc aagatccaat tgatttttcg caagaaggtg atatttcatt acctacacag 120

ctaaaaccca atgctaatta tcaaaaaatg ccaatgattt ctatggcatt gccaattgat 180

tcacaaattc aatctgcgat tttacagcaa caatgggcat tattacctag attattaagg 240

caatatcaac aacagggaca ttatgatcct gcgttgtatc attatgcgtt agctgcctat 300

tatttcaata cgttacagta tgataaagct attctgcatt atcaaacatt attagattta 360

caccctgaag tcatttaccc tcgctttgat atggcagtga ttttttttga aaattatcaa 420

tatttacaag ccaagcaaca atttgaacgt ttaatgctta aagcagatgg caaattaaaa 480

acattgattg aagcctattt gcaagaaatt aaacatcgtc agcaatggca gccctatgtg 540

aattttcaat atgtgaaaac agataatgtg aataatgctt cttctgaacg agagataact 600

attaatggta aaccgcttgt aaaagacgaa gaatcacttc ctcaatcagc acaaggtgtt 660

cggtatgcgt ttgaacttga acgaataaaa aatataacag gcaatcattt ttggcaaacg 720

acattaggat ataacggtgt ttactattgg gataatcaat attataacga acaaacttta 780

catttttcat tgggttatat gtggcgagat gctcagtttg ttggaaaaat tattcctttt 840

gttgaacaga attggtttgg cgttcatcgt tacaatcatc aatttggcgt aaagttgttt 900

agccaaattc aactttctga acactggctt tggcagaatc gtttggcaaa tatgagaaaa 960

cattatgctg atactagttt ggcagatcgt tataatggta atgaaaacac tgtttcgacc 1020

actataattt ggcaagataa tacacattgg caatcttggc ttaatttaga attggtgtcc 1080

gatcgtttaa aagagaagtc ttcatcatcg ttgaaatggg caagtggttt tggtattact 1140

tattatcaaa aacaatgggg tacacaaatc aatgttcgtt atatagatcg taattttgct 1200

gatcatcact atttaatgca tttaaaacgg cacgacagag aatatcaact aaatggtgcg 1260

atttggtatc aaaaattatc ttggagaggc ttcttgccta aattacatat ccgctatcaa 1320

cggataaaca gcaatattcc tgcactttat agccgaaaaa atcaggaact ctttttacg 1380

atagagaagc aattttag 1398

<210> 194

<211> 465

<212> PRT

<213> G. anatis SLAM 3

<400> 194

Met Lys Lys Leu Leu Ile Thr Ser Phe Val Ile Phe Ala Tyr Ser Leu
1 5 10 15

Asn Ala Glu Ser Leu Leu Arg Gln Asp Pro Ile Asp Phe Ser Gln Glu
20 25 30

Gly Asp Ile Ser Leu Pro Thr Gln Leu Lys Pro Asn Ala Asn Tyr Gln
35 40 45

Lys Met Pro Met Ile Ser Met Ala Leu Pro Ile Asp Ser Gln Ile Gln
50 55 60

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

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

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

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

Leu Ser Glu His Trp Leu Trp Gln Asn Arg Leu Ala Asn Met Arg Lys

305 310 315 320

His Tyr Ala Asp Thr Ser Leu Ala Asp Arg Tyr Asn Gly Asn Glu Asn

325 330 335

Thr Val Ser Thr Thr Ile Ile Trp Gln Asp Asn Thr His Trp Gln Ser

340 345 350

Trp Leu Asn Leu Glu Leu Val Ser Asp Arg Leu Lys Glu Lys Ser Ser

355 360 365

Ser Ser Leu Lys Trp Ala Ser Gly Phe Gly Ile Thr Tyr Tyr Gln Lys

370 375 380

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

385 390 395 400

Asp His His Tyr Leu Met His Leu Lys Arg His Asp Arg Glu Tyr Gln

405 410 415

Leu Asn Gly Ala Ile Trp Tyr Gln Lys Leu Ser Trp Arg Gly Phe Leu

420 425 430

Pro Lys Leu His Ile Arg Tyr Gln Arg Ile Asn Ser Asn Ile Pro Ala

435 440 445

Leu Tyr Ser Arg Lys Asn Gln Glu Leu Phe Phe Thr Ile Glu Lys Gln

450 455 460

Phe

465

<210> 195

<211> 1446

<212> DNA

<213> H. aegyptius SLAM 1

<400> 195

atgaaaaatg gcgtaaaaca aatttctctc ttatcattaa taggcttatc attaccgaat 60

gtagcttggg cagatgttgc acgtcctaaa aatgatacat tgacaaatac gattcaaagt 120

gcggaattaa aaacctcctc tttttcttct atgcctaaga aagaaatacc aaataggcat 180

attatttctc tttccaaaag ccaattagca caacatccaa gacttgtttt gcgtgggtta 240

attcttgctt tatatcaaaa taacactcag gcagttcaac tgttattacc actatataaa 300

caatttcctc agcaagataa tttcttactc acttgggcaa aggctattga agcgcgtgaa 360

caaggcgatt taactcaatc tattgcttat tatcgtgaat tattcgctct agacgcatct 420

ttactacctt tgcgttatca attagctcaa gccctatttt ttaactatga aaatgaatct 480

gccaaaattc aatttgaaaa attacgtaca gaggtagatg atgaaaaatt tttaggtgtt 540

attgatcagt atcttttaac actaaatcag cggaatcaat ggatatggca agtaggctta 600

aatttttaa atgatgataa tttgaataac gctccaaaaa gtggcacaaa aattggtaat 660

tggaccgctt gggaaaaaga aagtgggaag ggggtagggt attctttatc agtagaaaaa 720

aaatggccgt gggcagatca tttttttagt aaaactatgt ttaatgggaa tggaaaatat 780

tattgggata ataaaaaata caatgaggct acttttcgta taggtggtgg tttaggttat 840

caaactgcct tagttgaagt ctcgttgttt ccttttcaag aaaaacgctg gtatgcaggc 900

ggtagctctg gaacgaatac aatgaagcaa tatgcggata aattgggtat tcgtttagaa 960

aacgtagatt ggctaagtaa aacttggcaa atttctaccg cacttgagta tggaaaatct 1020

cgttataaaa cccgaaaaca tttagatggt gattattatt tcatttcatc aacactattt 1080

tatttaccta aaagcactca attttggttt gttggcatgg attttcatcg agaaaataca 1140

caagcattag ataatgctta tcaacaaaag acattgagat ttggttgggg gcaggattgg 1200

tcttatggta tttcatcacg ttttacttttt agttatgcca accgagtgta tagagagaaa 1260

gatttgattg ggatacagca aaaaaatcgt gaatacacaa ccacaattac tttatggcat 1320

cgaaatatac attttatggg attaacacct aaattatcgt gggattatca aaaatccact 1380

agtaatcatg ctttttatcg ttatgataaa aatagaattt atctcgaaat tggaaaaata 1440

ttttaa 1446

<210> 196

<211> 481

<212> PRT

<213> H. aegyptius SLAM 1

<400> 196

Met Lys Asn Gly Val Lys Gln Ile Ser Leu Leu Ser Leu Ile Gly Leu

1 5 10 15

Ser Leu Pro Asn Val Ala Trp Ala Asp Val Ala Arg Pro Lys Asn Asp

20 25 30

Thr Leu Thr Asn Thr Ile Gln Ser Ala Glu Leu Lys Thr Ser Ser Phe

35 40 45

Ser Ser Met Pro Lys Lys Glu Ile Pro Asn Arg His Ile Ile Ser Leu

50 55 60

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

65 70 75 80

Ile Leu Ala Leu Tyr Gln Asn Asn Thr Gln Ala Val Gln Leu Leu Leu

85 90 95

Pro Leu Tyr Lys Gln Phe Pro Gln Gln Asp Asn Phe Leu Leu Thr Trp

100 105 110

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

115 120 125

Ala Tyr Tyr Arg Glu Leu Phe Ala Leu Asp Ala Ser Leu Leu Pro Leu

130 135 140

Arg Tyr Gln Leu Ala Gln Ala Leu Phe Phe Asn Tyr Glu Asn Glu Ser

145 150 155 160

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

165 170 175

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

180 185 190

Gln Trp Ile Trp Gln Val Gly Leu Asn Phe Leu Asn Asp Asp Asn Leu

195 200 205

Asn Asn Ala Pro Lys Ser Gly Thr Lys Ile Gly Asn Trp Thr Ala Trp

210 215 220

Glu Lys Glu Ser Gly Lys Gly Val Gly Tyr Ser Leu Ser Val Glu Lys

225 230 235 240

Lys Trp Pro Trp Ala Asp His Phe Phe Ser Lys Thr Met Phe Asn Gly

245 250 255

Asn Gly Lys Tyr Tyr Trp Asp Asn Lys Lys Tyr Asn Glu Ala Thr Phe

260 265 270

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

275 280 285

Leu Phe Pro Phe Gln Glu Lys Arg Trp Tyr Ala Gly Gly Ser Ser Gly

290 295 300

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

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

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

<210> 197
<211> 1542
<212> DNA

<213> H. haemolyticus SLAM 1
<400> 197
ttggcggatt tttgtccgcc atttttcaac ttattgtttg tttataaata tttacttaaa 60
gttactcatt ttatgaaaag tattgctctc ttttttactg cacttttccc cgctcttgct 120
ttagcagaaa caacggcacc agatattcgt caaacaccaa ttaaaaccga acttgaacct 180

caaattaatg tcgccaaact tgaaaaacgc gaacaaaatt taccgcactt aggtacagaa 240

caagcagaac aaattgaaat tacccttgag caacttaaac aaaaccccgc tttaacccac 300

gaattattaa gccgtgccat ttacgcacgc aatccaggaa tgataaaaaa attgctggaa 360

atttaccgca cttttccaaa tcgtgacccg attatggaac gctttgcgga aggaaaattg 420

gctgcgataa cggaaaacta tactgtagct attgataaat atcgcgaaat tttagccaaa 480

aatccaaatt taaaccctgt acgaattgaa ctggctatcg ctttattcaa tcaaaaacaa 540

gacggtgctg ctaaagacca atttgaaaaa gcacaaaccg cagaggattt accgcctcaa 600

gttaagcgtt taatggatgc ttatttagag gctttaaaag aacgtgatag ctggaatgtg 660

gatttttctt ttaattatgt acgtgatacc aatgtcaaca atgtcggcga gggaaaaacg 720

gtcgtattaa ataatggtgg caccttaaca cgttcggaat cgatgatgcc acaaacagca 780

cacggcttag cgtactcact ggatatttcc agagatttta atttatgggg ttctcattac 840

ctcacggtgg gcaatgagtt tgggggaaag agctactggg ataatcataa atttgatgat 900

atttccaacc gcacttttgt tggctatgca cataaaaccg caaagcaaaa tttccgtatt 960

aaaccctttt atgaaaaacg ttggtatggc ggcgaaagtt accgttggtc taatggggca 1020

agggtggaat tttctcgctg gttaagtcca aactggcaac tttttacggc gggagagttt 1080

tcaaaacaac gttatttaga cagtacatca caaaacggta ataacaaact gatttccgca 1140

accttactgt gggcaagaac accgaaacag ttttttctacc tcggttctga ttttatggca 1200

gaaagaacga aggttcgtca atatggttca gacagtaaaa gcttacgttt aggttggggg 1260

caagaatgga attggggcat ttcctcacgt ctcggcttat ccataatgaa acgtgaattt 1320

aaagatattg ccaaacttgg taatctcaat ttgttttctt ttggaaaacg tcgagaagat 1380

aaaatttacg gcataaattt atccctatgg aaacgcgatt ggcatatttg gggaattaca 1440

ccaaaactcc aattaagctg gcgtaaacaa gatagcaata tcccagaaat gtattcttat 1500

acacagaaga atgtgaatat gttgtttgaa aagacattct ga 1542

<210> 198

<211> 513

<212> PRT

<213> H. haemolyticus SLAM 1

<400> 198

Met Ala Asp Phe Cys Pro Pro Phe Phe Asn Leu Leu Phe Val Tyr Lys

1 5 10 15

Tyr Leu Leu Lys Val Thr His Phe Met Lys Ser Ile Ala Leu Phe Phe

20 25 30

Thr Ala Leu Phe Pro Ala Leu Ala Leu Ala Glu Thr Thr Ala Pro Asp

35 40 45

Ile Arg Gln Thr Pro Ile Lys Thr Glu Leu Glu Pro Gln Ile Asn Val

50 55 60

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

65 70 75 80

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

85 90 95

Ala Leu Thr His Glu Leu Leu Ser Arg Ala Ile Tyr Ala Arg Asn Pro

100 105 110

Gly Met Ile Lys Lys Leu Leu Glu Ile Tyr Arg Thr Phe Pro Asn Arg

115 120 125

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

130 135 140

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

145 150 155 160

Asn Pro Asn Leu Asn Pro Val Arg Ile Glu Leu Ala Ile Ala Leu Phe

165 170 175

Asn Gln Lys Gln Asp Gly Ala Ala Lys Asp Gln Phe Glu Lys Ala Gln

180 185 190

Thr Ala Glu Asp Leu Pro Pro Gln Val Lys Arg Leu Met Asp Ala Tyr

195 200 205

Leu Glu Ala Leu Lys Glu Arg Asp Ser Trp Asn Val Asp Phe Ser Phe

210 215 220

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

225 230 235 240

Val Val Leu Asn Asn Gly Gly Thr Leu Thr Arg Ser Glu Ser Met Met

245 250 255

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

260 265 270

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

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

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

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

<210> 199

<211> 1446

<212> DNA

<213> H. influenzae SLAM 1

<400> 199

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tcggttgcta cagaaaaatc tccacaacca catgatgggc gtttagatga gcagctacat 120

ttggccaaac caaatttacc acaaaaacca accgcacttt tgaccaataa taatccatca 180

aagttatcta ttacaaaaga agaattagcc aaacacccag acttgattat tcgcggtctt 240

atccctgccg tattacaaaa taatggtgag gcagtacaac ttttattacc gctatatcag 300

cctttaccta aaaaagatcc gttcttgtta gaatgggctg aagcgattga tttacgagaa 360

aaaggacatt tttctgattc tgttaaagcc taccgacact tattttcaca aaaaactgat 420

cttttacctt tgcgctatca attagctcaa gccttgtttc taaataatga taatgaggcg 480

gcaaaagatc aatttcaaaa attaagagca gagcaagttt cccctgattc tgtaaaaata 540

attgaacaat atctttctgc cttaaatcaa cgagatcaat ggaaaatcca aggtggattt 600

agtttttaa atgaaagtaa tattaataat gcgccaaaag ccggcacaaa aattggcaac 660

tggacagctt gggaaaaaga aagtgccaga ggattttcgt attttgggaa tgctgaaaaa 720

aaatggtcat tacctcacaa ccactttaca aaattgtcct tggaaggtag tgggaaatat 780

tattgggata acaagaaata taatgaattt aacgcgagag ctggtgcagg tcttggatac 840

caaactgcgc gatttgaagt ctccttgatg ccatttactg aaaaacgttg gtatgtgggc 900

ggctcatcag gcggaaatgc gatgaaacaa tactctaaaa attcaggtgc tagattggat 960

ttatccaatt ggctaaatga aaaatggcaa atttcgaccg cacttgagta tggtgaacaa 1020

cgctatgaaa ctcgtaaaca tctaaatgga aataactatc tagcttccgc tacgctactt 1080

tacctggcga aaagtggaca gtattggttt ggcggagctg attataatcg cgaaaacact 1140

cgagatttag ataatgctta tcaacgaaaa aatgtccgat taggatgggg acaagaatgg 1200

aaagctggta tatcaactcg tttaatcctg aattatgcac gacgtgccta taaagaaaaa 1260

gatcttatcg gtattcgtca aaaaaataag gaatatgctt cagtcttcac tatctggcat 1320

agaaactttc atatttgggg aattacaccg aaattatctt ggtcgtatca aaaggtaaca 1380

agtaatcatc ctttttatga atatgataaa aatcgaattt acgtagaaat cagcaaaaca 1440

ttttga 1446

<210> 200

<211> 481

<212> PRT

<213> H. influenzae SLAM 1

<400> 200

Met Ser Ile Gln Thr Lys Phe Ile Leu Phe Leu Ser Ser Ser Leu Phe
1 5 10 15

Leu Thr Pro Tyr Ser Val Ala Thr Glu Lys Ser Pro Gln Pro His Asp
20 25 30

Gly Arg Leu Asp Glu Gln Leu His Leu Ala Lys Pro Asn Leu Pro Gln
35 40 45

Lys Pro Thr Ala Leu Leu Thr Asn Asn Asn Pro Ser Lys Leu Ser Ile
50 55 60

Thr Lys Glu Glu Leu Ala Lys His Pro Asp Leu Ile Ile Arg Gly Leu
65 70 75 80

Ile Pro Ala Val Leu Gln Asn Asn Gly Glu Ala Val Gln Leu Leu Leu
85 90 95

Pro Leu Tyr Gln Pro Leu Pro Lys Lys Asp Pro Phe Leu Leu Glu Trp
100 105 110

Ala Glu Ala Ile Asp Leu Arg Glu Lys Gly His Phe Ser Asp Ser Val
115 120 125

Lys Ala Tyr Arg His Leu Phe Ser Gln Lys Thr Asp Leu Leu Pro Leu
130 135 140

Arg Tyr Gln Leu Ala Gln Ala Leu Phe Leu Asn Asn Asp Asn Glu Ala
145 150 155 160

Ala Lys Asp Gln Phe Gln Lys Leu Arg Ala Glu Gln Val Ser Pro Asp
165 170 175

Ser Val Lys Ile Ile Glu Gln Tyr Leu Ser Ala Leu Asn Gln Arg Asp
180 185 190

Gln Trp Lys Ile Gln Gly Gly Phe Ser Phe Leu Asn Glu Ser Asn Ile
195 200 205

Asn Asn Ala Pro Lys Ala Gly Thr Lys Ile Gly Asn Trp Thr Ala Trp

210 215 220

Glu Lys Glu Ser Ala Arg Gly Phe Ser Tyr Phe Gly Asn Ala Glu Lys
225 230 235 240

Lys Trp Ser Leu Pro His Asn His Phe Thr Lys Leu Ser Leu Glu Gly
245 250 255

Ser Gly Lys Tyr Tyr Trp Asp Asn Lys Lys Tyr Asn Glu Phe Asn Ala
260 265 270

Arg Ala Gly Ala Gly Leu Gly Tyr Gln Thr Ala Arg Phe Glu Val Ser
275 280 285

Leu Met Pro Phe Thr Glu Lys Arg Trp Tyr Val Gly Gly Ser Ser Gly
290 295 300

Gly Asn Ala Met Lys Gln Tyr Ser Lys Asn Ser Gly Ala Arg Leu Asp
305 310 315 320

Leu Ser Asn Trp Leu Asn Glu Lys Trp Gln Ile Ser Thr Ala Leu Glu
325 330 335

Tyr Gly Glu Gln Arg Tyr Glu Thr Arg Lys His Leu Asn Gly Asn Asn
340 345 350

Tyr Leu Ala Ser Ala Thr Leu Leu Tyr Leu Ala Lys Ser Gly Gln Tyr
355 360 365

Trp Phe Gly Gly Ala Asp Tyr Asn Arg Glu Asn Thr Arg Asp Leu Asp
370 375 380

Asn Ala Tyr Gln Arg Lys Asn Val Arg Leu Gly Trp Gly Gln Glu Trp
385 390 395 400

Lys Ala Gly Ile Ser Thr Arg Leu Ile Leu Asn Tyr Ala Arg Arg Ala
405 410 415

Tyr Lys Glu Lys Asp Leu Ile Gly Ile Arg Gln Lys Asn Lys Glu Tyr
420 425 430

Ala Ser Val Phe Thr Ile Trp His Arg Asn Phe His Ile Trp Gly Ile
435 440 445

Thr Pro Lys Leu Ser Trp Ser Tyr Gln Lys Val Thr Ser Asn His Pro
450 455 460

Phe Tyr Glu Tyr Asp Lys Asn Arg Ile Tyr Val Glu Ile Ser Lys Thr

465 470 475 480

Phe

<210> 201

<211> 1461

<212> DNA

<213> H. influenzae SLAM 2

<400> 201

atgaaaaatg gcgtaaaaca aatttctttc ttatcattaa taggcttatc attaataggc 60

ttatcattaa ccaatgtagc ttgggcaaaa gttgcacgtc ctaaaaatga tacattgaca 120

aatacaattc aaagtgcgga attaaaaacc tcctcttttt cttctatgcc taagaaagaa 180

ataccaaata ggcatattat ttctctttcc aaaagccaat tagcacaaca tccaagactt 240

gttttgcgtg ggttaattct tgctttatat caaaataaca ctcaggcagt gcaactgtta 300

ttaccactat ataaacaatt tcctcagcaa gataatttct tactcacttg ggcaaaggct 360

attgaagcgc gtgaacaagg cgatttaact caatctattg cttattatcg tgaattattc 420

gctcgagacg tatctttact acctttgcgt tatcaattag ctcaagccct atttttaac 480

tatgaaaatg aatctgccaa aattcaattt gaaaaattac gtacagaggt agatgatgaa 540

aaatttttag gtgttattga tcagtatctt ttaacactaa atcagcggaa tcaatggata 600

tggcaagtag gcttaaattt tttaaatgat gataatttga ataacgctcc aaaaagtggc 660

acaaaaattg gtaattggac cgcttgggaa aaagaaagtg ggaagggggt agggtattct 720

ttatcagtag aaaaaaaatg gccatgggca gatcattttt ttagtaaaac tatgtttaat 780

gggaatggaa aatattattg ggataataaa aaatacaatg aggctacttt gcgtataggt 840

ggtggtttag gctatcaaac tgccttagtt gaagtctcgt tgtttccttt tcaagaaaaa 900

cgctggtatg caggcggtag ctctggaacg aatacaatga agcaatatgc ggataaattg 960

ggtattcgtt tagaaaacgt agattggcta agtaaaactt ggcaaatttc taccgcactt 1020

gagtatggaa aatctcgtta taaaatccga aaacatttag atggtaatta ttatttcatt 1080

tcatcaacac tattttattt acctaaaagc actcaatttt ggtttgttgg catggatttt 1140

catcgagaaa atacacaagc attagataat gcttatcaac aaaagacatt gagatttggt 1200

tgggggcagg attggtctca tggtatttca tcacgtttta cttttagtta tgccaaccga 1260

gtgtatagag agaaagattt gattgggata cagcaaaaaa atcgtgaata cacaaccaca 1320

attactttat ggcatcgaaa tatacatttt atgggattaa cacctaaatt atcgtgggat 1380

tatcaaaaat ccactagtaa tcatgctttt tatcgttatg ataaaaatag aatttatctc 1440

gaaattggaa aaatatttta a 1461

<210> 202

<211> 486

<212> PRT

<213> H. influenzae SLAM 2

<400> 202

Met Lys Asn Gly Val Lys Gln Ile Ser Phe Leu Ser Leu Ile Gly Leu

1 5 10 15

Ser Leu Ile Gly Leu Ser Leu Thr Asn Val Ala Trp Ala Lys Val Ala

20 25 30

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

35 40 45

Lys Thr Ser Ser Phe Ser Ser Met Pro Lys Lys Glu Ile Pro Asn Arg

50 55 60

His Ile Ile Ser Leu Ser Lys Ser Gln Leu Ala Gln His Pro Arg Leu

65 70 75 80

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

85 90 95

Val Gln Leu Leu Leu Pro Leu Tyr Lys Gln Phe Pro Gln Gln Asp Asn

100 105 110

Phe Leu Leu Thr Trp Ala Lys Ala Ile Glu Ala Arg Glu Gln Gly Asp

115 120 125

Leu Thr Gln Ser Ile Ala Tyr Tyr Arg Glu Leu Phe Ala Arg Asp Val

130 135 140

Ser Leu Leu Pro Leu Arg Tyr Gln Leu Ala Gln Ala Leu Phe Phe Asn

145 150 155 160

Tyr Glu Asn Glu Ser Ala Lys Ile Gln Phe Glu Lys Leu Arg Thr Glu

165 170 175

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

180 185 190

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

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

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

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

435 440 445

His Phe Met Gly Leu Thr Pro Lys Leu Ser Trp Asp Tyr Gln Lys Ser

450 455 460

Thr Ser Asn His Ala Phe Tyr Arg Tyr Asp Lys Asn Arg Ile Tyr Leu

465 470 475 480

Glu Ile Gly Lys Ile Phe

485

<210> 203

<211> 1251

<212> DNA

<213> H. influenzae SLAM 3

<400> 203

atgaaaaata taatagtctt tttatcacta tgtttaatta gttctaatat ttatagtgaa 60

acgagagcaa ttaattataa ttcatctgat ataaaacaaa atccagcaat aatagaaatg 120

ttattgctgg atgccattga tgaagacaat attaatggaa tagaatcatt attgatagat 180

taccagagat tacataatgc tagacttgat ctaattgcta ttgccaaatt taaaattggt 240

caataccagt ttaataatta tcaaaataat aaatctttaa aaaattttca attagctaaa 300

ttaatattta attttccgcc acttcatttt tacatcatag aacagtacct atccgtttta 360

aaagcaagag aaagttggca attttcctta ggtgggaatt atttacaaac taagaacgtg 420

aataatacgt ctaatgagcg acatattgaa aacacaggct ttgtgaaaaa tgaggatatg 480

ttgccacaat cggcacatgg ctttgcttat tattttgatg ctcagaaaaa ttggaacata 540

gcaggttcgc attatctgca ttttgcgaat aacctatatg gcaaaaatta ttggaataat 600

cataattatg atgaaatcac taaccgcact tatttaggct atcaatatca aaatgctaaa 660

tataaattgg tattaaaacc gttttatgag cgtcaatggt tgggcggtca tcgttataac 720

tgggcaaatg gtgctagagc ggaatatagt ttaaatcttt caaaaaattg gcagatttca 780

accgcacttg aattaagcca gctacgttat tttacccaag cagatcgtaa tggaacaatt 840

aagttagctt ctgtaacctt tatttggcag ccatctgata aaggttatta ttacttaggt 900

tcggatttta ttcgcgaaac cacgcgtata aaacaatata gcaatgatat gaaagcatta 960

cgattaggtt ggcggcaaaa ttggggttat gcaattgcaa gtcaaattaa tggctctatt 1020

gcgttgaaac agtataagga ttttgcttct cttggtggga ttttgccgtt aaataaaatt 1080

cgtcgagata aaatctattc tctgaattta actttatgga aacaagattg gcagtattta 1140

ggttttacgc cgaaagtgca attccgttgg aaaaaacaag aaagtaacct tccttcaatg 1200

ttttcttatt cagaaaaata tgtgcagatg ttagtagaaa aggattttta a 1251

<210> 204

<211> 416

<212> PRT

<213> H. influenzae SLAM 3

<400> 204

Met Lys Asn Ile Ile Val Phe Leu Ser Leu Cys Leu Ile Ser Ser Asn
1 5 10 15

Ile Tyr Ser Glu Thr Arg Ala Ile Asn Tyr Asn Ser Ser Asp Ile Lys
20 25 30

Gln Asn Pro Ala Ile Ile Glu Met Leu Leu Leu Asp Ala Ile Asp Glu
35 40 45

Asp Asn Ile Asn Gly Ile Glu Ser Leu Leu Ile Asp Tyr Gln Arg Leu
50 55 60

His Asn Ala Arg Leu Asp Leu Ile Ala Ile Ala Lys Phe Lys Ile Gly
65 70 75 80

Gln Tyr Gln Phe Asn Asn Tyr Gln Asn Asn Lys Ser Leu Lys Asn Phe
85 90 95

Gln Leu Ala Lys Leu Ile Phe Asn Phe Pro Pro Leu His Phe Tyr Ile
100 105 110

Ile Glu Gln Tyr Leu Ser Val Leu Lys Ala Arg Glu Ser Trp Gln Phe
115 120 125

Ser Leu Gly Gly Asn Tyr Leu Gln Thr Lys Asn Val Asn Asn Thr Ser
130 135 140

Asn Glu Arg His Ile Glu Asn Thr Gly Phe Val Lys Asn Glu Asp Met
145 150 155 160

Leu Pro Gln Ser Ala His Gly Phe Ala Tyr Tyr Phe Asp Ala Gln Lys
165 170 175

Asn Trp Asn Ile Ala Gly Ser His Tyr Leu His Phe Ala Asn Asn Leu
180 185 190

Tyr Gly Lys Asn Tyr Trp Asn Asn His Asn Tyr Asp Glu Ile Thr Asn

195 200 205

Arg Thr Tyr Leu Gly Tyr Gln Tyr Gln Asn Ala Lys Tyr Lys Leu Val

210 215 220

Leu Lys Pro Phe Tyr Glu Arg Gln Trp Leu Gly Gly His Arg Tyr Asn

225 230 235 240

Trp Ala Asn Gly Ala Arg Ala Glu Tyr Ser Leu Asn Leu Ser Lys Asn

245 250 255

Trp Gln Ile Ser Thr Ala Leu Glu Leu Ser Gln Leu Arg Tyr Phe Thr

260 265 270

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

275 280 285

Trp Gln Pro Ser Asp Lys Gly Tyr Tyr Tyr Leu Gly Ser Asp Phe Ile

290 295 300

Arg Glu Thr Thr Arg Ile Lys Gln Tyr Ser Asn Asp Met Lys Ala Leu

305 310 315 320

Arg Leu Gly Trp Arg Gln Asn Trp Gly Tyr Ala Ile Ala Ser Gln Ile

325 330 335

Asn Gly Ser Ile Ala Leu Lys Gln Tyr Lys Asp Phe Ala Ser Leu Gly

340 345 350

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

355 360 365

Asn Leu Thr Leu Trp Lys Gln Asp Trp Gln Tyr Leu Gly Phe Thr Pro

370 375 380

Lys Val Gln Phe Arg Trp Lys Lys Gln Glu Ser Asn Leu Pro Ser Met

385 390 395 400

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

405 410 415

<210> 205

<211> 1464

<212> DNA

<213> H. parahaemolyticus SLAM 1

<400> 205

atgaaacttt cccactcaat tgtatttgca atctttggcc taaatctgac ctctttcgca 60

caggcagaaa tagtgcaacc gcaagaaaag aaaatggctg agcctaaaaa tgatttaacc 120

gaacgcttcc aagtggctca accaaaacct aaaactcagc ctgatacaga acaaacagaa 180

acatcaggct cggtgtcgat gacaaaagaa gaattagctc agcaccctga tttaatcgta 240

cgaggtttaa ttccagctgt gttacaaaac aacgaacaag cggtcgaatt attgttgccg 300

atgtaccaaa acttgccaaa gcaagatcca ttcttacgtg agtgggcaga agcgatttcg 360

gctaaagcac aaggcaattt tagccttgca gtagaacgtt accgctcgct ctttgcacaa 420

aaatcggata ttcctgcttt gcgttatcag ctcgctcaag ccctcttttt aaataacaat 480

aatgaggcag caaaagatca attccagaaa ttgcgtgcgg aaaatttatc gcccgattca 540

gtggcaatta tcgaccaata tttgactgct ttaaataaac gtgatcagtg gaaatttagc 600

ggtggaatga gcttccttaa cgagacgaat atcaacaatg cacctaaagc gggcacgaga 660

gtaggcggtt gggaagcatg gaaaaaagag agtgcacagg gcttttctta ctacttcaac 720

actgagaaaa aatggtcgtt gccaaatcag tttttcacca aaatagcgtt ggatacttcg 780

ggaaaatatt attgggataa caaaaaatat aacgagctta atgtgcggac aggtgttggc 840

ttaggctatc aaaccgcacg ttttgaaatt gctcttaccc cctttaccga gaaacgttgg 900

tatgcgggtg gttcatcggg cagtgaatcg cttaaacaat attcaaaaaa ctcaggtgtg 960

cagcttgaaa gcagttactg gctgaatgaa aaatggcaac tttcaaatgt attggaatat 1020

ggtgaacaac gctacgactg gcgtaagcac ctaaacggca acaactattt gtggtcaaac 1080

acgctcttat atgtgccaaa aagcgggcaa tattggtttg caggtttgga ttacaatcgt 1140

gaaaatactc gcgataaaga caatgcttac caacgtacta gtgcacgttt aggctggggg 1200

caagaatggg gctggggaat ttctagccgc atctcgtttt cttatgcgaa gcgaacttat 1260

caggcacatc ctgctccaga tttaatcggc aaaatacaaa aaaatgatga atattcttct 1320

gctttaacgc tctggcatcg tgacttgcat ttctttggcg tgacaccaaa agtgacgtgg 1380

caatatcaga aagtaagcag taaccaccca ttttatagct acgataaaaa tcgggtttat 1440

tttgagatga gtaaaacatt ttaa 1464

<210> 206

<211> 487

<212> PRT

<213> H. parahaemolyticus SLAM 1

<400> 206

Met Lys Leu Ser His Ser Ile Val Phe Ala Ile Phe Gly Leu Asn Leu

1 5 10 15

Thr Ser Phe Ala Gln Ala Glu Ile Val Gln Pro Gln Glu Lys Lys Met

20 25 30

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

35 40 45

Lys Pro Lys Thr Gln Pro Asp Thr Glu Gln Thr Glu Thr Ser Gly Ser

50 55 60

Val Ser Met Thr Lys Glu Glu Leu Ala Gln His Pro Asp Leu Ile Val

65 70 75 80

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

85 90 95

Leu Leu Leu Pro Met Tyr Gln Asn Leu Pro Lys Gln Asp Pro Phe Leu

100 105 110

Arg Glu Trp Ala Glu Ala Ile Ser Ala Lys Ala Gln Gly Asn Phe Ser

115 120 125

Leu Ala Val Glu Arg Tyr Arg Ser Leu Phe Ala Gln Lys Ser Asp Ile

130 135 140

Pro Ala Leu Arg Tyr Gln Leu Ala Gln Ala Leu Phe Leu Asn Asn Asn

145 150 155 160

Asn Glu Ala Ala Lys Asp Gln Phe Gln Lys Leu Arg Ala Glu Asn Leu

165 170 175

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

180 185 190

Lys Arg Asp Gln Trp Lys Phe Ser Gly Gly Met Ser Phe Leu Asn Glu

195 200 205

Thr Asn Ile Asn Asn Ala Pro Lys Ala Gly Thr Arg Val Gly Gly Trp

210 215 220

Glu Ala Trp Lys Lys Glu Ser Ala Gln Gly Phe Ser Tyr Tyr Phe Asn

225 230 235 240

Thr Glu Lys Lys Trp Ser Leu Pro Asn Gln Phe Phe Thr Lys Ile Ala

245 250 255

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

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

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

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

<210> 207

<211> 1425

<212> DNA

<213> H. parahaemolyticus SLAM 2

<400> 207

atgaaaaaac tcgcaaactt tcttattttt ctaccgcttg cagttcaagc ggaaaccttt 60

cacgcacctc aacctgtttt ctttgaaaac aatactttgc ccaaacagac tgaaccacaa 120

ataaaaacgc aactacaaac agaaaatccg cctgcccctt cgtttgccct ttctgatgca 180

gacagcacca aaaccaagct agagaagttg attaactatg gtgtattaaa acagcaatgg 240

catttgttga agcagattct gccgttgtat caacagcagg cggattatga tgaaacgctt 300

tatcgttacg caatgggggc gatgttgcgg gcggaaaaag aatatccaca ggcaatttcg 360

ctttatcagc agattttagc cgagaagcca gagttagctt atccgcggtt tgatttgggg 420

atgatgctgt ttgagaataa acaatatcgc caagcaaaag cggagttgga acgtgctaag 480

cccgaacttt caccacaaat gcagcaactt accgaacatt atattcaggc gatgatagag 540

cggcaaagtt ggcagcctga tatggagctg caatataccc aaaccgataa cgtgaacaat 600

gcttcttctc agcaagatat tgtgttaggc gacttgcggt ttaaaaaaga tgcggaatcg 660

ctgccacaaa aagcccacgg cttccgttat ggtgtgggcg tgaaccgtga attgaatgtg 720

ggcggcaacc attttgttac cacaaatggt cgctttagtg gcgtgcatta ttgggataag 780

caagattata gcgaaaaatc actttatgct tcgcttggtt atcgttaccg ttcggcattg 840

caagcggtcg gattttcccc atttttgaa cagaactggc tcggttcacc acgttatagc 900

aaaaattacg gtgcagttgc agattttcgt caagaattga ccgcttactg ggcaatttca 960

ggatcttttt cgcatacgca aaaacgctat gcacaagaaa gcgtggctcg ccgtcataat 1020

ggttacttaa atggtgtttc attttcgtta agctaccaag ccaagccgaa ttggttgctg 1080

tttggtggca tggaagacag tgttgatcgt agcaaagata aagcggaatc ttcgcttcgc 1140

cgtggggtga atatcggttc agtgtgggaa atgaaggatt ttgtgagccg cgtgagcgtg 1200

cgttatgtaa aacgtgattt ccaagcggaa aatttctatt tcccaatgaa aaaacgccaa 1260

gataaagaat acagttttaa cgccaccatt tggcataaca aactacaatg gcaaggtttt 1320

gtaccgaagc taaattatcg ctaccgcaaa attgatagca atattccaga attttattct 1380

agaaaaagtg gcgagtggtt tgtgtcagta gagaaagatt tttag 1425

<210> 208

<211> 474

<212> PRT

<213> H. parahaemolyticus SLAM 2

<400> 208

Met Lys Lys Leu Ala Asn Phe Leu Ile Phe Leu Pro Leu Ala Val Gln
1 5 10 15
Ala Glu Thr Phe His Ala Pro Gln Pro Val Phe Phe Glu Asn Asn Thr

20 25 30
Leu Pro Lys Gln Thr Glu Pro Gln Ile Lys Thr Gln Leu Gln Thr Glu
35 40 45
Asn Pro Pro Ala Pro Ser Phe Ala Leu Ser Asp Ala Asp Ser Thr Lys
50 55 60
Thr Lys Leu Glu Lys Leu Ile Asn Tyr Gly Val Leu Lys Gln Gln Trp
65 70 75 80
His Leu Leu Lys Gln Ile Leu Pro Leu Tyr Gln Gln Gln Ala Asp Tyr

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

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

210 215 220
Ala His Gly Phe Arg Tyr Gly Val Gly Val Asn Arg Glu Leu Asn Val
225 230 235 240

Gly Gly Asn His Phe Val Thr Thr Asn Gly Arg Phe Ser Gly Val His
245 250 255
Tyr Trp Asp Lys Gln Asp Tyr Ser Glu Lys Ser Leu Tyr Ala Ser Leu
260 265 270
Gly Tyr Arg Tyr Arg Ser Ala Leu Gln Ala Val Gly Phe Ser Pro Phe

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

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

405 410 415
Lys Lys Arg Gln Asp Lys Glu Tyr Ser Phe Asn Ala Thr Ile Trp His
420 425 430
Asn Lys Leu Gln Trp Gln Gly Phe Val Pro Lys Leu Asn Tyr Arg Tyr
435 440 445
Arg Lys Ile Asp Ser Asn Ile Pro Glu Phe Tyr Ser Arg Lys Ser Gly
450 455 460
Glu Trp Phe Val Ser Val Glu Lys Asp Phe
465 470

<210> 209

<211> 1254

<212> DNA

<213> H. parahaemolyticus SLAM 3

<400> 209

atgaaaaaca cacttctttt tattttagtc tcaagtattt gttgcaatat ttttgctaac 60

gaaaaacaag aaaacaccta ttctatttcc gatttagaaa aagatcctaa aacaaccgaa 120

aaattacttt cagatatgct aagtattgat cgaatggatt tagtagatcg tttattaccg 180

atttatcaaa tttttccaga aaacaatcca agattggtta attacgccaa aataagacaa 240

gtaagattat tattcttaga ttatcaaaat aataatgcca aaaaggcttt tcagttattg 300

caaatggaag aaaatttaaa tcatgaagag cggtcgatta ttcaaaatta tttgcaagca 360

attgaaaacc gagaacgttg gcaattttct ttaggtggga attatttaca aactaagaat 420

gtgaataata catctaatga gcgacatatc gaaaacacgg gttttgtgaa aaatgatgat 480

atgttgccac aatcggcaca cggctttgct tattattttg atgctcagaa aaattggaac 540

atagcaggtt cgcattatct gtattttacg aataatctat atggcaaaaa ttattgggat 600

aatcataatt atgatgaaat cactaaccgc acttatttag gctatcaata tcaaaatgct 660

aaatataaat tggtattaaa accgttttat gagcgacaat ggttgggcgg ttatcggtat 720

aactgggcaa atggggcaag ggcggaatat gggctgagtt ttgcaaaaca ttggcaaatt 780

tcgaccgctt ttgagttcag tcagcctcgt tatttcactc aacctgatcg caatggtaac 840

attaaactgg cttccaccac gtttatttgg caacccaccg aaaaaggtta ttactattta 900

ggtacggatt ttattcgaga aaccacacgt ataaaacaat atagtaatga tatgaaagcc 960

ttgagaatag gttggaggca aaattggggc tatgtgattg ctactcaagt caatggttca 1020

attgcgttaa aacaatataa agattttgct tctcttggtg gaattttgcc attaaataaa 1080

attcgtcgtg ataaaatcta ttctctgaat ttaactttat ggaaacaaga ttggcagtat 1140

ttaggtttta cgccgaaagt gcaattccgt tggaaaaaac aagaaagtaa cattccttca 1200

atgttttctt attcagaaaa atatgtgcag atgttggtgg aaaaggattt ttaa 1254

<210> 210

<211> 417

<212> PRT

<213> H. parahaemolyticus SLAM 3

<400> 210

Met Lys Asn Thr Leu Leu Phe Ile Leu Val Ser Ser Ile Cys Cys Asn

1 5 10 15

Ile Phe Ala Asn Glu Lys Gln Glu Asn Thr Tyr Ser Ile Ser Asp Leu
20 25 30
Glu Lys Asp Pro Lys Thr Thr Glu Lys Leu Leu Ser Asp Met Leu Ser
35 40 45

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

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

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

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

260 265 270

Thr Gln Pro Asp Arg Asn Gly Asn Ile Lys Leu Ala Ser Thr Thr Phe

275 280 285

Ile Trp Gln Pro Thr Glu Lys Gly Tyr Tyr Tyr Leu Gly Thr Asp Phe

290 295 300

Ile Arg Glu Thr Thr Arg Ile Lys Gln Tyr Ser Asn Asp Met Lys Ala

305 310 315 320

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

325 330 335

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

340 345 350

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

355 360 365

Leu Asn Leu Thr Leu Trp Lys Gln Asp Trp Gln Tyr Leu Gly Phe Thr

370 375 380

Pro Lys Val Gln Phe Arg Trp Lys Lys Gln Glu Ser Asn Ile Pro Ser

385 390 395 400

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

405 410 415

Phe

<210> 211

<211> 1461

<212> DNA

<213> H. parainfluenzae SLAM 1

<400> 211

ttgctttatt tctctttcga taaaaaaatg aaatttacaa aaacttttt atatacagta 60

ttaagcataa catgtgctca gtgggcaaat gccgaggtag cacaatctaa aaatgacaca 120

ttagacaaaa atattcaggt tgcagcgcca aagcttcaag cacctgcgat ccagccgaag 180

acaaataatg aaggctcagt ctcaatgact aaagaagagc tagctcgtca tcctgattta 240

atcgtacgtg ggatgattcc ttctgtatta caaaataacg aagaagcagt ttcacttctg 300

ttgcctttat atcgagaact tccagaaaaa gatcctgtgt tattgagctg ggctgaagct 360

attgatgcgc gtcataaagg caactatagt gaagctgcac aacgctatcg tacgctattc 420

acccaacatt ctgatagcct tccattacgt tatcagcttg ctcaagcact ctttttaaat 480

aatgataacg aagcagcaaa agatcagttc caaaaattac gtgcggagca aatgacgcct 540

gaaatgactg ccgttattga tcaatattta tctgcattaa atcaacgcga tcaatggaaa 600

ttttatggtg gtgtaagtta cctcaatgaa agcaatatca acaatgcacc caaagcaggt 660

actcatattg gtaactggaa agcttggagt aaagaaagtg cacaagggct ttcttattca 720

ttaggtgttg agaaaaaatg gtctcttgca cataactttt tcaccaaatt aggcttagat 780

ggaaatggta aatactactg gaataacaaa aaatataacg aattaaatgc gcgcttaggt 840

tggggattag gttatcaaac ttcccattta gaattggctt taacaccatt taccgaaaaa 900

cgttggtata gtggtggctc aaacggtagc gatgcactca aacaatactc taaaaactct 960

ggcgtacgtt ttgatattag ctactggctt aatcctcgtt ggcaaatttc atctgctttg 1020

gaatatggcg aacaacgcta tgattggcga aaacatttaa acggcaacaa ttatttattt 1080

tccaacacat tactctatgt tccgaaaagc ggacaacatt ggtttgctgg ggtagattat 1140

tctcgtgaaa atactcgaga caaagataac gcctaccaac gagcaggtgt acgccttggt 1200

tggggacaag aatggccatg gggaatatca agccgagtca cgctttcata tgctaaacgt 1260

cattatcaag cggctgattt ctttaacatc cgtcagaata atagagaata tgcttcaacg 1320

ttaacattat ggcatcgcga tctctatttc tgggggatta cgcctaaaat tacatggtcc 1380

taccaaaaag taaaaagtaa tcatcctttc tatggttacg ataaaaatcg tgtattctta 1440

gaaatgagta aaacatttta a 1461

<210> 212

<211> 486

<212> PRT

<213> H. parainfluenzae SLAM 1

<400> 212

Met Leu Tyr Phe Ser Phe Asp Lys Lys Met Lys Phe Thr Lys Thr Phe

1 5 10 15

Leu Tyr Thr Val Leu Ser Ile Thr Cys Ala Gln Trp Ala Asn Ala Glu

20 25 30

Val Ala Gln Ser Lys Asn Asp Thr Leu Asp Lys Asn Ile Gln Val Ala

35 40 45

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

50 55 60

Gly Ser Val Ser Met Thr Lys Glu Glu Leu Ala Arg His Pro Asp Leu

65 70 75 80

Ile Val Arg Gly Met Ile Pro Ser Val Leu Gln Asn Asn Glu Glu Ala

85 90 95

Val Ser Leu Leu Leu Pro Leu Tyr Arg Glu Leu Pro Glu Lys Asp Pro

100 105 110

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

115 120 125

Tyr Ser Glu Ala Ala Gln Arg Tyr Arg Thr Leu Phe Thr Gln His Ser

130 135 140

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

145 150 155 160

Asn Asp Asn Glu Ala Ala Lys Asp Gln Phe Gln Lys Leu Arg Ala Glu

165 170 175

Gln Met Thr Pro Glu Met Thr Ala Val Ile Asp Gln Tyr Leu Ser Ala

180 185 190

Leu Asn Gln Arg Asp Gln Trp Lys Phe Tyr Gly Gly Val Ser Tyr Leu

195 200 205

Asn Glu Ser Asn Ile Asn Asn Ala Pro Lys Ala Gly Thr His Ile Gly

210 215 220

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

225 230 235 240

Leu Gly Val Glu Lys Lys Trp Ser Leu Ala His Asn Phe Phe Thr Lys

245 250 255

Leu Gly Leu Asp Gly Asn Gly Lys Tyr Tyr Trp Asn Asn Lys Lys Tyr

260 265 270

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

275 280 285

His Leu Glu Leu Ala Leu Thr Pro Phe Thr Glu Lys Arg Trp Tyr Ser

290 295 300

Gly Gly Ser Asn Gly Ser Asp Ala Leu Lys Gln Tyr Ser Lys Asn Ser

305 310 315 320

Gly Val Arg Phe Asp Ile Ser Tyr Trp Leu Asn Pro Arg Trp Gln Ile

325 330 335

Ser Ser Ala Leu Glu Tyr Gly Glu Gln Arg Tyr Asp Trp Arg Lys His

340 345 350

Leu Asn Gly Asn Asn Tyr Leu Phe Ser Asn Thr Leu Leu Tyr Val Pro

355 360 365

Lys Ser Gly Gln His Trp Phe Ala Gly Val Asp Tyr Ser Arg Glu Asn

370 375 380

Thr Arg Asp Lys Asp Asn Ala Tyr Gln Arg Ala Gly Val Arg Leu Gly

385 390 395 400

Trp Gly Gln Glu Trp Pro Trp Gly Ile Ser Ser Arg Val Thr Leu Ser

405 410 415

Tyr Ala Lys Arg His Tyr Gln Ala Ala Asp Phe Phe Asn Ile Arg Gln

420 425 430

Asn Asn Arg Glu Tyr Ala Ser Thr Leu Thr Leu Trp His Arg Asp Leu

435 440 445

Tyr Phe Trp Gly Ile Thr Pro Lys Ile Thr Trp Ser Tyr Gln Lys Val

450 455 460

Lys Ser Asn His Pro Phe Tyr Gly Tyr Asp Lys Asn Arg Val Phe Leu

465 470 475 480

Glu Met Ser Lys Thr Phe

485

<210> 213

<211> 1409

<212> DNA

<213> H. parainfluenzae SLAM 2

<400> 213

agaatcaaaa tgatcaagca aaacttaatc aagccattaa aactgagcaa caaacattgc 60

aaaaagcgct tttgaataaa caaagtttag aagagtcaaa tgtcagtcgt aaggatgatt 120

acactcgttt tacgggcaaa tatttagtag aacacccaga aattttagaa aaaattcttg 180

tagaatcact tattaatacg aataagcaag tacttcctac acttattgct ttatataaac 240

gtgtgcctaa tagagatgaa tccctacttg aatggggaaa tgcaattctg ttaactgata 300

ccaatttaaa tgattctgta tcagaatata gaaagctcct ggctaatttt cctgataata 360

attttattcg ttttcagtta gctcgagttt tatttttaa tcaggaattt gacgcgtcaa 420

agaatcaatt tgagaaatta cgtgctgcag ataatgtatc ggctcaagat agagaagtgt 480

ttaaccaatt tatctcagca attaatgaaa aaagccaatg gacttattct ttcggtatta 540

cttatcttaa tgataaaaat ttaagtaact ctgcaaaaga ggggactatc gttgttttac 600

ctaatggtca aacagcggtt tataacacac ctcgtcagaa agggaatggg gtaggtattt 660

ctcttggtgc caataaacaa tgggcattat caggcggaaa atacattgtg ttgaacacgg 720

gaatgaatac taaatattat tggaataata aaaattataa tgatttaaca ggtgtgtttg 780

gtcttggttt aggatattct gatgctcgat ttaatataga agtacaacct tatgttaata 840

aacgttggta ttctggtggt gtgaatggct cagaaagttt aaaacaatat tatgatacct 900

atggtgtatc gctttccact tcctattggt taaatcaaag ctttaagtat tcattttact 960

acgattatgg atatgagaaa tataaacagg aaaattatgc tactcaatat caaggcggta 1020

cgcatttaat tagtaatagt ttgatgtatg ttccttcacc aacccaatat tgggcattat 1080

ctttagattt tatgacgaaa aatgcaagag ataaaagtaa ttccttctta agagaaggtg 1140

cgcgcttaag ctggggacaa gaatggcctt taggtatttc tactaataca tcctttggta 1200

ttgcaaaaag aaattataaa gaagcgtctt tcttaggaaa acaaaagaat aatgaatata 1260

atgcttccat ctccatttgg aataaaaaaa ttcattatgc tgggttcacg ccgcgcttaa 1320

cgtggattta tactaaaacg aacagtaata tttctctata tacatatgat aaaaatcaaa 1380

tggttataga agcgacgaga acattctaa 1409

<210> 214

<211> 492

<212> PRT

<213> H. parainfluenzae SLAM 2

<400> 214

Met Lys Gln Pro Leu Leu Tyr Gly Ile Val Phe Ser Leu Leu Met Pro
1 5 10 15

Gln Cys Val Asp Ala Asn Glu Gln Asn Gln Asn Asp Gln Ala Lys Leu
20 25 30

Asn Gln Ala Ile Lys Thr Glu Gln Gln Thr Leu Gln Lys Ala Leu Leu

35 40 45

Asn Lys Gln Ser Leu Glu Glu Ser Asn Val Ser Arg Lys Asp Asp Tyr

50 55 60

Thr Arg Phe Thr Gly Lys Tyr Leu Val Glu His Pro Glu Ile Leu Glu

65 70 75 80

Lys Ile Leu Val Glu Ser Leu Ile Asn Thr Asn Lys Gln Val Leu Pro

85 90 95

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

100 105 110

Leu Glu Trp Gly Asn Ala Ile Leu Leu Thr Asp Thr Asn Leu Asn Asp

115 120 125

Ser Val Ser Glu Tyr Arg Lys Leu Leu Ala Asn Phe Pro Asp Asn Asn

130 135 140

Phe Ile Arg Phe Gln Leu Ala Arg Val Leu Phe Phe Asn Gln Glu Phe

145 150 155 160

Asp Ala Ser Lys Asn Gln Phe Glu Lys Leu Arg Ala Ala Asp Asn Val

165 170 175

Ser Ala Gln Asp Arg Glu Val Phe Asn Gln Phe Ile Ser Ala Ile Asn

180 185 190

Glu Lys Ser Gln Trp Thr Tyr Ser Phe Gly Ile Thr Tyr Leu Asn Asp

195 200 205

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

210 215 220

Asn Gly Gln Thr Ala Val Tyr Asn Thr Pro Arg Gln Lys Gly Asn Gly

225 230 235 240

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

245 250 255

Lys Tyr Ile Val Leu Asn Thr Gly Met Asn Thr Lys Tyr Tyr Trp Asn

260 265 270

Asn Lys Asn Tyr Asn Asp Leu Thr Gly Val Phe Gly Leu Gly Leu Gly

275 280 285

Tyr Ser Asp Ala Arg Phe Asn Ile Glu Val Gln Pro Tyr Val Asn Lys
290 295 300
Arg Trp Tyr Ser Gly Gly Val Asn Gly Ser Glu Ser Leu Lys Gln Tyr
305 310 315 320

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

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

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

<210> 215

<211> 1440

<212> DNA

<213> H. paraphrohaemolyticus SLAM 1

<400> 215

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caagctgaag tagcccagcc taaaaatgat ctgaccgaac attttcaagt tgctcagccg 120
aaaataaaga gtgctcctgt tcctgaacaa actgagaaat ctggcactgt gtcgatgacc 180
aaagaagagt tggctcagca ccccgattta attgtgcgcg ggttaattcc agctgtgttg 240
caaaacaacg aacaagcggt tgaattatta ctgccgatgt acaaaaactt gccgaatcaa 300
gatccattct tgcgtgactg ggcagaggcg atttctgcta aatcacaggg caattttgcg 360
gatgctgtag cacgctatcg ttctcttttt gcacaaaaat cagatattcc tgccttgcgt 420
tatcaactcg ctcaagccct ttttttaaat aacaataatg aggcggctaa agatcaattc 480

caaaaattgc gtgcagaaaa tttatcgccc gattcagttg caattatcga ccaatatttg 540
accgctttaa ataaacgcga tcagtggaaa tttagcggtg gaatgagctt ccttaatgaa 600
actaacatca ataacgcacc gaaagcgggt acaaaagtag gcagttggga agcctggaaa 660
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aatcaatttt tcaccaaaat ggaactgaat gcttcgggta aatattattg gaataacaaa 780
aaatataatg aactcaatgt acgtgcaggt gcaggcttag gatatcaaac tgcacgtttt 840
gaaattgccc tcactccatt taccgaaaaa cgttggtatg cgggtggttc atccggtagt 900

gaatcgctta aacaatattc aaaaaactca ggcgttcagc ttgaaagcag ttactggttg 960
aatgaaaaat ggcaactttc aagcgtgttg gaatatggcg aacagcgtta tgattggcgt 1020
aagcacttaa acggcaacaa ctatttgtgg tcaaacacgc tcttatatgt accaaaaagc 1080
gggcaatatt ggtttgttgg cgtagattac aaccgagaaa atacccgcga taaagacaac 1140
gcttaccaac gcaccactgc tcgtttaggc tgggggcaag agtggggctg gggcatctca 1200
agccgtgttt ccctttctta tgcgaaacgg acttatcagg ctcatcctgc gcccgattta 1260
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ttacacttct ttggtgtgac gccaaaagtg acttggcaat atcagaaagt aagcagtaac 1380
cacccgtttt atagctatga caaaaatcgg gtttattttg agatgagtaa aacgttctag 1440
<210> 216
<211> 479
<212> PRT
<213> H. paraphrohaemolyticus SLAM 1
<400> 216
Met Lys Phe Ser Pro Ala Val Leu Phe Ala Ile Leu Gly Ile Asn Leu
1 5 10 15

Thr Ala Leu Ala Gln Ala Glu Val Ala Gln Pro Lys Asn Asp Leu Thr
20 25 30
Glu His Phe Gln Val Ala Gln Pro Lys Ile Lys Ser Ala Pro Val Pro

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

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

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

225 230 235 240
Asn Gln Phe Phe Thr Lys Met Glu Leu Asn Ala Ser Gly Lys Tyr Tyr
245 250 255
Trp Asn Asn Lys Lys Tyr Asn Glu Leu Asn Val Arg Ala Gly Ala Gly

260 265 270

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

275 280 285

Glu Lys Arg Trp Tyr Ala Gly Gly Ser Ser Gly Ser Glu Ser Leu Lys

290 295 300

Gln Tyr Ser Lys Asn Ser Gly Val Gln Leu Glu Ser Ser Tyr Trp Leu

305 310 315 320

Asn Glu Lys Trp Gln Leu Ser Ser Val Leu Glu Tyr Gly Glu Gln Arg

325 330 335

Tyr Asp Trp Arg Lys His Leu Asn Gly Asn Asn Tyr Leu Trp Ser Asn

340 345 350

Thr Leu Leu Tyr Val Pro Lys Ser Gly Gln Tyr Trp Phe Val Gly Val

355 360 365

Asp Tyr Asn Arg Glu Asn Thr Arg Asp Lys Asp Asn Ala Tyr Gln Arg

370 375 380

Thr Thr Ala Arg Leu Gly Trp Gly Gln Glu Trp Gly Trp Gly Ile Ser

385 390 395 400

Ser Arg Val Ser Leu Ser Tyr Ala Lys Arg Thr Tyr Gln Ala His Pro

405 410 415

Ala Pro Asp Leu Ile Gly Lys Ile Gln Lys Asn Asp Glu Tyr Ser Thr

420 425 430

Ala Leu Thr Phe Trp His Arg Asp Leu His Phe Phe Gly Val Thr Pro

435 440 445

Lys Val Thr Trp Gln Tyr Gln Lys Val Ser Ser Asn His Pro Phe Tyr

450 455 460

Ser Tyr Asp Lys Asn Arg Val Tyr Phe Glu Met Ser Lys Thr Phe

465 470 475

<210> 217

<211> 1425

<212> DNA

<213> H. paraphrohaemolyticus SLAM 2

<400> 217

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cacgcacctc aacctgtatt ctttgagaac aacgttttgc caaaacaggc agagccgcaa 120

ataaaaacgc agtctaaagc agagagtgta cccacatctt catttgccct ttctgatgca 180

gatagcacca aaaccaagct cgagaagttg attaacaatg gtgtagtaaa gcaacaatgg 240

catttgttga agcagctact gccgttgtat caacagcagg cgaattatga tgaaacgctt 300

tatcgttacg caatgggggc gatgttgcgg gcagaaaaag aatacccaca ggtaatttcg 360

ctttatcagc agattttagc cgagaagcca gagttagctt atccgcgttt tgatttgggt 420

gtgatgttgt ttgaaaacaa gcaatatcgc caggcgaaag cagagttaga acgtgctaag 480

cccgaacttt caccacaaat gcagcagctt accgaacgtt atatgcaagc aatggcggag 540

cggcaaagct ggcagcctga tatggagcta caatataccc aaaccgataa cataaacaac 600

gcctcttctc agcaagatat tatattggga ggattgagat ttaaaaaaga tgcggactcc 660

ttgccgcaaa aggcacacgg ttttcgctac agtgtgggtg taaaccgtga attgaacata 720

tccggcaatc attttgttac agcaaatggt cgttttggtg gggtgcatta ttgggataac 780

caagattata gcgaaaaatc gctgtatgcc tcgctcggtt atcgataccg ttctgcattg 840

caagcagtcg gattttcccc atttttgaa cagaattggc tcggctcacc atgttatagc 900

aaaaattttg gtgcagttgc agattttcgt cgagaattga ctgcttactg ggcaatgtca 960

ggatcttttt cgcatacgca aaaacgctat gcacaagaaa gcgtggctcg ccgtcataat 1020

ggttacttaa acggtgtttc actttcgtta agctatcaag ccaagccgaa ttggttgctt 1080

tttagtggtg tggaaggcag tgttgatcat agtaaagata aagcagaatc ttctcttcgc 1140

cgtggggtga atattggttc ggtgtgggag attaaagagt ttgtcagccg tgttagctta 1200

cgttatgtga agcgagattt tcgtgcggag aatttttatt ttccaaccaa aaaacgtcaa 1260

gataaagaat atagcttgaa tgtgtcggtg tggcataacc gtttgcaatg gcaaggtttt 1320

gtgccgaagt tgaattatcg ctaccgtaaa attgatagca atattcctgc gttctattcc 1380

agagaaagta gcgagtggtt tgtgtcagta gagaaagatt tttag 1425

<210> 218

<211> 474

<212> PRT

<213> H. paraphrohaemolyticus SLAM 2

<400> 218

Met Lys Lys Leu Ala Asn Phe Leu Ile Ile Leu Pro Leu Ala Thr Gln

1 5 10 15

Ala Glu Thr Phe His Ala Pro Gln Pro Val Phe Phe Glu Asn Asn Val

20 25 30

Leu Pro Lys Gln Ala Glu Pro Gln Ile Lys Thr Gln Ser Lys Ala Glu

35 40 45

Ser Val Pro Thr Ser Ser Phe Ala Leu Ser Asp Ala Asp Ser Thr Lys

50 55 60

Thr Lys Leu Glu Lys Leu Ile Asn Asn Gly Val Val Lys Gln Gln Trp

65 70 75 80

His Leu Leu Lys Gln Leu Leu Pro Leu Tyr Gln Gln Gln Ala Asn Tyr

85 90 95

Asp Glu Thr Leu Tyr Arg Tyr Ala Met Gly Ala Met Leu Arg Ala Glu

100 105 110

Lys Glu Tyr Pro Gln Val Ile Ser Leu Tyr Gln Gln Ile Leu Ala Glu

115 120 125

Lys Pro Glu Leu Ala Tyr Pro Arg Phe Asp Leu Gly Val Met Leu Phe

130 135 140

Glu Asn Lys Gln Tyr Arg Gln Ala Lys Ala Glu Leu Glu Arg Ala Lys

145 150 155 160

Pro Glu Leu Ser Pro Gln Met Gln Gln Leu Thr Glu Arg Tyr Met Gln

165 170 175

Ala Met Ala Glu Arg Gln Ser Trp Gln Pro Asp Met Glu Leu Gln Tyr

180 185 190

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

195 200 205

Leu Gly Gly Leu Arg Phe Lys Lys Asp Ala Asp Ser Leu Pro Gln Lys

210 215 220

Ala His Gly Phe Arg Tyr Ser Val Gly Val Asn Arg Glu Leu Asn Ile

225 230 235 240

Ser Gly Asn His Phe Val Thr Ala Asn Gly Arg Phe Gly Gly Val His

245 250 255

Tyr Trp Asp Asn Gln Asp Tyr Ser Glu Lys Ser Leu Tyr Ala Ser Leu

260 265 270

Gly Tyr Arg Tyr Arg Ser Ala Leu Gln Ala Val Gly Phe Ser Pro Phe

275 280 285

Phe Glu Gln Asn Trp Leu Gly Ser Pro Cys Tyr Ser Lys Asn Phe Gly

290 295 300

Ala Val Ala Asp Phe Arg Arg Glu Leu Thr Ala Tyr Trp Ala Met Ser

305 310 315 320

Gly Ser Phe Ser His Thr Gln Lys Arg Tyr Ala Gln Glu Ser Val Ala

325 330 335

Arg Arg His Asn Gly Tyr Leu Asn Gly Val Ser Leu Ser Leu Ser Tyr

340 345 350

Gln Ala Lys Pro Asn Trp Leu Leu Phe Ser Gly Val Glu Gly Ser Val

355 360 365

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

370 375 380

Ile Gly Ser Val Trp Glu Ile Lys Glu Phe Val Ser Arg Val Ser Leu

385 390 395 400

Arg Tyr Val Lys Arg Asp Phe Arg Ala Glu Asn Phe Tyr Phe Pro Thr

405 410 415

Lys Lys Arg Gln Asp Lys Glu Tyr Ser Leu Asn Val Ser Val Trp His

420 425 430

Asn Arg Leu Gln Trp Gln Gly Phe Val Pro Lys Leu Asn Tyr Arg Tyr

435 440 445

Arg Lys Ile Asp Ser Asn Ile Pro Ala Phe Tyr Ser Arg Glu Ser Ser

450 455 460

Glu Trp Phe Val Ser Val Glu Lys Asp Phe

465 470

<210> 219

<211> 1401

<212> DNA

<213> H. parasuis SLAM 1

<400> 219

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ttggaaatca aatccgccga gccaacatta ccagtacaag cggttatttt ttcagaaaaa 120

tcagcaaata atggggaaat cactttaacc caagagctgc tcagtaagcc cgaacttact 180

cgtcaaatgt taaatcgggc gattgatagc cgacaatttc atttattgcc tgagctggtg 240

cggatttatc aacaaacgcc taatcctgat ttggtgctga ttgattatgc taacggtatt 300

attttggcaa gtcaggggga ctataaaacg gcaatcgatc tctatcgtgg cattattgcg 360

aagcacccta attttcagcc cgtgcgtttt cgtttagcac aaatgttgtt tgaagatcgg 420

caaaacgaag ccgcacttgc acaatttcgt aagctacaag cggacggatt gccgccacaa 480

attgcaaatg gggtggaaca atatattgct gccattcaga aacgttcgga ttggtcattc 540

gactttggtg tgaattattt gcacgaaagc aatgttaata atgcctcaag ctcgccttat 600

gttcgagtgg ggaatgtgcc gtttaagaaa acggaagaat cattaccgca atcagcaaat 660

gggttgagct accatctgaa tttggctaag aattggaatg ttagcggatc ccattatcta 720

cattttgaga accaatttag tggaaaatcc tattgggata atcatcaatt tgacgatcag 780

caaaaccgtt caagtcttgg ctatcaatat caaaatgctc aaagtcgtct tgctttttg 840

ccttattatg aaatgcgttg gtatggtaat catcgctata atcacggcta tggcgttcgg 900

ggagaagtag agcattggct tacatcacaa tggcagcttt ctacggctgg cgaaatgggc 960

aagctcaaac atcggggcga aaatcagctt gcagatagca caacattatt tggttctgct 1020

acgctactct atgcctttga tgcgaaaagt tatctctatg gtggtgtaga tttgttgcga 1080

gatcggacgt tagaacgttc tttagcctca aaacgttata cagggcgaat tggttggggg 1140

caagaatggt ggggcggaat ttccagccgt attcagctca gttatggcaa acgtgaattt 1200

gaccaagctc accgcatttt taatcagata cgcaaagata gagagttagg tttgaatgtt 1260

acactttggc atcgtaacct gcatttttgg ggaattacac cgaaaatcag ctatcaatat 1320

cagcgagtga actcaaattt agtggatctt tattcgtata aacgaaatcg agtttatttg 1380

agttttgaga aaagtttcta g 1401

<210> 220

<211> 466

<212> PRT

<213> H. parasuis SLAM 1

<400> 220

Met Lys Lys His Leu Pro Leu Thr Leu Phe Ile Pro Leu Val Ala Asn

1 5 10 15

Ala Ala Pro Glu Leu Glu Ile Lys Ser Ala Glu Pro Thr Leu Pro Val
20 25 30

Gln Ala Val Ile Phe Ser Glu Lys Ser Ala Asn Asn Gly Glu Ile Thr
35 40 45

Leu Thr Gln Glu Leu Leu Ser Lys Pro Glu Leu Thr Arg Gln Met Leu
50 55 60

Asn Arg Ala Ile Asp Ser Arg Gln Phe His Leu Leu Pro Glu Leu Val
65 70 75 80

Arg Ile Tyr Gln Gln Thr Pro Asn Pro Asp Leu Val Leu Ile Asp Tyr
85 90 95

Ala Asn Gly Ile Ile Leu Ala Ser Gln Gly Asp Tyr Lys Thr Ala Ile
100 105 110

Asp Leu Tyr Arg Gly Ile Ile Ala Lys His Pro Asn Phe Gln Pro Val
115 120 125

Arg Phe Arg Leu Ala Gln Met Leu Phe Glu Asp Arg Gln Asn Glu Ala
130 135 140

Ala Leu Ala Gln Phe Arg Lys Leu Gln Ala Asp Gly Leu Pro Pro Gln
145 150 155 160

Ile Ala Asn Gly Val Glu Gln Tyr Ile Ala Ala Ile Gln Lys Arg Ser
165 170 175

Asp Trp Ser Phe Asp Phe Gly Val Asn Tyr Leu His Glu Ser Asn Val
180 185 190

Asn Asn Ala Ser Ser Ser Pro Tyr Val Arg Val Gly Asn Val Pro Phe
195 200 205

Lys Lys Thr Glu Glu Ser Leu Pro Gln Ser Ala Asn Gly Leu Ser Tyr
210 215 220

His Leu Asn Leu Ala Lys Asn Trp Asn Val Ser Gly Ser His Tyr Leu
225 230 235 240

His Phe Glu Asn Gln Phe Ser Gly Lys Ser Tyr Trp Asp Asn His Gln
245 250 255

Phe Asp Asp Gln Gln Asn Arg Ser Ser Leu Gly Tyr Gln Tyr Gln Asn
260 265 270

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

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

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

Ser Phe
465

<210> 221
<211> 1461
<212> DNA

<213> H. parasuis SLAM 2

<400> 221

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aaactatctc aggatagtat tactgaacat ctaaatgata atagagtcca agcagaaaaa 120

gccgatatcc tcattcacag ccatcaattt aaggttcatc aaatcgctaa ggaggaaacg 180

gataagagta gtattacaat gacttcaaaa gagttggtaa aatatccaga tttagtgata 240

agagcattat tgcctgcggt aatgcaaggt aatattgaca atgtcgaatt gctttatccc 300

atttaccaac agcttcctgc acaatttcac gatccaattc tcaccaaatg ggcatcggca 360

attgtggcaa agaaaaatca gcaatatacg gaagcgatca agttatatcg tcagatcctt 420

gccgaacaag cagatattca gcctgttcgt ttacaacttg cggtagccct atttgaaaat 480

aacgaattag aggcttcaga agatcagttt aaaaaactgc gttctgaacc gcttatcccc 540

gaaattaccc aacttatcga tcaatatctt aatgcgataa accaacgaga tcgttggacg 600

ttttcgggtg gcgtgactta tcttaacgat cctaatatca ataatgcacc gaaagcagga 660

acaacctacg gcaactggca cgcaccaaaa cgaaaatcgg cagaaggtgt cggttttaat 720

ttcgatctcg gtaaaaaatg gtcgtgggga aatggtttct ttaatgaact acgtcttgct 780

accaacggca aatactactg ggataataaa aaatacaacg aaatgagctt acgaggcagt 840

gtggggctag gttttcaaaa tgcaaaatat aacctgaggc tgttgccatt tatggaacaa 900

acactttatg caggtggctc taatcaaagt gataccttaa aacgtttttc taaatcaggc 960

ggtttaaccc ttgaaacaaa ctattggtta tcacctaaat ggcaactcaa cactaactat 1020

gaatatgccg aacaacgcta tgcaagtcgc ttgcacctca atggcaatta tcactttatc 1080

tctggtgggc tagtttattt agccaatgca aaccaatatt ggtttgcaaa tttaaactac 1140

aatcgcaccg ctactcgtga taaagatgat agctttttcc gtcggggaat tagtttaggt 1200

tggggacaag aatggggcaa agggttttct actcgccttt ccgtaagtgt agctcaaaaa 1260

cgctataaaa aagaggcgat tttccgcatt attcaacgta ataaagaata tggcttcaat 1320

gcatcaattt ggcatcgtgc cgtgcattta tgggggatca ctcctcgttt aacctacaat 1380

tttactaaaa cgcaaagtaa ccacgttctt tatagctatg ataaacatag ggtgtttatt 1440

gagttgagca aacaaattta a 1461

<210> 222

<211> 486

<212> PRT

<213> H. pittmaniae SLAM 2

<400> 222

Met Asn His Ser Phe Ile Ser Ala Thr Leu Leu Leu Val Leu Ala Asn

1 5 10 15

Tyr Ser Ile Ala Lys Leu Ser Gln Asp Ser Ile Thr Glu His Leu Asn

20 25 30

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

35 40 45

Gln Phe Lys Val His Gln Ile Ala Lys Glu Glu Thr Asp Lys Ser Ser

50 55 60

Ile Thr Met Thr Ser Lys Glu Leu Val Lys Tyr Pro Asp Leu Val Ile

65 70 75 80

Arg Ala Leu Leu Pro Ala Val Met Gln Gly Asn Ile Asp Asn Val Glu

85 90 95

Leu Leu Tyr Pro Ile Tyr Gln Gln Leu Pro Ala Gln Phe His Asp Pro

100 105 110

Ile Leu Thr Lys Trp Ala Ser Ala Ile Val Ala Lys Lys Asn Gln Gln

115 120 125

Tyr Thr Glu Ala Ile Lys Leu Tyr Arg Gln Ile Leu Ala Glu Gln Ala

130 135 140

Asp Ile Gln Pro Val Arg Leu Gln Leu Ala Val Ala Leu Phe Glu Asn

145 150 155 160

Asn Glu Leu Glu Ala Ser Glu Asp Gln Phe Lys Lys Leu Arg Ser Glu

165 170 175

Pro Leu Ile Pro Glu Ile Thr Gln Leu Ile Asp Gln Tyr Leu Asn Ala

180 185 190

Ile Asn Gln Arg Asp Arg Trp Thr Phe Ser Gly Gly Val Thr Tyr Leu

195 200 205

Asn Asp Pro Asn Ile Asn Asn Ala Pro Lys Ala Gly Thr Thr Tyr Gly

210 215 220

Asn Trp His Ala Pro Lys Arg Lys Ser Ala Glu Gly Val Gly Phe Asn

225 230 235 240

Phe Asp Leu Gly Lys Lys Trp Ser Trp Gly Asn Gly Phe Phe Asn Glu

245 250 255

Leu Arg Leu Ala Thr Asn Gly Lys Tyr Tyr Trp Asp Asn Lys Lys Tyr

260 265 270

Asn Glu Met Ser Leu Arg Gly Ser Val Gly Leu Gly Phe Gln Asn Ala

275 280 285

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

290 295 300

Gly Gly Ser Asn Gln Ser Asp Thr Leu Lys Arg Phe Ser Lys Ser Gly

305 310 315 320

Gly Leu Thr Leu Glu Thr Asn Tyr Trp Leu Ser Pro Lys Trp Gln Leu

325 330 335

Asn Thr Asn Tyr Glu Tyr Ala Glu Gln Arg Tyr Ala Ser Arg Leu His

340 345 350

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

355 360 365

Asn Ala Asn Gln Tyr Trp Phe Ala Asn Leu Asn Tyr Asn Arg Thr Ala

370 375 380

Thr Arg Asp Lys Asp Asp Ser Phe Phe Arg Arg Gly Ile Ser Leu Gly

385 390 395 400

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

405 410 415

Val Ala Gln Lys Arg Tyr Lys Lys Glu Ala Ile Phe Arg Ile Ile Gln

420 425 430

Arg Asn Lys Glu Tyr Gly Phe Asn Ala Ser Ile Trp His Arg Ala Val

435 440 445

His Leu Trp Gly Ile Thr Pro Arg Leu Thr Tyr Asn Phe Thr Lys Thr

450 455 460

Gln Ser Asn His Val Leu Tyr Ser Tyr Asp Lys His Arg Val Phe Ile

465 470 475 480

Glu Leu Ser Lys Gln Ile

485

<210> 223

<211> 1434

<212> DNA

<213> H. pittmaniae SLAM 1

<400> 223

atgaagttga atgcattaat gtgttgttta ctagcaatac tatccacacc tctggttcag 60

gctgaagttg cacagtcaaa gaatgatagt ttagatgagc gtttgtccat tgctcggccg 120

tctcagcctc aatccctttc acaagcagcg caaaaaacat caggccaaac tctcaatctc 180

agcaagcagg aactggcaaa tcgcccagat cttattgtgc gggcattgat tccggcggtg 240

ttagaaaata acgctaatgc ggtgaaattg ctcctgccgt tgtatcaaaa tgtgccgcag 300

caggatccat ttttattgca atgggcacaa gctattgatg cccgtgagca agggcaatat 360

gagctggcga ttcgtcatta tcgtcgtctg tttgcccaag caccggaaaa tttggcaatt 420

cgttatcaat tggcgcaagc tttgttttta aataatgata atgaagcggc tcaggatcaa 480

ttccaaaaat tacgagctac tcagcaagat cctgaaaact tgcgattgtt tgatgcttat 540

ttgaatgcgc tcaatcaacg tgatcgttgg aagatttccg gcgggctttc atttctcaat 600

gaaagtaata taaataatgc accgaaggcg ggaacccgta ttggtaactg gcaggcatgg 660

gagcgggaaa gcgcaagggg attatcttat tctctcaatg ttgagaaaaa atggtcactg 720

gctaatcatt tgtttagcaa agtactgttg gaaggcaatg gtaaatatta ttgggataac 780

aaaaagtata atgaatttac agcccgagtt ggtgtcggct taggttatca aaatgcccgg 840

acagaatttt ccgcgattcc ctttacggag cgtcgttggt atgctggcgg ctcaagaggc 900

agtaagtcat taaaacgtta ttcccaaaat agtgggttac gcctagaact gaatcattgg 960

ctcaatccgc aatggcaata tgccggcgca ttggaatatg gtgaacagcg ttacgttact 1020

cgcaagcacc tcaatggtaa caattatctc tggtcaaata cgctgattta ttatccccaa 1080

aatggtcagt attggtttgc gggtgtggat tatagtcggg aaaatactcg tgatgcggat 1140

aacgcctacc aacgtaaaaa tgtgcgtttg gggtgggggc aggaatggtc ttggggaatt 1200

tctactcgcg tgtccttagg ctatgcgaga cgaacctaca aaggtgccga tcttttccaa 1260

attcgtcaga aaaataacga gtacagcggc gctttcagta tttggcaccg cgatctctat 1320

tttgggggaa tcacccctcg gttaacttgg gcatatcaaa aaatcgatag taatcatccg 1380

ttttatagtt atgacaaaaa tcggatttac ttagaaatga gcaaaacctt ctaa 1434

<210> 224

<211> 477

<212> PRT

<213> H. pittmaniae SLAM 1

<400> 224

Met Lys Leu Asn Ala Leu Met Cys Cys Leu Leu Ala Ile Leu Ser Thr
1 5 10 15

Pro Leu Val Gln Ala Glu Val Ala Gln Ser Lys Asn Asp Ser Leu Asp
20 25 30

Glu Arg Leu Ser Ile Ala Arg Pro Ser Gln Pro Gln Ser Leu Ser Gln
35 40 45

Ala Ala Gln Lys Thr Ser Gly Gln Thr Leu Asn Leu Ser Lys Gln Glu

50 55 60

Leu Ala Asn Arg Pro Asp Leu Ile Val Arg Ala Leu Ile Pro Ala Val
65 70 75 80

Leu Glu Asn Asn Ala Asn Ala Val Lys Leu Leu Leu Pro Leu Tyr Gln
85 90 95

Asn Val Pro Gln Gln Asp Pro Phe Leu Leu Gln Trp Ala Gln Ala Ile
100 105 110

Asp Ala Arg Glu Gln Gly Gln Tyr Glu Leu Ala Ile Arg His Tyr Arg

115 120 125

Arg Leu Phe Ala Gln Ala Pro Glu Asn Leu Ala Ile Arg Tyr Gln Leu
130 135 140

Ala Gln Ala Leu Phe Leu Asn Asn Asp Asn Glu Ala Ala Gln Asp Gln
145 150 155 160

Phe Gln Lys Leu Arg Ala Thr Gln Gln Asp Pro Glu Asn Leu Arg Leu
165 170 175

Phe Asp Ala Tyr Leu Asn Ala Leu Asn Gln Arg Asp Arg Trp Lys Ile

180 185 190

Ser Gly Gly Leu Ser Phe Leu Asn Glu Ser Asn Ile Asn Asn Ala Pro
195 200 205

Lys Ala Gly Thr Arg Ile Gly Asn Trp Gln Ala Trp Glu Arg Glu Ser
210 215 220

Ala Arg Gly Leu Ser Tyr Ser Leu Asn Val Glu Lys Lys Trp Ser Leu

225 230 235 240

Ala Asn His Leu Phe Ser Lys Val Leu Leu Glu Gly Asn Gly Lys Tyr

245 250 255

Tyr Trp Asp Asn Lys Lys Tyr Asn Glu Phe Thr Ala Arg Val Gly Val

260 265 270

Gly Leu Gly Tyr Gln Asn Ala Arg Thr Glu Phe Ser Ala Ile Pro Phe

275 280 285

Thr Glu Arg Arg Trp Tyr Ala Gly Gly Ser Arg Gly Ser Lys Ser Leu

290 295 300

Lys Arg Tyr Ser Gln Asn Ser Gly Leu Arg Leu Glu Leu Asn His Trp

305 310 315 320

Leu Asn Pro Gln Trp Gln Tyr Ala Gly Ala Leu Glu Tyr Gly Glu Gln

325 330 335

Arg Tyr Val Thr Arg Lys His Leu Asn Gly Asn Asn Tyr Leu Trp Ser

340 345 350

Asn Thr Leu Ile Tyr Tyr Pro Gln Asn Gly Gln Tyr Trp Phe Ala Gly

355 360 365

Val Asp Tyr Ser Arg Glu Asn Thr Arg Asp Ala Asp Asn Ala Tyr Gln

370 375 380

Arg Lys Asn Val Arg Leu Gly Trp Gly Gln Glu Trp Ser Trp Gly Ile

385 390 395 400

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

405 410 415

Asp Leu Phe Gln Ile Arg Gln Lys Asn Asn Glu Tyr Ser Gly Ala Phe

420 425 430

Ser Ile Trp His Arg Asp Leu Tyr Phe Gly Gly Ile Thr Pro Arg Leu

435 440 445

Thr Trp Ala Tyr Gln Lys Ile Asp Ser Asn His Pro Phe Tyr Ser Tyr

450 455 460

Asp Lys Asn Arg Ile Tyr Leu Glu Met Ser Lys Thr Phe

465 470 475

<210> 225

<211> 1458

<212> DNA

<213> H. somni SLAM 1

<400> 225

atgaaactca ctttatcagc cattcttctt ctttttccgg tttccgtact ggcgcacagt 60

cccaaaagtc cgagcgaaca tttggacgat caccgcattg cagatgagcg ggtacgtgaa 120

aacattcaat atgccttggc gacacaacct aaacaaaccg ttgtgccgaa cattcagcca 180

cagcaaacgg ttgcattaag cgaaagccag ttacagcaac atcctgattt acttgagcgt 240

gcattgatag cggctttatt gcaaggtaat ggtgagaatg cctctttgct gttaccgcac 300

tatcaaaagt tgcctgaaaa cctgcaagac ccgacttttc acctttgggc aaaagccttg 360

attgcgcgtt ggcgtcatca atatacacag tccgtgcgtt tataccgcca agccttggca 420

caacaacctg attggtcggt tttgcgttta cagaccgccg ccgccctctt gtccaataaa 480

gaattcgatg cggcagaagc tcagtttcgc aaggtgcaaa gcgaaaatca gctacccgcc 540

ggacttgccc aagaaattga atcagttttg ctgtatatca aacggcaaag ccgttggcaa 600

ttcagtggca acactaccta tattaacgac aaaaatatta acaacgctcc caaaaatcct 660

gatctgggcg gaggttggcg aggtgatcag gctgagtccg gtcaagggtt agccgttaat 720

ttgggcacca ataaaaaatg gttttggaaa aatggattat ttaatgaatg gcgtttagac 780

agcaacagta aattttattg gaacaacaaa cgattcaacg aagccaatgt gcgtgcttca 840

atgggtatcg gttatcaaaa tgctaaaaat agcattaccg ttctgccatt ttttgagcaa 900

gcgtggtatg caggggggcaa gaaaggcaat gagaccttac gacgtttttc caacagtcga 960

ggtattgcac tagaagcaac ccacactttt agccccaaat ggcaggggag tctgacagct 1020

gagacggcac aaaatcgtta tcggacacgt aagcatttaa acggtaatac gcactttgtt 1080

tctttatcgg cggtgtatca acacaatccg agtcaagctt ggtttggagg aatagactgg 1140

catcgcaaca acgcacgaga tggcgatgat tcttttgacc gtatcggggt acgggcaggc 1200

tggttgcaag actggaaagg actttccaca cgcttaatta cttcttatgg caaaaaaaac 1260

tatcgcagtg caggcttttt caacaaaacc caacgtaatc gagagttggg cgtacaggtc 1320

agtgtatggc atcgagccgt acactggcaa ggtttaacac cacggttaac atggtcatac 1380

actaaaacgg atagtaacat accattgttc cgttacaaca aacagcgcct gtttctggaa 1440

attaataagc agttttga 1458

<210> 226

<211> 485

<212> PRT

<213> H. somni SLAM 1

<400> 226

Met Lys Leu Thr Leu Ser Ala Ile Leu Leu Leu Phe Pro Val Ser Val
1 5 10 15

Leu Ala His Ser Pro Lys Ser Pro Ser Glu His Leu Asp Asp His Arg
20 25 30

Ile Ala Asp Glu Arg Val Arg Glu Asn Ile Gln Tyr Ala Leu Ala Thr
35 40 45

Gln Pro Lys Gln Thr Val Val Pro Asn Ile Gln Pro Gln Gln Thr Val
50 55 60

Ala Leu Ser Glu Ser Gln Leu Gln Gln His Pro Asp Leu Leu Glu Arg
65 70 75 80

Ala Leu Ile Ala Ala Leu Leu Gln Gly Asn Gly Glu Asn Ala Ser Leu
85 90 95

Leu Leu Pro His Tyr Gln Lys Leu Pro Glu Asn Leu Gln Asp Pro Thr
100 105 110

Phe His Leu Trp Ala Lys Ala Leu Ile Ala Arg Trp Arg His Gln Tyr
115 120 125

Thr Gln Ser Val Arg Leu Tyr Arg Gln Ala Leu Ala Gln Gln Pro Asp
130 135 140

Trp Ser Val Leu Arg Leu Gln Thr Ala Ala Ala Leu Leu Ser Asn Lys
145 150 155 160

Glu Phe Asp Ala Ala Glu Ala Gln Phe Arg Lys Val Gln Ser Glu Asn
165 170 175

Gln Leu Pro Ala Gly Leu Ala Gln Glu Ile Glu Ser Val Leu Leu Tyr
180 185 190

Ile Lys Arg Gln Ser Arg Trp Gln Phe Ser Gly Asn Thr Thr Tyr Ile
195 200 205

Asn Asp Lys Asn Ile Asn Asn Ala Pro Lys Asn Pro Asp Leu Gly Gly
210 215 220

Gly Trp Arg Gly Asp Gln Ala Glu Ser Gly Gln Gly Leu Ala Val Asn

225 230 235 240

Leu Gly Thr Asn Lys Lys Trp Phe Trp Lys Asn Gly Leu Phe Asn Glu

245 250 255

Trp Arg Leu Asp Ser Asn Ser Lys Phe Tyr Trp Asn Asn Lys Arg Phe

260 265 270

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

275 280 285

Lys Asn Ser Ile Thr Val Leu Pro Phe Phe Glu Gln Ala Trp Tyr Ala

290 295 300

Gly Gly Lys Lys Gly Asn Glu Thr Leu Arg Arg Phe Ser Asn Ser Arg

305 310 315 320

Gly Ile Ala Leu Glu Ala Thr His Thr Phe Ser Pro Lys Trp Gln Gly

325 330 335

Ser Leu Thr Ala Glu Thr Ala Gln Asn Arg Tyr Arg Thr Arg Lys His

340 345 350

Leu Asn Gly Asn Thr His Phe Val Ser Leu Ser Ala Val Tyr Gln His

355 360 365

Asn Pro Ser Gln Ala Trp Phe Gly Gly Ile Asp Trp His Arg Asn Asn

370 375 380

Ala Arg Asp Gly Asp Asp Ser Phe Asp Arg Ile Gly Val Arg Ala Gly

385 390 395 400

Trp Leu Gln Asp Trp Lys Gly Leu Ser Thr Arg Leu Ile Thr Ser Tyr

405 410 415

Gly Lys Lys Asn Tyr Arg Ser Ala Gly Phe Phe Asn Lys Thr Gln Arg

420 425 430

Asn Arg Glu Leu Gly Val Gln Val Ser Val Trp His Arg Ala Val His

435 440 445

Trp Gln Gly Leu Thr Pro Arg Leu Thr Trp Ser Tyr Thr Lys Thr Asp

450 455 460

Ser Asn Ile Pro Leu Phe Arg Tyr Asn Lys Gln Arg Leu Phe Leu Glu

465 470 475 480

Ile Asn Lys Gln Phe

485

<210

> 227

<211> 1254

<212> DNA

<213> H. somni SLAM 2

<400> 227

atgaaaaaat tgatatttat tttatttgtt agttgttata ttcctgttgt aacagcaaat 60

ttccaacaag aaagaaatta cagtataaga ttatcgagaa atgatacaaa gttaacagaa 120

agcctgttag taagtatgtt gaaatcacag caatttcatg cagcggagaa aatgctagct 180

atttatcaaa atattgataa tccgagccct caattaatca attacacaaa gatttatctt 240

gctcagcaat actacagaaa taaacaatat aaaagagcac tttctctttt tttagaatta 300

aagaaacaag ctaatttaac agataaagag aaagttatta ttgagcagta tctttctatt 360

cttgaggagc aagaaagttg gcaattttca ttctctgcaa attatcttcg caataaaaac 420

gtaaataatg catcttctga acgacaaata gaagatactg gatttagtaa gaatgatgat 480

atgttgccac aatctgcaac agggttggct tattattttt ctgctgaacg aaattggaat 540

ttagtagatt ctcattattt gcacttctcc aatgagcttt ttggtaagta ttattgggat 600

aataaagatt tcgatgaaag taataaccgc acttatattg gttatattta tcaaaatgca 660

aaattaaaat ttgcctctaa agccttttac gaacgtcaat ggtttgcaag acaccgttat 720

aattgggcaa atggattgag gactgaatta gagtattcat tagcaccaaa atggaaaata 780

tcgacggcga tagaacttag ccagcctcat tatttcaaac aaagagaaaa gaatggcaca 840

agtaaactta tttcattcac cttaatttgg caaccaaatc atcttagtta tttatattgg 900

ggaatagatt ttattcgtga aaaaacacaa ctaaaacaat atagcaatga tactaaaggg 960

ttaagattag gttggagtag aatttggacg ggaaatttta tcactcaaat caattcctct 1020

atttcttggc gaaattataa agataaagcg tctttaggcg gaatccttcc tcttgataaa 1080

attcgtaaag ataaaattta taatgctaat ttaacagttt ggaaatctga ttggaactgg 1140

tctggattta ctcctaagct ccaattcaaa tataagaagc aaaaaagtaa tatcgcttct 1200

gtttttttctt atactgaaaa gaatgtacag ttggttatcg aaaaaacttt ttag 1254

<210> 228

<211> 417

<212> PRT

<213> H. somni SLAM 2

<400> 228

Met Lys Lys Leu Ile Phe Ile Leu Phe Val Ser Cys Tyr Ile Pro Val
1 5 10 15

Val Thr Ala Asn Phe Gln Gln Glu Arg Asn Tyr Ser Ile Arg Leu Ser
20 25 30

Arg Asn Asp Thr Lys Leu Thr Glu Ser Leu Leu Val Ser Met Leu Lys
35 40 45

Ser Gln Gln Phe His Ala Ala Glu Lys Met Leu Ala Ile Tyr Gln Asn
50 55 60

Ile Asp Asn Pro Ser Pro Gln Leu Ile Asn Tyr Thr Lys Ile Tyr Leu
65 70 75 80

Ala Gln Gln Tyr Tyr Arg Asn Lys Gln Tyr Lys Arg Ala Leu Ser Leu
85 90 95

Phe Leu Glu Leu Lys Lys Gln Ala Asn Leu Thr Asp Lys Glu Lys Val
100 105 110

Ile Ile Glu Gln Tyr Leu Ser Ile Leu Glu Glu Gln Glu Ser Trp Gln
115 120 125

Phe Ser Phe Ser Ala Asn Tyr Leu Arg Asn Lys Asn Val Asn Asn Ala
130 135 140

Ser Ser Glu Arg Gln Ile Glu Asp Thr Gly Phe Ser Lys Asn Asp Asp
145 150 155 160

Met Leu Pro Gln Ser Ala Thr Gly Leu Ala Tyr Tyr Phe Ser Ala Glu
165 170 175

Arg Asn Trp Asn Leu Val Asp Ser His Tyr Leu His Phe Ser Asn Glu
180 185 190

Leu Phe Gly Lys Tyr Tyr Trp Asp Asn Lys Asp Phe Asp Glu Ser Asn
195 200 205

Asn Arg Thr Tyr Ile Gly Tyr Ile Tyr Gln Asn Ala Lys Leu Lys Phe
210 215 220

Ala Ser Lys Ala Phe Tyr Glu Arg Gln Trp Phe Ala Arg His Arg Tyr

225 230 235 240

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

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

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

<210> 229
<211> 1434
<212> DNA
<213> H. sputorum SLAM 1
<400> 229
atgaaattca caaaaacttt tttatattct gtactcggta tgacgtgcgc aaacttagcc 60

aatgctgaag tcgcacaatc taaaaatgac aatctagatg ataacattca ggttgccaca 120

cccaaatttc aagcgcccac tgttcagcct aaagtgaata atcaaggctc agtttctatg 180

actaaagctg agttggcaca acatccagat ttaattatac ggggaatgat tcctgcggta 240

ttacaaaata atgaagaagt tgtctcatta ctattaccct tatatcgaga aatccctcaa 300

aaagatcccg tcttgctgag ttgggcagaa gcgattgata cgcgccatca agggaattat 360

agtgaagctg cgcagcgtta tcgtaccttg tttactcagc attctgatat cttaccgcta 420

cgttatcagc ttgctcaggc actttttttg aataatgata atgaagcggc aaaagatcaa 480

tttcaaaaat tacgtgcaga agagatggcg ccagaaatga cagccgtcat tgaccaatat 540

ttatcggcat taaatcagcg tgaccagtgg aaatttagtg gcggtgtcag ttttctgaat 600

gaaacgaata tcaataatgc acctaaagct ggtacgcata ttggtagctg gcaagcctgg 660

aaaaaagaaa gtgcacaagg gctttcctat tcattaggtt tggataaaaa atggtcttta 720

ccaaataact tttttactca acttggactt gatggtcaag gtaagtatta ctgggataat 780

aaaaaatata atgagttaaa tgtacgccta ggctggggat taggctatca aacctctcgt 840

ttggaattat ctttaacgcc atttactgaa aaacgttggt atagtggcgg ctctagcgga 900

agtgatgcac taaaacagta ttcaaaaaat tctggtgccc gttttgatat cagttactgg 960

cttaaccctc gttggcaaat ttcctctgca ttagaatatg gcgagcaacg ttatgattgg 1020

cgtaagcatt taaacggcaa taattacttg ttctctaaca cattactcta tgttccgaaa 1080

agtggccaat attggtttgc agggttagat tattctcgtg aaaacacgcg agataaagat 1140

aatgcttatc aacgaatggg tagtcgactt ggttggggac aagaatggcc gtggggcata 1200

tctagccgaa ttacgctttc ttatgctaaa cgtcattatc aagcggtaga tttctttaat 1260

attcgccaga aaaaccgaga atatgcttca acattaaccc tgtggcatcg cgatctctat 1320

ttctggggca ttacacctaa aatcacttgg tcttatcaaa aggtgaaaag taatcatcct 1380

ttctatggct atgataaaaa ccgtgtattc ttagaaatga gcaaaacatt ctag 1434

<210> 230

<211> 477

<212> PRT

<213> H. sputorum SLAM 1

<400> 230

Met Lys Phe Thr Lys Thr Phe Leu Tyr Ser Val Leu Gly Met Thr Cys

1 5 10 15

Ala Asn Leu Ala Asn Ala Glu Val Ala Gln Ser Lys Asn Asp Asn Leu

20 25 30

Asp Asp Asn Ile Gln Val Ala Thr Pro Lys Phe Gln Ala Pro Thr Val

35 40 45

Gln Pro Lys Val Asn Asn Gln Gly Ser Val Ser Met Thr Lys Ala Glu

50 55 60

Leu Ala Gln His Pro Asp Leu Ile Ile Arg Gly Met Ile Pro Ala Val

65 70 75 80

Leu Gln Asn Asn Glu Glu Val Val Ser Leu Leu Leu Pro Leu Tyr Arg

85 90 95

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

100 105 110

Asp Thr Arg His Gln Gly Asn Tyr Ser Glu Ala Ala Gln Arg Tyr Arg

115 120 125

Thr Leu Phe Thr Gln His Ser Asp Ile Leu Pro Leu Arg Tyr Gln Leu

130 135 140

Ala Gln Ala Leu Phe Leu Asn Asn Asp Asn Glu Ala Ala Lys Asp Gln

145 150 155 160

Phe Gln Lys Leu Arg Ala Glu Glu Met Ala Pro Glu Met Thr Ala Val

165 170 175

Ile Asp Gln Tyr Leu Ser Ala Leu Asn Gln Arg Asp Gln Trp Lys Phe

180 185 190

Ser Gly Gly Val Ser Phe Leu Asn Glu Thr Asn Ile Asn Asn Ala Pro

195 200 205

Lys Ala Gly Thr His Ile Gly Ser Trp Gln Ala Trp Lys Lys Glu Ser

210 215 220

Ala Gln Gly Leu Ser Tyr Ser Leu Gly Leu Asp Lys Lys Trp Ser Leu

225 230 235 240

Pro Asn Asn Phe Phe Thr Gln Leu Gly Leu Asp Gly Gln Gly Lys Tyr

245 250 255

Tyr Trp Asp Asn Lys Lys Tyr Asn Glu Leu Asn Val Arg Leu Gly Trp

260 265 270

Gly Leu Gly Tyr Gln Thr Ser Arg Leu Glu Leu Ser Leu Thr Pro Phe

275 280 285

Thr Glu Lys Arg Trp Tyr Ser Gly Gly Ser Ser Gly Ser Asp Ala Leu

290 295 300

Lys Gln Tyr Ser Lys Asn Ser Gly Ala Arg Phe Asp Ile Ser Tyr Trp

305 310 315 320

Leu Asn Pro Arg Trp Gln Ile Ser Ser Ala Leu Glu Tyr Gly Glu Gln

325 330 335

Arg Tyr Asp Trp Arg Lys His Leu Asn Gly Asn Asn Tyr Leu Phe Ser

340 345 350

Asn Thr Leu Leu Tyr Val Pro Lys Ser Gly Gln Tyr Trp Phe Ala Gly

355 360 365

Leu Asp Tyr Ser Arg Glu Asn Thr Arg Asp Lys Asp Asn Ala Tyr Gln

370 375 380

Arg Met Gly Ser Arg Leu Gly Trp Gly Gln Glu Trp Pro Trp Gly Ile

385 390 395 400

Ser Ser Arg Ile Thr Leu Ser Tyr Ala Lys Arg His Tyr Gln Ala Val

405 410 415

Asp Phe Phe Asn Ile Arg Gln Lys Asn Arg Glu Tyr Ala Ser Thr Leu

420 425 430

Thr Leu Trp His Arg Asp Leu Tyr Phe Trp Gly Ile Thr Pro Lys Ile

435 440 445

Thr Trp Ser Tyr Gln Lys Val Lys Ser Asn His Pro Phe Tyr Gly Tyr

450 455 460

Asp Lys Asn Arg Val Phe Leu Glu Met Ser Lys Thr Phe

465 470 475

<210> 231

<211> 1308

<212> DNA

<213> H. sputorum SLAM 2

<400

> 231

atgcgtaagc ttttttattc tcttttcttt tgttcaactt ttgtctgggc ttcatctaat 60

ggttcaatta ccgcattaga agaacaactt aaacaagcga tttatcaaaa taatgcagag 120

caaattcaat cctttctttc tcaatatcaa caacaaacgc aacaggatcc cttgctgctt 180

tcttatgcgg aagcgaaact agcgagtttg cgccaagatt atgcccttgc aattcgtatt 240

taccgaaaaa tgttgagcga acgtccagcg ctcacttcta tccgaatgga acttgccaaa 300

gtgttatttg cagaccgtca agacatcgcg gcgagattgc aatttgataa ggtaaaaagc 360

gttaaaaatt tgcctgcttc ggcttatcag cagattgatc gttatattga cgcacttaat 420

tcgtataata cttggctgat tgatgcgagt gtttcctatc ttaaaacgga taacgtggaa 480

aatgtctcct ctgcgacaag cattgaaaat acaggtttta ttaagggtga acgtatgttg 540

ccacaaaagg ctcatggttt ttcctacaac ctgagtttta gccgtgattt taatattgtg 600

ggttctcact atgtaggttt tagtaatgaa actaacggaa aaagctattg ggacaatcat 660

caattcgatg atctttttaa ccgtacttct gtggggtatg cctacaagaa aaatgaggca 720

acattcaggc tacagccgtt ttatgaaaaa cgttggtatg gcggcgaagc attccattgg 780

tcaaatggga tcgaaatgag ttatagctat tggctttcta aaaattggca aaatcagacc 840

gcacttgaat atgaaaaacg ccgttttttt atcgagaatc cccaagctgg taatattaaa 900

accgcctcaa ataccttgat ttggtatcga aaccctgaac aaatctttta tacagggata 960

gctttttctc aacaaaaact ccttgagcgt caatatagtt cagatataaa aaatgtgcgg 1020

attggctggt tacaagaata tgcttggggg atttccacaa aactcaatct atcatttacc 1080

catcgccaat ttaaagatca agcggttctc ggcggtattt tacctttggg caagacgagg 1140

aaagatcata tttacaccat ttttgcacaa gtgtggaaac gtgattggca tttatggggc 1200

attacgccta aactcaattt tgaatggcga aaacaaaaaa gtaatttaga tacaatgtat 1260

tcctataaaa tgcacaacct gactttgagt tttgagaaaa ctttttaa 1308

<210> 232

<211> 435

<212> PRT

<213> H. sputorum SLAM 2

<400> 232

Met Arg Lys Leu Phe Tyr Ser Leu Phe Phe Cys Ser Thr Phe Val Trp

1 5 10 15

Ala Ser Ser Asn Gly Ser Ile Thr Ala Leu Glu Glu Gln Leu Lys Gln

20 25 30

Ala Ile Tyr Gln Asn Asn Ala Glu Gln Ile Gln Ser Phe Leu Ser Gln

35 40 45

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

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

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

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

Phe Phe Ile Glu Asn Pro Gln Ala Gly Asn Ile Lys Thr Ala Ser Asn
290 295 300

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

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

Lys Thr Phe
435

<210> 233
<211> 1491
<212> DNA
<213> Haemophilus sp. C1 SLAM 1
<400> 233
atgaaaaaaa cattcctatt tctcaccgtt ctttttccca tttttgcctc ggcagaaatc 60
ttagtgcaag atgttcgtca aatcccagta aatactgact ttgataataa aattaatatt 120
gcgaaacctg aaaaacgaga accaaattta ccgcacttag gtacagaaca agccgaacaa 180
attcaaatta cccttgagca acttaaacaa aacccagttt taacccacga attattaact 240
cgtgccattt atgcccgcaa tccagaaatg attaaaaaat tgctggaaat ttaccgcact 300
tttccaaatc gtgacccgat tatggaacgc tttgcggaag ggaaattggc tgcgataacg 360

gaaaactata ctgtagccat tgataaatat cgtgaaattt tagccaaaaa tccaaattta 420

aatcctgtgc gaattgaact ggctatcgct ttattcaatc aaaaacaaga tggtgctgcc 480

aaagaccaat ttgaaaaagc gcaaactgca gggaatttac cgcctcaagt taagcgttta 540

atggatgctt atttagaggc tttaaaagaa cgtgatagct ggaatgtgga tttttctttt 600

aactatgtgc gagataccaa tgtgaataat gtcggcagtg gacgccgttt agttctacgt 660

aatggtgggg taattactcg ccctgaatca atgttgcctc aaactgcaca cggattggcg 720

tattcactgg atatttcgag agatttcaat ttatggcgtt ctcattacct cacagtgggt 780

aatgcgttcg ggggcaagag ttattgggat aatcatgaat ttgatgatat ttccaaccgc 840

acttttgttg gctatgcgca taaaaccacg aagcaaaatt tccgtattaa acctttttat 900

gaaaaacgtt ggtatggtgg cgaaagttac cgttggtcta acggggcaag ggtagaattt 960

tctcgttggt taagcccgaa ttggcagatt tctacggcgg gagaattttc caaacaacgt 1020

tatctcgaca gtacatcaca aaacggcaat aacaaactaa tttcagcaac cttactttgg 1080

gcaagaacac caaaacagtt tttctatctc ggttctgatt ttatggcaga aagaacgaag 1140

gttcgtcaat atagttcaga cactaaaagt ttacgtttag gttggggaca agagtgggga 1200

tggcttggtt tttcttctcg tttaaattta tcttttacgc aaaggcaata caaagatgta 1260

ttaactttgg gttcatacca aaccccgtta ggcttgcttg atctttccgt aggtaaaaaa 1320

cgaaaagata aaatttacgg tgtgaattta tccctatgga aacgtgactg gcatatttgg 1380

gggattacgc caaaactcca attaagctgg cgtaaacaag atagtaatat tccagaaatg 1440

tattcttaca ctcagaagaa tgtgaatgtg ttatttgaga aaacctttta a 1491

<210> 234

<211> 496

<212> PRT

<213> Haemophilus sp. C1 SLAM 1

<400> 234

Met Lys Lys Thr Phe Leu Phe Leu Thr Val Leu Phe Pro Ile Phe Ala

1 5 10 15

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

20 25 30

Asp Phe Asp Asn Lys Ile Asn Ile Ala Lys Pro Glu Lys Arg Glu Pro

35 40 45

Asn Leu Pro His Leu Gly Thr Glu Gln Ala Glu Gln Ile Gln Ile Thr

50 55 60

Leu Glu Gln Leu Lys Gln Asn Pro Val Leu Thr His Glu Leu Leu Thr

65 70 75 80

Arg Ala Ile Tyr Ala Arg Asn Pro Glu Met Ile Lys Lys Leu Leu Glu

85 90 95

Ile Tyr Arg Thr Phe Pro Asn Arg Asp Pro Ile Met Glu Arg Phe Ala

100 105 110

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

115 120 125

Lys Tyr Arg Glu Ile Leu Ala Lys Asn Pro Asn Leu Asn Pro Val Arg

130 135 140

Ile Glu Leu Ala Ile Ala Leu Phe Asn Gln Lys Gln Asp Gly Ala Ala

145 150 155 160

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

165 170 175

Val Lys Arg Leu Met Asp Ala Tyr Leu Glu Ala Leu Lys Glu Arg Asp

180 185 190

Ser Trp Asn Val Asp Phe Ser Phe Asn Tyr Val Arg Asp Thr Asn Val

195 200 205

Asn Asn Val Gly Ser Gly Arg Arg Leu Val Leu Arg Asn Gly Gly Val

210 215 220

Ile Thr Arg Pro Glu Ser Met Leu Pro Gln Thr Ala His Gly Leu Ala

225 230 235 240

Tyr Ser Leu Asp Ile Ser Arg Asp Phe Asn Leu Trp Arg Ser His Tyr

245 250 255

Leu Thr Val Gly Asn Ala Phe Gly Gly Lys Ser Tyr Trp Asp Asn His

260 265 270

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

275 280 285

Thr Thr Lys Gln Asn Phe Arg Ile Lys Pro Phe Tyr Glu Lys Arg Trp

290 295 300

Tyr Gly Gly Glu Ser Tyr Arg Trp Ser Asn Gly Ala Arg Val Glu Phe

305 310 315 320

Ser Arg Trp Leu Ser Pro Asn Trp Gln Ile Ser Thr Ala Gly Glu Phe

325 330 335

Ser Lys Gln Arg Tyr Leu Asp Ser Thr Ser Gln Asn Gly Asn Asn Lys

340 345 350

Leu Ile Ser Ala Thr Leu Leu Trp Ala Arg Thr Pro Lys Gln Phe Phe

355 360 365

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

370 375 380

Ser Ser Asp Thr Lys Ser Leu Arg Leu Gly Trp Gly Gln Glu Trp Gly

385 390 395 400

Trp Leu Gly Phe Ser Ser Arg Leu Asn Leu Ser Phe Thr Gln Arg Gln

405 410 415

Tyr Lys Asp Val Leu Thr Leu Gly Ser Tyr Gln Thr Pro Leu Gly Leu

420 425 430

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

435 440 445

Asn Leu Ser Leu Trp Lys Arg Asp Trp His Ile Trp Gly Ile Thr Pro

450 455 460

Lys Leu Gln Leu Ser Trp Arg Lys Gln Asp Ser Asn Ile Pro Glu Met

465 470 475 480

Tyr Ser Tyr Thr Gln Lys Asn Val Asn Val Leu Phe Glu Lys Thr Phe

485 490 495

<210> 235

<211> 1506

<212> DNA

<213> Haemophilus sp. FF7 SLAM 1

<400> 235

atggtttctt tctatattaa tcaccgccat ataacgggca taatttttca ttttctccca 60

ccgttattaa tagccgcttg tacaacggct ttggcagcgg tacaaacgcc aaataatcat 120

gatgccgttc aactttggca gcaacacagc cagataagcc gacaacagca acaggaaagt 180

caggtggatg aacaagcaat tgatgcgcag acaaccgaaa atgaactctc tttcgacggt 240

caatcagtgg ttattgaaca taacgccgaa gcggtcgggc aggtactatt cttcgcctta 300

aaccgacagt tatgggatga ggcggaaaaa cttctgattc gttatcgaac tttcaaggat 360

catcatctcg aattggtttt atttgctgaa gccgcactgg cgcgccaaaa aggcgacatg 420

gatacggcgg aacagcgcta tcgtcaacta ctgcaggcag atccgagctt tatccgcgct 480

cagttggatc tggcacgcgt gctgtttgaa aataaaaaaa gccgagaatc caccgcactt 540

tttaatcaac tggcgacatt accactgccg aatagcgtcc ggtacagtat cgacagctac 600

cgtcaggcat tggcacagcg acaaaaatgg cagctgtctt tcagcttagg gtatcagtac 660

gctaccaata tcaatcaatc ttccgaacgc agtttctgca cgctgaacca aggcactcac 720

tgcttcgctc gctttacctc gccgcctgcc gccaatgcgc agggctggcg ttatgatgtc 780

agtgcacaga aacagacggc attatccggt catcacggca tgtactttta tctgaacagc 840

tacggccatt tttatccgca tgccggagaa tatgccgaag acagcagcaa agtttacctt 900

ggctatcgtt atcagaacat gaaaaccgaa ctgaccctga cgcccttgtt tgaatataat 960

cgcctaggca accgcactta ttcgcgggcg tggggcgtac aaagcacact gaaccgccga 1020

atcggtacgc agcattggct gaatatacaa atggaacaaa aaaggctgca atattcaccg 1080

cactataacg cactacgcat ggcggatctg agtgcgcttt atacgacttt gtattacacc 1140

gtttccgacc aaacaacctt gtttggcggg cttgacgggc aatatcgaca taccacgaat 1200

gacgctgaca attattatct gtatgggcta cgcgcaggca taaaccgaca atttgagttc 1260

gggctggatg cgactctgct ggcgttattg cgccgttatg actaccaggg cttcaatgca 1320

tcgttaaacc agacccgacg ggataatcaa caggtttatc tggccatatt aaaaatgccg 1380

acatggcagt tttacggcat gacgccgagt ctatggctga aacacaccga taatcggagt 1440

aatgttgact ggctgtattc ctataaacag aatgaaattc aactgaattt cgagtggcaa 1500

ttttaa 1506

<210> 236

<211> 488

<212> PRT

<213> Haemophilus sp. FF7 SLAM 1

<400> 236

Met Ile Phe His Phe Leu Pro Pro Leu Leu Ile Ala Ala Cys Thr Thr

1 5 10 15

Ala Leu Ala Ala Val Gln Thr Pro Asn Asn His Asp Ala Val Gln Leu

20 25 30

Trp Gln Gln His Ser Gln Ile Ser Arg Gln Gln Gln Gln Glu Ser Gln

35 40 45

Val Asp Glu Gln Ala Ile Asp Ala Gln Thr Thr Glu Asn Glu Leu Ser

50 55 60

Phe Asp Gly Gln Ser Val Val Ile Glu His Asn Ala Glu Ala Val Gly

65 70 75 80

Gln Val Leu Phe Phe Ala Leu Asn Arg Gln Leu Trp Asp Glu Ala Glu

85 90 95

Lys Leu Leu Ile Arg Tyr Arg Thr Phe Lys Asp His His Leu Glu Leu

100 105 110

Val Leu Phe Ala Glu Ala Ala Leu Ala Arg Gln Lys Gly Asp Met Asp

115 120 125

Thr Ala Glu Gln Arg Tyr Arg Gln Leu Leu Gln Ala Asp Pro Ser Phe

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Gln Arg Gln Lys Trp Gln Leu Ser Phe Ser Leu Gly Tyr Gln Tyr Ala

195 200 205

Thr Asn Ile Asn Gln Ser Ser Glu Arg Ser Phe Cys Thr Leu Asn Gln

210 215 220

Gly Thr His Cys Phe Ala Arg Phe Thr Ser Pro Pro Ala Ala Asn Ala

225 230 235 240

Gln Gly Trp Arg Tyr Asp Val Ser Ala Gln Lys Gln Thr Ala Leu Ser

245 250 255

Gly His His Gly Met Tyr Phe Tyr Leu Asn Ser Tyr Gly His Phe Tyr

260 265 270

Pro His Ala Gly Glu Tyr Ala Glu Asp Ser Ser Lys Val Tyr Leu Gly

275 280 285

Tyr Arg Tyr Gln Asn Met Lys Thr Glu Leu Thr Leu Thr Pro Leu Phe

290 295 300

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

305 310 315 320

Gln Ser Thr Leu Asn Arg Arg Ile Gly Thr Gln His Trp Leu Asn Ile

325 330 335

Gln Met Glu Gln Lys Arg Leu Gln Tyr Ser Pro His Tyr Asn Ala Leu

340 345 350

Arg Met Ala Asp Leu Ser Ala Leu Tyr Thr Thr Leu Tyr Tyr Thr Val

355 360 365

Ser Asp Gln Thr Thr Leu Phe Gly Gly Leu Asp Gly Gln Tyr Arg His

370 375 380

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

385 390 395 400

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

405 410 415

Leu Arg Arg Tyr Asp Tyr Gln Gly Phe Asn Ala Ser Leu Asn Gln Thr

420 425 430

Arg Arg Asp Asn Gln Gln Val Tyr Leu Ala Ile Leu Lys Met Pro Thr

435 440 445

Trp Gln Phe Tyr Gly Met Thr Pro Ser Leu Trp Leu Lys His Thr Asp

450 455 460

Asn Arg Ser Asn Val Asp Trp Leu Tyr Ser Tyr Lys Gln Asn Glu Ile

465 470 475 480

Gln Leu Asn Phe Glu Trp Gln Phe

485

<210> 237

<211> 1470

<212> DNA

<213> Haemophilus sp. oral taxon 851 SLAM 1

<400> 237

atgaaaagta ttgctttctt ttttactgca cttttccccg ctcttgcttt agcagaaaca 60

acggcactag atattcgtca aacaccaatt aaaaccgaac ttgaaccaca aattaatgtc 120

gccaaacttg aaaaacgcga acaaaattta ccgcccttag gcacagagca agtcgaacaa 180

attcaaatta cccttgagca acttaaacaa aaccccgctt taacccacaa attattaacc 240

cgtgccattt acgcacgcaa tccagaaatg ataaaaaaat tgctggaaat ttaccgcact 300

tttccaaatc gtgacccgat tatggaacgc tttgcggaag gaaaattggc tgcgataacg 360

gaaaactata ctgtagctat tgataaatat cgcgaaattt tagccaaaaa tccaaattta 420

aaccctgtac gaattgaact ggctatcgct ttattcaatc aaaaacaaga cggtgctgct 480

aaagaccaat ttgaaaaagc acaaaccgca gaggatttac cgcctcaagt taagcgttta 540

atggatgctt atttagaggc tttaaaagaa cgtgatagct ggaatgtgga cttttctttt 600

aattatgtac gtgataccaa tgtcaacaat gtcggcgagg gtaaaacggt cgcattaaat 660

aatggtggca ccttaacacg ttccgaatcg atgatgccac aaacagcaca cggtttggcg 720

tattcactcg atatttcgag agatttcaat ttatggagct ctaattacct cacggtgggc 780

aatgagtttg ggggaaagag ctactgggat aatcataaat ttgatgatat ttccaaccgc 840

acttttgttg gctatgcaca taaaaccgca aagcaaaatt tccgtattaa acctttttat 900

gaaaaacgtt ggtatggcgg cgaaagttac cgttggtcta atggggcaag ggtggaattt 960

tctcgttggt taagtccaaa ctggcaactt tttacggcgg gagagttttc aaaacaacgt 1020

tatttagaca gtacatcaca aaacggtaat aacaaactga tttccgcaac cttactgtgg 1080

gcaagaactc cgaaacagtt tttctacttc ggttctgatt tcatggcaga aagaacgaag 1140

gttcgtcaat atggttcaga cagtaaaagc ttacgtttag gttgggggca agaatggaat 1200

tggggcattt cctcacgtct cggcttatcc ataatgaaac gtgaatttaa agatattgcc 1260

aaacttggta atctcaattt gttttctttt ggaaaacgtc gagaagataa aatttacggc 1320

ataaatttat ccctatggaa acgcgattgg catatttggg gaattacacc aaaactccaa 1380

ttaagctggc gtaaacaaga tagcaatatc ccagaaatgt attcttacac acagaagaat 1440

gtgaatatgt tgtttgaaaa gacattctga 1470

<210> 238

<211> 489

<212> PRT

<213> Haemophilus sp. oral taxon 851 SLAM 1

<400> 238

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

Tyr Ser Leu Asp Ile Ser Arg Asp Phe Asn Leu Trp Ser Ser Asn Tyr

245 250 255

Leu Thr Val Gly Asn Glu Phe Gly Gly Lys Ser Tyr Trp Asp Asn His

260 265 270

Lys Phe Asp Asp Ile Ser Asn Arg Thr Phe Val Gly Tyr Ala His Lys

275 280 285

Thr Ala Lys Gln Asn Phe Arg Ile Lys Pro Phe Tyr Glu Lys Arg Trp

290 295 300

Tyr Gly Gly Glu Ser Tyr Arg Trp Ser Asn Gly Ala Arg Val Glu Phe

305 310 315 320

Ser Arg Trp Leu Ser Pro Asn Trp Gln Leu Phe Thr Ala Gly Glu Phe

325 330 335

Ser Lys Gln Arg Tyr Leu Asp Ser Thr Ser Gln Asn Gly Asn Asn Lys

340 345 350

Leu Ile Ser Ala Thr Leu Leu Trp Ala Arg Thr Pro Lys Gln Phe Phe

355 360 365

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

370 375 380

Gly Ser Asp Ser Lys Ser Leu Arg Leu Gly Trp Gly Gln Glu Trp Asn

385 390 395 400

Trp Gly Ile Ser Ser Arg Leu Gly Leu Ser Ile Met Lys Arg Glu Phe

405 410 415

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

420 425 430

Arg Arg Glu Asp Lys Ile Tyr Gly Ile Asn Leu Ser Leu Trp Lys Arg

435 440 445

Asp Trp His Ile Trp Gly Ile Thr Pro Lys Leu Gln Leu Ser Trp Arg

450 455 460

Lys Gln Asp Ser Asn Ile Pro Glu Met Tyr Ser Tyr Thr Gln Lys Asn

465 470 475 480

Val Asn Met Leu Phe Glu Lys Thr Phe

485

<210> 239

<211> 1422

<212> DNA

<213> K. denitrificans SLAM 1

<400> 239

atggatttct tttggacgcg gttgcggcat atcgtttggc tggcgttgcc cctgcaggct 60

gcttttgccg cgccgcccga acctcgcccc gaaccggata cgggcttcga cattacgccg 120

caggccgccc cgaaggtgga aagcccggcc gtgccgcagg acgggcgatt gaaaatccgc 180

cgcgaagagc tgctgcaacg ccccgagctt ctgcagcagg cattgagtta tgccgtgctc 240

gccaacgaca aagacggcgt ggaacttttg ctgccgctgt atttgcaaca gcaggcaccg 300

cgcgacgaat tgctggtcac gttggcacag gccgttttgg cgcgcgcaga aggcgattac 360

cgccgtgccg ttgccttata tcgcgccgcg ttggaaaccg accccgattt gcccaccgtt 420

cggttggcat tggcgcaatc actgtttgaa aaccgcgccg acaaagccgc acggcaagaa 480

ttggaacgct tccgccaaac gcccgatttg gcacccgaat acgcccaaat cggcgaacaa 540

tatgcacagg cattggacaa gcgcgaccgc tggacgtttg gcggcaccgt cagctatctc 600

cgcgacggca acgtgaacaa cgccccgcac caacgcgaat accgcacccg caggggcgta 660

tggcggctgc cgaaagccga gtccgcacaa ggatttgcct accgcttgga agtcgaacgc 720

gattggaatc tccacggcaa tgcctattgg cgcgtccatt tgggcggcga aggcaaatgg 780

tattgggaca accaccgcta tgacgaccac aacgcccgca tcgccaccgg ctttgcctat 840

aaaaccgccc gcaccgaagc cgccatcacc ccgtattttg aacgccgctg gtacggcaca 900

cacccttatt cgcgcgaata cggcgtgcgt gccgaagggc aatattggct caccccgcga 960

aacaaaatcc tgggcgcatt tgaatttggc cggcaacgcc acgaccgccg ccgctggctg 1020

gacggccgcc aatataccgc ctccgccact tggttgttcg cacgccgccc cgaccaatat 1080

ttcagcttcg gcgcagatgg cgcaagcaaa caggcggaag acgccgccga atcctacacc 1140

cgccaaggcc tgcgcttcgg ctggacgcaa caatggccgt ccgggctcgc cacatccgcc 1200

catatcggca tcggccgccg ccgctaccac gccgcagact ggttcggcat cctgcgccgc 1260

gaccgcgaat tttccgccag catgtccgtg tcacaccgca aaatccaatt tgccggcatt 1320

accccgcaaa tcgtcggcgt gtggcaatgt gtccgcagca accatttttt ctatcctttc 1380

cgcaaaggca acgtgtttat ccagttcggc cggacatttt ga 1422

<210> 240

<211> 473

<212> PRT

<213> K. denitrificans SLAM 1

<400> 240

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

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

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

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

Lys Ala Glu Ser Ala Gln Gly Phe Ala Tyr Arg Leu Glu Val Glu Arg

225 230 235 240

Asp Trp Asn Leu His Gly Asn Ala Tyr Trp Arg Val His Leu Gly Gly

245 250 255

Glu Gly Lys Trp Tyr Trp Asp Asn His Arg Tyr Asp Asp His Asn Ala

260 265 270

Arg Ile Ala Thr Gly Phe Ala Tyr Lys Thr Ala Arg Thr Glu Ala Ala

275 280 285

Ile Thr Pro Tyr Phe Glu Arg Arg Trp Tyr Gly Thr His Pro Tyr Ser

290 295 300

Arg Glu Tyr Gly Val Arg Ala Glu Gly Gln Tyr Trp Leu Thr Pro Arg

305 310 315 320

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

325 330 335

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

340 345 350

Phe Ala Arg Arg Pro Asp Gln Tyr Phe Ser Phe Gly Ala Asp Gly Ala

355 360 365

Ser Lys Gln Ala Glu Asp Ala Ala Glu Ser Tyr Thr Arg Gln Gly Leu

370 375 380

Arg Phe Gly Trp Thr Gln Gln Trp Pro Ser Gly Leu Ala Thr Ser Ala

385 390 395 400

His Ile Gly Ile Gly Arg Arg Arg Tyr His Ala Ala Asp Trp Phe Gly

405 410 415

Ile Leu Arg Arg Asp Arg Glu Phe Ser Ala Ser Met Ser Val Ser His

420 425 430

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

435 440 445

Gln Cys Val Arg Ser Asn His Phe Phe Tyr Pro Phe Arg Lys Gly Asn

450 455 460

Val Phe Ile Gln Phe Gly Arg Thr Phe

465 470

<210> 241

<211> 1410

<212> DNA

<213> K. denitrificans SLAM 2

<400> 241

atgcgttaca ttccttttct tctgctcgcc gccgcatccg ccgtgtctgc cgcgcctgtc 60

ggcacaccgc tcaaccccat tcccgattta aaccaaaaca gcattcggga acacgtgcag 120

gacaccgaaa agcagcctgc acccgaacca caagcccccg tccaaatgag cgaagagcag 180

cttttgcagc agcctgcact actgctcaat gccttggaca ccgccgtggg ccagcaaaac 240

accgacaata tccgcttcct gctgccgctt taccgcaggc tgcctgccga acagcaagac 300

cccgtgttgg cagaatatgc cgaagccatc ctcctacgcg cagacggccg ccatgacgcc 360

gccgaacaaa aactgcgcca aattctggaa agaaaccccg aattttcccc cgtgcgcctg 420

caactggcgc taacccaatc gcaaaacggc aaacagcgcg aagccgccgc cgaaatcgcc 480

cgaatccggc aaacgcccga actgcccgcc cccgtcgccc aatacctcga ccaatacgaa 540

caatacctga accgagaacg cgcctggcaa ttcagcggca acgcctatta cctgcaagac 600

aacaacgtgg cgcgcgcccc cgaacagcgc acctacggcg catggcagtt taacgaaccc 660

caatccgcgc acggcatcgg ctacgaattt tcggcacaga aaaccacgcc cgtcaaaggc 720

cactgggcgg cacgcgtgca ggctgccctc tacggcaaat tttactggga tgcacatgat 780

tacgacgact tggtcgcccg cgccgaagcc ggccccgtgt ggcgcgacgc acggcaggaa 840

atctatgccg ccccgtttta cgaacaacgc tggtacggca ccgaaccctt ttcccgccaa 900

ttcggcggca gcatccacta ttcgcgcacc ctgtcgccga attggcaaat gtatgccgcc 960

tggcagtccg gctacaaaca acacaacgag cgcaccttcc tcaacggcac cagccacacc 1020

ggttcgctca ccctgctcta ccgcacatcg ccgcagcaat atttcgtgat gggcatcggc 1080

ggcgggcagg aaaacgccaa agacctgtcg gacgcatacc gcaaaagcag cctgcacggc 1140

ggctggacgc gccactgggg cagcagccgc gccttcgcca catcgctcaa catcagcgtg 1200

cagcgcagaa actaccgcgg ccccgacatc ttcaatatcc agcgccgcga caccgaatac 1260

ttcacccgcc tggcgctgtc gcacagccgc ctctcctgga aaggcttcac cccgcgcctg 1320

aactggacct ggtcgcacat ccacagcaac catttctatt accgctataa caaccaccgc 1380

gtgtttttgg atgtattcaa gcagttctga 1410

<210> 242

<211> 469

<212> PRT

<213> K. denitrificans SLAM 2

<400> 242

Met Arg Tyr Ile Pro Phe Leu Leu Leu Ala Ala Ala Ser Ala Val Ser
1 5 10 15

Ala Ala Pro Val Gly Thr Pro Leu Asn Pro Ile Pro Asp Leu Asn Gln
20 25 30

Asn Ser Ile Arg Glu His Val Gln Asp Thr Glu Lys Gln Pro Ala Pro

35 40 45

Glu Pro Gln Ala Pro Val Gln Met Ser Glu Glu Gln Leu Leu Gln Gln
50 55 60

Pro Ala Leu Leu Leu Asn Ala Leu Asp Thr Ala Val Gly Gln Gln Asn
65 70 75 80

Thr Asp Asn Ile Arg Phe Leu Leu Pro Leu Tyr Arg Arg Leu Pro Ala
85 90 95

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

100 105 110

Arg Ala Asp Gly Arg His Asp Ala Ala Glu Gln Lys Leu Arg Gln Ile
115 120 125

Leu Glu Arg Asn Pro Glu Phe Ser Pro Val Arg Leu Gln Leu Ala Leu
130 135 140

Thr Gln Ser Gln Asn Gly Lys Gln Arg Glu Ala Ala Ala Glu Ile Ala
145 150 155 160

Arg Ile Arg Gln Thr Pro Glu Leu Pro Ala Pro Val Ala Gln Tyr Leu

165 170 175

Asp Gln Tyr Glu Gln Tyr Leu Asn Arg Glu Arg Ala Trp Gln Phe Ser
180 185 190

Gly Asn Ala Tyr Tyr Leu Gln Asp Asn Asn Val Ala Arg Ala Pro Glu
195 200 205

Gln Arg Thr Tyr Gly Ala Trp Gln Phe Asn Glu Pro Gln Ser Ala His
210 215 220

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

225 230 235 240

His Trp Ala Ala Arg Val Gln Ala Ala Leu Tyr Gly Lys Phe Tyr Trp

245 250 255

Asp Ala His Asp Tyr Asp Asp Leu Val Ala Arg Ala Glu Ala Gly Pro

260 265 270

Val Trp Arg Asp Ala Arg Gln Glu Ile Tyr Ala Ala Pro Phe Tyr Glu

275 280 285

Gln Arg Trp Tyr Gly Thr Glu Pro Phe Ser Arg Gln Phe Gly Gly Ser

290 295 300

Ile His Tyr Ser Arg Thr Leu Ser Pro Asn Trp Gln Met Tyr Ala Ala

305 310 315 320

Trp Gln Ser Gly Tyr Lys Gln His Asn Glu Arg Thr Phe Leu Asn Gly

325 330 335

Thr Ser His Thr Gly Ser Leu Thr Leu Leu Tyr Arg Thr Ser Pro Gln

340 345 350

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

355 360 365

Leu Ser Asp Ala Tyr Arg Lys Ser Ser Leu His Gly Gly Trp Thr Arg

370 375 380

His Trp Gly Ser Ser Arg Ala Phe Ala Thr Ser Leu Asn Ile Ser Val

385 390 395 400

Gln Arg Arg Asn Tyr Arg Gly Pro Asp Ile Phe Asn Ile Gln Arg Arg

405 410 415

Asp Thr Glu Tyr Phe Thr Arg Leu Ala Leu Ser His Ser Arg Leu Ser

420 425 430

Trp Lys Gly Phe Thr Pro Arg Leu Asn Trp Thr Trp Ser His Ile His

435 440 445

Ser Asn His Phe Tyr Tyr Arg Tyr Asn Asn His Arg Val Phe Leu Asp

450 455 460

Val Phe Lys Gln Phe

465

<210> 243

<211> 1428

<212> DNA

<213> K. denitrificans SLAM 3

<400> 243

atgaacatcc gccctatttt ctggctgctg cccgccctat tcgccgcaca agtgcaggct 60

gccccgttgc cgcccaaagt ggaacagtcg ctcaccgcac cggaagaaca cttcgacaaa 120

cagccgcccg cagacgtgcc cgcaccaccc caaccgccgc aacaaagcga atccggcagt 180

ctgaccattt catcggaaga actgcaaaag cagcctgcac ttttgaaaca ggcgttttat 240

tcggccatcg ccgccaacaa cacgcccgcc gtgcgcctgc tgctgccctt gtaccgccgc 300

ctgcccgacg gcaacgaaga agtgccgatt gcactgtccg aagccataat tgcgcgcgca 360

gacggccatt acgcccaagc catcgaaaaa ttccgctttg ccttggacaa gcagcccgat 420

atgcccgtgg cgcaaatgtc gctggcgcaa accctgcaca gcgactaccg ctacccgtcc 480

gccgccaaag catttgaaga aatcgcgcag cgcaccgatt tgccgcccga attccaccaa 540

gtcgcccaaa cctacctgaa cagcatcaaa gcgcgggaag actggaaatt ccaagtgaac 600

ggcaattacc tggacgacaa aaacgtgggc aacacgcccg accgctacat catcggcgca 660

tggtcgctca atccgcccga atccgcacac ggcatctcgt attacggcag cgtgtcgcgc 720

gaaaaatggc tggccgacca cttcaccctg cgttacggcg ccgacctata cggcaaaacc 780

tattgggaca accaccgttt cgacgatttg gccgtgcgcg tgaaagccgg attcggttat 840

cagacaggcc gttccgaaac cgtggtgcag ccctatttcg agcgccgctg gttcggcagc 900

gacggctatt cgcgcgagtt gggcattggc atcgactggt cgtattggct aaccgcgcgc 960

aaccagctga tgctttccgc cgcgcacgcc acacagaatt atgacgaccg ccgctatttg 1020

gaaggccgcc tgcgcaccgc gtccgccaca tggttgtttg tgcccagcgg cacgcagtat 1080

tggacgctcg gcacggactg gacgcgcaaa accgcacaag acgccagcga tgcctaccgc 1140

cgccaagccg ttcgtgtcgg ctggacgcag caatggccgg cacagttcgg cacgtcggtg 1200

aatctgtcgt gggcgaaacg cacctacgac cgcccgaatt ttccgttcaa ctacatccgc 1260

atcgaccacg aacgttccgc cgctgtgtcg ctttggaacc gcaaagtcca atggtggggc 1320

atcatgccgc gcctggtgtg gcgttggcag caaacgcgca gcaaccaccc gttttacggc 1380

gattacacca aacgcgatgt gtttatccag ttgaacaagg cgttttaa 1428

<210> 244

<211> 475

<212> PRT

<213> K. denitrificans SLAM 3

<400> 244

Met Asn Ile Arg Pro Ile Phe Trp Leu Leu Pro Ala Leu Phe Ala Ala
1 5 10 15

Gln Val Gln Ala Ala Pro Leu Pro Pro Lys Val Glu Gln Ser Leu Thr
20 25 30

Ala Pro Glu Glu His Phe Asp Lys Gln Pro Pro Ala Asp Val Pro Ala
35 40 45

Pro Pro Gln Pro Pro Gln Gln Ser Glu Ser Gly Ser Leu Thr Ile Ser
50 55 60

Ser Glu Glu Leu Gln Lys Gln Pro Ala Leu Leu Lys Gln Ala Phe Tyr
65 70 75 80

Ser Ala Ile Ala Ala Asn Asn Thr Pro Ala Val Arg Leu Leu Leu Pro
85 90 95

Leu Tyr Arg Arg Leu Pro Asp Gly Asn Glu Glu Val Pro Ile Ala Leu
100 105 110

Ser Glu Ala Ile Ile Ala Arg Ala Asp Gly His Tyr Ala Gln Ala Ile
115 120 125

Glu Lys Phe Arg Phe Ala Leu Asp Lys Gln Pro Asp Met Pro Val Ala
130 135 140

Gln Met Ser Leu Ala Gln Thr Leu His Ser Asp Tyr Arg Tyr Pro Ser
145 150 155 160

Ala Ala Lys Ala Phe Glu Glu Ile Ala Gln Arg Thr Asp Leu Pro Pro
165 170 175

Glu Phe His Gln Val Ala Gln Thr Tyr Leu Asn Ser Ile Lys Ala Arg
180 185 190

Glu Asp Trp Lys Phe Gln Val Asn Gly Asn Tyr Leu Asp Asp Lys Asn
195 200 205

Val Gly Asn Thr Pro Asp Arg Tyr Ile Ile Gly Ala Trp Ser Leu Asn
210 215 220

Pro Pro Glu Ser Ala His Gly Ile Ser Tyr Tyr Gly Ser Val Ser Arg

225 230 235 240

Glu Lys Trp Leu Ala Asp His Phe Thr Leu Arg Tyr Gly Ala Asp Leu

245 250 255

Tyr Gly Lys Thr Tyr Trp Asp Asn His Arg Phe Asp Asp Leu Ala Val

260 265 270

Arg Val Lys Ala Gly Phe Gly Tyr Gln Thr Gly Arg Ser Glu Thr Val

275 280 285

Val Gln Pro Tyr Phe Glu Arg Arg Trp Phe Gly Ser Asp Gly Tyr Ser

290 295 300

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

305 310 315 320

Asn Gln Leu Met Leu Ser Ala Ala His Ala Thr Gln Asn Tyr Asp Asp

325 330 335

Arg Arg Tyr Leu Glu Gly Arg Leu Arg Thr Ala Ser Ala Thr Trp Leu

340 345 350

Phe Val Pro Ser Gly Thr Gln Tyr Trp Thr Leu Gly Thr Asp Trp Thr

355 360 365

Arg Lys Thr Ala Gln Asp Ala Ser Asp Ala Tyr Arg Arg Gln Ala Val

370 375 380

Arg Val Gly Trp Thr Gln Gln Trp Pro Ala Gln Phe Gly Thr Ser Val

385 390 395 400

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

405 410 415

Asn Tyr Ile Arg Ile Asp His Glu Arg Ser Ala Ala Val Ser Leu Trp

420 425 430

Asn Arg Lys Val Gln Trp Trp Gly Ile Met Pro Arg Leu Val Trp Arg

435 440 445

Trp Gln Gln Thr Arg Ser Asn His Pro Phe Tyr Gly Asp Tyr Thr Lys

450 455 460

Arg Asp Val Phe Ile Gln Leu Asn Lys Ala Phe

465 470 475

<210> 245

<211> 1458

<212> DNA

<213> K. denitrificans SLAM 4

<400> 245

atgataccca tcttccgcca tcccaccatt ctggcactgt gcctgctcag ccttccgctc 60

ggcacgattg ccgcgccgcc aaccctcgtg ccgcacgatg acaatccgcc atggccgcag 120

ccgccccagc ccattcaaac ggacgacagc atcgccccga aaacacccca aagcagtacc 180

caaccctcca agcacctaac cgaaaccgac ctgcgcgcca atcccgccct gaccgaacac 240

ctgatcaatc aggccatcct cagtcaccaa tgggatttgc tggccgacct gctggatttg 300

taccgcacca tgccgaacca cgataccgtt ttgtacgatt acggcaaagg tgccctattg 360

cgcgggcagg acaagcttga gcaggcaatc aggcattatg ccgccattgt gcagcggcgg 420

ccggaactgt cttatgtccg gttcgactac atggcgatgc tgtttgaaaa ccaccaatac 480

cgccaggccg atcaacaggc cgaacaattg gaacagtccg acctgctgcc ggaagcaaaa 540

caactggtgg cgcaataccg ccaagccatg caaaaacggc aggcgtggca agccgatgcc 600

tcgctgcaat acgaacggaa cgacaacgtc aataacgcct cctctgcccg cgaactgcgc 660

ttgggctcac gcgtgtgggt gcgtgatgaa gcctcgttgc cccagaaagc caccggcctg 720

cgttacagtg ccgcgctcga ccgatccgtg aacattggcg gcaaccactt cctcaccggc 780

ggtgttagtt tggacggtgt gttttactgg gatcggcgcg agtacaacga agaaaacctа 840

cgtgtgcagg ctggttaccg cttccgcaat atccgcagca gctggcagat acagccctat 900

accgaattca gctggttttc aggtagccca tacagccgcc aatacggcat acaggggcaa 960

tatagccgcc aaatcggctc aaaatggcaa atcagcgtga tggccacccg cagttggcgg 1020

cattaccgca gcaaaaacgt tgcacaaagc tacaacggcc cgcaaaccca attaactgcc 1080

accgccgcct ggatgcccat cgcaaacagc ctgctctata tcggtttaga ctggctggaa 1140

caccaaaccc gcgacccgtc ggaagcctcc gtccgacgcg gcatccgctt cgggctgatg 1200

cgggaatggc cgcaattcgg cctgcgtgca gacatccgct tgggcaggcg gcagttccgc 1260

caaacgcact tctttttccc cgtggtgcgc tccgaccgag aaacccagct caacttgtcg 1320

ctgtggcatc ccaaactgca atggcacggc ctgatgcccc gcctaaccta ccgccatctg 1380

aacatcaaca gcaatattcc ggaactctac caacgccgca gccgccaatg gtttatcgag 1440

gtggaacgtc ggttttga 1458

<210> 246

<211> 485

<212> PRT

<213> K. denitrificans SLAM 4

<400> 246

Met Ile Pro Ile Phe Arg His Pro Thr Ile Leu Ala Leu Cys Leu Leu
1 5 10 15

Ser Leu Pro Leu Gly Thr Ile Ala Ala Pro Pro Thr Leu Val Pro His
20 25 30

Asp Asp Asn Pro Pro Trp Pro Gln Pro Pro Gln Pro Ile Gln Thr Asp
35 40 45

Asp Ser Ile Ala Pro Lys Thr Pro Gln Ser Ser Thr Gln Pro Ser Lys
50 55 60

His Leu Thr Glu Thr Asp Leu Arg Ala Asn Pro Ala Leu Thr Glu His
65 70 75 80

Leu Ile Asn Gln Ala Ile Leu Ser His Gln Trp Asp Leu Leu Ala Asp
85 90 95

Leu Leu Asp Leu Tyr Arg Thr Met Pro Asn His Asp Thr Val Leu Tyr
100 105 110

Asp Tyr Gly Lys Gly Ala Leu Leu Arg Gly Gln Asp Lys Leu Glu Gln
115 120 125

Ala Ile Arg His Tyr Ala Ala Ile Val Gln Arg Arg Pro Glu Leu Ser
130 135 140

Tyr Val Arg Phe Asp Tyr Met Ala Met Leu Phe Glu Asn His Gln Tyr
145 150 155 160

Arg Gln Ala Asp Gln Gln Ala Glu Gln Leu Glu Gln Ser Asp Leu Leu
165 170 175

Pro Glu Ala Lys Gln Leu Val Ala Gln Tyr Arg Gln Ala Met Gln Lys
180 185 190

Arg Gln Ala Trp Gln Ala Asp Ala Ser Leu Gln Tyr Glu Arg Asn Asp
195 200 205

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

210 215 220

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

225 230 235 240

Arg Tyr Ser Ala Ala Leu Asp Arg Ser Val Asn Ile Gly Gly Asn His

245 250 255

Phe Leu Thr Gly Gly Val Ser Leu Asp Gly Val Phe Tyr Trp Asp Arg

260 265 270

Arg Glu Tyr Asn Glu Glu Asn Leu Arg Val Gln Ala Gly Tyr Arg Phe

275 280 285

Arg Asn Ile Arg Ser Ser Trp Gln Ile Gln Pro Tyr Thr Glu Phe Ser

290 295 300

Trp Phe Ser Gly Ser Pro Tyr Ser Arg Gln Tyr Gly Ile Gln Gly Gln

305 310 315 320

Tyr Ser Arg Gln Ile Gly Ser Lys Trp Gln Ile Ser Val Met Ala Thr

325 330 335

Arg Ser Trp Arg His Tyr Arg Ser Lys Asn Val Ala Gln Ser Tyr Asn

340 345 350

Gly Pro Gln Thr Gln Leu Thr Ala Thr Ala Ala Trp Met Pro Ile Ala

355 360 365

Asn Ser Leu Leu Tyr Ile Gly Leu Asp Trp Leu Glu His Gln Thr Arg

370 375 380

Asp Pro Ser Glu Ala Ser Val Arg Arg Gly Ile Arg Phe Gly Leu Met

385 390 395 400

Arg Glu Trp Pro Gln Phe Gly Leu Arg Ala Asp Ile Arg Leu Gly Arg

405 410 415

Arg Gln Phe Arg Gln Thr His Phe Phe Phe Pro Val Val Arg Ser Asp

420 425 430

Arg Glu Thr Gln Leu Asn Leu Ser Leu Trp His Pro Lys Leu Gln Trp

435 440 445

His Gly Leu Met Pro Arg Leu Thr Tyr Arg His Leu Asn Ile Asn Ser

450 455 460

Asn Ile Pro Glu Leu Tyr Gln Arg Arg Ser Arg Gln Trp Phe Ile Glu

465 470 475 480

Val Glu Arg Arg Phe

485

<210> 247

<211> 1539

<212> DNA

<213> K. denitrificans SLAM 5

<400> 247

gtgaaaacta ttcgtaaaat tatttcagga ttggtattgg gcatttcggt gggcgcggtg 60

gcggaacctt tgccgcaaac ggccgcagaa caggccggcg aatcgctgca acagcaaccg 120

tggctgcaat cgttggaggc ggacggcgcg ggtgaaaagc agcctgcact tgaacggaaa 180

ggtgctgcgc ctgttgtggt gcgcaatcag gatttgcgcg aacaccccga actgttggcg 240

gccatgctgc ggcaggcggt ggatgcgcgc cacgagcctt tgctcggcgc gctgctgcct 300

acctatttga cgttgccgca agagcagcag gacgcgaaac ttcggcagca tgcgcaagcc 360

gaactggcac ggttgcgcgg agattatccc accgccacgg cgcattatca ggccgtgcag 420

cggcaatatc cggacgatgt gcgtttgcag ttggactcgg cggcaacgct ggcggaagac 480

cgacaatggc gcgaggcaga agccttgttt gcccaagcgg cgcaaacgcc cgaactgccc 540

gacacggtgg cggaaaacat ccgcctgtac cgcaacggaa tccgccaaaa tacgcaatgg 600

caggttcagg gcggcgtgca gttgtcgtac gacaagaaca tcaatgacgc gccgcaggcc 660

tattgcacgc ctttgggctg cgtgcgcgaa cggcaggaaa atgcgtgggg gctgcgctac 720

cgcgtgtatg ccgaaaagaa cacgccgatt cgcggccatc acaacctgct gttccgcatg 780

aatgcgtctg ggacgacgta ttacctgtcg caacgcagcg cgtatgatta tgcgttggca 840

cgcgcatcgc tgggctaccg tttccaagat gcgcggcaat cgctggaaat tctgccgttt 900

tatcaggcgc aattttcagg cagccgccag ttccccgaca aagcgccgcg acaaaagcgc 960

gtgttgccgt atatgttggg gcatgccgtc ggggtgcagg ctgcttttga acggcagctc 1020

gcaccgaaat ggacaggctt cgtatcgctg gaaggaatgc ggcaggattt ccgcgaggcg 1080

gaacgcgcgc gtcatcaaaa cgggatggtg tggaatgcgt ttgcatcgct gtcgtaccgc 1140

atccgcccgc agcatctctt gttcgcgggc tacggctggg gcagcctgca cccggacaac 1200

gacatggtgg gcggccgcgc caattcttcg ggctatgtgc ggcacagcgt gcaggccggc 1260

tggctggcgc aatggacggc tttgggcaac ctgaacacgg aagtccgcgg gcaatatacg 1320

cagcggcgct atcgcggttc ggcattggac acggcgtttt tgcggcggcc gcagcgcaac 1380

aacgaacgtt cgctgacggt ggcgctgtcg tatccgaaat ggcgcgtgtg gggcgctgtg 1440

ccgaagttgg tttggcagga gaaccgcatc gacagcacgc acgattgggc cgaccgcagg 1500

cagcgcaatg tgtggctgga atgggaaaag cggttttag 1539

<210> 248

<211> 512

<212> PRT

<213> K. denitrificans SLAM 5

<400> 248

Met Lys Thr Ile Arg Lys Ile Ile Ser Gly Leu Val Leu Gly Ile Ser

1 5 10 15

Val Gly Ala Val Ala Glu Pro Leu Pro Gln Thr Ala Ala Glu Gln Ala

20 25 30

Gly Glu Ser Leu Gln Gln Gln Pro Trp Leu Gln Ser Leu Glu Ala Asp

35 40 45

Gly Ala Gly Glu Lys Gln Pro Ala Leu Glu Arg Lys Gly Ala Ala Pro

50 55 60

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

65 70 75 80

Ala Met Leu Arg Gln Ala Val Asp Ala Arg His Glu Pro Leu Leu Gly

85 90 95

Ala Leu Leu Pro Thr Tyr Leu Thr Leu Pro Gln Glu Gln Gln Asp Ala

100 105 110

Lys Leu Arg Gln His Ala Gln Ala Glu Leu Ala Arg Leu Arg Gly Asp

115 120 125

Tyr Pro Thr Ala Thr Ala His Tyr Gln Ala Val Gln Arg Gln Tyr Pro

130 135 140

Asp Asp Val Arg Leu Gln Leu Asp Ser Ala Ala Thr Leu Ala Glu Asp

145 150 155 160

Arg Gln Trp Arg Glu Ala Glu Ala Leu Phe Ala Gln Ala Ala Gln Thr

165 170 175

Pro Glu Leu Pro Asp Thr Val Ala Glu Asn Ile Arg Leu Tyr Arg Asn

180 185 190

Gly Ile Arg Gln Asn Thr Gln Trp Gln Val Gln Gly Gly Val Gln Leu

195 200 205

Ser Tyr Asp Lys Asn Ile Asn Asp Ala Pro Gln Ala Tyr Cys Thr Pro

210 215 220

Leu Gly Cys Val Arg Glu Arg Gln Glu Asn Ala Trp Gly Leu Arg Tyr

225 230 235 240

Arg Val Tyr Ala Glu Lys Asn Thr Pro Ile Arg Gly His His Asn Leu

245 250 255

Leu Phe Arg Met Asn Ala Ser Gly Thr Thr Tyr Tyr Leu Ser Gln Arg

260 265 270

Ser Ala Tyr Asp Tyr Ala Leu Ala Arg Ala Ser Leu Gly Tyr Arg Phe

275 280 285

Gln Asp Ala Arg Gln Ser Leu Glu Ile Leu Pro Phe Tyr Gln Ala Gln

290 295 300

Phe Ser Gly Ser Arg Gln Phe Pro Asp Lys Ala Pro Arg Gln Lys Arg

305 310 315 320

Val Leu Pro Tyr Met Leu Gly His Ala Val Gly Val Gln Ala Ala Phe

325 330 335

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

340 345 350

Met Arg Gln Asp Phe Arg Glu Ala Glu Arg Ala Arg His Gln Asn Gly

355 360 365

Met Val Trp Asn Ala Phe Ala Ser Leu Ser Tyr Arg Ile Arg Pro Gln

370 375 380

His Leu Leu Phe Ala Gly Tyr Gly Trp Gly Ser Leu His Pro Asp Asn

385 390 395 400

Asp Met Val Gly Gly Arg Ala Asn Ser Ser Gly Tyr Val Arg His Ser

405 410 415

Val Gln Ala Gly Trp Leu Ala Gln Trp Thr Ala Leu Gly Asn Leu Asn

420 425 430

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

435 440 445

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

450 455 460

Leu Thr Val Ala Leu Ser Tyr Pro Lys Trp Arg Val Trp Gly Ala Val

465 470 475 480

Pro Lys Leu Val Trp Gln Glu Asn Arg Ile Asp Ser Thr His Asp Trp

485 490 495

Ala Asp Arg Arg Gln Arg Asn Val Trp Leu Glu Trp Glu Lys Arg Phe

500 505 510

<210> 249

<211> 1434

<212> DNA

<213> K. kingae SLAM 1

<400> 249

atgtattcca aactattact taccagtgcg ctgtggctgg caacggcatc gatttatgcc 60

gaaacgctgc cacccaaagt tgaacagatg ctgaacgaat cgtcgcccga aaccgaattc 120

aatcgcacgc ccgacatcaa acccaccgaa aacacgccac ctacaaacga tgcggatggc 180

gaaacactca atatttcatc ggaagaactg caaaagcagc ctgcactttt aaaacgcgct 240

ttttttggtg cattggcaac aggcaatgtg gctggtgtca aaattctgct gccctggtat 300

cgcaatctac cagacggcaa cgacgaattt gcgctcaatt tagcagatgc catgctcgcg 360

caggacaagg gcgattacga taacgcggta gaatcgtatc aaaaagtatt ggcacaacag 420

cccgatgcgc cgtctatcca aatgggacta gcacaaactt tgttcgccga ccaccgcaac 480

agcgaagcca aacaaatctt gaccgaattg cacaatcgca gcgatttacc cgaaaatttc 540

cgccaatacg caggcagcta tctgtccgcc ataaaaaaac gcaacgattg gacatttaac 600

atcaatgcgt attacacgca agacaacaac atcaatagca cccccaatca acgcaaagtc 660

ggcaactgga cactgggtga acccgaatca gcacacggca ttgcgtatta tggcaacgtc 720

aataaagaca cctatttggg caaacaatgg tcattgcgct ttggcacaga cgtgtttggc 780

aaatattatt gggacaaccg caaatacgac gatttatcgg cgcgtgtcaa actgggcgta 840

gcgcatcaaa ccgcgcgaag tgaaacagcg attttgccgt attttgaacg ccgttggtat 900

ggtggcaaag aatacgctgc cgaaaaaggg ctaacgctgg aatggtcata ctggttcacg 960

cccaaaaatc aagttttgct gtcgggcgaa catagctggc aaaaacacga cacgcgctca 1020

tttttggacg gcaaaaacag caatttgtcg gctacatggc tgtttttatc atcagaaaaa 1080

caatactgga cgctgggcat agacctgacc cgcaaaaccg cgcaagacag cagcgacgct 1140

tatcgccgca aaggcatacg tttaggctgg acgcaatatt ggggcaacac cgtgggcagc 1200

tcattgggca ttggcactgc acaacgtgtt tacgatgcgc ccaacttccc gttcaactac 1260

attcgcaaag accgcgaaca ttttgcatcg cttagcttgt ggaacaaccg ctggcaattt 1320

gggggcatca caccacgcct agtattccgt tggacaaaag tcagcagcaa tcatccgttt 1380

tacggcgatt acagcaagaa aaatgtcttt atccaaatga acaaagcctt ttaa 1434

<210> 250

<211> 477

<212> PRT

<213> K. kingae SLAM 1

<400> 250

Met Tyr Ser Lys Leu Leu Leu Thr Ser Ala Leu Trp Leu Ala Thr Ala

1 5 10 15

Ser Ile Tyr Ala Glu Thr Leu Pro Pro Lys Val Glu Gln Met Leu Asn

20 25 30

Glu Ser Ser Pro Glu Thr Glu Phe Asn Arg Thr Pro Asp Ile Lys Pro

35 40 45

Thr Glu Asn Thr Pro Pro Thr Asn Asp Ala Asp Gly Glu Thr Leu Asn

50 55 60

Ile Ser Ser Glu Glu Leu Gln Lys Gln Pro Ala Leu Leu Lys Arg Ala

65 70 75 80

Phe Phe Gly Ala Leu Ala Thr Gly Asn Val Ala Gly Val Lys Ile Leu

85 90 95

Leu Pro Trp Tyr Arg Asn Leu Pro Asp Gly Asn Asp Glu Phe Ala Leu

100 105 110

Asn Leu Ala Asp Ala Met Leu Ala Gln Asp Lys Gly Asp Tyr Asp Asn

115 120 125

Ala Val Glu Ser Tyr Gln Lys Val Leu Ala Gln Gln Pro Asp Ala Pro

130 135 140

Ser Ile Gln Met Gly Leu Ala Gln Thr Leu Phe Ala Asp His Arg Asn

145 150 155 160

Ser Glu Ala Lys Gln Ile Leu Thr Glu Leu His Asn Arg Ser Asp Leu

165 170 175

Pro Glu Asn Phe Arg Gln Tyr Ala Gly Ser Tyr Leu Ser Ala Ile Lys

180 185 190

Lys Arg Asn Asp Trp Thr Phe Asn Ile Asn Ala Tyr Tyr Thr Gln Asp

195 200 205

Asn Asn Ile Asn Ser Thr Pro Asn Gln Arg Lys Val Gly Asn Trp Thr

210 215 220

Leu Gly Glu Pro Glu Ser Ala His Gly Ile Ala Tyr Tyr Gly Asn Val

225 230 235 240

Asn Lys Asp Thr Tyr Leu Gly Lys Gln Trp Ser Leu Arg Phe Gly Thr

245 250 255

Asp Val Phe Gly Lys Tyr Tyr Trp Asp Asn Arg Lys Tyr Asp Asp Leu

260 265 270

Ser Ala Arg Val Lys Leu Gly Val Ala His Gln Thr Ala Arg Ser Glu

275 280 285

Thr Ala Ile Leu Pro Tyr Phe Glu Arg Arg Trp Tyr Gly Gly Lys Glu

290 295 300

Tyr Ala Ala Glu Lys Gly Leu Thr Leu Glu Trp Ser Tyr Trp Phe Thr

305 310 315 320

Pro Lys Asn Gln Val Leu Leu Ser Gly Glu His Ser Trp Gln Lys His

325 330 335

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

340 345 350

Trp Leu Phe Leu Ser Ser Glu Lys Gln Tyr Trp Thr Leu Gly Ile Asp

355 360 365

Leu Thr Arg Lys Thr Ala Gln Asp Ser Ser Asp Ala Tyr Arg Arg Lys

370 375 380

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

385 390 395 400

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

405 410 415

Pro Phe Asn Tyr Ile Arg Lys Asp Arg Glu His Phe Ala Ser Leu Ser

420 425 430

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

435 440 445

Phe Arg Trp Thr Lys Val Ser Ser Asn His Pro Phe Tyr Gly Asp Tyr

450 455 460

Ser Lys Lys Asn Val Phe Ile Gln Met Asn Lys Ala Phe

465 470 475

<210> 251

<211> 1452

<212> DNA

<213> K. kingae SLAM 2

<400> 251

atgcgccact tggctatttt gacattactc gcgcccactt atttgcttgc caacacattt 60

gatgcaccgc cagtccccat agaaacaagc gcacccatca cgcgctcaac tctcatttcg 120

ccaaccgaat cgcccgacgc gcaggctgct ttgccgactt ctgcacctgt caaaaacatc 180

acgctcaacg aacaagattt actccgcaat cgtcctttgt tggaagagct gattggtcaa 240

gccatcaaaa ccaaagacgc ggcgtttttg caagatttgt tgtcgctgta tcaaaaacat 300

ccagagcgcg acctaatctt gcaagactac gcgcaaagtg ccttgcttta tctacacggc 360

aagctcagtc aagctattga tttacaacaa aatttggttg agcaacaccc cgatttgcct 420

tatatgcgaa tgaacttggc aaccatgcaa ctggaagaca aacgctttgc cgatgccgag 480

cagcagtttg aacacttggc gcagcaaaca gagcagcctg cacttcgcgc cattgccaac 540

gcgcacttaa aatcgttggc acatatgcag caatggcagt ttgacggaca gttggaatat 600

gaccgcaaca ataatgtaaa caacgcatcg gcagaacgtg aaatcgtcat caatggtgcg 660

cggctgcaaa aaagtgagca gtcgttaccc aaatctgccg aaggtttgcg ctatggcgtg 720

tcggtgtcgc gttttgtacc gcttgctggc aaccatgcgc tgtcgttttc gggtagcgta 780

aacgggcgac attattggga caaccacgaa tacagtcagc ataatgttta catatcaggc 840

agttatatct accaaaacaa aaactggacg ttccgcacca cgccttttgc gctgcaatcg 900

tggttgggcg gcgcacgtta tacgcaaagt tggggcgcga gccaaagtgc ggcgtatcaa 960

tttttgcctg cgtggcgtgt gcagttgagc gtgtcggggc gcaaaacgcg ctatcacgat 1020

gcggatttgc gtgattttga cagccgttat gtgtcgctta cgcctgtgct ggtgtattcg 1080

cgtcctacgt ttggcgtgca ttttggcgtg acggtgggca agaatcaggc gcgaaaagag 1140

tcgctgtcgt ctaaaagctg gcaggtgttt ggtggcgtga gcaaacagtt taattatttt 1200

ggcgcatcgg cttcgctgtc gtacggcaag gaacgctaca accaagcacc cgaattgcgg 1260

gttacgccct atccgtttcg ccgagatgac aaaatcattc aaaccgatgt ggcgatttgg 1320

aatccaaaat ggcattattg gggcttgatg ccgaagttga atttttcgcg ttatcaaatc 1380

gttagcaata tgcctgcgtt ttattcacgc aaaagccaac gtgtgtattt gagcgtggaa 1440

aagcggtttt ga 1452

<210> 252

<211> 483

<212> PRT

<213> K. kingae SLAM 2

<400> 252

Met Arg His Leu Ala Ile Leu Thr Leu Leu Ala Pro Thr Tyr Leu Leu

1 5 10 15

Ala Asn Thr Phe Asp Ala Pro Pro Val Pro Ile Glu Thr Ser Ala Pro

20 25 30

Ile Thr Arg Ser Thr Leu Ile Ser Pro Thr Glu Ser Pro Asp Ala Gln

35 40 45

Ala Ala Leu Pro Thr Ser Ala Pro Val Lys Asn Ile Thr Leu Asn Glu

50 55 60

Gln Asp Leu Leu Arg Asn Arg Pro Leu Leu Glu Glu Leu Ile Gly Gln

65 70 75 80

Ala Ile Lys Thr Lys Asp Ala Ala Phe Leu Gln Asp Leu Leu Ser Leu

85 90 95

Tyr Gln Lys His Pro Glu Arg Asp Leu Ile Leu Gln Asp Tyr Ala Gln

100 105 110

Ser Ala Leu Leu Tyr Leu His Gly Lys Leu Ser Gln Ala Ile Asp Leu

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

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

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

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

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

370 375 380

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

435 440 445

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

<210> 253
<211> 1608
<212> DNA
<213> K. kingae SLAM 3
<400> 253
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tgggtatatc aaatgaataa acagcatcta ttttggttat ggttagctgt gagtctgtca 120
gcagttgcag cagatgacga tgaactgcct gctccgtttg tagcaaagcg tacggacaat 180
aatgcggcag aagttatcgc tattgcaaaa gccccaacca ccacacacgc tgacccacaa 240
gtattgcaac aaccgtttga cgatgtgaat acacaactgg aatatgtgtt agagccactg 300
cccaattcag cacaaaccga gccgttgccc gaattagcgc cattggaaat gcagcccaaa 360
gtcagcacgc aacaacaaat agacgaccaa atcaatcaag cgttgttggc aaaaaaatgg 420
gacgaactag aacgcttatt agcaaccgag ccacaagaag gatacgatga aatcttgtgg 480

gtttatgcca aaggcacgtt gttgcgtcaa aagcaaaaat attcacaggc gattgccgaa 540
taccgcaaag tggttgccac gcagccagaa ttgggttatc cgcgtttgga tttaggcatt 600

atgttgtttg aaaacaagca atataacgaa gcggaagccg aattgaccca agccaaagcg 660

gacattaatc cagaagctgg ggcgcaaaaa gtggcagatg cctacttatc gcgcatggaa 720

aacgaacaaa gttggcagcc tagtatgggc ttgcaataca cgcaaaccga taatgtaaac 780

aacgcagcca atagcacgga tttatattac aacggcagac attttgtaaa aaataccgat 840

gctttgccca aatcggcgca cggttttaac tatcatttgg gcgtagaaaa agacaccaat 900

ttagcaggta atcattatgt tagattgggc gtgagtggta gcggtgtgca ttattgggat 960

aactcagatt acgatgagaa ctctgtgcaa ttcaatgtgg gctaccgttt tcaaagttgg 1020

cgacatcaat ttggcgttat gccttttttc acgcaaaact ggttgggcgg agaacgctac 1080

aatcaacgct ttggcgtaac cagcaattac cgctatcgct ttaatccaca atggtctatt 1140

tctgccgcgc atacttattc caacacgcaa tatcataacg acagagttgc ccaatattac 1200

gatggtcata acaacaacgt aggcttaaca ttgatatgga atcccacgcc cagttggttg 1260

ctgtttagcg gtgtaaatgg cagctacgac aatttgaacg acaaagcaga aagctccaaa 1320

cgccgcagca ttgtgagcgg catcgtgtac gataaccaac aatggggcgg acgcgctaat 1380

tttaattatg ccaatcgccg cttccaaggc gcacactttt tgtatggcaa tcatcgtgcc 1440

gacaaggaat atcaagtcag cgcagcggtg tggcaccata aattgtcgtg gcgcaatatt 1500

acgccgcgtt tgaactatcg ctatttgaag gtagatagca atatgtctgc gctgtattca 1560

cgcaccagcg gcgaatggtt tattagtgcg gaaaaaacgt tccattaa 1608

<210> 254

<211> 534

<212> PRT

<213> K. kingae SLAM 3

<400> 254

Met Gln Ala Ala Phe Leu Arg Glu Asn Thr Gln Lys Gln Pro Ala Lys

1 5 10 15

Tyr Leu Thr Leu Trp Val Tyr Gln Met Asn Lys Gln His Leu Phe Trp

20 25 30

Leu Trp Leu Ala Val Ser Leu Ser Ala Val Ala Ala Asp Asp Asp Glu

35 40 45

Leu Pro Ala Pro Phe Val Ala Lys Arg Thr Asp Asn Asn Ala Ala Glu

50 55 60

Val Ile Ala Ile Ala Lys Ala Pro Thr Thr Thr His Ala Asp Pro Gln

65 70 75 80

Val Leu Gln Gln Pro Phe Asp Asp Val Asn Thr Gln Leu Glu Tyr Val

85 90 95

Leu Glu Pro Leu Pro Asn Ser Ala Gln Thr Glu Pro Leu Pro Glu Leu

100 105 110

Ala Pro Leu Glu Met Gln Pro Lys Val Ser Thr Gln Gln Gln Ile Asp

115 120 125

Asp Gln Ile Asn Gln Ala Leu Leu Ala Lys Lys Trp Asp Glu Leu Glu

130 135 140

Arg Leu Leu Ala Thr Glu Pro Gln Glu Gly Tyr Asp Glu Ile Leu Trp

145 150 155 160

Val Tyr Ala Lys Gly Thr Leu Leu Arg Gln Lys Gln Lys Tyr Ser Gln

165 170 175

Ala Ile Ala Glu Tyr Arg Lys Val Val Ala Thr Gln Pro Glu Leu Gly

180 185 190

Tyr Pro Arg Leu Asp Leu Gly Ile Met Leu Phe Glu Asn Lys Gln Tyr

195 200 205

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

210 215 220

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

225 230 235 240

Asn Glu Gln Ser Trp Gln Pro Ser Met Gly Leu Gln Tyr Thr Gln Thr

245 250 255

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

260 265 270

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

275 280 285

Phe Asn Tyr His Leu Gly Val Glu Lys Asp Thr Asn Leu Ala Gly Asn

290 295 300

His Tyr Val Arg Leu Gly Val Ser Gly Ser Gly Val His Tyr Trp Asp

305 310 315 320

Asn Ser Asp Tyr Asp Glu Asn Ser Val Gln Phe Asn Val Gly Tyr Arg

325 330 335

Phe Gln Ser Trp Arg His Gln Phe Gly Val Met Pro Phe Phe Thr Gln

340 345 350

Asn Trp Leu Gly Gly Glu Arg Tyr Asn Gln Arg Phe Gly Val Thr Ser

355 360 365

Asn Tyr Arg Tyr Arg Phe Asn Pro Gln Trp Ser Ile Ser Ala Ala His

370 375 380

Thr Tyr Ser Asn Thr Gln Tyr His Asn Asp Arg Val Ala Gln Tyr Tyr

385 390 395 400

Asp Gly His Asn Asn Asn Val Gly Leu Thr Leu Ile Trp Asn Pro Thr

405 410 415

Pro Ser Trp Leu Leu Phe Ser Gly Val Asn Gly Ser Tyr Asp Asn Leu

420 425 430

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

435 440 445

Val Tyr Asp Asn Gln Gln Trp Gly Gly Arg Ala Asn Phe Asn Tyr Ala

450 455 460

Asn Arg Arg Phe Gln Gly Ala His Phe Leu Tyr Gly Asn His Arg Ala

465 470 475 480

Asp Lys Glu Tyr Gln Val Ser Ala Ala Val Trp His His Lys Leu Ser

485 490 495

Trp Arg Asn Ile Thr Pro Arg Leu Asn Tyr Arg Tyr Leu Lys Val Asp

500 505 510

Ser Asn Met Ser Ala Leu Tyr Ser Arg Thr Ser Gly Glu Trp Phe Ile

515 520 525

Ser Ala Glu Lys Thr Phe

530

<210> 255

<211> 1698

<212> DNA

<213> K. kingae SLAM 4

<400> 255

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tttttaggtg atttttcttt gtatcgcaaa aaaatgaaag ccattctcaa attgaatgct 120

aaaataccgc tatccaaaca taaccgcatt tttttgatga tgaccacaca caccacccca 180

ttcaatcgca ccatattaac gattttatta ttcggcggac ttttatcgtc acacgtagcc 240

cacgccaacg acaacccgac cgaactcaaa cagccagccg attccgcgca gcaaaaatcg 300

tggctcaacc agcttaatca acaagccaag cagcctgcac cgcaatcagg cagcgcaaat 360

acatcgccca atcatgtaac cgatgccgat ttaatcaagc agcctgcact tttggcgcaa 420

ctgttgcaac aagccttgaa cacgcccgaa accgagttga ttcaatcgct ggcaaacgcc 480

tatcgccaaa ccgaaaaccc cgatgctttg ctgctggcgc gagcagacgg catggtgctt 540

cgtggacaaa atcgcctgtc cgatgccatt gccgcctacg agcgcattgt gcaaacccac 600

aacgacacgc gcacacgctt ggatttggca gccatgcaat ttgaaaacaa acaatggcgc 660

gatgccgacc agcaatttga atccgctaaa caaaacgaag ccttgcccga tgcggtgttg 720

cacaatgtgg cgcgatacca aaacgcgatt gcccagcagc aagcgtggca gtttgaggca 780

ggcatcagcc ccattcgcaa tcaaaacgtg aacgatgcgc ccgaaaagcc gtattgcttg 840

tatggcattt attgcagcac cacgcgccca attaaggcga ctggtattgg ctattctttt 900

gattttgcga aacaatattc gctgcgtggc aatcattcgc tggtgttgcg cggtcaggta 960

agcggcacgc attatatcaa ccacgcgcaa tataacgatg cgtttttgcg tgtgctggct 1020

ggttggcaat ggcaggacaa aacgcgcacg attggcgtgt tgccgtttta ccaagcgcaa 1080

ttttcgggca gcgataattt tgatagcaag ccgactcaat cgggtagggt gctgccgtat 1140

atgctggcac acggcaacgg cttgcaactg aattatgcgc aacaatatgg cacgcgctgg 1200

caaagttatc actcgctgga aggctatcgc acgttttacc gcgaaactgc tcgcgcccaa 1260

aaacaagacg gctggacgca cagcacttat cattcgctcg cctttcgcgc cacgtccaat 1320

atgacgtggt ttacgggcta tcaatattcg cggttcgcgc ccaaaaatcg cgatttggca 1380

ggcagtcgca acaacgcggc attccaacgc cacgctatta gtttgggctg gttgcaacgc 1440

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gcgttgtcgc acgataaatt gcaatatcgc ggattgcagc cgagcttgaa tgtgcagttt 1620

aaccgcattc gcagcaatcg gccgtgggcg caacgcaaat cgcatacagt ttatttgggc 1680

ttggataagt cgttttga 1698

<210> 256

<211> 565

<212> PRT

<213> K. kingae SLAM 4

<400> 256

Met Ser Glu Ile Lys Thr Lys Gln Pro Ala Leu Tyr Val Asp Glu Lys
1 5 10 15

Val Gln Ala Ala Phe Leu Gly Asp Phe Ser Leu Tyr Arg Lys Lys Met
20 25 30

Lys Ala Ile Leu Lys Leu Asn Ala Lys Ile Pro Leu Ser Lys His Asn
35 40 45

Arg Ile Phe Leu Met Met Thr Thr His Thr Thr Pro Phe Asn Arg Thr
50 55 60

Ile Leu Thr Ile Leu Leu Phe Gly Gly Leu Leu Ser Ser His Val Ala
65 70 75 80

His Ala Asn Asp Asn Pro Thr Glu Leu Lys Gln Pro Ala Asp Ser Ala
85 90 95

Gln Gln Lys Ser Trp Leu Asn Gln Leu Asn Gln Gln Ala Lys Gln Pro
100 105 110

Ala Pro Gln Ser Gly Ser Ala Asn Thr Ser Pro Asn His Val Thr Asp
115 120 125

Ala Asp Leu Ile Lys Gln Pro Ala Leu Leu Ala Gln Leu Leu Gln Gln
130 135 140

Ala Leu Asn Thr Pro Glu Thr Glu Leu Ile Gln Ser Leu Ala Asn Ala
145 150 155 160

Tyr Arg Gln Thr Glu Asn Pro Asp Ala Leu Leu Leu Ala Arg Ala Asp
165 170 175

Gly Met Val Leu Arg Gly Gln Asn Arg Leu Ser Asp Ala Ile Ala Ala
180 185 190

Tyr Glu Arg Ile Val Gln Thr His Asn Asp Thr Arg Thr Arg Leu Asp
195 200 205

Leu Ala Ala Met Gln Phe Glu Asn Lys Gln Trp Arg Asp Ala Asp Gln

210 215 220

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

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

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

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

Asn Ala Ala Phe Gln Arg His Ala Ile Ser Leu Gly Trp Leu Gln Arg
465 470 475 480

Trp Gln Thr Leu Gly Gly Leu Asn Ser Arg Val Val Tyr Ser Tyr Ala
485 490 495

Lys Arg Arg Tyr Ser Gly Ile Ala Thr Leu Ser Asn Glu Ala Gln Arg
500 505 510

Asn His Glu Thr Ser Leu Gln Leu Ala Leu Ser His Asp Lys Leu Gln
515 520 525

Tyr Arg Gly Leu Gln Pro Ser Leu Asn Val Gln Phe Asn Arg Ile Arg
530 535 540

Ser Asn Arg Pro Trp Ala Gln Arg Lys Ser His Thr Val Tyr Leu Gly
545 550 555 560

Leu Asp Lys Ser Phe
565

<210> 257

<211> 1428

<212> DNA

<213> K. oralis SLAM 1

<400> 257

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caaaccgaac gccaaaatca gcaaaagcaa gcggcgcaaa atggtgaaaa aacatcggtt 180

tccatgacag aagaagagct gttgcaacgc cctgatttgc tcaaaaacgc gctggacacg 240

gcaaatgcgc agcacaatat tgaaaacatt cgtttttttgc tgccgttgta tcgcaggctg 300

cctgccgagc agcaggattc tgtgctggcg cgctattcgg aagggctggt gtggctggcg 360

gatgataagc atgaggcggc ggagaaatta tttaacgaaa ttttggcgga acatcctgat 420

tacgcgcctg tgcgcttgca gttggcgttg agccagtcac aaaacggcaa gcagcgcgag 480

gcggcaaatg aattgaaaac cttgaagcaa acgcctgatt tgcctgcgcc tgtggcgcaa 540

tatattgacc agtttgacgc gcatttgcaa aaaagcaagg cgtggcagtt caacgccaat 600

gcgtattatc tgcaagacag caatgtgggg cgcacgcccg agcagcgcac ttatggctat 660

tggcgttttg ccgagcctaa atcggcgcac ggcgtgggct atgagctatc ggcgcaaaaa 720

accacgccga ttaaggggca ttgggcggcg cgggtgaatg catcggcgta tggtaagttt 780

tattgggatg cgcacgatta tgatgatttg gttacacggc tggaagcggg gcctgtatgg 840

cgcgatgcga agcaggaggt ttcgttgttg ccgttttatg agaaacgctg gtatggcggc 900

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tcgctgcatg gtagcgtgca aaagcgtaag tatcgcgcgg aggatttttt caatatcaag 1260

cgcaacgaga aggagtattt cacgcgcttg tcgctgtcgc ataaaaagct ggcgtggcgc 1320

gggtttgagc cgcgtttgaa ctggacgtgg tcgcacgtgg acagcaacca tttttattat 1380

aagtatgaca atcatcgggt gtttttggat gtgtctaagc agttttaa 1428

<210> 258

<211> 475

<212> PRT

<213> K. oralis SLAM 1

<400> 258

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1 5 10 15

Phe Tyr Thr Gln Ala Ala Pro Val Ala Thr Pro Leu Asn Pro Val Ala
20 25 30

Asp Leu Thr Glu Glu Gln Ile Gln Gln Thr Glu Arg Gln Asn Gln Gln
35 40 45

Lys Gln Ala Ala Gln Asn Gly Glu Lys Thr Ser Val Ser Met Thr Glu
50 55 60

Glu Glu Leu Leu Gln Arg Pro Asp Leu Leu Lys Asn Ala Leu Asp Thr
65 70 75 80

Ala Asn Ala Gln His Asn Ile Glu Asn Ile Arg Phe Leu Leu Pro Leu
85 90 95

Tyr Arg Arg Leu Pro Ala Glu Gln Gln Asp Ser Val Leu Ala Arg Tyr
100 105 110

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

115 120 125

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

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

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

Trp Gln Val Phe Thr Ala Trp Gln Ser Gly Tyr Lys Lys His Asp Lys
325 330 335
Arg Thr Phe Leu Asp Gly Ala Ser His Leu Gly Thr Val Ser Leu Leu
340 345 350
Tyr Arg Thr Ser Pro Tyr Gln Tyr Phe Val Val Ser Trp Gly Gly Gly
355 360 365

Glu Asn Ser Ala Lys Asp Lys Ser Glu Ala Tyr Arg Phe Gly Asn Leu
370 375 380

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

Thr Trp Ser His Val Asp Ser Asn His Phe Tyr Tyr Lys Tyr Asp Asn
450 455 460
His Arg Val Phe Leu Asp Val Ser Lys Gln Phe
465 470 475

<210> 259
<211> 1491
<212> DNA
<213> K. oralis SLAM 2
<400> 259

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gccaacaagc cgtcttccaa cgcccccgct ccccttttct ttgacgaccg cgaaatcgcc 180

cttatcccca acgagatgct gccccagcct gccgagccgg ccgcgagcct tgccgacaat 240
gcgaccgaag acgacaacac gctggaagcg caaatcaacc gcgccatcat cgcccgcgat 300
tgggcaacgc tgcccgcgct gctggaacgc taccacgccg agccgcagca cgacccaacg 360
ctttacgatt acgcgctggg tgcattgcgc cgctcgcagt tgcgccacga tgaagccacc 420
gccctgtatc gcggcattgt gcaaaggcag cctgaattgg cctatccgcg ctttgatttg 480
ggcgtgatgc tgtttgaaga caagcaatac aacgaagcca aacgcgagct ggaacgcgcc 540
aagtccgatt tgtcgcccgc catgcaagcc gttgccgagc gttatcttgc cgccattgcc 600

caagcgcaaa attggcagcc tgaaatgtcg ctgcaatacg aaaccaccga taatgtgaac 660
aacgccgccg atgcgcgcga aattgaaatc aacgggcgca tttggcgcaa aaccgaagaa 720

agcctgccgc aaagcgcgca aggtttgcgc tatggcttgg gcgtggagcg cgagcgcaat 780

ttaggcgggc accattttat ttatgggcgc gttcatggcg atggcgtggc ttattgggat 840

aaacatgaat acgacgagca aagcgtgaat atcgcgctgg gctacaaaaa ccgcaccgtc 900

aaacgcgcgt tgggcatcgt gccgtttttt gagcaaaact ggctgggcgg cagccgatac 960

agccacaacg caggcgtgca ggccgatttt tcgcaccagc tgggcaaacg ctggcgcgtg 1020

atgctgaacg cgggctatat agccaagcga tacgatgagc cctccaccgc acagcggtac 1080

aacggcaaaa tgccgctggc aagcgccacg ctgatgtatt acgcgccgca aaattggctg 1140

ctgtatggcg gggtggattg gtcgcacgac atcacgcaag atgcggagca ggcttcggtg 1200

cgcaaaggcg tgcggctggg cacggcaaaa acgtttgcca acgggctggg attgcgcaca 1260

catttgcgtt atgcacggcg cacgtttgat gcggcgggta cgctggttta tctgtatccc 1320

cgccaagacg atgagtatca ggcgaatgtg tcgttgtggc atgacaaatt gtcgtggaag 1380

agctttacgc cgcatttgaa tttccgctat ttggcgattg acagcaatat gaaagggttt 1440

tattcacgca aaaacgcgca atggttttta agcgtggagc gggggtttta g 1491

<210> 260

<211> 496

<212> PRT

<213> K. oralis SLAM 2

<400> 260

Met Ala Leu His Thr Pro Thr Gln Met Asn Lys Leu Pro Leu Leu Leu
1 5 10 15

Leu Pro Leu Ser Leu Leu Ala Leu Ala Asp Thr Pro Thr Ala Leu Asn
20 25 30

Gly Ala Pro Pro Ala His Arg Ile Ala Asn Lys Pro Ser Ser Asn Ala
35 40 45

Pro Ala Pro Leu Phe Phe Asp Asp Arg Glu Ile Ala Leu Ile Pro Asn
50 55 60

Glu Met Leu Pro Gln Pro Ala Glu Pro Ala Ala Ser Leu Ala Asp Asn
65 70 75 80

Ala Thr Glu Asp Asp Asn Thr Leu Glu Ala Gln Ile Asn Arg Ala Ile
85 90 95

Ile Ala Arg Asp Trp Ala Thr Leu Pro Ala Leu Leu Glu Arg Tyr His

100 105 110

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

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

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

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

Glu Pro Ser Thr Ala Gln Arg Tyr Asn Gly Lys Met Pro Leu Ala Ser
355 360 365

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

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

<210> 261
<211> 1410
<212> DNA
<213> Kingella sp. Sch538 SLAM 1
<400> 261
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gttagcaccc ctttaaacca aatccccgat ttaaaccaag agcaaatcag ccagcaaact 120
gaaaccgttg tgcagcctga aaacgccaag caacattcag cgtccatgac cgcagacgat 180
ttgctcaagc agcctgaatt attgcaaaac gcgctggata ctgccatcaa tcagcaaaat 240
gtaaacaata tccgctttct gctgtcgatt taccgcaagc agcctgaaaa ccagcaagat 300
gccgttttat tgaaatacgc agagagcttt gtgcaacgcg cagacggtca gcaagatgaa 360

gcagaacaaa atttgcgtga actggtgcaa gcgcaccccg aatttgcgcc gattcgtttg 420
caatacgcgc tgactttgtt gcaaaacggc gagcaaaaag aagccgcgca agaagtcgcc 480

aaaatccgcg aaacgctcga attacccgaa gatgtcagcc aatatctcaa ccaatttgac 540

gcgcatctga aaaacgaaaa agcgtggcaa ttcaacgcta acgcgtatta tttgaatgaa 600

ggcaacgtag gtcgcgcgcc tgaacaacgc acttatggca attggcaatt tccagagcct 660

aaaaaagcgc acggtttcgg ctacgagtta tccgctcaaa aaaccgttcc cattaaaggg 720

cattgggcgg cgcgtgtgaa tgcttcggtt tacggcaaat tttattggga tgcgcatgat 780

tacgatgatt tagtcgcgca taccgaagcg ggcgcggtgt ggcgcaatgc caagcaagaa 840

gtgtctctga tgccgtttta cgaaaaacgc tggtatggca ctgagccgta ttcgcaaact 900

tcgggcgcga ttttgcgtta ttcgcgcact ttgtcgccta gctggcaggt ttatggtgcg 960

tggcaatcag attacaaacg ccatgatgac cgtctgcatt taaacggggc tgaccattcg 1020

gcttcggtgt cggtgctgta tcgcagcagt ccgcagcagt attttgtgat tggggctggg 1080

gctgggcgca gcaacgcaaa agatttgtcg gacgcgtatg tttacagcaa tgcgcgtgtg 1140

agctggacgc gaaattggcg cagcctgaaa aatttatcca ccactttgag cgtgtcggca 1200

caacgccgca attatcgtgc gcctgatttt ttcaatatcc gcagacatga caaggaatat 1260

ttcacgcgct tatctgtgtc tcacccaaaa ttatcttggg gcgggtttgt gccgcgcttg 1320

aactggactt ggtctcatgt gaatagcgac catttttatt atcgctataa tcagaatcgg 1380

gtttttgttg atgtgatgaa gcagttttga 1410

<210> 262

<211> 469

<212> PRT

<213> Kingella sp. Sch538 SLAM 1

<400> 262

Met Lys Lys Thr Ser Leu Leu Phe Leu Thr Leu Thr Ala Thr Ala Val
1 5 10 15

Gln Ala Ala Pro Val Ser Thr Pro Leu Asn Gln Ile Pro Asp Leu Asn
20 25 30

Gln Glu Gln Ile Ser Gln Gln Thr Glu Thr Val Val Gln Pro Glu Asn
35 40 45

Ala Lys Gln His Ser Ala Ser Met Thr Ala Asp Asp Leu Leu Lys Gln
50 55 60

Pro Glu Leu Leu Gln Asn Ala Leu Asp Thr Ala Ile Asn Gln Gln Asn
65 70 75 80

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

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

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

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

325 330 335

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

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

Val Met Lys Gln Phe
465

<210> 263
<211> 1605
<212> DNA
<213> Kingella sp. Sch538 SLAM 2
<400> 263
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gatgatgaag acttgcccac ttccgccact gccaaacgca aagaaaacaa cacggtggaa 120
accatcccca ttgccaaagc tgccacagcc acgcataacg acccacaagt atttcagcag 180
ccgtttgatg atgtgaacac gcaagaagaa tatgaattaa aaccgttgcc caatttgcca 240
aaaaacgatt tagcagacgt gcaacaggaa tatgaattgc agccgttgcc gaatccagcg 300

aaaaaagatg ttatccctga attaacacag cctgaagcat cgcagcctga aaaccaacaa 360
accagcacac aacaattaga cgaccaaatc aaccaagcgt tagtcgccaa aaaatgggac 420

gagctggaaa aactattggc agtagaacag caagcaggac aagacgaaac gctgcgagct 480

tatgccaaag gcgcactatt gcgtcaaaaa caagaatatc cacaggcaat cgcagaatat 540

cgcaaagtag tcgccgcgca gcctgaattg ggctatccgc gtttagactt gggcatcatg 600

ttgtttgaaa acaagcaatt ccgtgaagcc aaagccgaat taaccgaagc caaagcgcgt 660

atcaatccag aagcaagagc gcaaaaaatc gtcgatgcgt atttagaagg tatggaaaaa 720

gagcaaagct ggcagccgaa tatgggctta caatacacgc aaaccgataa tgtgaacaac 780

gcatcggata gcgtagaact gttttataac ggcagacgtt ttgtgaaaga taccgatgcc 840

ttaccaaagt cagcgcacgg tttcaactac aatctgggac tggaaaaaga caccaactta 900

gcaggcaacc attatgcacg agtgagcata aacggcagcg gcgtacatta ttgggataac 960

tcggattacg atgaaaactc gttgcaattg agtgcaggtt atcgctacca aagctggcgt 1020

taccaactcg gcttctcgcc atttttcgcg caaaactggc tcggcggtga acgctataat 1080

caacgctttg gcgtaaccag caattatcgt tatcgcttta atccgaagtg gtcgatttcc 1140

gccgcgcata cctattttaa tacgcgttac cgcagcgata atgtcgccaa atattacaac 1200

ggctacaaca acaatgtggg cttaacgctg atgtggaacc caacgccaag atggttgctg 1260

tttggtggcg tgaatgccag ccatgacaag ctaaaagaca aagccgaaag ctcaaaacgc 1320

gcaggcttca ccagtggcgt ggtgtacgat aaccaaaaat ggggtgcacg aaccaacttc 1380

aattttgcca accgccgttt ccaagatgcg cacttcttgt atggcagtca tcgtgcagac 1440

aaagagtacc aaatcagcgc agccgtatgg catcacaaat taacgtggca cggcatcacg 1500

ccacgtttga actatcgcta tttgaaaatt gatagcaata tgccagcact ctattcacgc 1560

aaaaacggcg aatggtttat cagcgcggaa aaaattttcc attaa 1605

<210> 264

<211> 404

<212> PRT

<213> Kingella sp. Sch538 SLAM 2

<400> 264

Met Asn Gln Ala Leu Val Ala Lys Lys Trp Asp Glu Leu Glu Lys Leu
1 5 10 15

Leu Ala Val Glu Gln Gln Ala Gly Gln Asp Glu Thr Leu Arg Ala Tyr
20 25 30

Ala Lys Gly Ala Leu Leu Arg Gln Lys Gln Glu Tyr Pro Gln Ala Ile
35 40 45

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

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

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

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

290 295 300

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

Gly Ile Thr Pro Arg Leu Asn Tyr Arg Tyr Leu Lys Ile Asp Ser Asn
370 375 380
Met Pro Ala Leu Tyr Ser Arg Lys Asn Gly Glu Trp Phe Ile Ser Ala
385 390 395 400
Glu Lys Ile Phe

<210> 265
<211> 1416
<212> DNA
<213> L. adecarboxylata SLAM 1
<400> 265
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gcgccgccgg aaaccgactc gattcctgct gctccccact ttgaacgact ggccacgcca 120

gagaagcgca ccgcgcctgg cgataaaacg ctgcatgtga ccaatgcgca actggcggaa 180
cagcctgagc tggcgatggc gctgctcgat caggccatac gcgaagaaaa gtggccgatg 240
gttcgtgcca tattaccagt ctatgcggcg tcaccgaatc ctgattctac cctgattcat 300
tttgccaaag ctggccttgc gcgcagtcag gggaattatg cagaggcgat tgaacactat 360
cgcgccattc tgagtcgtca tcctgacttt gctgcagtgc gtctggattt agcgcgtgcc 420
atgtttgaaa atcgtcagtt tgacgcggct gattatcagt ttcgtcgtgt attacaaagc 480
aatccgcctg agaatattca gcaggttatt gcacagtatc ttgagcgcat tcagaaaggc 540

agcgcattga cgggttcatt cagcgtgagt tatttgaatg acagtaatgt gaataatgca 600
tcatcgggta aaaccattcg ggttggcgat cgtctgttta ttcgtaataa ggatagtttc 660

ccacagcgcg gagaaggttt ctggttcaat ggcgcattac aaaaagatgt tcagctcttt 720

gatcagcatg gcttgcgatt tcttggtacg gtaaacggta aaagttactg gaataatcat 780

gattttgatg atgtgactag ccgggcttat gccggatatc aatggcgtaa tttccggcag 840

caatttgccc tgttgccgtt ttatgaaaaa agatggtatg gcaccgaggc ctattcttct 900

ggccccggcg tccgcgcgga atacagttat ttactgacgc ccacctggca ggtgagtcag 960

gcgctggaat atcagaaact ggattatgat gatgaagatt atcgcttctt gcgcggtcaa 1020

aatcgttact cttccacaac cctgtcccat gccttcagta accgggtgtc aggctttgcc 1080

ggcgtcgatc tgcttgagca gcagacctcc actcgcagtg aatctaacca tcgggtcggt 1140

ttgcgcagcg gggtgcaggt tgatatgccc tggcaactct cttttgccgc caccacggcc 1200

attgccagac gcaattacca ggccgacagt gatatctttt cgacgcgacg caaagataac 1260

gaacagatct ataacctctc gctctggcat cgcgacctct atttctttgg ggtgatgccg 1320

aaactgaatt tcagctataa gcgggtcgat agcaatatca atttctatga ttatcaacag 1380

aggtatatca cgctttctct ggataagaat ttttaa 1416

<210> 266

<211> 471

<212> PRT

<213> L. adecarboxylata SLAM 1

<400> 266

Met Asn Ile Leu Arg Thr Gly Ala Leu Ser Leu Leu Cys Pro Leu Ser
1 5 10 15

Val Ala Phe Ala Ala Pro Pro Glu Thr Asp Ser Ile Pro Ala Ala Pro
20 25 30

His Phe Glu Arg Leu Ala Thr Pro Glu Lys Arg Thr Ala Pro Gly Asp
35 40 45

Lys Thr Leu His Val Thr Asn Ala Gln Leu Ala Glu Gln Pro Glu Leu
50 55 60

Ala Met Ala Leu Leu Asp Gln Ala Ile Arg Glu Glu Lys Trp Pro Met
65 70 75 80

Val Arg Ala Ile Leu Pro Val Tyr Ala Ala Ser Pro Asn Pro Asp Ser
85 90 95

Thr Leu Ile His Phe Ala Lys Ala Gly Leu Ala Arg Ser Gln Gly Asn

100 105 110

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

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

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

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

Ser Asn Arg Val Ser Gly Phe Ala Gly Val Asp Leu Leu Glu Gln Gln
355 360 365

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

Leu Tyr Phe Phe Gly Val Met Pro Lys Leu Asn Phe Ser Tyr Lys Arg
435 440 445
Val Asp Ser Asn Ile Asn Phe Tyr Asp Tyr Gln Gln Arg Tyr Ile Thr
450 455 460
Leu Ser Leu Asp Lys Asn Phe
465 470

<210> 267
<211> 1296
<212> DNA
<213> L. oryzae SLAM 1
<400> 267
atgagtgcat tggcactcgc catcgcgcta cttggacaat ccgcctgtgc aggcgatatg 60
tccacactac tgcagtccgc taaaacgcaa ccggcggatg aagcctatca attgctatct 120

gcggaagaag cacaatttgc aggtgaacca gacttcgact atgcccttgg ggtagcggca 180
ctagaaagtg gccactacac cgcggccagc tttgcgctgg aacgcgtcgt cgcaaacgaa 240
ccggacaatg cagccgccta tctggatctt ggccgggcct actatggcat gggtgatctg 300
gacgctgcca aaacggcctt tgacgaggta gcctcccata atccgccaga agcggtacgc 360
aagctgctgc aaagctacca aggacaactc acaccacctg ccagcagcga actgaaggca 420
atgatctata tcgggacggg gcatgacagc aatgccaatg gcggattaag ccaagacatc 480
tatacattcc ccgcagcacc tgctctccca gtcacaatgc cgtcaacagc attggccaag 540

tccgacaatt acgcttttgc aggagcgcag ctctcttacc ggacagtgat cagtaatggc 600

ctcgttctgg acgccagcct gaatgcggca ggcaaatcct ttgatcagct agacactcag 660

gacagtcata ccatcggact cggtggtggc ctgacctggc aaacgggaga taaccggcta 720

cggcttggcg tcaataccag caaagagtgg ctgaaccatc aacactacgt cactacggat 780

ggcgcacgga tcgactggtc ccacctgctg gatagccaaa gcgaaatctc cttgtatggc 840

aactacaacc ggtatgacta cacctcatcc gggagtgatg ttcatcgtgt gacattaggc 900

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tatgcaggca aaaccctgac agatgctgga acacctgact atgtcggtaa ccggttcttc 1020

ggtttcatgc tgggtggcat ctggcatacc agcgagcaaa ccgacattta cctctccggt 1080

gcttatgaga gacgcatcta ttcggccgat acacccgcct atctggctcg gcgaaaagac 1140

aatcaatggg atatccggct aggcatgaac taccgctttt acccacgctt cacgttgacc 1200

ccgcaaatca gctggacccg caatggcagt aatcaggata tcagccaata ccagcgcacc 1260

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<210> 268

<211> 412

<212> PRT

<213> L. oryzae SLAM 1

<400> 268

Met Ser Thr Leu Leu Gln Ser Ala Lys Thr Gln Pro Ala Asp Glu Ala
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Tyr Gln Leu Leu Ser Ala Glu Glu Ala Gln Phe Ala Gly Glu Pro Asp
20 25 30

Phe Asp Tyr Ala Leu Gly Val Ala Ala Leu Glu Ser Gly His Tyr Thr
35 40 45

Ala Ala Ser Phe Ala Leu Glu Arg Val Val Ala Asn Glu Pro Asp Asn
50 55 60

Ala Ala Ala Tyr Leu Asp Leu Gly Arg Ala Tyr Tyr Gly Met Gly Asp
65 70 75 80

Leu Asp Ala Ala Lys Thr Ala Phe Asp Glu Val Ala Ser His Asn Pro
85 90 95

Pro Glu Ala Val Arg Lys Leu Leu Gln Ser Tyr Gln Gly Gln Leu Thr
100 105 110

Pro Pro Ala Ser Ser Glu Leu Lys Ala Met Ile Tyr Ile Gly Thr Gly

115 120 125

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

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

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

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

Gly Met Asn Tyr Arg Phe Tyr Pro Arg Phe Thr Leu Thr Pro Gln Ile
370 375 380

Ser Trp Thr Arg Asn Gly Ser Asn Gln Asp Ile Ser Gln Tyr Gln Arg
385 390 395 400
Thr Arg Phe Asp Leu Thr Leu Lys Tyr Asp Phe Gln
405 410

<210> 269
<211> 1509
<212> DNA
<213> M. aminisulfidivorans SLAM 1
<400> 269

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ctccgcttaa accaaggaat cgagttacgc gctgatcaac aagagcagga aatcctgaaa 180

gatgaggact atttgcgagg tgaacggccc agtttaatca ttgatggtca gtcatacacc 240
gttcagcaca acagtaatga tgtcggccgt gccttgtatg tgtcattgca gaaaaaacag 300
tggtcgtcgg tgaagttttt tctgcaagaa tatgaagaat ttgctgatgc agatcctatg 360
ctgctcgcct atgcacgggg tgctattgca cgaatggaag gtgatctgga acaggcagaa 420
acagaatacc gccagcttat cgacttaaaa cccgactttt tgcccggtca gttagaactc 480
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caacagacat taaatcctgc cgatgcacgt cagcaaggcg ttagcaccac ggtagatagt 600

tttttgcagg ctttagataa acgccagtca tggcaaggtt ccttttccat tggcccaacc 660
tgggtcgata acttaaacca atcctctgaa agctacagtt gcttactcta ttttggcaat 720
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caagaagact atgctgctta taacggtgat atctggtcag cttacgccac cgcctggtat 1140
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gtggaaccct atgcctatca gcaaataggc atcagagctg gtctgtccaa aaaattcaat 1260

gaagacatta acgccgtgct ttttgcctct gtgcgtcaac gcaaacatga tgaatttaat 1320

gccttacttg gtgagcagcg tgaagatatt gagcaaaact acacacttat cgtgcgtttc 1380

cccggactga gtttttatgg gctggaacct aatctcaccc tgaagcatcg aaaagtgcat 1440

agcaatgtga actggcttta ttcctatgaa cgtaatgctg tgagcctccg acttgagaaa 1500

caattttaa 1509

<210> 270

<211> 502

<212> PRT

<213> M. aminisulfidivorans SLAM 1

<400> 270

Met Ile Phe Asp Val Tyr Gln Ser Tyr Arg Tyr Pro Ile Ser Val Trp

1 5 10 15

Ile Ala Phe Leu Cys Leu Thr Val Leu Ser Ile Thr Ser Gln Asn Ser

20 25 30

Trp Ala Asp Asp Lys Asp Thr Ser Leu Arg Leu Asn Gln Gly Ile Glu

35 40 45

Leu Arg Ala Asp Gln Gln Glu Gln Glu Ile Leu Lys Asp Glu Asp Tyr

50 55 60

Leu Arg Gly Glu Arg Pro Ser Leu Ile Ile Asp Gly Gln Ser Tyr Thr

65 70 75 80

Val Gln His Asn Ser Asn Asp Val Gly Arg Ala Leu Tyr Val Ser Leu

85 90 95

Gln Lys Lys Gln Trp Ser Ser Val Lys Phe Phe Leu Gln Glu Tyr Glu

100 105 110

Glu Phe Ala Asp Ala Asp Pro Met Leu Leu Ala Tyr Ala Arg Gly Ala

115 120 125

Ile Ala Arg Met Glu Gly Asp Leu Glu Gln Ala Glu Thr Glu Tyr Arg

130 135 140

Gln Leu Ile Asp Leu Lys Pro Asp Phe Leu Pro Gly Gln Leu Glu Leu

145 150 155 160

Ala Arg Val Leu Phe Glu Asn Arg Lys Asp Ala Glu Ser Asp Gln Val

165 170 175

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

180 185 190

Gly Val Ser Thr Thr Val Asp Ser Phe Leu Gln Ala Leu Asp Lys Arg

195 200 205

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

210 215 220

Leu Asn Gln Ser Ser Glu Ser Tyr Ser Cys Leu Leu Tyr Phe Gly Asn

225 230 235 240

Val Cys Phe Tyr Glu Arg Glu Thr Pro Glu Ala Val Lys Ala His Gly

245 250 255

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

260 265 270

His Gly Val Phe Phe Arg Ser Leu Leu Phe Gly Gln Ser Tyr Lys Asp

275 280 285

His Ser Asp Phe Asn Glu Ser Gln Ile Thr Ser Gln Leu Gly Tyr Ser

290 295 300

Tyr His Ala Gln Arg Asn Gln Phe Ser Phe Ala Pro Ser Phe Asp Phe

305 310 315 320

Ser Arg Tyr Gly Gln Arg Ser Met Tyr Gly Ala Trp Gly Leu His Ser

325 330 335

Glu Trp Leu His Tyr Val Ser Asp Arg Met Leu Phe Lys Leu Glu Ala

340 345 350

Asp Tyr Lys Asp Gln Gln Tyr Arg Gln Glu Asp Tyr Ala Ala Tyr Asn

355 360 365

Gly Asp Ile Trp Ser Ala Tyr Ala Thr Ala Trp Tyr Val Phe Pro His

370 375 380

Leu Trp Thr Val Phe Gly Gly Val Asp Trp Thr Gln Lys Gln Ala Glu

385 390 395 400

Val Glu Pro Tyr Ala Tyr Gln Gln Ile Gly Ile Arg Ala Gly Leu Ser

405 410 415

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

420 425 430

Gln Arg Lys His Asp Glu Phe Asn Ala Leu Leu Gly Glu Gln Arg Glu

435 440 445

Asp Ile Glu Gln Asn Tyr Thr Leu Ile Val Arg Phe Pro Gly Leu Ser

450 455 460

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

465 470 475 480

Ser Asn Val Asn Trp Leu Tyr Ser Tyr Glu Arg Asn Ala Val Ser Leu

485 490 495

Arg Leu Glu Lys Gln Phe

500

<210> 271

<211> 1266

<212> DNA

<213> M. caprae SLAM 1

<400> 271

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ctttcggtgc tggtggctaa tgatgtggct ggaactcagt tattattgcc catctaccaa 120

aaacagccga gtgaaatcat tgaatctgaa atggttgact ggggcagtgc cgtgctggca 180

ggtgcggaaa gcagacatgg tcaagccagc aaaatctacc aatttttgca taaccaatac 240

cccaataatg atctttttgc cgttagactg attcagagtt tgtttgccaa tcgtcaatat 300

ctagaagcca aacaactgct tgcagagcaa ccagattata ttgtccgtga aatgcgtgcc 360

taccaaaaag ccttaacaaa tttaaccaag ccatcggtgt atttttctgg caatgtaatt 420

gttgataaaa acattaacaa tgcacccaat cagaccgatt tgggtggtgg ctggacggca 480

aacgctgctg agcaagcaca tggtgtcgcc atcaatgcag gtatggaaaa gaaagtttta 540

ctcaaaggtg gcatgacgct agaaccttct gttacgatga gtggcaagct ctttcgtgat 600

gctaagcatt ataatgaaac gcagcttcgc ctaggggtca acactgtcaa aaaccatact 660

gggggtagct tatctgtttc gccttttgtg gagactgctt ggtatgctgg tggtaaaaag 720

ggtgttaatg aattaaagca tttttcggac acgctgggtg tgagtattgg cagtcaaaga 780

cagcttggta aaaaaagcca gcttgctact aatgttgaat ttgccaaaca tcatcataac 840

atcagacatc atttatcagg tcatagtgtc agtgccaaag cgagcttttc tacgcgtcct 900

aactggctgg gagaaagtgg ttgggtcagt gttggtgcag attatcgaca ggcaaaaacc 960

cgggataaag atgactccta tacccgtgtc ggcatacaag gttcaattac caagcggtgg 1020

catgatttcg gtgtgagtgg cagtttgaat ttttcccaaa gacgctatca tggaccgatg 1080

ccgatttttа atcaaataca aacaagtgat gagtatttta ccaacatcag tgtttggcat 1140

aataagctga gctacttagg gctaacgccg aaattgactt ggcaatacca aaaaaatgac 1200

agcaacatcg cactgtacaa ctacgataaa agtcgtgtgt tcttagaggt gagtcgccaa 1260

ttttaa 1266

<210> 272

<211> 421

<212> PRT

<213> M. caprae SLAM 1

<400> 272

Met Leu Ser Val Asp Glu Gln Met Leu Leu Thr Asn Pro Thr Leu Leu
1 5 10 15

Ser Arg Ala Met Leu Ser Val Leu Val Ala Asn Asp Val Ala Gly Thr
20 25 30

Gln Leu Leu Leu Pro Ile Tyr Gln Lys Gln Pro Ser Glu Ile Ile Glu
35 40 45

Ser Glu Met Val Asp Trp Gly Ser Ala Val Leu Ala Gly Ala Glu Ser
50 55 60

Arg His Gly Gln Ala Ser Lys Ile Tyr Gln Phe Leu His Asn Gln Tyr
65 70 75 80

Pro Asn Asn Asp Leu Phe Ala Val Arg Leu Ile Gln Ser Leu Phe Ala
85 90 95

Asn Arg Gln Tyr Leu Glu Ala Lys Gln Leu Leu Ala Glu Gln Pro Asp
100 105 110

Tyr Ile Val Arg Glu Met Arg Ala Tyr Gln Lys Ala Leu Thr Asn Leu
115 120 125

Thr Lys Pro Ser Val Tyr Phe Ser Gly Asn Val Ile Val Asp Lys Asn
130 135 140

Ile Asn Asn Ala Pro Asn Gln Thr Asp Leu Gly Gly Gly Trp Thr Ala
145 150 155 160

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

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

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

Gln Arg Arg Tyr His Gly Pro Met Pro Ile Phe Asn Gln Ile Gln Thr
355 360 365
Ser Asp Glu Tyr Phe Thr Asn Ile Ser Val Trp His Asn Lys Leu Ser
370 375 380
Tyr Leu Gly Leu Thr Pro Lys Leu Thr Trp Gln Tyr Gln Lys Asn Asp

385 390 395 400

Ser Asn Ile Ala Leu Tyr Asn Tyr Asp Lys Ser Arg Val Phe Leu Glu

405 410 415

Val Ser Arg Gln Phe

420

<210> 273

<211> 1512

<212> DNA

<213> M. catarrhalis SLAM 1

<400> 273

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atggctggct tgacttttct aatcgctcat atcagccatg ccgatgatgg tcgcaccgac 120

aatcaagagc caatcaatca agaaatagcc acccttgaac ccatcattaa ccatgctcag 180

cctgagttat tgtcccatga tgcattaaca ccaaaaatag aaccaatact ggcacaaaca 240

ccaaatcctg ccgaagatac gctcatcgcc gatgaggcgt tactgcttga taaccctgat 300

ttgctcaatc acgccctaaa ttctgctgtc atgaccaatc atatggcagg cgttcacgca 360

ttattgccca tttatcaaaa actgcccaaa gaccatcaaa atggcatttt acttgggtat 420

gccaatgcct tggctgcttt ggataagggc aacgccaaaa aagccattga tgagctgcgt 480

cgcatcatcg ccatcatgcc tgaatataat gtggtgcgtt ttcatctggc aagggcatta 540

tttatggaca aacaaaatga agccgccctt gaccagttta ataaattaca tgctgacaac 600

ttgccagagg aggtgcggca ggttgttggg cagtacagac aagcgttaaa acaacgagat 660

tcatggacat ggcaagtagg catgaatctg gccaaagaag acaacatcaa tcaaaccccc 720

aaaaacacca cgcaaggtca atggactttt gacaaaccca ttgacgccat caccctaagc 780

taccaattgg gggcggataa aaagtggtct ttgcccaaag gggcatatgt gggagcgaac 840

gcccaaatct atggcaaaca tcatcaaaat cacaaaaaat acaacgacca ttggggcaga 900

ctgggggcaa atttgggctt tgctgatgcc aaaaaagacc ttagcattga gacctatggt 960

gaaaaaagat tttatgggca tgagcgttat accgacacca tcggcatacg catgtcggtt 1020

gattatagaa tcaacccaaa atttcaaagc ctaaacgcca tagacatatc acgcctaacc 1080

aaccatcgga cgcctagggc tgacagtaat aacactttat acagcacctc attgatttat 1140

tacccaaatg ccacacgcta ttatcttttg ggggcagact tttatgatga aaaagtgcca 1200

caagacccat ctgacagcta tcaacgccgt ggcatacgca cagcgtgggg gcaagaatgg 1260

gcgggtggtc tttcaagccg tgcccaaatc agcatcaaca aacgccatta ccaaggggca 1320

aacctaacca gcggtggaca aattcgccat gataaacaga tgcaagcgtc tttatcgctt 1380

tggcacagag acattcacaa atggggcatc acgccacggc tgaccatcag cacaaacatc 1440

aacaaaagca atgacatcaa ggcaaattat cacaaaaatc aaatgtttgt tgagtttagt 1500

cgcatttttt ga 1512

<210> 274

<211> 503

<212> PRT

<213> M. catarrhalis SLAM 1

<400> 274

Met Thr Ile Thr Pro Val Tyr Thr Thr Phe Thr Pro Thr Lys Thr Pro

1 5 10 15

Ile Lys Phe Phe Met Ala Gly Leu Thr Phe Leu Ile Ala His Ile Ser

20 25 30

His Ala Asp Asp Gly Arg Thr Asp Asn Gln Glu Pro Ile Asn Gln Glu

35 40 45

Ile Ala Thr Leu Glu Pro Ile Ile Asn His Ala Gln Pro Glu Leu Leu

50 55 60

Ser His Asp Ala Leu Thr Pro Lys Ile Glu Pro Ile Leu Ala Gln Thr

65 70 75 80

Pro Asn Pro Ala Glu Asp Thr Leu Ile Ala Asp Glu Ala Leu Leu Leu

85 90 95

Asp Asn Pro Asp Leu Leu Asn His Ala Leu Asn Ser Ala Val Met Thr

100 105 110

Asn His Met Ala Gly Val His Ala Leu Leu Pro Ile Tyr Gln Lys Leu

115 120 125

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

130 135 140

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

145 150 155 160

Arg Ile Ile Ala Ile Met Pro Glu Tyr Asn Val Val Arg Phe His Leu

165 170 175

Ala Arg Ala Leu Phe Met Asp Lys Gln Asn Glu Ala Ala Leu Asp Gln

180 185 190

Phe Asn Lys Leu His Ala Asp Asn Leu Pro Glu Glu Val Arg Gln Val

195 200 205

Val Gly Gln Tyr Arg Gln Ala Leu Lys Gln Arg Asp Ser Trp Thr Trp

210 215 220

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

225 230 235 240

Lys Asn Thr Thr Gln Gly Gln Trp Thr Phe Asp Lys Pro Ile Asp Ala

245 250 255

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

260 265 270

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

275 280 285

Gln Asn His Lys Lys Tyr Asn Asp His Trp Gly Arg Leu Gly Ala Asn

290 295 300

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

305 310 315 320

Glu Lys Arg Phe Tyr Gly His Glu Arg Tyr Thr Asp Thr Ile Gly Ile

325 330 335

Arg Met Ser Val Asp Tyr Arg Ile Asn Pro Lys Phe Gln Ser Leu Asn

340 345 350

Ala Ile Asp Ile Ser Arg Leu Thr Asn His Arg Thr Pro Arg Ala Asp

355 360 365

Ser Asn Asn Thr Leu Tyr Ser Thr Ser Leu Ile Tyr Tyr Pro Asn Ala

370 375 380

Thr Arg Tyr Tyr Leu Leu Gly Ala Asp Phe Tyr Asp Glu Lys Val Pro

385 390 395 400

Gln Asp Pro Ser Asp Ser Tyr Gln Arg Arg Gly Ile Arg Thr Ala Trp

405 410 415

Gly Gln Glu Trp Ala Gly Gly Leu Ser Ser Arg Ala Gln Ile Ser Ile

420 425 430

Asn Lys Arg His Tyr Gln Gly Ala Asn Leu Thr Ser Gly Gly Gln Ile

435 440 445

Arg His Asp Lys Gln Met Gln Ala Ser Leu Ser Leu Trp His Arg Asp

450 455 460

Ile His Lys Trp Gly Ile Thr Pro Arg Leu Thr Ile Ser Thr Asn Ile

465 470 475 480

Asn Lys Ser Asn Asp Ile Lys Ala Asn Tyr His Lys Asn Gln Met Phe

485 490 495

Val Glu Phe Ser Arg Ile Phe

500

<210> 275

<211> 1626

<212> DNA

<213> M. catarrhalis SLAM 2

<400> 275

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gtgctgttat tgctttgtgt tgatacatta acagcacagg cgtacgccca cagccatcat 120

acgcccattc atacacccac gcatgagctg ccatctgctg atgctttatc agatgaaggc 180

ttgggtaagg atttgggcag tttggacagt ttggatagcc cagatggttt aggtgatggt 240

ttaggcgatg gtttgggtga tggcttaaaa agtgataaaa ccccttacc catcaacgcc 300

ttgaccgccc atcagaccaa tgagagccag cctgccccac cgagcgtaga tgtcaatttt 360

ttacttgccc agccagaggc attttatcat gtctttcatc aagcgattgt gcaagatgat 420

gtggcaacat tacgcttgtt attgccattt tatgaccgcc tgcctgatga ttatcaagat 480

gatgttttgt tgttatttgc ccaaagcaaa cttgccctaa gtgatggtaa taccaaactg 540

gcattaaatc tgctgaccga tttgagcaac aaagagccga cgcttacggc ggtgaaatta 600

caacttgcct ctttgcttct gaccaacaag cacgataaac acgcccaaat ggtgctagat 660

gaactcaaag atgatgccca ctttttaaaa ttaagcaaaa aagagcaaag atgggtgcta 720

tcgcaaagtc gctatttaca taaaaaatat aaaatgggct tggatttggg catcaactat 780

ctgcatttgg ataatatcaa cgccgcctcc accatcaccc agcccaacat taaaaaagat 840

gccccaaaac ctgctcatgg gcttgcctta tcgcttggtg tgaataaata cacgccgctt 900

agtcatggca tgagtattta tacagcccta gatgttgatg gtaaatttta tgatgacaaa 960

agccacaatg aactggcggt ttttgctcat gctggactaa gaaaagatca ccaaaaaggt 1020

tatgttgatg tcgtaccttt tgttgggcgt atttttgcca ccaatcagca gcatggcaga 1080

ttatccccca gaaaagacag tcagggcgtg gcgtttggca gccatcatcg gatcaatgat 1140

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agtcatgcca caaagataca ttttggggtg ttgcaaagat tgccaaatgg tctgaccgtg 1380

caaggtagag tgagtgctga gcgtgagcgt tatcatggta aattattgcg tctggttaat 1440

cctgatgatg tgtatcgcac agataaaacc ctaaccctac aaacctccat ttggcacaaa 1500

gacattcact ggcttggatt aacgccaaag ctgacttatc gttacagtaa aaataacagt 1560

aacttaccag cactttatag ccataacaaa caaaattttt atttggagct tggtcggtcg 1620

ttttaa 1626

<210> 276

<211> 541

<212> PRT

<213> M. catarrhalis SLAM 2

<400> 276

Met Thr Cys Leu Pro Lys Thr Asn Pro Ala Leu Lys Val Lys His Arg
1 5 10 15

Phe Leu Lys Gln Val Leu Leu Leu Leu Cys Val Asp Thr Leu Thr Ala
20 25 30

Gln Ala Tyr Ala His Ser His His Thr Pro Ile His Thr Pro Thr His
35 40 45

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

Leu Gly Ser Leu Asp Ser Leu Asp Ser Pro Asp Gly Leu Gly Asp Gly
65 70 75 80

Leu Gly Asp Gly Leu Gly Asp Gly Leu Lys Ser Asp Lys Thr Pro Leu
85 90 95

Pro Ile Asn Ala Leu Thr Ala His Gln Thr Asn Glu Ser Gln Pro Ala

100 105 110

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

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

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

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

Ala Thr Asn Gln Gln His Gly Arg Leu Ser Pro Arg Lys Asp Ser Gln
355 360 365

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

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

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

<210> 277
<211> 1449
<212> DNA
<213> M. flagellatus SLAM 1
<400> 277

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gataatcgcc gtaaccagcc tacgcttgag gagcagattc aggcagagcc tgcgattatg 180

ctaggtgatg atcaaaacag caccgcaaca ttggcgcagg aaattttcgt ccagatcaac 240

cagcagaact gggtcaaggt caagcaactg ctaagctatt acctggtttc cccgcaccgc 300

gaccccagcc tggtggcgta tgcagaggct aatctagctg aagcgcaggg caacctgtcc 360

ctggcattgg agaaatacga gcggacattg tcgtatcttc cggatttcac gcgcggcaag 420

atggattatg cgcgagcctt gttcaagaat ggcgaggaca aggaggccaa acagattttt 480

ctttccgtca tgacgcccga tctccccttg ccggtgcagc ataatctcaa tttataccta 540

gatgcgcttg aaaggcgcaa cgagtggaag ttttatgccg cgctggatta tttcaaggat 600

gacaatatca acctgacttc cggggcgtcg ctctgtctgc tctcaatcag cagtgatcta 660

tgtgcggccc gatggtctgc gccaggggca ttgccgagcc atggagtgaa ctatacgttc 720

actgcggaga aattcacgcc cttaaaaggc cgccatgggt tgatgttccg ctcgctggtc 780

tatggttcgg actatacgca ggataatctg tacaacatcg ggatggcgaa catggcgctt 840

ggctatgctt atcgcacgcc caaccatcgc ttgtttatcg cccccacctt tgaagcctat 900

tggcagagca accgcagact ctacaccgca ggcggcatga tggcggagct gcgtagccag 960

ttgacgccga ggtggcagaa taccttcagc atcaactggc aggatatcca gtatgtgagg 1020

gaggaggaaa gggacaacga cgccaagcaa tatttggtga cgctgaacca gttatatgcg 1080

ttatccgaca agacattgct gttcggcggt gtggactata tccgtcgtaa gctggatcct 1140

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tcatggtttg acgtgaccat gtcagcctcc aggcgctggc ggaaatatga tgaatacaat 1260

ccgatatacg gcgggttgcg ccaggacacc gaggatttct acagcctggc attggggttc 1320

ccccgtttgc aggtgcaagg tgtcaagcct tcactgtatg tgcagcattt cgatactgac 1380

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tcgttctga 1449

<210> 278

<211> 482

<212> PRT

<213> M. flagellatus SLAM 1

<400> 278

Met Lys Ala Leu Leu Phe Pro Leu Ile Val Leu Cys Leu Ser Ser Thr

1 5 10 15

Ala Trp Ala Asn Asp Phe Phe Asp Asn Ser Ala Asn Gln Trp Gln Phe

20 25 30

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

35 40 45

Leu Glu Glu Gln Ile Gln Ala Glu Pro Ala Ile Met Leu Gly Asp Asp

50 55 60

Gln Asn Ser Thr Ala Thr Leu Ala Gln Glu Ile Phe Val Gln Ile Asn

65 70 75 80

Gln Gln Asn Trp Val Lys Val Lys Gln Leu Leu Ser Tyr Tyr Leu Val

85 90 95

Ser Pro His Arg Asp Pro Ser Leu Val Ala Tyr Ala Glu Ala Asn Leu

100 105 110

Ala Glu Ala Gln Gly Asn Leu Ser Leu Ala Leu Glu Lys Tyr Glu Arg

115 120 125

Thr Leu Ser Tyr Leu Pro Asp Phe Thr Arg Gly Lys Met Asp Tyr Ala

130 135 140

Arg Ala Leu Phe Lys Asn Gly Glu Asp Lys Glu Ala Lys Gln Ile Phe

145 150 155 160

Leu Ser Val Met Thr Pro Asp Leu Pro Leu Pro Val Gln His Asn Leu

165 170 175

Asn Leu Tyr Leu Asp Ala Leu Glu Arg Arg Asn Glu Trp Lys Phe Tyr

180 185 190

Ala Ala Leu Asp Tyr Phe Lys Asp Asp Asn Ile Asn Leu Thr Ser Gly

195 200 205

Ala Ser Leu Cys Leu Leu Ser Ile Ser Ser Asp Leu Cys Ala Ala Arg

210 215 220

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

225 230 235 240

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

245 250 255

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

260 265 270

Ile Gly Met Ala Asn Met Ala Leu Gly Tyr Ala Tyr Arg Thr Pro Asn

275 280 285

His Arg Leu Phe Ile Ala Pro Thr Phe Glu Ala Tyr Trp Gln Ser Asn

290 295 300

Arg Arg Leu Tyr Thr Ala Gly Gly Met Met Ala Glu Leu Arg Ser Gln

305 310 315 320

Leu Thr Pro Arg Trp Gln Asn Thr Phe Ser Ile Asn Trp Gln Asp Ile

325 330 335

Gln Tyr Val Arg Glu Glu Glu Arg Asp Asn Asp Ala Lys Gln Tyr Leu

340 345 350

Val Thr Leu Asn Gln Leu Tyr Ala Leu Ser Asp Lys Thr Leu Leu Phe

355 360 365

Gly Gly Val Asp Tyr Ile Arg Arg Lys Leu Asp Pro Phe Pro Met Ala

370 375 380

Ser Phe Glu Arg Ser Gly Val Arg Val Gly Met Phe His Thr Val Ser

385 390 395 400

Ser Trp Phe Asp Val Thr Met Ser Ala Ser Arg Arg Trp Arg Lys Tyr

405 410 415

Asp Glu Tyr Asn Pro Ile Tyr Gly Gly Leu Arg Gln Asp Thr Glu Asp

420 425 430

Phe Tyr Ser Leu Ala Leu Gly Phe Pro Arg Leu Gln Val Gln Gly Val

435 440 445

Lys Pro Ser Leu Tyr Val Gln His Phe Asp Thr Asp Ser Ser Leu Pro

450 455 460

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

465 470 475 480

Ser Phe

<210> 279

<211> 1329

<212> DNA

<213> M. flagellatus SLAM 2

<400> 279

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ctggagccgg tggagtccga gtattccggc gaccctgcat atgacatgct attcggcctg 180

gcggcgattg acagcggtca tgtgacgcgc ggcgtgttcg cgcttgagcg cgtgcttgcg 240

gtccagccgt ataacggcaa tgccagggcg cagattgcgc gcgcgtattt tcttctgggc 300

gagcaagaag ctgcccgcgc tgagttcagg aatgtgctca accagcaacc gcctgaagag 360

atcacccagg tgatcaatcg ctacatgagc gcgatcgaca aggcccaggg gttgacgacg 420

gcattctctg cgtatcttga aggcggagtg ggtcatgatt cgaatgtgaa cagtgccacg 480

gccgccagtt ctgttaccgt cgctgtccct gcgctgggcg gcttgattgt ggatattggc 540

cttgaccgtc aagcccgcga gtcgagcgat aactatacca atcttgctgg aggcatttcg 600

tttcgcaccc cattggcaag acggtttgcg ttgtttgccg gtatcaatgc gtctcagcgg 660

ttgaatcggc atcaggatgc ctttgatctg ggaatgctgg atgcgaatgt tgggctgagt 720

tatcgtcagc accgggatac ctataccgta gccgcgcagg cgaatagcct cagcctcgat 780

gaccagactt atcgtcgggc atacggcatc aacatgcaat ggcagcgcga cattgatacc 840

aagaatcaag tcaacctgtt tgcccaggtt tcgcgcctgg cctatcccga caacaggatt 900

cgggatgctg accgatatat tgtaggcgga gggtgggctc atgtcttcga tggggacctg 960

acgccttttat tgtttgtgag tggctatgga ggaaaggaac aggcaaggaa cgagtatgcg 1020

gacttcctca gctatcgtgt ccatggtgtg cgcagcgggg gccagctgac tctcaggccg 1080

aatcttgtcg cgttcacaac attgggatac gagaaccgcc gacatgatga gccggaaaca 1140

ttccctttc ttttcgcgac acgcgaggac aagcagctgg atgccagtgt gggattaagg 1200

tatctgccgg gatacaattg gattatcaag ccgcaattca cttttattcg taatgactcc 1260

acggttgaac tctacagctt tgaccgttat atggtctcgg tcagcgtccg acgtgagttc 1320

aactggtag 1329

<210> 280

<211> 442

<212> PRT

<213> M. flagellatus SLAM 2

<400> 280

Met Ala Gly Val Ile Leu Leu Leu Met Gly Glu Gly Leu Ala Cys Ala

1 5 10 15

His Asp Thr Ala Leu Leu Asp Lys Ala Gly Arg Leu Met Ala Ser Arg
20 25 30
Asp Tyr Ala Ala Ala Tyr Ala Leu Leu Glu Pro Val Glu Ser Glu Tyr
35 40 45
Ser Gly Asp Pro Ala Tyr Asp Met Leu Phe Gly Leu Ala Ala Ile Asp
50 55 60
Ser Gly His Val Thr Arg Gly Val Phe Ala Leu Glu Arg Val Leu Ala
65 70 75 80

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

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

Phe Ala Leu Phe Ala Gly Ile Asn Ala Ser Gln Arg Leu Asn Arg His
210 215 220
Gln Asp Ala Phe Asp Leu Gly Met Leu Asp Ala Asn Val Gly Leu Ser
225 230 235 240
Tyr Arg Gln His Arg Asp Thr Tyr Thr Val Ala Ala Gln Ala Asn Ser
245 250 255

Leu Ser Leu Asp Asp Gln Thr Tyr Arg Arg Ala Tyr Gly Ile Asn Met
260 265 270

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

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

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

<210> 281
<211> 1449
<212> DNA
<213> M. granulomatis SLAM 1
<400> 281
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aaaacgcagc aaattcaaga gcaattagat aaccaaagaa tgcaacaaaa ccggtatatg 120

gagcccgctg aacatcgcgt taagccatta aacataaagg ctaaaaacca gggtaagaga 180

gtttccatta ctcctcagga gttatcaaga cagcctcaac tgcttaattc agcaatgctc 240

acggcattag tcatgaatca cacacataat gtgatatttt tacgacctat ttatcagcaa 300

ctgcctgaaa atgagcaaaa tgaacagatc ttattatggg ctgaagcaat acaacaaaaa 360

tctgaacgta actattcaga ctcaattcgc ctatatcgta cgctcattgc acaaaaccca 420

caaagccagc ctattaggtt tcaattagct actgccttgt ttgagaatag agaaaccgaa 480

gctgcagaag aacaattccg caaactccaa acagagcaat taccggcaga aattgctcat 540

attattgagc agtatttaaa cgcaatcaat aaacaggata aatggaattt tcaaggcggt 600

ctaacctatt taaatgatcc gaatattaac aatgctccgg attcaggcat aacatataag 660

ggttggacac ctcccaaaaa agaatccgca caaggaattg gctttaattt tgatgctgat 720

aaaaaatggt cttggggtaa tggtttcttc catcaattcc gcctaaatgg caacggaaaa 780

tattattgga ataacaaaaa atacaatgaa tattctttgc gggaaagtct aggtttaggt 840

tatcaaaatg cgaagcacag aatcatattt ctgccttttt tagagcaaat gtggtatagc 900

ggtggttcaa gccaaagcac aagcaccaaa cgttattcta aagcaggtgg aataaatgcc 960

cgctggcatt attggctaac acctcaatgg caatcggtgc tgaattacga atacgctgag 1020

cagcgttata cacgccgcaa acatctaaat ggtaactatc actttgttgc accatcgctt 1080

tattactatc ctaacagcca gcaatattgg tttgttggtg caaactttaa ccgtaccagc 1140

actagagatt tagacgacag ctttattcgc cgaggtctta ccttaggttg gggccaagaa 1200

tggaaaaatg gattgtccag ccaattaagc gtgagttatg ctctaaaaca atatagaggt 1260

ccaaactttt tcaatatcat acaaaaaaac aaagagtacg gtattcaagc aagtctgtgg 1320

catagagcag tgcatttttg gggaattaca ccacgtttaa catggagtta cacaaaagtg 1380

aaaagcaacc acccattcaa taattatgat aaaaatcgca tataccttga tttttctcat 1440

acattctaa 1449

<210> 282

<211> 482

<212> PRT

<213> M. granulomatis SLAM 1

<400> 282

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

1 5 10 15

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

20 25 30

Arg Met Gln Gln Asn Arg Tyr Met Glu Pro Ala Glu His Arg Val Lys

35 40 45

Pro Leu Asn Ile Lys Ala Lys Asn Gln Gly Lys Arg Val Ser Ile Thr

50 55 60

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

65 70 75 80

Thr Ala Leu Val Met Asn His Thr His Asn Val Ile Phe Leu Arg Pro

85 90 95

Ile Tyr Gln Gln Leu Pro Glu Asn Glu Gln Asn Glu Gln Ile Leu Leu

100 105 110

Trp Ala Glu Ala Ile Gln Gln Lys Ser Glu Arg Asn Tyr Ser Asp Ser

115 120 125

Ile Arg Leu Tyr Arg Thr Leu Ile Ala Gln Asn Pro Gln Ser Gln Pro

130 135 140

Ile Arg Phe Gln Leu Ala Thr Ala Leu Phe Glu Asn Arg Glu Thr Glu

145 150 155 160

Ala Ala Glu Glu Gln Phe Arg Lys Leu Gln Thr Glu Gln Leu Pro Ala

165 170 175

Glu Ile Ala His Ile Ile Glu Gln Tyr Leu Asn Ala Ile Asn Lys Gln

180 185 190

Asp Lys Trp Asn Phe Gln Gly Gly Leu Thr Tyr Leu Asn Asp Pro Asn

195 200 205

Ile Asn Asn Ala Pro Asp Ser Gly Ile Thr Tyr Lys Gly Trp Thr Pro

210 215 220

Pro Lys Lys Glu Ser Ala Gln Gly Ile Gly Phe Asn Phe Asp Ala Asp

225 230 235 240

Lys Lys Trp Ser Trp Gly Asn Gly Phe Phe His Gln Phe Arg Leu Asn

245 250 255

Gly Asn Gly Lys Tyr Tyr Trp Asn Asn Lys Lys Tyr Asn Glu Tyr Ser

260 265 270

Leu Arg Glu Ser Leu Gly Leu Gly Tyr Gln Asn Ala Lys His Arg Ile

275 280 285

Ile Phe Leu Pro Phe Leu Glu Gln Met Trp Tyr Ser Gly Gly Ser Ser

290 295 300

Gln Ser Thr Ser Thr Lys Arg Tyr Ser Lys Ala Gly Gly Ile Asn Ala

305 310 315 320

Arg Trp His Tyr Trp Leu Thr Pro Gln Trp Gln Ser Val Leu Asn Tyr

325 330 335

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

340 345 350

Tyr His Phe Val Ala Pro Ser Leu Tyr Tyr Tyr Pro Asn Ser Gln Gln

355 360 365

Tyr Trp Phe Val Gly Ala Asn Phe Asn Arg Thr Ser Thr Arg Asp Leu

370 375 380

Asp Asp Ser Phe Ile Arg Arg Gly Leu Thr Leu Gly Trp Gly Gln Glu

385 390 395 400

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

405 410 415

Gln Tyr Arg Gly Pro Asn Phe Phe Asn Ile Ile Gln Lys Asn Lys Glu

420 425 430

Tyr Gly Ile Gln Ala Ser Leu Trp His Arg Ala Val His Phe Trp Gly

435 440 445

Ile Thr Pro Arg Leu Thr Trp Ser Tyr Thr Lys Val Lys Ser Asn His

450 455 460

Pro Phe Asn Asn Tyr Asp Lys Asn Arg Ile Tyr Leu Asp Phe Ser His

465 470 475 480

Thr Phe

<210> 283

<211> 1302

<212> DNA

<213> M. granulomatis SLAM 2

<400> 283

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cagaaattat tacaagagta tcaagagcaa actgattcag atccaaaact tattgcttat 180

gcacaggcaa aatcggcgtt tattcagcaa gattattcaa ccgctattgc gatttatcgc 240

aaaataatca gtagtcaccc tgagctaaat tccattcgaa tagaattagc catcgcccta 300

tttgcagatc gacaagataa tgcatctaaa tcacagtttg aaaaagtgaa agctgcttca 360

ggcttgccag atagtgcgta tcagataatt caagcttatt tagatacgat aaatcagcgt 420

aatgaatggc aatttagcct gaatttatct tactcgagaa ccgataatgt tgataatgtt 480

tctagcgatt caactataga gaatacaggt tttaccaagc acaaaaatat gctgcctaaa 540

aaagcacacg gtattgccta taatattgat ttcggcaaag attttaattt ggtcggctcc 600

cactatttaa gctttcataa tgaaacaaac ggcaaaacat attgggataa tcaccgcttt 660

gatgatcttt caaaccgtat tttggttggc tatgcctata aaaagcaaga tagcattttc 720

cggtttcaac ctttctatga taaacgttgg tatggtaata gctcttttca ttggtcgaac 780

ggcatacagc ttagttatga ttttagactg tctaatcaat ggcaaaatca aacgttattt 840

gcatttgaga agcggtcatt ttttgatgaa aatttgcaag ccgggaatat taaaacagta 900

tcaaatacac ttatttggca acccaaaccg cagcaactct tttatttagg tggagcaatt 960

tccaaagaaa acacgagaga gaaacaatat ggttcaacta gccgaaatat tcgcttggga 1020

tggttacaag aataccaatg ggggatttct actcaattca gtttttcttt tacccatcga 1080

aaatttcacg atgaagcggt atttgcaagc attattcctc ttaataaaat tagacgcgat 1140

catatttata atattaatgc caaaatttgg aaacgagatt ggcatttatg gggaattaca 1200

ccaaaactga gttttgtttg gaaaaagcaa cgaagcaatt tgaaaacttt gtattcctac 1260

tatgatcagc aactgaattt attatttgag aaaagttttt aa 1302

<210> 284

<211> 433

<212> PRT

<213> M. granulomatis SLAM 2

<400> 284

Met Arg Phe Ser Phe Leu Phe Leu Thr Leu Cys Ile Thr His Thr Val

1 5 10 15

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

20 25 30

Tyr Leu Gln Arg Leu Asp Asp Ile Gln Lys Leu Leu Gln Glu Tyr Gln

35 40 45

Glu Gln Thr Asp Ser Asp Pro Lys Leu Ile Ala Tyr Ala Gln Ala Lys

50 55 60

Ser Ala Phe Ile Gln Gln Asp Tyr Ser Thr Ala Ile Ala Ile Tyr Arg

65 70 75 80

Lys Ile Ile Ser Ser His Pro Glu Leu Asn Ser Ile Arg Ile Glu Leu

85 90 95

Ala Ile Ala Leu Phe Ala Asp Arg Gln Asp Asn Ala Ser Lys Ser Gln

100 105 110

Phe Glu Lys Val Lys Ala Ala Ser Gly Leu Pro Asp Ser Ala Tyr Gln

115 120 125

Ile Ile Gln Ala Tyr Leu Asp Thr Ile Asn Gln Arg Asn Glu Trp Gln

130 135 140

Phe Ser Leu Asn Leu Ser Tyr Ser Arg Thr Asp Asn Val Asp Asn Val

145 150 155 160

Ser Ser Asp Ser Thr Ile Glu Asn Thr Gly Phe Thr Lys His Lys Asn

165 170 175

Met Leu Pro Lys Lys Ala His Gly Ile Ala Tyr Asn Ile Asp Phe Gly

180 185 190

Lys Asp Phe Asn Leu Val Gly Ser His Tyr Leu Ser Phe His Asn Glu

195 200 205

Thr Asn Gly Lys Thr Tyr Trp Asp Asn His Arg Phe Asp Asp Leu Ser

210 215 220

Asn Arg Ile Leu Val Gly Tyr Ala Tyr Lys Lys Gln Asp Ser Ile Phe

225 230 235 240

Arg Phe Gln Pro Phe Tyr Asp Lys Arg Trp Tyr Gly Asn Ser Ser Phe

245 250 255

His Trp Ser Asn Gly Ile Gln Leu Ser Tyr Asp Phe Arg Leu Ser Asn

260 265 270

Gln Trp Gln Asn Gln Thr Leu Phe Ala Phe Glu Lys Arg Ser Phe Phe

275 280 285

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

290 295 300

Ile Trp Gln Pro Lys Pro Gln Gln Leu Phe Tyr Leu Gly Gly Ala Ile

305 310 315 320

Ser Lys Glu Asn Thr Arg Glu Lys Gln Tyr Gly Ser Thr Ser Arg Asn

325 330 335

Ile Arg Leu Gly Trp Leu Gln Glu Tyr Gln Trp Gly Ile Ser Thr Gln

340 345 350

Phe Ser Phe Ser Phe Thr His Arg Lys Phe His Asp Glu Ala Val Phe

355 360 365

Ala Ser Ile Ile Pro Leu Asn Lys Ile Arg Arg Asp His Ile Tyr Asn

370 375 380

Ile Asn Ala Lys Ile Trp Lys Arg Asp Trp His Leu Trp Gly Ile Thr

385 390 395 400

Pro Lys Leu Ser Phe Val Trp Lys Lys Gln Arg Ser Asn Leu Lys Thr

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Leu Tyr Ser Tyr Tyr Asp Gln Gln Leu Asn Leu Leu Phe Glu Lys Ser

420 425 430

Phe

<210> 285

<211> 1407

<212> DNA

<213> M. granulomatis SLAM 3

<400> 285

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caaaaagttg caaaaaacag cttaaaatca accgcttact tgtctgagaa taagacgact 180

gaaagtatag aacaacaaat taaccaagcg attttaacgc aagattggat aaggttagaa 240

aaattactga cagattattc aacgcaaaaa caatttgatc cattactgct ggattatgca 300

tcggctgccc tagcctatgc aaaaaaggat catcgttctg ctatttttta ctatcggcag 360

ctgctgaaaa aacagccgga gttaatctat ccccgttttg atttagcttt aattttaaaa 420

gaagattacc gctatagaga ggcagagaag gaatttgaac agcttaaaac gactgctcca 480

cataatttac aaaccacagt gaattcgttg ctaacccaaa ttcatgaaga agagagctgg 540

cagccggatt tctacttgca atatatccaa accaataatg tgaataatgc agcctcatcc 600

cctattgtga atgtaaacgg gcgaattttc cgtaaaagtg aggatagtct acctcaatcg 660

gcaaaagggа taaaatatgg tgttgggtta agcaaagtgc gaaatgtagg tggcaaccac 720

tttttaggaa cagagcttgc ttataatggt gtctattatt ggaataatca ggattatagt 780

gagcagtcgg tttctataaa gccaagctat agttacagaa cggcacatta tcgtattggg 840

ttttcaccgt ttatagaaca gaattggctg ggaagctcac gttataacta ccagtttggc 900

ggaagaataa atgcgcttaa acgttttgaa caaagcttag tttcagtctc attcagccat 960

ttgcaaaaac gctattttgc ccctaaaacg gcagagcgcc ataatagtta ccagaaccaa 1020

gtaattgttg gaacccaatg gcaagcggtt aaaaattggc gatttttgc aaatctgatt 1080

gccagtcgtg aaattgcacg agaaaaagca caatcttcaa ataagtggtt ggcaaatgta 1140

ggcgtgattt accaaactcc aagttgggca acctcagcca gtttaggcta tggaaaacgt 1200

tattttgcgg ataaacatta tttattcggc tataaacggc aagataagga atatcaagcc 1260

aatattgcgg tgtggaataa aaattggcat tggcaaggca ttgtgccgaa actgaatttt 1320

cgctaccaaa gaatagacag caacattgct gatttttact ctcgtagcaa taaagaactc 1380

ttttttacag tcgaaaaatt attttag 1407

<210> 286

<211> 468

<212> PRT

<213> M. granulomatis SLAM 3

<400> 286

Met Asn Lys Lys Leu Phe Leu Leu Leu Leu Phe Ser Pro Trp Val Asn

1 5 10 15

Ala Glu Thr Ile Val Glu Phe His Gln Asp Pro Lys Glu Phe Asn Tyr

20 25 30

Asp Arg Gln Ala Val Lys Phe Glu Gln Lys Val Ala Lys Asn Ser Leu

35 40 45

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

50 55 60

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

115 120 125

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

180 185 190

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

245 250 255

Gln Asp Tyr Ser Glu Gln Ser Val Ser Ile Lys Pro Ser Tyr Ser Tyr
260 265 270
Arg Thr Ala His Tyr Arg Ile Gly Phe Ser Pro Phe Ile Glu Gln Asn
275 280 285
Trp Leu Gly Ser Ser Arg Tyr Asn Tyr Gln Phe Gly Gly Arg Ile Asn

290 295 300

Ala Leu Lys Arg Phe Glu Gln Ser Leu Val Ser Val Ser Phe Ser His

305 310 315 320

Leu Gln Lys Arg Tyr Phe Ala Pro Lys Thr Ala Glu Arg His Asn Ser

325 330 335

Tyr Gln Asn Gln Val Ile Val Gly Thr Gln Trp Gln Ala Val Lys Asn

340 345 350

Trp Arg Phe Phe Ala Asn Leu Ile Ala Ser Arg Glu Ile Ala Arg Glu

355 360 365

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

370 375 380

Gln Thr Pro Ser Trp Ala Thr Ser Ala Ser Leu Gly Tyr Gly Lys Arg

385 390 395 400

Tyr Phe Ala Asp Lys His Tyr Leu Phe Gly Tyr Lys Arg Gln Asp Lys

405 410 415

Glu Tyr Gln Ala Asn Ile Ala Val Trp Asn Lys Asn Trp His Trp Gln

420 425 430

Gly Ile Val Pro Lys Leu Asn Phe Arg Tyr Gln Arg Ile Asp Ser Asn

435 440 445

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

450 455 460

Glu Lys Leu Phe

465

<210> 287

<211> 1395

<212> DNA

<213> M. haemolytica SLAM 1

<400> 287

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gaaattgcaa aaaaggattt aaaattaacc gcttacttgg aggaagataa ttctcttaaa 180

ggtattgaac agcacattaa ccaagcgatt cttagacaag attgggcgaa gctggaaagg 240

ctgcttggcg attatgcaaa gcaagagcaa tttgatccgc tacttttaga ctatgctttg 300

gcggcattgg cttatgctaa aaaagattat cgctctgcgg cgttttatta tcagcagttg 360

ctgaaaaaac agcctgattt aacctaccct cgttttgatt tggctctgat tttaaaagag 420

gattatcgct acagggaagc agagcaagaa tttaagcaac tcaaaaccga tgatttacgc 480

aatgcggtga acagtgcgtt ggctcaaata gaggaggaag agagctggaa gccggatttt 540

tatttgcaat atactcaaac caacaatgtg aataatgctt cttcgtcgcc aacggtaaat 600

gtaaacgggc ggatttttat taaagaatca gacagcttgc cgcagtcggc aaaaggcgta 660

agatatggcg ttggcttgag taaaatgcga aatatcggcg gtaatcattt tgtgggagtc 720

gatcttggct ataacggcgt ttattactgg aataaccacg attatagcga acagtcggtc 780

tcactaacac caaaatatag ctacagaacg gcaacttatc gtatcggggt ttcgcccttt 840

attgagcaga attggctggg tagctcacgg tataactatc aatttggtag cagtatcaat 900

gctgttaaac tttttgaacg agggctgatt tccggctcat tcagccatct gcaaaaacgt 960

tatagtgaac agcatattgc cgaccgttac aatggttatc gcaaccaact cacgctaggt 1020

acgcaatggc aagcggtcaa aaattggcga ttttttgcaa atcttaacgc tagccgtgaa 1080

attacccgtg agaaagctca atcttccaat aagtggctgg cgaccattgg cgtaatttac 1140

caaaccccaa gctgggcaag ttcggtaagt gtcggatatg gcaagcgtta ttttgctgat 1200

aaacattatc tgtttggcta taaacgccaa gataaggaat atcaagcgaa tgtggcggtg 1260

tggaatcgaa gttggcactg gcaagggatt gtgccgaaat tgaatttccg ttatcaaaaa 1320

atcgatagca atattgccga tttctactct cgtagcaata aagaagtctt tatgacctta 1380

gagaaactat tttaa 1395

<210> 288

<211> 464

<212> PRT

<213> M. haemolytica SLAM 1

<400> 288

Met Tyr Lys Lys His Phe Leu Phe Leu Leu Val Ser Pro Leu Val Met

1 5 10 15

Ala Glu Thr Val Glu Phe Gln Gln Asp Pro Lys Glu Phe Asp Gly Gln

20 25 30

Arg Gln Ala Val Lys Phe Glu Gln Glu Ile Ala Lys Lys Asp Leu Lys

35 40 45

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

50 55 60

His Ile Asn Gln Ala Ile Leu Arg Gln Asp Trp Ala Lys Leu Glu Arg

65 70 75 80

Leu Leu Gly Asp Tyr Ala Lys Gln Glu Gln Phe Asp Pro Leu Leu Leu

85 90 95

Asp Tyr Ala Leu Ala Ala Leu Ala Tyr Ala Lys Lys Asp Tyr Arg Ser

100 105 110

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

115 120 125

Tyr Pro Arg Phe Asp Leu Ala Leu Ile Leu Lys Glu Asp Tyr Arg Tyr

130 135 140

Arg Glu Ala Glu Gln Glu Phe Lys Gln Leu Lys Thr Asp Asp Leu Arg

145 150 155 160

Asn Ala Val Asn Ser Ala Leu Ala Gln Ile Glu Glu Glu Glu Ser Trp

165 170 175

Lys Pro Asp Phe Tyr Leu Gln Tyr Thr Gln Thr Asn Asn Val Asn Asn

180 185 190

Ala Ser Ser Ser Pro Thr Val Asn Val Asn Gly Arg Ile Phe Ile Lys

195 200 205

Glu Ser Asp Ser Leu Pro Gln Ser Ala Lys Gly Val Arg Tyr Gly Val

210 215 220

Gly Leu Ser Lys Met Arg Asn Ile Gly Gly Asn His Phe Val Gly Val

225 230 235 240

Asp Leu Gly Tyr Asn Gly Val Tyr Tyr Trp Asn Asn His Asp Tyr Ser

245 250 255

Glu Gln Ser Val Ser Leu Thr Pro Lys Tyr Ser Tyr Arg Thr Ala Thr

260 265 270

Tyr Arg Ile Gly Val Ser Pro Phe Ile Glu Gln Asn Trp Leu Gly Ser

275 280 285

Ser Arg Tyr Asn Tyr Gln Phe Gly Ser Ser Ile Asn Ala Val Lys Leu

290 295 300

Phe Glu Arg Gly Leu Ile Ser Gly Ser Phe Ser His Leu Gln Lys Arg

305 310 315 320

Tyr Ser Glu Gln His Ile Ala Asp Arg Tyr Asn Gly Tyr Arg Asn Gln

325 330 335

Leu Thr Leu Gly Thr Gln Trp Gln Ala Val Lys Asn Trp Arg Phe Phe

340 345 350

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

355 360 365

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

370 375 380

Trp Ala Ser Ser Val Ser Val Gly Tyr Gly Lys Arg Tyr Phe Ala Asp

385 390 395 400

Lys His Tyr Leu Phe Gly Tyr Lys Arg Gln Asp Lys Glu Tyr Gln Ala

405 410 415

Asn Val Ala Val Trp Asn Arg Ser Trp His Trp Gln Gly Ile Val Pro

420 425 430

Lys Leu Asn Phe Arg Tyr Gln Lys Ile Asp Ser Asn Ile Ala Asp Phe

435 440 445

Tyr Ser Arg Ser Asn Lys Glu Val Phe Met Thr Leu Glu Lys Leu Phe

450 455 460

<210> 289

<211> 1410

<212> DNA

<213> M. haemolytica SLAM 2

<400> 289

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attgaacaca acactgaccc gatttccttt gagcgtcagc cgcaagcggt taaatttgag 120

caaaatgttg taaaaaattc acaaaaaccg accgcttatc agcctgcgta ttcagtcaat 180

cagaatgttg aacagcaaat taaccaagcg attctcagcc aagattgggc aacgcttgaa 240

ccgcttttaa gccgttatcc gcaaactgaa aattttgacc cgttgttgtg gcactatgcg 300

caagccgcac ttgcctatgc gaaaaaagat catcaaaccg cagtttttca ctatcgccaa 360

ctgttagcta agcccccgag tttggtttac cctcgttttg atttggcgtt gattttggca 420

gaagatcagc aatttcgtgc ggcagagcag gaatttaagg ctattcaagc ccatttaccg 480

ccggaacttg ctaaaattgc ccgcaatact caagtccaaa ttgctgaaaa tgaggcgtgg 540

cagcccgatt tttatctgca atatacccaa acagataacg tgaataatgc ctcatcttcg 600

ccgattgtga atgtaaatgg gcggattttc cgcaaaaatg cagacagttt gccacaatca 660

gcaaaaggcg tgcgttatgg cttagggttg agtaaattgc acaacgtgaa aggcaatcat 720

tttgtcggtt taacgctcaa ttatagcggg atttactatt gggataaccg agattaccgt 780

gagcaatccg tatccgtttc gccgaattat agctaccgca ccgtcgctta tcggctgact 840

ttttcgcctt ttattgagca aaattggctg gggagtagcc gttataatgt tcaatttggg 900

gcaacactca acggtttgcg ttaccttaat tcgcaatggt tggtgtcggg gagttttacc 960

catttgcaaa aacggtattt tgaggagcta accgcaagcc gttataacag ctatcagcac 1020

caactcagtg gcggtgtgca gtggcaagcg gtcaaaaatg ggcggttttt tgcaaattta 1080

gacggcgtgc gtgaaattgc acgggaaaaa gcacaaagct cgaataagtg gctggctcga 1140

gtgggggcgg tttttcaagg cgaacgctgg gcaacgcagg caagtatcgg ctttggcaag 1200

cgatattttg ccgacaagca ctatttgttt ggctataagc ggttagacac ggaatatcaa 1260

gccaatttag cggtttggaa ccgcacttgg cattggcagg gcattgtgcc gaagctgaat 1320

ttccgttatc aaaaaattga cagcaatatt gctgattttt actctcgcca aaacaaggaa 1380

gtctttttca ctttagaaaa gctattttag 1410

<210> 290

<211> 469

<212> PRT

<213> M. haemolytica SLAM 2

<400> 290

Met Lys Lys Tyr Pro Leu Leu Phe Ser Leu Phe Ser Pro Val Val Trp
1 5 10 15

Ala Glu Lys Val Ile Glu His Asn Thr Asp Pro Ile Ser Phe Glu Arg
20 25 30

Gln Pro Gln Ala Val Lys Phe Glu Gln Asn Val Val Lys Asn Ser Gln
35 40 45

Lys Pro Thr Ala Tyr Gln Pro Ala Tyr Ser Val Asn Gln Asn Val Glu

50 55 60

Gln Gln Ile Asn Gln Ala Ile Leu Ser Gln Asp Trp Ala Thr Leu Glu

65 70 75 80

Pro Leu Leu Ser Arg Tyr Pro Gln Thr Glu Asn Phe Asp Pro Leu Leu

85 90 95

Trp His Tyr Ala Gln Ala Ala Leu Ala Tyr Ala Lys Lys Asp His Gln

100 105 110

Thr Ala Val Phe His Tyr Arg Gln Leu Leu Ala Lys Pro Pro Ser Leu

115 120 125

Val Tyr Pro Arg Phe Asp Leu Ala Leu Ile Leu Ala Glu Asp Gln Gln

130 135 140

Phe Arg Ala Ala Glu Gln Glu Phe Lys Ala Ile Gln Ala His Leu Pro

145 150 155 160

Pro Glu Leu Ala Lys Ile Ala Arg Asn Thr Gln Val Gln Ile Ala Glu

165 170 175

Asn Glu Ala Trp Gln Pro Asp Phe Tyr Leu Gln Tyr Thr Gln Thr Asp

180 185 190

Asn Val Asn Asn Ala Ser Ser Ser Pro Ile Val Asn Val Asn Gly Arg

195 200 205

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

210 215 220

Arg Tyr Gly Leu Gly Leu Ser Lys Leu His Asn Val Lys Gly Asn His

225 230 235 240

Phe Val Gly Leu Thr Leu Asn Tyr Ser Gly Ile Tyr Tyr Trp Asp Asn

245 250 255

Arg Asp Tyr Arg Glu Gln Ser Val Ser Val Ser Pro Asn Tyr Ser Tyr

260 265 270

Arg Thr Val Ala Tyr Arg Leu Thr Phe Ser Pro Phe Ile Glu Gln Asn

275 280 285

Trp Leu Gly Ser Ser Arg Tyr Asn Val Gln Phe Gly Ala Thr Leu Asn

290 295 300

Gly Leu Arg Tyr Leu Asn Ser Gln Trp Leu Val Ser Gly Ser Phe Thr

305 310 315 320

His Leu Gln Lys Arg Tyr Phe Glu Glu Leu Thr Ala Ser Arg Tyr Asn

325 330 335

Ser Tyr Gln His Gln Leu Ser Gly Gly Val Gln Trp Gln Ala Val Lys

340 345 350

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

355 360 365

Glu Lys Ala Gln Ser Ser Asn Lys Trp Leu Ala Arg Val Gly Ala Val

370 375 380

Phe Gln Gly Glu Arg Trp Ala Thr Gln Ala Ser Ile Gly Phe Gly Lys

385 390 395 400

Arg Tyr Phe Ala Asp Lys His Tyr Leu Phe Gly Tyr Lys Arg Leu Asp

405 410 415

Thr Glu Tyr Gln Ala Asn Leu Ala Val Trp Asn Arg Thr Trp His Trp

420 425 430

Gln Gly Ile Val Pro Lys Leu Asn Phe Arg Tyr Gln Lys Ile Asp Ser

435 440 445

Asn Ile Ala Asp Phe Tyr Ser Arg Gln Asn Lys Glu Val Phe Phe Thr

450 455 460

Leu Glu Lys Leu Phe

465

<210> 291

<211> 1413

<212> DNA

<213> M. haemolytica SLAM 3

<400> 291

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actacacagg cttatattga gcatactgca cagccaacta caacccccca aagggtcaag 120

atcgaaaaat cagtgcctat ttttaacgaa actgaattac gtgctaatca attattgacc 180

gaaaagctac ttatccaagc tatttatagt cgtaggcttg ctaacatgga aaaattaact 240

gcgatttatc gggattttac ccacattgac ccggttttac tgcgttatgc acaaggtaaa 300

attgccctac tgaaaggcga ttacgcacag gcaattcagc acttccaaac cattcttgcc 360

aaacaaccca aactaaacac tgtaagaatt gagctggcga ttgctctatt gtacgatcag 420

caacttaatc aagcccaagc acaatttgaa aaagccaaaa gtgccgaaca tctaccgcct 480

aaagttcacg cattaattga gcaatatcag caacatctgg caaaaaaaca ggaatggaaa 540

tttagttttt cagccaatta tgtgcgagac ggcaacatta accgaacctc gaaacagccg 600

aacattgagc aaaccggcta tgtaaaacaa cctaatttgt tgccccaaac cgcacatggt 660

gttcactatg cgtttggatt acagagagat ttcaacctgt tcgactcaca ctatgtgagt 720

tttgacaacc aaacccaagg tgaactttat tgggataacc acgattatga tgaaattacc 780

aatcgcacct tgtttggata cgcttacaaa aaatccgacc aaaccacccg cttgttaccg 840

ttttatgaaa aacgctggaa acatcaccgt tcggaacgct ggacaaacgg aattcgactt 900

gaacacgcac aatggttttc accgcattgg caactcgcca ccgcattgga atacggcaaa 960

aaacgttatt ttgatttgcc gatttataac ggcagctaca aacttgcctc tgccacattg 1020

ctttggttac gcaatccaca acaatttttc tttgtcggca ctgatttcaa tcaagacaaa 1080

actcagttaa aacaatatag ctctgatact aaaggcatac gctttggctg gcaacgagaa 1140

tggcaagccc tcgagctttc cagtcgcctc acgcttggct atactgacag acgttacaaa 1200

gacaccgcta tattgggagg aaaacttaat cttggcagaa tccgccatga ccgtgtgcaa 1260

agtgctaacc tcacgctttg gaaacgagat tggcactggc tcggcctgat gccgaagctg 1320

caatttagtt acgccaaaca ccgtagcaac ctgccgagcc tctatgccta caccgataaa 1380

aacatcaatt taattattga aagtcggttc tag 1413

<210> 292

<211> 470

<212> PRT

<213> M. haemolytica SLAM 3

<400> 292

Met Lys Lys Ile Ala Leu Leu Ala Leu Phe Pro Met Met Leu Phe Ala

1 5 10 15

Arg Asp Pro Asn Thr Thr Gln Ala Tyr Ile Glu His Thr Ala Gln Pro

20 25 30

Thr Thr Thr Pro Gln Arg Val Lys Ile Glu Lys Ser Val Pro Ile Phe

35 40 45

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

50 55 60

Ile Gln Ala Ile Tyr Ser Arg Arg Leu Ala Asn Met Glu Lys Leu Thr
65 70 75 80

Ala Ile Tyr Arg Asp Phe Thr His Ile Asp Pro Val Leu Leu Arg Tyr
85 90 95

Ala Gln Gly Lys Ile Ala Leu Leu Lys Gly Asp Tyr Ala Gln Ala Ile
100 105 110

Gln His Phe Gln Thr Ile Leu Ala Lys Gln Pro Lys Leu Asn Thr Val

115 120 125

Arg Ile Glu Leu Ala Ile Ala Leu Leu Tyr Asp Gln Gln Leu Asn Gln
130 135 140

Ala Gln Ala Gln Phe Glu Lys Ala Lys Ser Ala Glu His Leu Pro Pro
145 150 155 160

Lys Val His Ala Leu Ile Glu Gln Tyr Gln Gln His Leu Ala Lys Lys
165 170 175

Gln Glu Trp Lys Phe Ser Phe Ser Ala Asn Tyr Val Arg Asp Gly Asn

180 185 190

Ile Asn Arg Thr Ser Lys Gln Pro Asn Ile Glu Gln Thr Gly Tyr Val
195 200 205

Lys Gln Pro Asn Leu Leu Pro Gln Thr Ala His Gly Val His Tyr Ala
210 215 220

Phe Gly Leu Gln Arg Asp Phe Asn Leu Phe Asp Ser His Tyr Val Ser
225 230 235 240

Phe Asp Asn Gln Thr Gln Gly Glu Leu Tyr Trp Asp Asn His Asp Tyr

245 250 255

Asp Glu Ile Thr Asn Arg Thr Leu Phe Gly Tyr Ala Tyr Lys Lys Ser
260 265 270

Asp Gln Thr Thr Arg Leu Leu Pro Phe Tyr Glu Lys Arg Trp Lys His
275 280 285

His Arg Ser Glu Arg Trp Thr Asn Gly Ile Arg Leu Glu His Ala Gln

290 295 300

Trp Phe Ser Pro His Trp Gln Leu Ala Thr Ala Leu Glu Tyr Gly Lys

305 310 315 320

Lys Arg Tyr Phe Asp Leu Pro Ile Tyr Asn Gly Ser Tyr Lys Leu Ala

325 330 335

Ser Ala Thr Leu Leu Trp Leu Arg Asn Pro Gln Gln Phe Phe Phe Val

340 345 350

Gly Thr Asp Phe Asn Gln Asp Lys Thr Gln Leu Lys Gln Tyr Ser Ser

355 360 365

Asp Thr Lys Gly Ile Arg Phe Gly Trp Gln Arg Glu Trp Gln Ala Leu

370 375 380

Glu Leu Ser Ser Arg Leu Thr Leu Gly Tyr Thr Asp Arg Arg Tyr Lys

385 390 395 400

Asp Thr Ala Ile Leu Gly Gly Lys Leu Asn Leu Gly Arg Ile Arg His

405 410 415

Asp Arg Val Gln Ser Ala Asn Leu Thr Leu Trp Lys Arg Asp Trp His

420 425 430

Trp Leu Gly Leu Met Pro Lys Leu Gln Phe Ser Tyr Ala Lys His Arg

435 440 445

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

450 455 460

Ile Ile Glu Ser Arg Phe

465 470

<210> 293

<211> 1455

<212> DNA

<213> M. haemolytica SLAM 4

<400> 293

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acaccggctc aacttcaaga aaaaatggat aaccagcgaa tgcagaaaaa cctacataca 120

ttagaaaagc ctgaacctca agccaaacca caagcggtta atgcacaggc tcaccggcaa 180

tcgatctcta tttcaagcca acagctgctt caacagcctg agttgctcaa ctcggcaatg 240

ctaactgcgt tggtcactaa ccacactgag aatgttcaat tcttactgcc tatttatcaa 300

caattacccg ccagtaaaca aaacagcgaa gttgtacaat gggcggaggc agttaatgcc 360

aaagcaaaac aaaattattc agaggcaata aaaggctacc gtcagctact ggcaaaatac 420

cctgaaaatc agccaatccg tatgcaatta gcggttgcat tgtttgaaaa tcgggaaaat 480

gaagccgcag aggctcaatt ttataagtta caagcggaca aattaccgca agaaattgca 540

aatgcggtca atagctattt ggaggcgatt ggcaagcaag atcaatggag ttttcaaggc 600

ggcttaacct atttgaatga cccgaatatc aacaatgctc caaatgcagg cacgacctat 660

ggcaactgga ctgcaccgaa aaaagaatcc gcccaagggg tcggctttca ctttgaggcg 720

gataaaaagt ggtcttgggg caatggtttc ttccacgagt ttcgtttaaa cggaaacggc 780

aaatattact ggaataacaa aaaatataac gaatattcgc tcagagaaag cctcggcttg 840

ggttatcaaa atgcaaaaca aaaaatcacc ttgttgccgt tttttgagca gatgtggtat 900

gccggtggct caagccaaac cgaaagcacc aaacgctact ccaacgcagg cggtgtgaat 960

gcccgctggc aatattggat tactccacag tggcaatctg caatcagcta cgaatatgcg 1020

gaacagcgtt acactcgccg ccaacattta gacggcaatt atcattttat tgccccgagc 1080

ctctattttt accctaacag ccggcaatat tggtttgtgg gggcgaattt taaccgcacc 1140

agcccccgtg atttagatga tagctttatt cgccgaggtg tttctattgg ttggggacaa 1200

gagtggaaaa acgggctttc aacccaatta agtgccagct acgcccgcaa acaataccga 1260

gccccaatgc cgattttcca aattacacaa cgtaacagtg aatatggtgt gcaagccagc 1320

atctggcaca gagccttgca ttttaagggt attacccctc gcttaacgtg gcaatataac 1380

aaggtaaaaa gcaatcatag cttctatagt tatgacaaaa accgtgtcta tattgagttt 1440

tcacatacgt tctaa 1455

<210> 294

<211> 484

<212> PRT

<213> M. haemolytica SLAM 4

<400> 294

Met Lys Lys Ile Val Ser Thr Leu Leu Ile Leu Thr Ser Asn Leu Ala

1 5 10 15

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

20 25 30

Arg Met Gln Lys Asn Leu His Thr Leu Glu Lys Pro Glu Pro Gln Ala

35 40 45

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

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

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

Asp Lys Lys Trp Ser Trp Gly Asn Gly Phe Phe His Glu Phe Arg Leu
245 250 255
Asn Gly Asn Gly Lys Tyr Tyr Trp Asn Asn Lys Lys Tyr Asn Glu Tyr
260 265 270
Ser Leu Arg Glu Ser Leu Gly Leu Gly Tyr Gln Asn Ala Lys Gln Lys
275 280 285

Ile Thr Leu Leu Pro Phe Phe Glu Gln Met Trp Tyr Ala Gly Gly Ser
290 295 300

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

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

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

<210> 295
<211> 1323
<212> DNA
<213> M. jannaschii SLAM 1
<400> 295

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caggggggata tggcggccgc ctatgattta gcgcagcaac ttcagcctga atatgagggc 180

gatcctgcgt ttgatctgca atatggcatt gcggctatcg ataacggcga tattggccag 240

gggatgtttg cgctggagcg ggtgctggta ttacggccgg atatgcatct ggcgcggctg 300

gagttggcgc ggggctattt cctgcagggc aatgatctgc gggcaaaaga gcagtttaac 360

gcggtgctgg agaataaccc accacctaag gtggtcgacc agattcaggc cttcctgaac 420

ctgatcgcca gccgggctga gaagagtcgc tggagcgccg gcggctcgct gcaactggcc 480

tggggctatg acgacaatat caatgccgcg ccggaatcac agaccacggt ggtgacacta 540

agcgatacgg cactggggcg tggcgaccag ttcactacga tgaagctgaa cggccatgct 600

gaatatcagg caaccaaggc tcagagctgg tttggtaatg ccaccctgga atcgcgctgg 660

tacgccgatg aagatccgca ggacttccgc aacctgcgcg gcttggttgg cagtcgctgg 720

ctggacggtc gcaatcgcta ccagttggcg ctgaacgcgc agaattatca gctggataat 780

aacgattacc gggacagcta cggggttggt ggccagtgga cctatgccct gagtaaaacc 840

gctatcgtga cgacgtcgct ggattacagc cagcttgatt atgatacggc ggactggaag 900

gacagtgatc tggtcagcct cggagtgaat ggcgttatcg tcggtaacgg ccactggacg 960

ccggtgtatt ttgccggagg ctttgccggc cgagaaaaac cggatagccc gggcgtgctg 1020

gcagatgccg gtgtcgaccg actgttcttc ggcggccaca tcggggccag gatagagcct 1080

tatgatggcc tgcagctgac cactaccctg gtggcccagc gcagtaacta ccgcggcacc 1140

gactttatct acaatatccg ccgcgatgac aactacctgg cactggcgct ggatgccagc 1200

tggaagctgc cgcacgactg gcgttttatc agcggtatca gctacagccg caatgactcc 1260

aatatcgaac tccatgatta cgaccgcacc caggttcgcc tcggtgtgca gtatcagttc 1320

tga 1323

<210> 296

<211> 419

<212> PRT

<213> M. jannaschii SLAM 1

<400> 296

Met Val Ser Thr Ala Gln Ala Asp Thr Gln Ile Glu Gln Leu Thr Ser

1 5 10 15

Leu Val Asn Gln Gly Asp Met Ala Ala Ala Tyr Asp Leu Ala Gln Gln

20 25 30

Leu Gln Pro Glu Tyr Glu Gly Asp Pro Ala Phe Asp Leu Gln Tyr Gly

35 40 45

Ile Ala Ala Ile Asp Asn Gly Asp Ile Gly Gln Gly Met Phe Ala Leu

50 55 60

Glu Arg Val Leu Val Leu Arg Pro Asp Met His Leu Ala Arg Leu Glu

65 70 75 80

Leu Ala Arg Gly Tyr Phe Leu Gln Gly Asn Asp Leu Arg Ala Lys Glu

85 90 95

Gln Phe Asn Ala Val Leu Glu Asn Asn Pro Pro Pro Lys Val Val Asp

100 105 110

Gln Ile Gln Ala Phe Leu Asn Leu Ile Ala Ser Arg Ala Glu Lys Ser

115 120 125

Arg Trp Ser Ala Gly Gly Ser Leu Gln Leu Ala Trp Gly Tyr Asp Asp

130 135 140

Asn Ile Asn Ala Ala Pro Glu Ser Gln Thr Thr Val Val Thr Leu Ser

145 150 155 160

Asp Thr Ala Leu Gly Arg Gly Asp Gln Phe Thr Thr Met Lys Leu Asn

165 170 175

Gly His Ala Glu Tyr Gln Ala Thr Lys Ala Gln Ser Trp Phe Gly Asn

180 185 190

Ala Thr Leu Glu Ser Arg Trp Tyr Ala Asp Glu Asp Pro Gln Asp Phe

195 200 205

Arg Asn Leu Arg Gly Leu Val Gly Ser Arg Trp Leu Asp Gly Arg Asn

210 215 220

Arg Tyr Gln Leu Ala Leu Asn Ala Gln Asn Tyr Gln Leu Asp Asn Asn

225 230 235 240

Asp Tyr Arg Asp Ser Tyr Gly Val Gly Gly Gln Trp Thr Tyr Ala Leu

245 250 255

Ser Lys Thr Ala Ile Val Thr Thr Ser Leu Asp Tyr Ser Gln Leu Asp

260 265 270

Tyr Asp Thr Ala Asp Trp Lys Asp Ser Asp Leu Val Ser Leu Gly Val

275 280 285

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

290 295 300

Gly Gly Phe Ala Gly Arg Glu Lys Pro Asp Ser Pro Gly Val Leu Ala

305 310 315 320

Asp Ala Gly Val Asp Arg Leu Phe Phe Gly Gly His Ile Gly Ala Arg

325 330 335

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

340 345 350

Arg Ser Asn Tyr Arg Gly Thr Asp Phe Ile Tyr Asn Ile Arg Arg Asp

355 360 365

Asp Asn Tyr Leu Ala Leu Ala Leu Asp Ala Ser Trp Lys Leu Pro His

370 375 380

Asp Trp Arg Phe Ile Ser Gly Ile Ser Tyr Ser Arg Asn Asp Ser Asn

385 390 395 400

Ile Glu Leu His Asp Tyr Asp Arg Thr Gln Val Arg Leu Gly Val Gln

405 410 415

Tyr Gln Phe

<210> 297

<211> 1386

<212> DNA

<213> M. lonarensis SLAM 1

<400> 297

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gagtatctgc gagggcagcg gcccaccctg accattgacg gtacgaccca taccatcgaa 120

cacaacgtca atgatgttgg acgggcgttg tatttgtcta ttcaacagcg gcaatggcca 180

gcggtgctgt attttctgga tgaatatctg acattccctg atgcagatcc gatgctgatt 240

gcctatgcac aaggttcgct ggccagatta cgaggcgaga tgaagctggc ggaaagcgag 300

ttcagaaaac tgcttgatat tcagcctgat tttctgctcg gacagctgga gttggcgcgg 360

gtgttatttg aaaaccgtaa agatgccgat tccgaagcca tgtttcagca gattgccgtg 420

actctggatc ccgctgatgc tcgtcatcag ggcgtgttga caacggtaga cagtttttg 480

caggcggttg acagacgcca atcctggcag ggctctgttg cgatgggtgc ggtctggtca 540

gataacctga atcagacatc cgagagttat acctgtctgc tctattacgg ttcagtgtgt 600

ctgtttgaac gccagacgcc agatgctatc aaagcgcatg ggcttgatta tgagatgacc 660

ttgaacaggc gctttgcatt gtcggggcat catggtgtgt tttttcgcgg gctgttgttt 720

gggcaaagtt ataaagagca ttctatttat aacgaaagcc aaatcagtac gcagttcggt 780

tacagctacc acaatatgcg taaccagtat tcgttggctc ccacctttga gttttctcgt 840

tacggcaatg attcgcttta tggtgcctgg ggtctgaatg cagagtggca gcactatttc 900

agcgataaag tgatgttcaa actggagaca agttataagg atcagcagta ccggaaaagc 960

gtacttgccg atcagtatga tggcgatatc tggtctgcgt ttgcgaccgc ctggtatgtc 1020

ttaccgaata actggacagt gtttggtggc ctggactgga cccggaaaaa agcccaaatc 1080

aaacaactcg cctacgaaca gctgggggtc agagcgggtg tggccaaaac ctttaatcag 1140

tacgtcaatg ccgtgttgtt tgcttcgtat cgtgagcgtg aacatgatgc gtttagccca 1200

ttgtttggtg aacaacgcaa ggatcgagaa caaaactata ccttgattgt gcgcttcccc 1260

ggtcttgcca tgtatggcat ggaacccaat ctgactttca agcaccgcaa ggtcgatagc 1320

aacattgact ggctgtatgc ctatgaacgc aacagtgtca gcctgaaact gcaaaaaaac 1380

ttctga 1386

<210> 298

<211> 461

<212> PRT

<213> M. lonarensis SLAM 1

<400> 298

Met Asn Gln Ser Ile Glu Leu Gln Ser Ser Gln Gln Glu Arg Gln Ile
1 5 10 15

Leu Lys Asp Glu Glu Tyr Leu Arg Gly Gln Arg Pro Thr Leu Thr Ile
20 25 30

Asp Gly Thr Thr His Thr Ile Glu His Asn Val Asn Asp Val Gly Arg
35 40 45

Ala Leu Tyr Leu Ser Ile Gln Gln Arg Gln Trp Pro Ala Val Leu Tyr
50 55 60

Phe Leu Asp Glu Tyr Leu Thr Phe Pro Asp Ala Asp Pro Met Leu Ile

65 70 75 80

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

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

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

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

Val Leu Ala Asp Gln Tyr Asp Gly Asp Ile Trp Ser Ala Phe Ala Thr
325 330 335

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

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

<210>
299

<211> 1542

<212> DNA

<213> M. macacae SLAM 1

<400> 299

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attttgcacc cagaagcggg cattgatagt ttgcaaaatg aacccattgc gactactttg 180
ccaattgaca attcaccaca aaccgagcaa attgcaccca ttgcaccaac tgaaataaac 240
gaaacgccaa ccgtggatat tgatttttta attaacaatc ccaatgcatt tgcgcatgtt 300
ttttatcaag cggtaataaa tgatgatgcc gaaacgttgc gtttattagt gccgttttat 360

catcaattgc caagggatta tcaagatgag attttattgt tatttgcgca aagtaaaatt 420
gctttaagcg ataataatca taaattggct ttgcaattat taaccgaatt aagccaaaaa 480

cagcccaatt taactgcggt aaaaatgcaa attgcttcat tgttattaaa aaataagcat 540

gaccaaaagg caactatcat tttaaatgaa ttaaaaacct ctgtgcattt taacaattta 600

acaacaacag aaaaaaaatg gctaataaaa caaagtgcaa ttttaacacg caaatataaa 660

ccgagcattg atattggtat gaacttgtta tatttagata atattaattc agcttctacc 720

accgagcaaa aaaatattag caaagaaaag ccaaaaagca cgcacggttt ggcgttgtct 780

ttggatttgg ataaatatac gccgcttaat catggattga gtttatatac tggtcttgat 840

attgatggca aattttaccg cgataacagt cataatgaag cgtctatttt tgccaatatt 900

ggcttgaaaa aaaataatac gcacggattt ttgtctatta cgccatttat tgggcgcaat 960

tttgccaccg acaacaaaca aaaccttgta ccaagaaaaa acagtattgg ggcggcgttt 1020

aattggcaac ataaatttaa taatgaatta aataaaacgt ggcaaaataa tttatttata 1080

cgtgccgaac atggcaatta tcaaaagtcg tatcaaggtt ataatggcaa ccgttatcat 1140

ttaagcgata ctattgtatt gcaaaataac cctaagcggc gttattcttt ggggataaat 1200

tatcaattga gcgatttaac agatgccgcc aaaagtagcc atactgtggg agtaaattta 1260

ggtattttgc aacaatttaa taatggcttt tttgtgcaag gcaaattaag cgccgagcgt 1320

gagcgttatc atggcaaatt attgcgcctt gttaatccga ataatgttta tcgcaccgat 1380

aaaaccataa cgctgcaaac ggctgtttgg cataaaaata ttaattggca gggtattacg 1440

ccgcggctta gttatcgtta tgtgaataat aaaagtaatt tgccagcgtt atatagttat 1500

aagaagcata gtgtgttttt ggagtttggg cggtcgtttt ag 1542

<210> 300

<211> 513

<212> PRT

<213> M. macacae SLAM 1

<400> 300

Met Asn Gly Phe Phe Ala Ile Lys Thr Ala Thr Gln Leu Thr Thr Lys
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Leu Thr Thr Leu Cys Cys Cys Leu Ala Tyr Phe Met Pro Val Phe Ala
20 25 30

Asp Asp Lys Ala Val Gln Pro Pro Ile Leu His Pro Glu Ala Gly Ile
35 40 45

Asp Ser Leu Gln Asn Glu Pro Ile Ala Thr Thr Leu Pro Ile Asp Asn
50 55 60

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

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

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

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

305 310 315 320

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

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

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

Phe

<210> 301
<211> 1365
<212> DNA
<213> M. mediterranea SLAM 1

<400> 301

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ctgaagcgcg gaccacgcgc ctttttgttc acgtttgccc ttgtggccct cacgattggc 120

gccccgcaat ggggcttcgc aaaaaagtcc accgttaccg gctttgacgc ggtgcgtgtg 180

ctggttgaat atggccagta tgaaaatgcg atggcactgg cgcaaagctt cgcgaccgac 240

gaaaagggca aggcgctcgc tgccgccttc acgcaggccc tcatactgga gcagcagggc 300

cggttgccgg aagcggcaag cgcgcttcgc gccatccttt cgcagaaccc cgaggcccgc 360

aacgtccggc gtgaacttgc cagcgttctc tacgaacagg gcgagggcaa cgcatcgctg 420

catcacttcg aacttctggc cggcagcgcc aatagtgccg atgagcgcgc gttctatgaa 480

cgccttgccg ccaaggcccg cacgattcgt ccctggtcgc ttggtggcta tctctcaatc 540

gcccccagca ccaacattac cgaagccccc gatgccgacc tcgtctatat cggcggcatt 600

cccatactgc ctgccaaaaa gaagagcggc atcggctatg gctatgggtt gaacggatcc 660

taccgttttg accttgatga aatttcatcg atcacggtag gtggcggggt gaacggcaac 720

tggtatcgcg acaccagttt caacacgagc tactttgaca gtttcgtcga ctatcgccgg 780

gaaatggggg actggacggt gactggcggc cttgtaggcc agtatgtgat gaagggcgaa 840

gaaccttatc gctggtcgct cggaccggct ttctcgctgc gtcacaatat gggacgaaag 900

ggcgtcacaa cgctgcgtgg catgtggcga aagctcgatt accacgaccg cgatgaactg 960

gacggcagcg aaaccgtgct ggggatcagc catctctatg ccatctcatc ggcaagctcg 1020

gtgcgtttcg ggggcaatat cggctatgtc gatgcggcga acgacaccaa cagctatctc 1080

cgcctttccc tgaacgcgca gtatttccgg gaatggagtt tcggcgcgat ttccgatatc 1140

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tcagatcagc gtatccaggc ctcgctcggc atcacgctgc gcaatctggc gatcaagggt 1260

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ttttcgaaga acacgctttc gacttatctg acgaagaggt tctga 1365

<210> 302

<211> 454

<212> PRT

<213> M. mediterranea SLAM 1

<400> 302

Met Thr Asn Arg Arg Leu Glu Pro Arg Ala Gly Lys Pro Ala Arg Gly

1 5 10 15

Leu Cys Leu Glu Leu Lys Arg Gly Pro Arg Ala Phe Leu Phe Thr Phe

20 25 30

Ala Leu Val Ala Leu Thr Ile Gly Ala Pro Gln Trp Gly Phe Ala Lys

35 40 45

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

50 55 60

Gly Gln Tyr Glu Asn Ala Met Ala Leu Ala Gln Ser Phe Ala Thr Asp

65 70 75 80

Glu Lys Gly Lys Ala Leu Ala Ala Ala Phe Thr Gln Ala Leu Ile Leu

85 90 95

Glu Gln Gln Gly Arg Leu Pro Glu Ala Ala Ser Ala Leu Arg Ala Ile

100 105 110

Leu Ser Gln Asn Pro Glu Ala Arg Asn Val Arg Arg Glu Leu Ala Ser

115 120 125

Val Leu Tyr Glu Gln Gly Glu Gly Asn Ala Ser Leu His His Phe Glu

130 135 140

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

145 150 155 160

Arg Leu Ala Ala Lys Ala Arg Thr Ile Arg Pro Trp Ser Leu Gly Gly

165 170 175

Tyr Leu Ser Ile Ala Pro Ser Thr Asn Ile Thr Glu Ala Pro Asp Ala

180 185 190

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

195 200 205

Ser Gly Ile Gly Tyr Gly Tyr Gly Leu Asn Gly Ser Tyr Arg Phe Asp

210 215 220

Leu Asp Glu Ile Ser Ser Ile Thr Val Gly Gly Gly Val Asn Gly Asn

225 230 235 240

Trp Tyr Arg Asp Thr Ser Phe Asn Thr Ser Tyr Phe Asp Ser Phe Val

245 250 255

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

260 265 270

Gly Gln Tyr Val Met Lys Gly Glu Glu Pro Tyr Arg Trp Ser Leu Gly

275 280 285

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

290 295 300

Leu Arg Gly Met Trp Arg Lys Leu Asp Tyr His Asp Arg Asp Glu Leu

305 310 315 320

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

325 330 335

Ser Ala Ser Ser Val Arg Phe Gly Gly Asn Ile Gly Tyr Val Asp Ala

340 345 350

Ala Asn Asp Thr Asn Ser Tyr Leu Arg Leu Ser Leu Asn Ala Gln Tyr

355 360 365

Phe Arg Glu Trp Ser Phe Gly Ala Ile Ser Asp Ile Ser Ile Phe Ala

370 375 380

Asp Asp Arg Lys Tyr Gln Asp Ile Thr Tyr Leu Ala Gly Glu Lys Arg

385 390 395 400

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

405 410 415

Ala Ile Lys Gly Phe Ala Pro Arg Ile Glu Tyr Ala Tyr Thr Gln Asn

420 425 430

Phe Ser Asn Val Asp Val Tyr Asp Phe Ser Lys Asn Thr Leu Ser Thr

435 440 445

Tyr Leu Thr Lys Arg Phe

450

<210> 303

<211> 1365

<212> DNA

<213> M. mediterranea SLAM 2

<400> 303

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ctgaagcgcg gaccacgcgc ctttttgttc acgtttgccc ttgtggccct cacgattggc 120

gccccgcaat ggggcttcgc aaaaaagtcc accgttaccg gctttgacgc ggtgcgtgtg 180

ctggttgaat atggccagta tgaaaatgcg atggcactgg cgcaaagctt cgcgaccgac 240

gaaaagggca aggcgctcgc tgccgccttc acgcaggccc tcatactgga gcagcagggc 300

cggttgccgg aagcggcaag cgcgcttcgc gccatccttt cgcagaaccc cgaggcccgc 360

aacgtccggc gtgaacttgc cagcgttctc tacgaacagg gcgagggcaa cgcatcgctg 420

catcacttcg aacttctggc cggcagcgcc aatagtgccg atgagcgcgc gttctatgaa 480

cgccttgccg ccaaggcccg cacgattcgt ccctggtcgc ttggtggcta tctctcaatc 540

gcccccagca ccaacattac cgaagccccc gatgccgacc tcgtctatat cggcggcatt 600

cccatactgc ctgccaaaaa gaagagcggc atcggctatg gctatgggtt gaacggatcc 660

taccgttttg accttgatga aatttcatcg atcacggtag gtggcggggt gaacggcaac 720

tggtatcgcg acaccagttt caacacgagc tactttgaca gtttcgtcga ctatcgccgg 780

gaaatggggg actggacggt gactggcggc cttgtaggcc agtatgtgat gaagggcgaa 840

gaaccttatc gctggtcgct cggaccggct ttctcgctgc gtcacaatat gggacgaaag 900

ggcgtcacaa cgctgcgtgg catgtggcga aagctcgatt accacgaccg cgatgaactg 960

gacggcagcg aaaccgtgct ggggatcagc catctctatg ccatctcatc ggcaagctcg 1020

gtgcgtttcg ggggcaatat cggctatgtc gatgcggcga acgacaccaa cagctatctc 1080

cgcctttccc tgaacgcgca gtatttccgg gaatggagtt tcggcgcgat ttccgatatc 1140

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<210> 304

<211> 454

<212> PRT

<213> M. mediterranea SLAM 2

<400> 304

Met Thr Asn Arg Arg Leu Glu Pro Arg Ala Gly Lys Pro Ala Arg Gly

1 5 10 15

Leu Cys Leu Glu Leu Lys Arg Gly Pro Arg Ala Phe Leu Phe Thr Phe

20 25 30

Ala Leu Val Ala Leu Thr Ile Gly Ala Pro Gln Trp Gly Phe Ala Lys

35 40 45

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

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

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

Trp Tyr Arg Asp Thr Ser Phe Asn Thr Ser Tyr Phe Asp Ser Phe Val
245 250 255
Asp Tyr Arg Arg Glu Met Gly Asp Trp Thr Val Thr Gly Gly Leu Val
260 265 270
Gly Gln Tyr Val Met Lys Gly Glu Glu Pro Tyr Arg Trp Ser Leu Gly
275 280 285

Pro Ala Phe Ser Leu Arg His Asn Met Gly Arg Lys Gly Val Thr Thr
290 295 300

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

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

Phe Ser Asn Val Asp Val Tyr Asp Phe Ser Lys Asn Thr Leu Ser Thr
435 440 445
Tyr Leu Thr Lys Arg Phe
450

<210> 305
<211> 1428
<212> DNA
<213> M. morosus SLAM 1
<400> 305
gtggaaaggc acagattaat agcttcaaga gatttgattt tttgtcttat attaatactt 60
ttaaaaagtc atactgtctt tgcggaacaa tatgtcttgc caggacaaga tcaaataacc 120
gttaccgccg tccctttaac aacccaacca aaagcgcaag agactctcaa cgccaaactg 180
catgaggcta tggccttgta ttataacggg tcgtatcgtt tggcattgcc catcctcaaa 240

gaagttgccg cccaaaacga tagtcgagag gtattgtatt ggttagggcg gtctgcgtat 300

gagacagggg aaacaggcct tgctatcgaa aaataccaac aaatcctggc gcgcgagccg 360

aaactttcta gagttcgttt agaactggcg gcagcttata aacaggcagg caatactgat 420

gcggcacaag cggaactgca aaaagtgctg gcagaaaatc ccgatgcaga agttaaggag 480

ttaattgaga aagccgtggt ggatatagaa gaaccacagg tcgagtccaa gcggtttttt 540

gcggctctcc gggcttcaat ggggccggaa tacgacagca atgttaacgt cgggcccagg 600

gatgagcgca ttttattggc aaataaccaa gcgctgacat ctaaaaacct tgacggatgg 660

ctgctcaaat ttaacctcaa cggcgacctg ctctacgatt ttggcaagcc aaatgggttt 720

gtttggcata accacattca atttctccat catgaatacc cagacagcac caatagtaac 780

tttaattaca cccagacaga tgtcaatacg gggcttgatt attatgaccg caggtttaag 840

gcgaaacttc cgtttgggtt tattgaccga cggttttcca ataatgacct atcccatgcc 900

tattatttca tgccgaatat tgaaattaac ctacgcgacg atacggattt tgccttatcg 960

taccgttatg aaaatgaaga ttttattgag cctcaatttg atgccttaag tggtataacg 1020

catacaggca cgtttgggcc acggtataaa tttgaggcct ttaatgcaga gcattcactg 1080

gcgttattcg gcacctatag tcggcgtaat gcccacacag accgtttttc ctatgacgaa 1140

tggtcaatgg ggccgtcgta cttcgcccgg tttaaaacgg ggacagagtt ttacctggat 1200

ttcaaatact taaatcgcga ttacgatgcc ccggcgttat tgtttgtgga taagggcagg 1260

cgtttggaca atcgctatac cttaaccttt tctctcagcc agacattcta caaagtctac 1320

ttcgtgtcct tgggttatac ctataccgac aatagctcga atgcaaaatt gttcgattac 1380

gacaaaaata tggtcgggct gaatgttggc acaaatttga atttctaa 1428

<210> 306

<211> 475

<212> PRT

<213> M. morosus SLAM 1

<400> 306

Met Glu Arg His Arg Leu Ile Ala Ser Arg Asp Leu Ile Phe Cys Leu
1 5 10 15

Ile Leu Ile Leu Leu Lys Ser His Thr Val Phe Ala Glu Gln Tyr Val
20 25 30

Leu Pro Gly Gln Asp Gln Ile Thr Val Thr Ala Val Pro Leu Thr Thr
35 40 45

Gln Pro Lys Ala Gln Glu Thr Leu Asn Ala Lys Leu His Glu Ala Met

50 55 60

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

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

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

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

Pro Asn Ile Glu Ile Asn Leu Arg Asp Asp Thr Asp Phe Ala Leu Ser
305 310 315 320

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

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

Thr Asp Asn Ser Ser Asn Ala Lys Leu Phe Asp Tyr Asp Lys Asn Met
450 455 460
Val Gly Leu Asn Val Gly Thr Asn Leu Asn Phe
465 470 475

<210> 307
<211> 1575
<212> DNA
<213> M. nitratireducenticrescens SLAM 1
<400> 307

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cgaattatgt tgcctgaatt acaactatct tttgtttctt cacggaaatt ggtgatctct 120
actgcattgt ttatcacact actgaccagc gtgaacagtt gggcggacga taaggatact 180

tctctgcggc tgaatcaaag tattgatctg caatcgaatg agcaagaacg acaaatcctc 240

aaagatgaag attacctgaa aggggagcgt ccgaccttaa cgattgatgg taagacttac 300

acaatcaaac acaatgtgaa cgatgtaggc cgtgcgttat atatgtcgat tcaacagaaa 360

caatggtctg cggtagggta ttttttggat gaatatctga ccttttccaa tgcggatcca 420

atgttgattg cttatgctca gggagcccta gccagacttc agggtaatat ggaaaaggcc 480

gaagcagaat ttaaaaccct gcttgatatc aaaccggatt ttatgctcgg tcagttggaa 540

ctggcccgag tattgtttga aaatcgtaaa gatgccgaat cggaggcgat gtttcagcaa 600

atcgctcagt cgcttaatcc ggctgatgcc aggcagcagg gtgtgctcac taccgttgat 660

agctttctgc aagcggttga taaacgtcag gcatggcaag gatctatcgc attaggccca 720

acctggtcgg ataatctaaa ccagacatct gaaagttaca gctgtctgtt ttattacggt 780

tcggtatgcc tgtttgaacg tgctacccct gaagcggtta aatcccatgg tatggattat 840

gaaataacgt taaataaacg ttttgctttg tccggtcatc atggtttgtt ttttcgttcg 900

ttatggtttg ggcaaagtta taaagatcat tcgctctaca acgaaagtca gcttagcacc 960

cagttcggct acagctacca caatatgcgt aatcagtatt ctttagcacc ttcatttgag 1020

tttgttcgtt atggtaatga ttcactatac ggggcttcgg gtctgcatgg tgaatggctg 1080

cattatctga gcgacaaagc gatgttcaag ctggaagcag attataaaaa tcagcaatac 1140

cggaaagaac ttattgccga ccagtacgac ggtggtatct ggtctactta tgcaacagcc 1200

tggtatggcc tgccaaataa ctggactgta tttggtggtc tggactggac ccgcaaaacc 1260

gccgaagtcg atcaaaatgc gtatgagcaa atcggcgtca gagcaggtgt cgccaaaacc 1320

tttaatgcgc atattaatgc ggtactgttc gcttcattac gggaacgtga acatgatgca 1380

tttaatgcgt tattggatga gcagcgtaag gatttcgaac aaaactatac cgttattctg 1440

cgttttccga ccctcgctgt ttacggcttg gagcccaatc tgacttttaa gcaccgcaaa 1500

gtgcacagca atgtggactg gctgtattcc tatgaccgca acagtgtcag cctgaaactg 1560

gaaaaacgtt tctaa 1575

<210> 308

<211> 524

<212> PRT

<213> M. nitratireducenticrescens SLAM 1

<400> 308

Met Asp Glu Ile Trp Pro Asp Ala Phe Gly His Leu Ala Phe Ser Phe

1 5 10 15

Tyr Tyr Gln Ser Arg Ile Met Leu Pro Glu Leu Gln Leu Ser Phe Val

20 25 30

Ser Ser Arg Lys Leu Val Ile Ser Thr Ala Leu Phe Ile Thr Leu Leu

35 40 45

Thr Ser Val Asn Ser Trp Ala Asp Asp Lys Asp Thr Ser Leu Arg Leu

50 55 60

Asn Gln Ser Ile Asp Leu Gln Ser Asn Glu Gln Glu Arg Gln Ile Leu

65 70 75 80

Lys Asp Glu Asp Tyr Leu Lys Gly Glu Arg Pro Thr Leu Thr Ile Asp

85 90 95

Gly Lys Thr Tyr Thr Ile Lys His Asn Val Asn Asp Val Gly Arg Ala

100 105 110

Leu Tyr Met Ser Ile Gln Gln Lys Gln Trp Ser Ala Val Gly Tyr Phe

115 120 125

Leu Asp Glu Tyr Leu Thr Phe Ser Asn Ala Asp Pro Met Leu Ile Ala

130 135 140

Tyr Ala Gln Gly Ala Leu Ala Arg Leu Gln Gly Asn Met Glu Lys Ala

145 150 155 160

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

165 170 175

Gly Gln Leu Glu Leu Ala Arg Val Leu Phe Glu Asn Arg Lys Asp Ala

180 185 190

Glu Ser Glu Ala Met Phe Gln Gln Ile Ala Gln Ser Leu Asn Pro Ala

195 200 205

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

210 215 220

Ala Val Asp Lys Arg Gln Ala Trp Gln Gly Ser Ile Ala Leu Gly Pro

225 230 235 240

Thr Trp Ser Asp Asn Leu Asn Gln Thr Ser Glu Ser Tyr Ser Cys Leu

245 250 255

Phe Tyr Tyr Gly Ser Val Cys Leu Phe Glu Arg Ala Thr Pro Glu Ala

260 265 270

Val Lys Ser His Gly Met Asp Tyr Glu Ile Thr Leu Asn Lys Arg Phe

275 280 285

Ala Leu Ser Gly His His Gly Leu Phe Phe Arg Ser Leu Trp Phe Gly

290 295 300

Gln Ser Tyr Lys Asp His Ser Leu Tyr Asn Glu Ser Gln Leu Ser Thr

305 310 315 320

Gln Phe Gly Tyr Ser Tyr His Asn Met Arg Asn Gln Tyr Ser Leu Ala

325 330 335

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

340 345 350

Ser Gly Leu His Gly Glu Trp Leu His Tyr Leu Ser Asp Lys Ala Met

355 360 365

Phe Lys Leu Glu Ala Asp Tyr Lys Asn Gln Gln Tyr Arg Lys Glu Leu

370 375 380

Ile Ala Asp Gln Tyr Asp Gly Gly Ile Trp Ser Thr Tyr Ala Thr Ala

385 390 395 400

Trp Tyr Gly Leu Pro Asn Asn Trp Thr Val Phe Gly Gly Leu Asp Trp

405 410 415

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

420 425 430

Val Arg Ala Gly Val Ala Lys Thr Phe Asn Ala His Ile Asn Ala Val

435 440 445

Leu Phe Ala Ser Leu Arg Glu Arg Glu His Asp Ala Phe Asn Ala Leu

450 455 460

Leu Asp Glu Gln Arg Lys Asp Phe Glu Gln Asn Tyr Thr Val Ile Leu

465 470 475 480

Arg Phe Pro Thr Leu Ala Val Tyr Gly Leu Glu Pro Asn Leu Thr Phe

485 490 495

Lys His Arg Lys Val His Ser Asn Val Asp Trp Leu Tyr Ser Tyr Asp

500 505 510

Arg Asn Ser Val Ser Leu Lys Leu Glu Lys Arg Phe

515 520

<210> 309

<211> 1326

<212> DNA

<213> M. thermotolerans

<400> 309

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tgtcaagccc agtcgctggt acaggatgcc gcggctcaca tcgaagcagg gcgttacgcc 120

gatgcctacc gcatgttgtc agccgaagag tcggaaagag ccggagatcc tcagttcgat 180

ctcttgctag gcatcgcggc gctcgaaacc ggtcggcata cgctcgcggt attcgcgctc 240

gagcgcgtgc tcgcggtgca gcccgacaac gcgcgcgcgc gcgccgagat cggccgcgcc 300

tatatggcgc tgggcgagtc ggaaggtgca aaacgtgaat tgcaggcggt gcggggccag 360

gacgtcccgc ccgaggtggt acgcgccatc gatcgtctgc tcgccgccat cgatcgtgcg 420

gccctgcagg ggaggaccgc attcagcggt tacgtagagg cggccgtggg gcgcgatacc 480

aatgtaaaca gcgcgacttc gctgacctcg gtcaccgtgc ccagtctggg cgcattcgtg 540

ctcgatacat ccagccgcag tcgcagcgcc tggttcagtg cgctgtccgg cggcgtcaac 600

gtgcgcgtgc ctgtcaatcc cgaatgggcg ttgatcgccg gcgcgtccgg tgccggcaga 660

ttcaatggcg gcgaatcgcg tttcgacacg accgcgctgg acgggaatgg cggcgttgtc 720

tggtcgcggg ggcagcatcg ggtaaccgcc ctgctgcagg ccggcatgtt cgaggttgat 780

caggaaaagt tgcgcgatta cacaggcggt ctgctgcagt ggcaatacac tcacgatgcg 840

cgcaaccaga cgacggtcta tgcgcagcag acgcggctgc gctacgaagg cagcaatgat 900

gtgcgtgacg taaaccgcaa catctatggc gtcgggcatg caatgctgct gcccgacgga 960

cagacgctgc tgttcgggag cgtctatctg ggcgcggaaa caggccgcaa cgatctgtcg 1020

tcgggcatca atatcgcggc caatgatgtg atcggcttcc gcttcggcgc acagcacagc 1080

ctggatgagc gctggcagtt gttcggtgcg ctgtcgcacg aggcgcgtga ttatcacgcc 1140

accgacccgg tgttcggcgt cgtcagggac gacacgctga catcgctgtc gctgggcgca 1200

agttatgaat tcgcgaagaa ctggctggcg acgccatcgc tgtcgttctc gcgcaacgat 1260

tcaagcatca gtctgaacga gtaccgtcgc ggcattgcgc agttcgcggt gcggcgcaca 1320

ttctag 1326

<210> 310

<211> 441

<212> PRT

<213> M. thermotolerans SLAM 1

<400> 310

Met Arg Ala Arg Arg Asn Ile Ser Leu Met Phe Ser Leu Phe Leu Gly
1 5 10 15

Leu Ser Val Pro Cys Gln Ala Gln Ser Leu Val Gln Asp Ala Ala Ala
20 25 30

His Ile Glu Ala Gly Arg Tyr Ala Asp Ala Tyr Arg Met Leu Ser Ala
35 40 45

Glu Glu Ser Glu Arg Ala Gly Asp Pro Gln Phe Asp Leu Leu Leu Gly
50 55 60

Ile Ala Ala Leu Glu Thr Gly Arg His Thr Leu Ala Val Phe Ala Leu
65 70 75 80

Glu Arg Val Leu Ala Val Gln Pro Asp Asn Ala Arg Ala Arg Ala Glu
85 90 95

Ile Gly Arg Ala Tyr Met Ala Leu Gly Glu Ser Glu Gly Ala Lys Arg
100 105 110

Glu Leu Gln Ala Val Arg Gly Gln Asp Val Pro Pro Glu Val Val Arg
115 120 125

Ala Ile Asp Arg Leu Leu Ala Ala Ile Asp Arg Ala Ala Leu Gln Gly
130 135 140

Arg Thr Ala Phe Ser Gly Tyr Val Glu Ala Ala Val Gly Arg Asp Thr
145 150 155 160

Asn Val Asn Ser Ala Thr Ser Leu Thr Ser Val Thr Val Pro Ser Leu
165 170 175

Gly Ala Phe Val Leu Asp Thr Ser Ser Arg Ser Arg Ser Ala Trp Phe
180 185 190

Ser Ala Leu Ser Gly Gly Val Asn Val Arg Val Pro Val Asn Pro Glu
195 200 205

Trp Ala Leu Ile Ala Gly Ala Ser Gly Ala Gly Arg Phe Asn Gly Gly
210 215 220

Glu Ser Arg Phe Asp Thr Thr Ala Leu Asp Gly Asn Gly Gly Val Val

225 230 235 240

Trp Ser Arg Gly Gln His Arg Val Thr Ala Leu Leu Gln Ala Gly Met

245 250 255

Phe Glu Val Asp Gln Glu Lys Leu Arg Asp Tyr Thr Gly Gly Leu Leu

260 265 270

Gln Trp Gln Tyr Thr His Asp Ala Arg Asn Gln Thr Thr Val Tyr Ala

275 280 285

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

290 295 300

Asn Arg Asn Ile Tyr Gly Val Gly His Ala Met Leu Leu Pro Asp Gly

305 310 315 320

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

325 330 335

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

340 345 350

Phe Arg Phe Gly Ala Gln His Ser Leu Asp Glu Arg Trp Gln Leu Phe

355 360 365

Gly Ala Leu Ser His Glu Ala Arg Asp Tyr His Ala Thr Asp Pro Val

370 375 380

Phe Gly Val Val Arg Asp Asp Thr Leu Thr Ser Leu Ser Leu Gly Ala

385 390 395 400

Ser Tyr Glu Phe Ala Lys Asn Trp Leu Ala Thr Pro Ser Leu Ser Phe

405 410 415

Ser Arg Asn Asp Ser Ser Ile Ser Leu Asn Glu Tyr Arg Arg Gly Ile

420 425 430

Ala Gln Phe Ala Val Arg Arg Thr Phe

435 440

<210> 311

<211> 1452

<212> DNA

<213> M. varigena SLAM 1

<400> 311

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gccccagctc caattcaaga gaaaatggat aatcagcgga tgcaacaaaa tcaatcgttt 120

gagacaccgg aacataaagt tgctcaagct cagcccaaag tgcaaaatag caatcagact 180

atttcaattt caagccaaga actcattcag cagcctgagt tattaaattc agcaatgctg 240

acggcattgg taacaggcaa taccgaaaac gtcctctttt tattgccgat ataccaaaaa 300

ctccctacat ctaagcaaaa tcgtgaaatg attacgtggg caaaggcaac agaggcaaaa 360

tcaaatcaag attatactca atctattaag ctctaccgag agttgctggc aagttatccg 420

gaaaatcagc cgatccgaat gcagcttgcg gtggcacttt ttgaaaaccg tgaaaatgaa 480

gccgcagaag cacaatttca taaattacaa gcggataaat tacctataaa aattacaaat 540

atcatcaatc attatttaga agccatcagt aaacaagaca aatgggtatt tcaaggcggc 600

ttaacttatt taaatgatcc aaatattaat aatgctccag cttcaggcac aacttacggc 660

agatggtcag ctccgaaaaa agagtctgct caagggattg ggctaagttt tgacgctgcg 720

aaaaaatggt cttggggaaa tggtttcttc cacgagtttc gcctaaacgg taatggcaaa 780

tattattgga ataataaaaa atataatgaa tattcgctta gagaaagttt cggattaggc 840

tatcaaagtg cgaaacaaaa aatcacagtt ttacctttct tagagcaaac ttggtatgcg 900

ggcggttcta ctcaaagtca aagcactaag cgttattcaa atgcaggtgg tgttaatact 960

cgttggcaat actggattac gccacaatgg caatcctcaa taacgtatga atatgccgag 1020

caacgttata cccgtcgcca gcacttagat ggaaattatc attttgtttc tccgagtatt 1080

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acccgagatt tagatgacag ctttattcgt cgaggtgttt cactaggttg ggggcaagag 1200

tggaagaatg ggctttcaag ccaattaagc gtgagctatg gtcgcaagca atatagagca 1260

ccaatgccta ttttccaaat tacccagcgt aataaagaat acggcgtaca agcgagtatc 1320

tggcacagag ccgtgcattt taaaggcatt actcctcgtt taacctggca atataacaaa 1380

gtaaaaagta atcacacttt ttatagttat gataaaaacc gtgtgtatat tgagttttca 1440

catacgttct aa 1452

<210> 312

<211> 483

<212> PRT

<213> M. varigena SLAM 1

<400> 312

Met Lys Lys Ile Ile Pro Ile Ala Phe Ser Leu Ala Ala His Phe Ala
1 5 10 15
Leu Ala Asp Thr Ala Pro Ala Pro Ile Gln Glu Lys Met Asp Asn Gln
20 25 30
Arg Met Gln Gln Asn Gln Ser Phe Glu Thr Pro Glu His Lys Val Ala
35 40 45
Gln Ala Gln Pro Lys Val Gln Asn Ser Asn Gln Thr Ile Ser Ile Ser

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

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

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

Lys Lys Trp Ser Trp Gly Asn Gly Phe Phe His Glu Phe Arg Leu Asn

245 250 255

Gly Asn Gly Lys Tyr Tyr Trp Asn Asn Lys Lys Tyr Asn Glu Tyr Ser

260 265 270

Leu Arg Glu Ser Phe Gly Leu Gly Tyr Gln Ser Ala Lys Gln Lys Ile

275 280 285

Thr Val Leu Pro Phe Leu Glu Gln Thr Trp Tyr Ala Gly Gly Ser Thr

290 295 300

Gln Ser Gln Ser Thr Lys Arg Tyr Ser Asn Ala Gly Gly Val Asn Thr

305 310 315 320

Arg Trp Gln Tyr Trp Ile Thr Pro Gln Trp Gln Ser Ser Ile Thr Tyr

325 330 335

Glu Tyr Ala Glu Gln Arg Tyr Thr Arg Arg Gln His Leu Asp Gly Asn

340 345 350

Tyr His Phe Val Ser Pro Ser Ile Tyr Tyr His Pro Ser Ser Gln Gln

355 360 365

Tyr Trp Phe Val Gly Ala Asn Phe Asn Arg Asn Ser Thr Arg Asp Leu

370 375 380

Asp Asp Ser Phe Ile Arg Arg Gly Val Ser Leu Gly Trp Gly Gln Glu

385 390 395 400

Trp Lys Asn Gly Leu Ser Ser Gln Leu Ser Val Ser Tyr Gly Arg Lys

405 410 415

Gln Tyr Arg Ala Pro Met Pro Ile Phe Gln Ile Thr Gln Arg Asn Lys

420 425 430

Glu Tyr Gly Val Gln Ala Ser Ile Trp His Arg Ala Val His Phe Lys

435 440 445

Gly Ile Thr Pro Arg Leu Thr Trp Gln Tyr Asn Lys Val Lys Ser Asn

450 455 460

His Thr Phe Tyr Ser Tyr Asp Lys Asn Arg Val Tyr Ile Glu Phe Ser

465 470 475 480

His Thr Phe

<210> 313

<211> 1410

<212> DNA

<213> M. varigena SLAM 2

<400> 313

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attgagcaca acacagatcc cgtttctttt gaacgccatt cacaagcggt caaatttgag 120

caaaattttg caaaaaagcc acaaaaaacg accgcttatc agcccaaata ttcgttaaat 180

cagaatgttg aacagcaaat taaccaagcg attttgagcc aaaattggga aaacttagca 240

ccgcttttaa gtcgttatca gcaaatgccc aatgttgatc cgttactttg gcattacgcc 300

caagcggcac ttgcctatgc ggaaaaagat catcattcag ccatttttca ctaccgccaa 360

ttactcgcca gaaatcccaa tttggtttat ccacgttttg atttagcgtt aattttggca 420

gaagatcagc aatttcgtga ggcggagcgt gaatttagcc atattcaagc ctatttaccg 480

cccgatttag gcaaaattgc ggcgaatact caaatgcaaa ttgcagaaaa tgagcgttgg 540

cagcctgatt tttacttgca atatacccag acaaataacg tgaataatgc ttcatcttcg 600

ccgattgtaa gcgtaaatgg gcggattttc cgtaaaaatg aagaaagtct tccacaatcg 660

gcaaaaggtg ttcgctatgg tttcggatta agcaaattgc agaatttgcg tggcaaccat 720

tttgtggggt tagggctgaa ttatagcggt atttattatt gggataatca agattaccgt 780

gagcaatctc tttctatttc gccaagttat agttaccgca aggctcgcta tcgctttagt 840

ttttcgccgt ttattgagca gaattggttg ggaagtagcc gttataatta ccaatttgga 900

gcaacggtaa gtggttttcg ttatctcaat tcgcaatggt tgatgtcagg tagttttacc 960

catttacaaa aacgctattt tgatgagcta accgcaagtc gttataacag ttatcagcac 1020

caaatcagta ctggactgca gtggcaagcg gtcaaaaatt ggcgattttt tgcaaattta 1080

gacggcagcc gtgaaatcgc tcgtgagaaa gctcaaacgt caaataagtg gttagcaaga 1140

gtcggggcag tttatcacgg cgaaaaatgg gcaactcagg caagtttagg ctttggaaaa 1200

cgctattttg ccgataagca ctatttattt ggctataaac ggcaagataa ggaatatcaa 1260

gttaatcttg cggtttggaa tcgtacttgg cattggcaag gcattgtgcc gaagttgaat 1320

ttccgttatc aaaaaatgga tagtaatatt gccgattttt actctcgaca aaataaagaa 1380

ctgtttttta cgttagagaa gctattttag 1410

<210> 314

<211> 469

<212> PRT

<213> M. varigena SLAM 2

<400> 314

Met Lys Lys Tyr Thr Leu Leu Phe Pro Leu Phe Ser Pro Phe Val Leu
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Ala Glu Thr Val Ile Glu His Asn Thr Asp Pro Val Ser Phe Glu Arg
20 25 30

His Ser Gln Ala Val Lys Phe Glu Gln Asn Phe Ala Lys Lys Pro Gln
35 40 45

Lys Thr Thr Ala Tyr Gln Pro Lys Tyr Ser Leu Asn Gln Asn Val Glu
50 55 60

Gln Gln Ile Asn Gln Ala Ile Leu Ser Gln Asn Trp Glu Asn Leu Ala
65 70 75 80

Pro Leu Leu Ser Arg Tyr Gln Gln Met Pro Asn Val Asp Pro Leu Leu
85 90 95

Trp His Tyr Ala Gln Ala Ala Leu Ala Tyr Ala Glu Lys Asp His His
100 105 110

Ser Ala Ile Phe His Tyr Arg Gln Leu Leu Ala Arg Asn Pro Asn Leu
115 120 125

Val Tyr Pro Arg Phe Asp Leu Ala Leu Ile Leu Ala Glu Asp Gln Gln
130 135 140

Phe Arg Glu Ala Glu Arg Glu Phe Ser His Ile Gln Ala Tyr Leu Pro
145 150 155 160

Pro Asp Leu Gly Lys Ile Ala Ala Asn Thr Gln Met Gln Ile Ala Glu
165 170 175

Asn Glu Arg Trp Gln Pro Asp Phe Tyr Leu Gln Tyr Thr Gln Thr Asn
180 185 190

Asn Val Asn Asn Ala Ser Ser Ser Pro Ile Val Ser Val Asn Gly Arg
195 200 205

Ile Phe Arg Lys Asn Glu Glu Ser Leu Pro Gln Ser Ala Lys Gly Val
210 215 220

Arg Tyr Gly Phe Gly Leu Ser Lys Leu Gln Asn Leu Arg Gly Asn His

225 230 235 240

Phe Val Gly Leu Gly Leu Asn Tyr Ser Gly Ile Tyr Tyr Trp Asp Asn

245 250 255

Gln Asp Tyr Arg Glu Gln Ser Leu Ser Ile Ser Pro Ser Tyr Ser Tyr

260 265 270

Arg Lys Ala Arg Tyr Arg Phe Ser Phe Ser Pro Phe Ile Glu Gln Asn

275 280 285

Trp Leu Gly Ser Ser Arg Tyr Asn Tyr Gln Phe Gly Ala Thr Val Ser

290 295 300

Gly Phe Arg Tyr Leu Asn Ser Gln Trp Leu Met Ser Gly Ser Phe Thr

305 310 315 320

His Leu Gln Lys Arg Tyr Phe Asp Glu Leu Thr Ala Ser Arg Tyr Asn

325 330 335

Ser Tyr Gln His Gln Ile Ser Thr Gly Leu Gln Trp Gln Ala Val Lys

340 345 350

Asn Trp Arg Phe Phe Ala Asn Leu Asp Gly Ser Arg Glu Ile Ala Arg

355 360 365

Glu Lys Ala Gln Thr Ser Asn Lys Trp Leu Ala Arg Val Gly Ala Val

370 375 380

Tyr His Gly Glu Lys Trp Ala Thr Gln Ala Ser Leu Gly Phe Gly Lys

385 390 395 400

Arg Tyr Phe Ala Asp Lys His Tyr Leu Phe Gly Tyr Lys Arg Gln Asp

405 410 415

Lys Glu Tyr Gln Val Asn Leu Ala Val Trp Asn Arg Thr Trp His Trp

420 425 430

Gln Gly Ile Val Pro Lys Leu Asn Phe Arg Tyr Gln Lys Met Asp Ser

435 440 445

Asn Ile Ala Asp Phe Tyr Ser Arg Gln Asn Lys Glu Leu Phe Phe Thr

450 455 460

Leu Glu Lys Leu Phe

465

<210> 315

<211> 1299

<212> DNA

<213> M. varigena SLAM 3

<400> 315

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attctactga aagattataa acaacaagaa aatgcagatc ctactgtaat cgcttatgca 180

aaagcgaagt ctgcctttat tcaacaagat taccaaacag caatttctat ttataggaat 240

atcattagtc aaaagccgga attaaattca atgcgtatgg agcttgcggt tgccttattt 300

gcagataagc aagataacga agctaagttg caatttgata aagtaaagag tgttcctgat 360

ttgcccggag tagcttacca aaaaattgag gcttatttag aggcgataaa tcaacgtaat 420

gaatggcaat ttgacctgaa tttttcttat cttaaaacgg ataatgtagc gaatgtatct 480

caccagccac agattgaaaa tacgggtttt attaaaaacg aaacgatgtt accacagaaa 540

gctaatggct ttgcttttaa tgtagatgta gcgaaagatt ttaatttatt taattctcac 600

tatttgagct ttcgaaatga agcaactggc aaaatttact gggataatca ccgttttgat 660

gatgtatcta atcgccttct gctaggttat gcctataaaa aatcagataa aacactacgc 720

attcagcctt tttatgataa acgttggttt ggtaataggt cttttcattg gtctaatggg 780

cttcaattta gttatgattt tgctatctct aatcaatgga aaaatcagac ggttttatca 840

tttgaaaagc ggtcgttttt tgatgaaaat ttgcaagccg gtaatataaa agctttctcc 900

aatactttgc tttggttgcc taatcctaaa caattatttt atgttggggg gacaatatca 960

aaagaaaata cgcgagaaaa acagtatggc tcaacaagca aaaatattcg cttaggctgg 1020

ttacaagaat atcaatgggg aatttctagt cagttgagtt tttcatttac ccaccgaaaa 1080

tttcacgatg aggcgatact cgtagggatt attcctctca ataaaatcag acaagataaa 1140

atctatagtg tgaatgctaa attttggaaa cgagattggt atttatgggg cattacgcct 1200

aaactgaata ttgtatggaa aaagcaacaa agtaatttag caagcctcta ttcttataca 1260

gataagcaaa ttacagtatt atttgaaaag agcttttaa 1299

<210> 316

<211> 432

<212> PRT

<213> M. varigena SLAM 3

<400> 316

Met Arg Phe Cys Ile Ser Leu Leu Ala Phe Phe Ser Ile Gln Met Val
1 5 10 15

Leu Ala Asn His Ser Lys Leu Glu Glu Gln Leu Lys Gln Ala Ile Tyr
20 25 30

Gln Gln Glu Phe Lys Lys Ile Gln Ile Leu Leu Lys Asp Tyr Lys Gln
35 40 45

Gln Glu Asn Ala Asp Pro Thr Val Ile Ala Tyr Ala Lys Ala Lys Ser

50 55 60

Ala Phe Ile Gln Gln Asp Tyr Gln Thr Ala Ile Ser Ile Tyr Arg Asn
65 70 75 80

Ile Ile Ser Gln Lys Pro Glu Leu Asn Ser Met Arg Met Glu Leu Ala
85 90 95

Val Ala Leu Phe Ala Asp Lys Gln Asp Asn Glu Ala Lys Leu Gln Phe
100 105 110

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

115 120 125

Ile Glu Ala Tyr Leu Glu Ala Ile Asn Gln Arg Asn Glu Trp Gln Phe
130 135 140

Asp Leu Asn Phe Ser Tyr Leu Lys Thr Asp Asn Val Ala Asn Val Ser
145 150 155 160

His Gln Pro Gln Ile Glu Asn Thr Gly Phe Ile Lys Asn Glu Thr Met
165 170 175

Leu Pro Gln Lys Ala Asn Gly Phe Ala Phe Asn Val Asp Val Ala Lys

180 185 190

Asp Phe Asn Leu Phe Asn Ser His Tyr Leu Ser Phe Arg Asn Glu Ala
195 200 205

Thr Gly Lys Ile Tyr Trp Asp Asn His Arg Phe Asp Asp Val Ser Asn
210 215 220

Arg Leu Leu Leu Gly Tyr Ala Tyr Lys Lys Ser Asp Lys Thr Leu Arg
225 230 235 240

Ile Gln Pro Phe Tyr Asp Lys Arg Trp Phe Gly Asn Arg Ser Phe His

245 250 255

Trp Ser Asn Gly Leu Gln Phe Ser Tyr Asp Phe Ala Ile Ser Asn Gln

260 265 270

Trp Lys Asn Gln Thr Val Leu Ser Phe Glu Lys Arg Ser Phe Phe Asp

275 280 285

Glu Asn Leu Gln Ala Gly Asn Ile Lys Ala Phe Ser Asn Thr Leu Leu

290 295 300

Trp Leu Pro Asn Pro Lys Gln Leu Phe Tyr Val Gly Gly Thr Ile Ser

305 310 315 320

Lys Glu Asn Thr Arg Glu Lys Gln Tyr Gly Ser Thr Ser Lys Asn Ile

325 330 335

Arg Leu Gly Trp Leu Gln Glu Tyr Gln Trp Gly Ile Ser Ser Gln Leu

340 345 350

Ser Phe Ser Phe Thr His Arg Lys Phe His Asp Glu Ala Ile Leu Val

355 360 365

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

370 375 380

Asn Ala Lys Phe Trp Lys Arg Asp Trp Tyr Leu Trp Gly Ile Thr Pro

385 390 395 400

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

405 410 415

Tyr Ser Tyr Thr Asp Lys Gln Ile Thr Val Leu Phe Glu Lys Ser Phe

420 425 430

<210> 317

<211> 2115

<212> DNA

<213> M. varigena SLAM 4

<400> 317

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caaaaaattg taaaaaacac gcaaaaatcg accgcttact tgcctgatga acaagtaaca 180

gaaagtgtag aacaacaaat taaccaagcg atcttaacgc aaaattggga aaagcttgaa 240

atattactga cagcgtattc aatgcaacag caagcagatc cgcttctact ggattatgct 300

tcagcggcgt tagcgtatgc taaaaaagat catcgctcgg caatttttta ctatcaacaa 360

ttgctcaaga aacaaccttc ttttatttat cctcgatttg atttagccct aattctaaaa 420

gaagatttcc gctaccgaga ggctcagaaa gaatttgagc aactgaaaac aactgctcca 480

cataatttac acgcgaccat aaataatgca ttggagcaaa tggcggaaga ggaacagtgg 540

aagcctgatt tctatctgat ggcactcggt ttgcaaaatt tccgactcaa aacattgtac 600

aatctgccca cttataccga taacatcccc aacattgcca tgaaaaaacg tctgctcctc 660

ctcgccatcc tgccccttc cctttacgcc gccgatgtgc cgcccaacgt aaaacccgag 720

cttcaagtca acactgccga accccaacag cccgaagcgc acaatatccc tgccgaacag 780

acaaacaggc cgtctgaaaa aatcatcgac gtcgatgccg acaccctgct tgccaacacc 840

gaattactgg cacgcgccat gtattccgcc gtcgtcgccc acaatatccc cggcatcaaa 900

gccgttttgc ccatttacga acaatggccc gaacacgacc gtgccatggc acgctatgcc 960

aaaggtttgc ttgcccaatc cgaagggcgc gccgccgaag ccgtcggcca ttaccgccgc 1020

tttatcgccg agcagcccga tgcctccgcc gtccgctggc agcttgcaac cgccttgttt 1080

gaagacaaac aaaacgaagc cgcggccgac cagttcgaca aactgcaaac cgaatccctc 1140

ccgcctgcct tgcaagaacg catcgaaacc taccgcaaag ccctgcgcga acgcgactta 1200

tggcaattca acgccggcct gaacatcacg cgcgaacaaa acatcaacca agcccccagc 1260

caacgccgtc tgggcaacca cctgagcgac gaacaatgcc gcgccgtgcg ccttgtctat 1320

cccgacgacg actgcttccg aggctggaca ttccccgaac ccatcgatgc caccgccgtc 1380

cattaccaaa tcggtgcaga aaaaaaatgg tcgttgccac gtggcttcta tgtcacggca 1440

ggcgcagacc attacggcaa aatctacccc aaacacacca actacaacga cctcaccaca 1500

cgcttctcgg caggcctagg ctatgccgac cagcgcagcg atatcggcat taccccgttc 1560

cacgaacgcc gcttctacgg caacgacccc tacacctaca ccaacggcgc acgcctccac 1620

tacaaccatt ggtggcaacc caagctacaa accctcagcg catttgaagc aggccgtctg 1680

aaaaacagcc gccgcgaaca ttccgacaac accagccaac tgctcagcaa ctccatcgtg 1740

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cgcgacgaca aaagcgacag cttcaaccgc tacgccctgc gcaccacatg gggacaagaa 1860

tggcccaaag gcctctccac cgtcctacgc ctcagcgccg cccaacgccg ttaccaagcc 1920

cccggcttct tcagtaacga acaaaaccgc cgcgacaaag aaacctccgc ctccctgagc 1980

gtatggcacc gcgccctcca tttcaaaggc atcaccccgc gcctgaccat tgcccacaac 2040

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<210> 318

<211> 461

<212> PRT

<213> M. varigena SLAM 4

<400> 318

Met Asn Lys Lys Leu Leu Leu Leu Leu Leu Phe Ser Pro Leu Val Lys
1 5 10 15

Ala Glu Thr Ile Val Glu Phe Asp Gln Asp Gln Lys Glu Phe Asn His
20 25 30

Asp Arg Gln Ala Val Glu Phe Glu Gln Lys Ile Val Lys Asn Thr Gln
35 40 45

Lys Ser Thr Ala Tyr Leu Pro Asp Glu Gln Val Thr Glu Ser Val Glu
50 55 60

Gln Gln Ile Asn Gln Ala Ile Leu Thr Gln Asn Trp Glu Lys Leu Glu
65 70 75 80

Ile Leu Leu Thr Ala Tyr Ser Met Gln Gln Gln Ala Asp Pro Leu Leu
85 90 95

Leu Asp Tyr Ala Ser Ala Ala Leu Ala Tyr Ala Lys Lys Asp His Arg
100 105 110

Ser Ala Ile Phe Tyr Tyr Gln Gln Leu Leu Lys Lys Gln Pro Ser Phe
115 120 125

Ile Tyr Pro Arg Phe Asp Leu Ala Leu Ile Leu Lys Glu Asp Phe Arg
130 135 140

Tyr Arg Glu Ala Gln Lys Glu Phe Glu Gln Leu Lys Thr Thr Ala Pro
145 150 155 160

His Asn Leu His Ala Thr Ile Asn Asn Ala Leu Glu Gln Met Ala Glu
165 170 175

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

180 185 190

Ser Pro Ile Val Asn Ile Asn Gly Arg Ile Phe His Lys Ala Glu Glu

195 200 205

Ser Leu Pro Gln Ser Ala Lys Gly Phe Arg Tyr Gly Val Gly Leu Ser

210 215 220

Lys Met Gln Asn Val Ser Gly Asn His Phe Ile Gly Ala Asp Leu Ala

225 230 235 240

Tyr Asn Gly Val Tyr Tyr Trp Asn Asn Gln Asp Tyr Ser Glu Gln Val

245 250 255

Leu Ser Ile Thr Pro Ser Tyr Ser Tyr Arg Lys Ala Thr Tyr Arg Ile

260 265 270

Gly Leu Ser Pro Phe Ile Glu Gln Asn Trp Leu Gly Ser Ser Arg Asp

275 280 285

Asn Tyr Gln Phe Gly Gly Arg Val Asn Val Met Lys Leu Leu Glu Arg

290 295 300

Gly Ile Val Ser Gly Ser Phe Ser His Thr Gln Lys Arg Tyr Phe Asp

305 310 315 320

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

325 330 335

Gly Thr Gln Trp Gln Ala Val Lys Asn Trp Arg Phe Phe Ala Asn Val

340 345 350

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

355 360 365

Trp Leu Ala Thr Ile Gly Val Ile His Gln Thr Gln Arg Trp Ser Ser

370 375 380

Ser Ala Ser Val Gly Tyr Gly Lys Arg Tyr Phe Ala Asp Lys His Tyr

385 390 395 400

Leu Leu Asp Tyr Lys Arg Gln Asp Lys Glu Tyr Gln Ala Asn Val Ala

405 410 415

Val Trp Asn Gln Asn Trp His Trp Asn Gly Ile Val Pro Lys Leu Asn

420 425 430

Phe Arg Tyr Gln Lys Ile Asp Ser Asn Ile Ala Asp Phe Tyr Ser Arg

435 440 445

Ser Asn Lys Glu Val Phe Leu Thr Val Glu Lys Val Phe

450 455 460

<210> 319

<211> 1494

<212> DNA

<213> M. viscosa SLAM 1

<400> 319

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gcaagtgaga tagaacaaga attgcttgcc gaagaaaatg aaaaagaaaa agaaaaaaac 180

caacaatctt cagccatgat tattgatggt gaaacttatc aagtgaatga cacgttgcca 240

gaattggggc aagcgctgta tttttcggtt cagtctcgtc aatggccgct cgcctcccaa 300

tatttagcca ggtaccaaaa gcttgacggc ttcgacccat tattagttca ctataccaaa 360

ggtgcgctgt atcgtgttaa aggtgaactt acactagctg aacaggaata ttctcaactt 420

ttagcactac aacccgactt tttacctgcg caattagaac tggcacgcgt gcaatttgaa 480

aatcaaaaaa acgctgacgc ctattcacta tttattctca tcaacgaaaa cttaccttct 540

aacaataccc gctctcaagg aatccgaaaa accgtaacaa gcttcattac ggctgcaaaa 600

cacagagact cttggaacgg atcatttagc tttggaccgt catataacga caaccttaac 660

cagtcatcac aatcctatac ttgcttggct cggcttccgt caggccaatg ccgagtagaa 720

agaagcacac cagaagctgt aaaagggaca ggtgtcgatt ttaatgccag cctgaacaag 780

cgtctctcat tatctggtca tcatggtatc gcctttagcg ggctggctta tggttccagc 840

tatttagata atgacaaatt caatgaacaa actttaatca ccagccttgg atacagctat 900

caaaatgcaa ataacaaatt caccttatcg ccacagttgg aatacagtgc ttcaggtaat 960

aaagcacttt acttcgctgg aggtttgaaa tttgactggt ttaaaagcct ggattcatca 1020

agtgcgatga agctagaaat tgaggcggaa tatcaagatt accgaccagt aaaccttgaa 1080

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tggctactat ttggcggttt ggattggacc caaaaagata acgatgaaaa ggtgcatgcc 1200

tatcaactct tcggcggaag attcggcgtt aaccgagcat ggggcgaact ggttgatgta 1260

aatctattta cttcctttag gcaacgtaaa tatggtgagt tcagcgcatt attggacgaa 1320

agaagaacag atcaagaaca aagttataca ctcatgctgt cctccaagtc gctctcatta 1380

tacggtatta cgccgctact tacgtggact cataagcgag taaaaagcaa cgttgactgg 1440

ctttatacct atcaacaaaa cgaaatcgcc ttaaagttag aaaaaagatt ttga 1494

<210> 320

<211> 497

<212> PRT

<213> M. viscosa SLAM 1

<400> 320

Met Asn Leu Ile Ser Ala Ser Lys Arg Ser Ile Leu Val Cys Leu Leu
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Phe Ser Phe Ser Tyr Tyr Ser Val Ala Asp Gln Asp Thr Lys Ile Gln
20 25 30

Ile Gln Gln Arg Asp Asn Leu Thr Ala Ser Glu Ile Glu Gln Glu Leu
35 40 45

Leu Ala Glu Glu Asn Glu Lys Glu Lys Glu Lys Asn Gln Gln Ser Ser
50 55 60

Ala Met Ile Ile Asp Gly Glu Thr Tyr Gln Val Asn Asp Thr Leu Pro
65 70 75 80

Glu Leu Gly Gln Ala Leu Tyr Phe Ser Val Gln Ser Arg Gln Trp Pro
85 90 95

Leu Ala Ser Gln Tyr Leu Ala Arg Tyr Gln Lys Leu Asp Gly Phe Asp
100 105 110

Pro Leu Leu Val His Tyr Thr Lys Gly Ala Leu Tyr Arg Val Lys Gly
115 120 125

Glu Leu Thr Leu Ala Glu Gln Glu Tyr Ser Gln Leu Leu Ala Leu Gln
130 135 140

Pro Asp Phe Leu Pro Ala Gln Leu Glu Leu Ala Arg Val Gln Phe Glu
145 150 155 160

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

Asn Leu Pro Ser Asn Asn Thr Arg Ser Gln Gly Ile Arg Lys Thr Val
180 185 190

Thr Ser Phe Ile Thr Ala Ala Lys His Arg Asp Ser Trp Asn Gly Ser
195 200 205

Phe Ser Phe Gly Pro Ser Tyr Asn Asp Asn Leu Asn Gln Ser Ser Gln
210 215 220

Ser Tyr Thr Cys Leu Ala Arg Leu Pro Ser Gly Gln Cys Arg Val Glu
225 230 235 240

Arg Ser Thr Pro Glu Ala Val Lys Gly Thr Gly Val Asp Phe Asn Ala
245 250 255

Ser Leu Asn Lys Arg Leu Ser Leu Ser Gly His His Gly Ile Ala Phe
260 265 270

Ser Gly Leu Ala Tyr Gly Ser Ser Tyr Leu Asp Asn Asp Lys Phe Asn
275 280 285

Glu Gln Thr Leu Ile Thr Ser Leu Gly Tyr Ser Tyr Gln Asn Ala Asn
290 295 300

Asn Lys Phe Thr Leu Ser Pro Gln Leu Glu Tyr Ser Ala Ser Gly Asn
305 310 315 320

Lys Ala Leu Tyr Phe Ala Gly Gly Leu Lys Phe Asp Trp Phe Lys Ser
325 330 335

Leu Asp Ser Ser Ser Ala Met Lys Leu Glu Ile Glu Ala Glu Tyr Gln
340 345 350

Asp Tyr Arg Pro Val Asn Leu Glu Tyr Gln Ser Asp Trp Gln Trp Ser
355 360 365

Ser Tyr Leu Ser Leu Trp His Gln Leu Pro Asp Asn Trp Leu Leu Phe
370 375 380

Gly Gly Leu Asp Trp Thr Gln Lys Asp Asn Asp Glu Lys Val His Ala
385 390 395 400

Tyr Gln Leu Phe Gly Gly Arg Phe Gly Val Asn Arg Ala Trp Gly Glu
405 410 415

Leu Val Asp Val Asn Leu Phe Thr Ser Phe Arg Gln Arg Lys Tyr Gly
420 425 430

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

435 440 445

Tyr Thr Leu Met Leu Ser Ser Lys Ser Leu Ser Leu Tyr Gly Ile Thr

450 455 460

Pro Leu Leu Thr Trp Thr His Lys Arg Val Lys Ser Asn Val Asp Trp

465 470 475 480

Leu Tyr Thr Tyr Gln Gln Asn Glu Ile Ala Leu Lys Leu Glu Lys Arg

485 490 495

Phe

<210> 321

<211> 1506

<212> DNA

<213> Marinomonas sp. D104 SLAM 1

<400> 321

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aggttaaacc aaagcataga acaacaaagc aattcaaagg aaagtgagtt actcaaagat 180

gaagattacc taccaggaaa acgcccagag ctgattctca atagcaagtc ttacaccgta 240

ggacacaatg ctaatgatat cgggcgtgca ctctacgttt ccatcaagca aaaacaatgg 300

aatgccgttg tttattttct caacgaatat caaaccctcc ctgatgctga ccctctttta 360

ctcgcttatg cgaaaggcgc gctggctaga atacaaggta atatggagca agccacgata 420

gaatatcgcc acctcctcga cctgaactct gaatttttgc cgggccaact ggaactggct 480

cgcgtcttat ttgaagatca tcaagacaaa gaagcggagg aaatgttcac tcagatatcc 540

gccatacttg atccagacaa cgcacaacaa gctggcgtaa accgcacagt agaaagtttc 600

cgtaaagcac ttgaacagcg ccgtgattgg tcgacttcca tcgcgcttgg tgcagtatgg 660

aatgataacc ttaaccaatc ctcagaaagc cgaacttgtc tgctgatgta tcaaaatcaa 720

tgtgtttatg aacgtaaaat ccctgacgcc atgtcagcaa cagggcttga ttacgaactt 780

accatcaaca aatacatgcc aattgtcggt cataatggac tgtattctcg ctctttgctg 840

tacggtaaaa gttatggtga ttacagtgat tacaatgaaa gtacgttagt aacacagcta 900

ggttatcgct accaagatat tggtgaccag atacaactcg ctccttcttt tgaattttcc 960

gcctatggca ataaagcgat gtacagtgcc ttaggcctcc atggcgaatg gactcgccgc 1020

ttttctaaca agcaaatgtt caaactccaa ggcgattaca aagaactgcg ctacaaaaag 1080

caaaactatg aacgttataa cggcccttcc tactcagcaa acgcaaccat gtggcaagtc 1140

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aaaccctatg gttatataca actcggcgta cggctggggg tctcaaaatc gttttctaat 1260

gttctaagcg caacattttt cacctctttc cgcgaacaaa cttacaaagc gtacagcagc 1320

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caactgtcca tcttaggttt tactccgagc ctaaccatca aacactcaaa tataaacagc 1440

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ttttag 1506

<210> 322

<211> 501

<212> PRT

<213> Marinomonas sp. D104 SLAM 1

<400> 322

Met Arg Phe Ser Lys Asn Thr Leu Cys Ser Leu Leu Asn Tyr Lys Thr
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Phe Gly Leu Val Leu Leu Phe Met Phe Ser Gln Pro Ala Thr Ala Asp
20 25 30

Asp His Asp Leu Asp Thr Gln Leu Arg Leu Asn Gln Ser Ile Glu Gln
35 40 45

Gln Ser Asn Ser Lys Glu Ser Glu Leu Leu Lys Asp Glu Asp Tyr Leu
50 55 60

Pro Gly Lys Arg Pro Glu Leu Ile Leu Asn Ser Lys Ser Tyr Thr Val
65 70 75 80

Gly His Asn Ala Asn Asp Ile Gly Arg Ala Leu Tyr Val Ser Ile Lys
85 90 95

Gln Lys Gln Trp Asn Ala Val Val Tyr Phe Leu Asn Glu Tyr Gln Thr
100 105 110

Leu Pro Asp Ala Asp Pro Leu Leu Leu Ala Tyr Ala Lys Gly Ala Leu
115 120 125

Ala Arg Ile Gln Gly Asn Met Glu Gln Ala Thr Ile Glu Tyr Arg His
130 135 140

Leu Leu Asp Leu Asn Ser Glu Phe Leu Pro Gly Gln Leu Glu Leu Ala
145 150 155 160
Arg Val Leu Phe Glu Asp His Gln Asp Lys Glu Ala Glu Glu Met Phe
165 170 175
Thr Gln Ile Ser Ala Ile Leu Asp Pro Asp Asn Ala Gln Gln Ala Gly
180 185 190

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

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

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

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

385 390 395 400

Lys Pro Tyr Gly Tyr Ile Gln Leu Gly Val Arg Leu Gly Val Ser Lys

405 410 415

Ser Phe Ser Asn Val Leu Ser Ala Thr Phe Phe Thr Ser Phe Arg Glu

420 425 430

Gln Thr Tyr Lys Ala Tyr Ser Ser Ile Leu Gly Ala Lys Arg Asn Asp

435 440 445

His Glu Ser Ser Tyr Thr Leu Ile Leu Lys Ser Pro Gln Leu Ser Ile

450 455 460

Leu Gly Phe Thr Pro Ser Leu Thr Ile Lys His Ser Asn Ile Asn Ser

465 470 475 480

Asn Val Asp Trp Leu Tyr Ser Arg Glu Asn Asn Gln Val Ser Leu Lys

485 490 495

Leu Glu Lys Thr Phe

500

<210> 323

<211> 1497

<212> DNA

<213> Marinomonas sp. MWYL1 SLAM 1

<400> 323

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caaaacatag aacaacaaaa caattcaaag gaaagtgagt tactcaaaga tgaagattac 180

ctatcaggaa aacgcccaga gctgattctt gatggcaagt cttacaccgt aggacacaat 240

gctagtgata ttgggcgtgc gctctatgtt tccattaaac aaaaacaatg gaatgccgtc 300

gtttactttc tcgatgaata ccgaacactt accgatgctg atccactttt actcgcttat 360

gcgaaaggcg cattagctcg aatccaaggt aatatggaac aagccgcaac agagtatcgc 420

cagctcctcg gcctgaaccc tgaattcttg ccaggtcaac tggaactggc ccgcgtacta 480

ttcgaagatc atcaagataa agaagcaaag gtagttttta cacaaatatc ggcaaagctc 540

gatcctgaca atgagcaaca gaccggcgtc tatcgtacgg tagaaagttt ccgtaaagca 600

cttgaacaac gccgtgattg gtcgacgtcc atcgcgcttg gtgcagtatg gaatgataac 660

cttaaccaat cttcagaaag tcgtacctgt ttactccttt cccaaggcca atgtatttat 720

gaacgaaaaa tccccgatgc tatttcagca acggggcttg attacgaact gacccttaac 780

aagcacacac ctattacgag tcataatgga ctgtattttc gctctttgct atatggtaaa 840

agctatgacg attacactga ctacaatgaa agtacgctaa ttacacagct aggttatcgc 900

taccaagatc tcgatgacca gatacaactc gctccttctt ttgaattttc cgcctatgga 960

aataaagcca tgtacagtgc cttaggcctg catggcgaat ggactcgtcg cttttctaac 1020

aagcaaatac ttaaagtcca aggcgattac aaagaactgc gctataaaaa gcaaaactac 1080

gaacgttata acggcccttc ctactcagca aatgcaacta tgtggcaagt cttaccgaat 1140

agctggacgt tatttggagg tgttgatggc ttagaccgac aagcggatga taaaccctat 1200

ggctacttac aacttggcgt acgactcggg gtctcaaaat cgttttctaa tgttctaagc 1260

acaacatttt tcacctcttt ccgcgaacaa acctacaaag cgtacagcag cattcttggc 1320

gcaaagcgaa atgaccatga aagtagttac acattgatct tgaaatcgcc tcaactgtcc 1380

atcttaggtt ttgctccgag cctaaccatc aaacactcaa atataaacag caatgtagat 1440

tggctttata gccgtgaaaa caaccaagtc agcctaaaaa tggagaaaaa tttctaa 1497

<210> 324

<211> 498

<212> PRT

<213> Marinomonas sp. MWYL1 SLAM 1

<400> 324

Met His Phe Leu Lys Ser Asn Phe Leu His Cys Lys Ile Val Gly Leu
1 5 10 15

Ala Leu Leu Phe Met Phe Ser Arg Ser Ala Thr Ala Asp Asp His Asp
20 25 30

Leu Asp Thr Gln Leu Arg Leu Asn Gln Asn Ile Glu Gln Gln Asn Asn
35 40 45

Ser Lys Glu Ser Glu Leu Leu Lys Asp Glu Asp Tyr Leu Ser Gly Lys
50 55 60

Arg Pro Glu Leu Ile Leu Asp Gly Lys Ser Tyr Thr Val Gly His Asn
65 70 75 80

Ala Ser Asp Ile Gly Arg Ala Leu Tyr Val Ser Ile Lys Gln Lys Gln
85 90 95

Trp Asn Ala Val Val Tyr Phe Leu Asp Glu Tyr Arg Thr Leu Thr Asp

100 105 110

Ala Asp Pro Leu Leu Leu Ala Tyr Ala Lys Gly Ala Leu Ala Arg Ile

115 120 125

Gln Gly Asn Met Glu Gln Ala Ala Thr Glu Tyr Arg Gln Leu Leu Gly

130 135 140

Leu Asn Pro Glu Phe Leu Pro Gly Gln Leu Glu Leu Ala Arg Val Leu

145 150 155 160

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

165 170 175

Ser Ala Lys Leu Asp Pro Asp Asn Glu Gln Gln Thr Gly Val Tyr Arg

180 185 190

Thr Val Glu Ser Phe Arg Lys Ala Leu Glu Gln Arg Arg Asp Trp Ser

195 200 205

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

210 215 220

Ser Glu Ser Arg Thr Cys Leu Leu Leu Ser Gln Gly Gln Cys Ile Tyr

225 230 235 240

Glu Arg Lys Ile Pro Asp Ala Ile Ser Ala Thr Gly Leu Asp Tyr Glu

245 250 255

Leu Thr Leu Asn Lys His Thr Pro Ile Thr Ser His Asn Gly Leu Tyr

260 265 270

Phe Arg Ser Leu Leu Tyr Gly Lys Ser Tyr Asp Asp Tyr Thr Asp Tyr

275 280 285

Asn Glu Ser Thr Leu Ile Thr Gln Leu Gly Tyr Arg Tyr Gln Asp Leu

290 295 300

Asp Asp Gln Ile Gln Leu Ala Pro Ser Phe Glu Phe Ser Ala Tyr Gly

305 310 315 320

Asn Lys Ala Met Tyr Ser Ala Leu Gly Leu His Gly Glu Trp Thr Arg

325 330 335

Arg Phe Ser Asn Lys Gln Ile Leu Lys Val Gln Gly Asp Tyr Lys Glu

340 345 350

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

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

Ala Pro Ser Leu Thr Ile Lys His Ser Asn Ile Asn Ser Asn Val Asp
465 470 475 480
Trp Leu Tyr Ser Arg Glu Asn Asn Gln Val Ser Leu Lys Met Glu Lys
485 490 495
Asn Phe

<210> 325
<211> 1317
<212> DNA
<213> Martelella sp. AD-3 SLAM 1
<400> 325
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atcaaggtgc tgatcgagag cggccagtat gagaaagcga tggcgctttc ggcgcagctt 180
tccgacgacc ctgagctttc cgcgctgtcg cagcaattca cctatgcgct tatcctgaag 240
catgagggcc acttcaggga agcggcgatc ctgatgcgcg gcgttctcga caagaagccg 300
gatttcaccc gcgtgcgcca ggagcttgcc cacacgctgg cgctgatggg cgagaagaag 360
gcggcgatct atcatttctc gcttctggcc gacaacgcgc cgagcgaatc gctccgctcc 420

ttctacgagg acttcatcga ccgggtgaat atcgaccgcc cctggacgct tggcggttac 480

ctcgccattg cgccaagcac caatatctcc aacgccacgg atcagagcct tgtccatgtc 540

ggcggcattc cgcttgcgcc cggcacgaag gcggaaagcg gcgtggggct caattacggc 600

gtcaacggca cctattcctt cgatctcgtc gacgacctgt cgctgacctt cggcggctcc 660

gtcaccggcc ttgcctacag ggaaaaggcc tataaccaga cccagttcgg cggcttctcg 720

cagctttcct ggcgcaacga cccgtggatt ttcagcggcg gcatggcggc ggaatatgtg 780

ctgatgggca atgagcctta ccgcgtcggc tatggtccgg tcttttccgt gcgacgctcc 840

ttcgggccct tcggcgtcac gtcggccaat ttctcgttcc agtggctcga ttatcacgac 900

atggatgcct atgatggcta ccaggccggc atgagcatca accatcgcta tgcgctgacg 960

ccatcgagca gcatccgcat gggcgggggg ttcaactatg tctccgccga aaaggacttc 1020

aattcctatt ccggctacaa catcaacgcc aaatatgccc gcgaatggtc gggcgggata 1080

ctgaccgaca tagaggtcga gggcacgctg cgggactatg agggcgattt tccgctgatg 1140

accaagtcgc ggcttgaccg caggctcgac atagccgtcg gcgccacctt tcgcacgctt 1200

gcgatgaaag gcttcgcgcc gcgcctcgaa tatgcctatt cgaagaattt ctccaatgtc 1260

gaactttacg aatacgacaa gagcacggtt tcgctgttcg tcaccaaaca gttctga 1317

<210> 326

<211> 438

<212> PRT

<213> Martelella sp. AD-3 SLAM 1

<400> 326

Met Arg His Phe Leu Ser Leu Met Arg Leu Arg Leu Ser Gly Gly Leu
1 5 10 15

Ala Gly Leu Ala Phe Leu Leu Thr Val Phe Ala Ala Gly Met Ala Phe
20 25 30

Ala Val Val Asn Pro Phe Pro Gln Ile Lys Val Leu Ile Glu Ser Gly
35 40 45

Gln Tyr Glu Lys Ala Met Ala Leu Ser Ala Gln Leu Ser Asp Asp Pro
50 55 60

Glu Leu Ser Ala Leu Ser Gln Gln Phe Thr Tyr Ala Leu Ile Leu Lys
65 70 75 80

His Glu Gly His Phe Arg Glu Ala Ala Ile Leu Met Arg Gly Val Leu

85 90 95

Asp Lys Lys Pro Asp Phe Thr Arg Val Arg Gln Glu Leu Ala His Thr

100 105 110

Leu Ala Leu Met Gly Glu Lys Lys Ala Ala Ile Tyr His Phe Ser Leu

115 120 125

Leu Ala Asp Asn Ala Pro Ser Glu Ser Leu Arg Ser Phe Tyr Glu Asp

130 135 140

Phe Ile Asp Arg Val Asn Ile Asp Arg Pro Trp Thr Leu Gly Gly Tyr

145 150 155 160

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

165 170 175

Leu Val His Val Gly Gly Ile Pro Leu Ala Pro Gly Thr Lys Ala Glu

180 185 190

Ser Gly Val Gly Leu Asn Tyr Gly Val Asn Gly Thr Tyr Ser Phe Asp

195 200 205

Leu Val Asp Asp Leu Ser Leu Thr Phe Gly Gly Ser Val Thr Gly Leu

210 215 220

Ala Tyr Arg Glu Lys Ala Tyr Asn Gln Thr Gln Phe Gly Gly Phe Ser

225 230 235 240

Gln Leu Ser Trp Arg Asn Asp Pro Trp Ile Phe Ser Gly Gly Met Ala

245 250 255

Ala Glu Tyr Val Leu Met Gly Asn Glu Pro Tyr Arg Val Gly Tyr Gly

260 265 270

Pro Val Phe Ser Val Arg Arg Ser Phe Gly Pro Phe Gly Val Thr Ser

275 280 285

Ala Asn Phe Ser Phe Gln Trp Leu Asp Tyr His Asp Met Asp Ala Tyr

290 295 300

Asp Gly Tyr Gln Ala Gly Met Ser Ile Asn His Arg Tyr Ala Leu Thr

305 310 315 320

Pro Ser Ser Ser Ile Arg Met Gly Gly Gly Phe Asn Tyr Val Ser Ala

325 330 335

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

Ala Arg Glu Trp Ser Gly Gly Ile Leu Thr Asp Ile Glu Val Glu Gly
355 360 365

Thr Leu Arg Asp Tyr Glu Gly Asp Phe Pro Leu Met Thr Lys Ser Arg
370 375 380

Leu Asp Arg Arg Leu Asp Ile Ala Val Gly Ala Thr Phe Arg Thr Leu
385 390 395 400

Ala Met Lys Gly Phe Ala Pro Arg Leu Glu Tyr Ala Tyr Ser Lys Asn
405 410 415

Phe Ser Asn Val Glu Leu Tyr Glu Tyr Asp Lys Ser Thr Val Ser Leu
420 425 430

Phe Val Thr Lys Gln Phe
435

<210> 327

<211> 1362

<212> DNA

<213> Martelella sp. AD-3 SLAM 2

<400> 327

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ccgcaagtgg gcttcgcaaa acagtccagc gtgaccggtt ttgacgcggt gcgcgtgctg 180

gtcgaatacg ggcgctacga agatgcaatg gcgctggcgg aaagctttgc cgccgacgaa 240

aagggcaaga cgcttgccgc tgccttcacg caggctctca ttctggagca gcagggccgg 300

ttgccggaag cggcaagcgc tcttcgcgcc attctttcgc aaaatccgaa agcccgcaac 360

gtccggcgcg aacttgccgg cgttctctac gaacagggcg agggcaacgc atcgctgcat 420

cacttcgaac ttctggccgg aagcgccagc agtgccgaag agcgcaggtt ctacgaacgc 480

ctcgccgcca gggcccgcac gatccgtccc tggtcgcttg gcggctatct ctccatagcc 540

cccagcacca acatcaccga agcccccgac gccgatctcg tctatgtcgg cggcattccc 600

atactgcctg ccaagaagaa aagcggcatc ggctatggct atggggtgga cggatcctac 660

cgtttcgacc tcgatgaaat ctcatcgatc accataggcg gcggggtgaa cgggaactgg 720

tatcgtgata ccagcttcaa cacgagctac ttcgacagtt tcgtcgatta tcgccgcgaa 780

atgggtgact ggacggtgac cggcggtgtg gtcggccagt atgtgatgaa gggcgaagag 840

ccttatcgct ggtcgctcgg cccggctttc tcgctgaggc acaatatggg ccgaaagggc 900
gttacaacgt tgcgcggcct gtggcgcaag cttgattacc acgaccgcga tgcgctcgac 960
ggcagcgaga ccgtgctggg aatcagccat ctctacgcca tctcgtccgc aagttcggtg 1020
cgtttcggcg gcaatgtcag ctttgttgac gccgcgaacg acaccaacag ctatgtccgg 1080
ttctccctga atgcgcaata tttccgggaa tggagtttcg gagcgatttc cgatatctcg 1140
attttcgcgg acgatcgccg atatcaggat ataacctatc tcgcgggcga aaaacgctcc 1200
gatcagcgta tccaggcctc gctgggcatc acgctgcgca atctggcggt caggggcttc 1260

gccccacgcc tcgaatatgc ctacacgcag aacttctcga atatcgatgt ctatgatttt 1320
tcgaagaaca cgatatcaac ctatctgacg aagaaattct ga 1362

<210> 328
<211> 453
<212> PRT
<213> Martelella sp. AD-3 SLAM 2
<400> 328

Met Thr Asp Arg Arg Ser Glu Pro Arg Ala Arg Asp Pro Ala Arg Gly
1 5 10 15
Leu Glu Gln Arg Leu Glu Arg Thr Lys Arg Phe Met Leu Ala Phe Ala
20 25 30
Leu Gly Leu Phe Thr Met Gly Ile Pro Gln Val Gly Phe Ala Lys Gln
35 40 45
Ser Ser Val Thr Gly Phe Asp Ala Val Arg Val Leu Val Glu Tyr Gly
50 55 60
Arg Tyr Glu Asp Ala Met Ala Leu Ala Glu Ser Phe Ala Ala Asp Glu
65 70 75 80
Lys Gly Lys Thr Leu Ala Ala Ala Phe Thr Gln Ala Leu Ile Leu Glu
85 90 95
Gln Gln Gly Arg Leu Pro Glu Ala Ala Ser Ala Leu Arg Ala Ile Leu
100 105 110
Ser Gln Asn Pro Lys Ala Arg Asn Val Arg Arg Glu Leu Ala Gly Val
115 120 125

Leu Tyr Glu Gln Gly Glu Gly Asn Ala Ser Leu His His Phe Glu Leu
130 135 140
Leu Ala Gly Ser Ala Ser Ser Ala Glu Glu Arg Arg Phe Tyr Glu Arg
145 150 155 160
Leu Ala Ala Arg Ala Arg Thr Ile Arg Pro Trp Ser Leu Gly Gly Tyr

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

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

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

355 360 365
Arg Glu Trp Ser Phe Gly Ala Ile Ser Asp Ile Ser Ile Phe Ala Asp

370 375 380

Asp Arg Arg Tyr Gln Asp Ile Thr Tyr Leu Ala Gly Glu Lys Arg Ser

385 390 395 400

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

405 410 415

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

420 425 430

Ser Asn Ile Asp Val Tyr Asp Phe Ser Lys Asn Thr Ile Ser Thr Tyr

435 440 445

Leu Thr Lys Lys Phe

450

<210> 329

<211> 1308

<212> DNA

<213> N. aromaticivorans SLAM 1

<400> 329

atggctgtgc ccgctgccga aaggccgcag gctcctgccg tcgaagccgg ggacgcccga 60

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ggcgattttg ccgctgccga atccgcctat cgcgcgctcg ccgcgaaccc ggatatcgac 180

ctgcgcaccg aagcgcgctt ccgcctcggc ctgatgctgg ccgatggcat gggtcgcccg 240

cgcgacgctg ccatcgaatt tcgccgcatc ctcgatgaaa agcccgatgc cgcgcgcgtc 300

cggctcgaac ttgcccgcat ggacgccatg cttggccgcc tcggcgcggc agagcgcgaa 360

tttcgcgccg cgcaggccac tggccagctc cccccggatg tagagcgcgc ggtgcgcttc 420

tatgcttctg ctttggctgc cgccaagccg ttcggcggca gcatcgaact tgccctcgcg 480

cccgacagca acatcaaccg cgctacccgt tcggatacgc tcggcaccgt catcggcgat 540

ttcacgctca gcgacgatgc caaggcgaaa tccggcatcg gccttgcggc gcgcgcgcag 600

gcctatgccc ggcttccgct cggccagaag gcccggcttc tcgcgcgtgt ttccggcagc 660

ggcgatttct accgcacccg cgcattcgac gattatgccc tcgcgctcca ggccgggccg 720

gaattcgtct cgggcgcgga tcgcttcacc ctttcggccg gtccctcatg gcgctggtac 780

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gatttcaacc gccgtgcagc cgaactgggg gtcacgtcgg cattctga 1308

<210> 330

<211> 435

<212> PRT

<213> N. aromaticivorans SLAM 1

<400> 330

Met Ala Val Pro Ala Ala Glu Arg Pro Gln Ala Pro Ala Val Glu Ala

1 5 10 15

Gly Asp Ala Arg Lys Ser Val Gln Leu Thr Pro Ala Gln Leu Phe Leu

20 25 30

Phe Ala Asp Ala Ala Arg Asp Ala Gly Asp Phe Ala Ala Ala Glu Ser

35 40 45

Ala Tyr Arg Ala Leu Ala Ala Asn Pro Asp Ile Asp Leu Arg Thr Glu

50 55 60

Ala Arg Phe Arg Leu Gly Leu Met Leu Ala Asp Gly Met Gly Arg Pro

65 70 75 80

Arg Asp Ala Ala Ile Glu Phe Arg Arg Ile Leu Asp Glu Lys Pro Asp

85 90 95

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

100 105 110

Arg Leu Gly Ala Ala Glu Arg Glu Phe Arg Ala Ala Gln Ala Thr Gly

115 120 125

Gln Leu Pro Pro Asp Val Glu Arg Ala Val Arg Phe Tyr Ala Ser Ala

130 135 140

Leu Ala Ala Ala Lys Pro Phe Gly Gly Ser Ile Glu Leu Ala Leu Ala

145 150 155 160

Pro Asp Ser Asn Ile Asn Arg Ala Thr Arg Ser Asp Thr Leu Gly Thr
165 170 175
Val Ile Gly Asp Phe Thr Leu Ser Asp Asp Ala Lys Ala Lys Ser Gly
180 185 190
Ile Gly Leu Ala Ala Arg Ala Gln Ala Tyr Ala Arg Leu Pro Leu Gly

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

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

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

385 390 395 400
Gly Leu Ala Pro Phe Val Arg Ala Arg Phe Glu Arg Asn Leu Ser Thr

405 410 415

Val Glu Leu Tyr Asp Phe Asn Arg Arg Ala Ala Glu Leu Gly Val Thr

420 425 430

Ser Ala Phe

435

<210> 331

<211> 1422

<212> DNA

<213> N. bacilliformis SLAM 1

<400> 331

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cccgaaccca cagccaaccg cctcaccccc aaccctaccg gccaaaccct caccatagac 180

aaccccgatc aactcctgca acagcccgaa ctcctccacc gcgccctctc ctccgccgcc 240

atcgccggca acgcccaagc cgtcaaactc ctcctgcccg tctaccgccg tctgcccgaa 300

cccaaagacc acaccctcct cgacctcgcc gaaggtatcg ccgcccacgc cgacggccac 360

tacacccgcg ccgtcaaaca cctgcaacgc gcccaccaaa ccatgcccca agccgtcatc 420

atccgcctgc gcctcgccca agccctcaaa gacgaccacc gcgacctcgc cgccgagagc 480

cactaccaaa ccctcctcga caccgacctc cctcccgaag cccgcaccgc cctgcaaagc 540

caactcgacg aaattcgcag ccgcagccgc tggcagaccg aactcaacgc caactacacc 600

cgcgacaaca acatcaacaa cgccccaagc caacgcaccg tccgctacgc cggtggcacc 660

tggatcctgc ccgaacccca aaaagcccaa ggcatcgcct acaatgccgg ccttgcccgt 720

gacatcaacc tccccggcca ctggcgcatc cgcagcgaaa ccgacgccta cggtaaaacc 780

tactgggaca accaccccta cgacgaccac accgtccgca ccgccctcgg catcgcctac 840

aaaagcggcc gcagcgaagc cgccctcctg ccttatcacc aacaccgctg gtacggcggc 900

gcgacctacg cccgcgaaaa cggcctccgc gcccaatggc agcggcagct ttccgaacgc 960

caccgcctca tcaccgccgc cgaaaccggc cgcccccgcc acccacaccg cccctccgcc 1020

gacggccgcg acagcagcct ctccgccacc tgggtctacc tgcaaagccc ccgccaatac 1080

ctcaccctcg gcgcagacct cgcccgcaaa cgcgcccgcg accccgacga agcctaccgc 1140

cgcaaagccc tccgcgcctc catcgtgcgc atctggggca aaggcctcgg caccgccctc 1200

accgccgcct acgcccgccg caaatacgac ggcgcattca tcgtccccac cctccgcagc 1260

gaccgcgaat acaccgccac cgccgccatc tggcacaacc gcctcagctt ccggggcatc 1320

acccccgcc tcgtaaccgt ctggcacaaa accgacagca acatcccctt ctacacctac 1380

cgcaaagcca acgccttcat ccaactgggc aaaaccttct ga 1422

<210> 332

<211> 473

<212> PRT

<213> N. bacilliformis SLAM 1

<400> 332

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

180 185 190

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

195 200 205

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

210 215 220

Glu Pro Gln Lys Ala Gln Gly Ile Ala Tyr Asn Ala Gly Leu Ala Arg

225 230 235 240

Asp Ile Asn Leu Pro Gly His Trp Arg Ile Arg Ser Glu Thr Asp Ala

245 250 255

Tyr Gly Lys Thr Tyr Trp Asp Asn His Pro Tyr Asp Asp His Thr Val

260 265 270

Arg Thr Ala Leu Gly Ile Ala Tyr Lys Ser Gly Arg Ser Glu Ala Ala

275 280 285

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

290 295 300

Arg Glu Asn Gly Leu Arg Ala Gln Trp Gln Arg Gln Leu Ser Glu Arg

305 310 315 320

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

325 330 335

Arg Pro Ser Ala Asp Gly Arg Asp Ser Ser Leu Ser Ala Thr Trp Val

340 345 350

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

355 360 365

Arg Lys Arg Ala Arg Asp Pro Asp Glu Ala Tyr Arg Arg Lys Ala Leu

370 375 380

Arg Ala Ser Ile Val Arg Ile Trp Gly Lys Gly Leu Gly Thr Ala Leu

385 390 395 400

Thr Ala Ala Tyr Ala Arg Arg Lys Tyr Asp Gly Ala Phe Ile Val Pro

405 410 415

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

420 425 430

Asn Arg Leu Ser Phe Arg Gly Ile Thr Pro Arg Leu Val Thr Val Trp

435 440 445

His Lys Thr Asp Ser Asn Ile Pro Phe Tyr Thr Tyr Arg Lys Ala Asn

450 455 460

Ala Phe Ile Gln Leu Gly Lys Thr Phe

465 470

<210> 333

<211> 1416

<212> DNA

<213> N. bacilliformis SLAM 2

<400> 333

atgcgctatc ccatcctgat actctgcgcc gccgcctgcg cggctgccgc cgatcccctt 60

tccacgccgc acgacgacaa ccccgacccc aaccgtagcc aaatccgcca aatgcagcac 120

gaagcccgtc tgcccgcgtc cgaacatgaa ggagacgacg gctctgtttc catgagcgaa 180

gacgagctga tcgcgcagcc cgatttgctg caaaacgtcc tcgacaccgc cgtggcgcgg 240

cagcaggttg aaaacatccg cttcctgctg ccgctttacc gccgtttgga cgaagaacgg 300

cgcgacgcgg tgctggaaga ctacgccgaa tccttcctgc tgcgcgaaga cgggcaatat 360

gcccgcgccg aagaaaagct gcgcggcatc cttgcgcaaa acccgggcta cgcccccgta 420

cgcctgcaac tcgcgctcac cctgtcgcaa agcggccaaa cgcgcgaagc cgccgccgaa 480

gtggcggaag tgaaggaaac ctccgaactg ccgcccgatg cggccgcctt tctcaacagc 540

ttttccgact acctcaaacg cgaccgcgcc tggcagtttg acgccaacgc ctactacctc 600

gccgatcgca atgtcggccg cgcgccgaaa gagcgcgaat acggcccctg gcgtttcccc 660

gaaccccgcg ccgcgcacgg gctgggctac gatgcctccg ccgtcaaaac cctgcccgta 720

aaaaaacact gggcggcgcg ggtgcaggct tccgtttacg gcaaattcta ttgggacgcg 780

cacgattacg acgatttgaa cgcccgcatc gaagccgggc cggtgtaccg cagcggcagc 840

ggcgaaaccg ccctgacgcc ctttgccgaa aaacgctggt acggcacgga agcctattcg 900

cacaccgcag gcggcgtgct gcgccgctcg cacaatctgt cgccgaaaac catgctgttt 960

gcaagctggc agacgggcta taaaaagcat gaagaacgcg actatctcga cggcgcaagc 1020

cacggcggcg cactctcgct ggtgtaccaa agctcgccgc agcagtattt cgtgttcggc 1080

gcgggcgcgg ggcgcgaaaa cgcccgcgac cctgcggaag cctaccgcca cgcaagcctg 1140

cgcgcaggct ggacgcgccg ctggtcaggc ggcgacggcc tgcttacttc gcttaacggc 1200

agcatccgcc gcagccttta ccgcagcgag gatttttca acatccgccg ccgcgacacg 1260

gaatatttcg tcctcgccgc cgtcggccac aaaaaactgt cgtggaaaag cttcaccccg 1320

cacctgaact ggacatggtc gtatctggca agcaaccatt tctactaccg ccgccacgaa 1380

aaccgcgtgt ttttggacgt gtccaaacag ttctga 1416

<210> 334

<211> 471

<212> PRT

<213> N. bacilliformis SLAM 2

<400> 334

Met Arg Tyr Pro Ile Leu Ile Leu Cys Ala Ala Ala Cys Ala Ala Ala
1 5 10 15

Ala Asp Pro Leu Ser Thr Pro His Asp Asp Asn Pro Asp Pro Asn Arg
20 25 30

Ser Gln Ile Arg Gln Met Gln His Glu Ala Arg Leu Pro Ala Ser Glu
35 40 45

His Glu Gly Asp Asp Gly Ser Val Ser Met Ser Glu Asp Glu Leu Ile
50 55 60

Ala Gln Pro Asp Leu Leu Gln Asn Val Leu Asp Thr Ala Val Ala Arg
65 70 75 80

Gln Gln Val Glu Asn Ile Arg Phe Leu Leu Pro Leu Tyr Arg Arg Leu
85 90 95

Asp Glu Glu Arg Arg Asp Ala Val Leu Glu Asp Tyr Ala Glu Ser Phe
100 105 110

Leu Leu Arg Glu Asp Gly Gln Tyr Ala Arg Ala Glu Glu Lys Leu Arg
115 120 125

Gly Ile Leu Ala Gln Asn Pro Gly Tyr Ala Pro Val Arg Leu Gln Leu
130 135 140

Ala Leu Thr Leu Ser Gln Ser Gly Gln Thr Arg Glu Ala Ala Ala Glu
145 150 155 160

Val Ala Glu Val Lys Glu Thr Ser Glu Leu Pro Pro Asp Ala Ala Ala
165 170 175

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

180 185 190

Phe Asp Ala Asn Ala Tyr Tyr Leu Ala Asp Arg Asn Val Gly Arg Ala

195 200 205

Pro Lys Glu Arg Glu Tyr Gly Pro Trp Arg Phe Pro Glu Pro Arg Ala

210 215 220

Ala His Gly Leu Gly Tyr Asp Ala Ser Ala Val Lys Thr Leu Pro Val

225 230 235 240

Lys Lys His Trp Ala Ala Arg Val Gln Ala Ser Val Tyr Gly Lys Phe

245 250 255

Tyr Trp Asp Ala His Asp Tyr Asp Asp Leu Asn Ala Arg Ile Glu Ala

260 265 270

Gly Pro Val Tyr Arg Ser Gly Ser Gly Glu Thr Ala Leu Thr Pro Phe

275 280 285

Ala Glu Lys Arg Trp Tyr Gly Thr Glu Ala Tyr Ser His Thr Ala Gly

290 295 300

Gly Val Leu Arg Arg Ser His Asn Leu Ser Pro Lys Thr Met Leu Phe

305 310 315 320

Ala Ser Trp Gln Thr Gly Tyr Lys Lys His Glu Glu Arg Asp Tyr Leu

325 330 335

Asp Gly Ala Ser His Gly Gly Ala Leu Ser Leu Val Tyr Gln Ser Ser

340 345 350

Pro Gln Gln Tyr Phe Val Phe Gly Ala Gly Ala Gly Arg Glu Asn Ala

355 360 365

Arg Asp Pro Ala Glu Ala Tyr Arg His Ala Ser Leu Arg Ala Gly Trp

370 375 380

Thr Arg Arg Trp Ser Gly Gly Asp Gly Leu Leu Thr Ser Leu Asn Gly

385 390 395 400

Ser Ile Arg Arg Ser Leu Tyr Arg Ser Glu Asp Phe Phe Asn Ile Arg

405 410 415

Arg Arg Asp Thr Glu Tyr Phe Val Leu Ala Ala Val Gly His Lys Lys

420 425 430

Leu Ser Trp Lys Ser Phe Thr Pro His Leu Asn Trp Thr Trp Ser Tyr
435 440 445

Leu Ala Ser Asn His Phe Tyr Tyr Arg Arg His Glu Asn Arg Val Phe
450 455 460

Leu Asp Val Ser Lys Gln Phe
465 470

<210> 335

<211> 1482

<212> DNA

<213> N. bacilliformis SLAM 3

<400> 335

atgaaaaaat atgccctgct gcccgccctg ctcttgtctg ccgccgcctt tgccgacgac 60

gacgacaccc gcctgctgct cgacaacgcg cgtttccaaa tgcgccagca gcaggccgaa 120

gccttttcag agtgcgaagc ctcccgccct cgggactgcc tctccgacag cggcagcatc 180

gaaatcgacg gcgaaaccta tctcgtgccg aacaccgcca acgatttgaa actgggcatt 240

tactacgcaa tcgacggcag gcagtggggc aaagtgcgcg aattcctcca acgctaccgc 300

aacttgtccg accacaagcc gcaactggtc ttgatggccg aaggcttgct ggcgcgctcg 360

gagggcaaaa ccgccgccgc gctggaaaaa atgcaggccg cacatgaaac cgcacccgag 420

gatgtgcgga tcaacttgga actggcgcgg ctctacggcg aggacaacca aacccgcgaa 480

tcgcaggcgc agtttgaaca agtcgtaaaa acagacatcc cgcccgaaac ccgcgaaatg 540

gtgcagggct atcttgccgc gctcgaccgc cgccgccgct ggcacggcag cctcagcatc 600

ggcggcggct acaacgacaa catcaaccag ggcaatggca agcgcgaatg cgtcggcatg 660

tttatggggc agtgtttcag ctaccgcagc ctgcccgagc cggtcggctc ggcgttttgg 720

cagtacagcg cggttgccgc caaaaaaatc cccctgcgcg gccaccacaa cctgctgctg 780

cgcggcctct cctacggcac caaataccgc cgcgacgaca cccagtccga accgcccgag 840

ccgtacagcg aaaacaccgc cgcgctgtat gcgggctacg aatacaccga tgcccgcaac 900

gatttcaccc ttacccccta tttcgagcac tactatcgcg gcagccgcag ccgttaccgc 960

gcatggggcg cggaagcggg ctgggagcgc aatctcaacg ccaaatggtc gctcaacgcc 1020

cgcgccgaag gccgccgcgt caaatacctc gaacaggagc ggcagtatta cagcgactac 1080

acgctttaca ccggcggcgt ggggctgggc tacacctttt cagacggcct cggcctttac 1140

ggcggcatcg acctcacccg ccgcaaatat ccctacgccg cgtccagcag caaggaatac 1200

accgcccgaa tcggcggcta caaaatgttc caaaacggca tctatttcaa cgccgccgcc 1260

ctctaccgca aaagccgcta cgacgcgggc agttacctca ccgcaggcga gccgcgccgc 1320

gaccgccaaa ccatcttcac cgccgccctc ggcgcatcga aactctcgtt taaaaacatc 1380

taccccgagc tgcgcttcaa acgcaccctt gcccgcagca attccgattt ctacgcctac 1440

cgccaaaacg aatacgccct ggctttgaaa taccgttttt aa 1482

<210> 336

<211> 493

<212> PRT

<213> N. bacilliformis SLAM 3

<400> 336

Met Lys Lys Tyr Ala Leu Leu Pro Ala Leu Leu Leu Ser Ala Ala Ala
1 5 10 15

Phe Ala Asp Asp Asp Asp Thr Arg Leu Leu Leu Asp Asn Ala Arg Phe
20 25 30

Gln Met Arg Gln Gln Gln Ala Glu Ala Phe Ser Glu Cys Glu Ala Ser
35 40 45

Arg Pro Arg Asp Cys Leu Ser Asp Ser Gly Ser Ile Glu Ile Asp Gly
50 55 60

Glu Thr Tyr Leu Val Pro Asn Thr Ala Asn Asp Leu Lys Leu Gly Ile
65 70 75 80

Tyr Tyr Ala Ile Asp Gly Arg Gln Trp Gly Lys Val Arg Glu Phe Leu
85 90 95

Gln Arg Tyr Arg Asn Leu Ser Asp His Lys Pro Gln Leu Val Leu Met
100 105 110

Ala Glu Gly Leu Leu Ala Arg Ser Glu Gly Lys Thr Ala Ala Ala Leu
115 120 125

Glu Lys Met Gln Ala Ala His Glu Thr Ala Pro Glu Asp Val Arg Ile
130 135 140

Asn Leu Glu Leu Ala Arg Leu Tyr Gly Glu Asp Asn Gln Thr Arg Glu
145 150 155 160

Ser Gln Ala Gln Phe Glu Gln Val Val Lys Thr Asp Ile Pro Pro Glu
165 170 175

Thr Arg Glu Met Val Gln Gly Tyr Leu Ala Ala Leu Asp Arg Arg Arg
180 185 190
Arg Trp His Gly Ser Leu Ser Ile Gly Gly Gly Tyr Asn Asp Asn Ile
195 200 205
Asn Gln Gly Asn Gly Lys Arg Glu Cys Val Gly Met Phe Met Gly Gln

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

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

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

405 410 415
Asn Ala Ala Ala Leu Tyr Arg Lys Ser Arg Tyr Asp Ala Gly Ser Tyr

420 425 430

Leu Thr Ala Gly Glu Pro Arg Arg Asp Arg Gln Thr Ile Phe Thr Ala

435 440 445

Ala Leu Gly Ala Ser Lys Leu Ser Phe Lys Asn Ile Tyr Pro Glu Leu

450 455 460

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

465 470 475 480

Arg Gln Asn Glu Tyr Ala Leu Ala Leu Lys Tyr Arg Phe

485 490

<210> 337

<211> 1260

<212> DNA

<213> N. bacilliformis SLAM 4

<400> 337

atgccgtgcc tgctgccttt gacggtgatt tgttcgagat tggccgattc tctgattttt 60

gcgggtgtat cgtcggcgtg ggcggaggcg gcgcggctgc tggcggccta ccgcgcaacg 120

gacggccacg atgaaaatct ggccgcgttc accgaggcga gcatcgcgcg tttgaacggc 180

gattatgcgg gggcgttgcg ccaatatgcc gatctgctgg cgcggcagcc ggattttgca 240

cgggcgcggc tggactatgc gaaaacgctg ttcgacgaca aacagacgcg cgaggcgcag 300

gcgcagtttg cccggttgca gcaggaagag ttgcccgagc ctgtgcagca gaacatcgcg 360

gcctatctca acgcggccaa agtgcgcggg gcgtggcacg gctcgcttgc cgtcggcggc 420

gtgcgcaaca gcaatgtgcg cgaaaccacc ggcgaaacct actgttttga cccctacggc 480

ctcacctgcg cgctcaccgc cgcgcccgaa gcggccgaag gattcaccta cgaagcctcg 540

gcggaaaaac accgtgctct ggccggacat cacggcctgt tcgcccgcgc cacgctttac 600

ggcacgcgtt acaagcattt ccccgacagc agcgaagaca cgctgaacgt gtcggcgggc 660

taccgctact cgtcggccaa aaacacctgg tcggccgcgc ccgtggccga gtggggcagg 720

gcggacagca gcctgctcta ccgcagcgcg gggctgcgcg gcgaatggca gcacgatttt 780

tccgagcgta ccgccctgag cgcggaggcc gaataccgcg aaatgcgcta cgccgaagac 840

tacgcgggca acgacggccg cctgttttca ctctacgcca cgctgatgca cgccccgtcc 900

gatgcctgga tgctctacgg cggcgcgaac gtgcaaaagc gcaaaacgca gagcgaggcc 960

accggctatc tgacgcacgg cttccaagcg ggggcgcaat accggcgcgg cgacgcgttt 1020

tccctgcgcc cgcacgccgc gctgcgctac cgccgctacg gcggtttcaa cccgtggata 1080

caggtgcgcc gcagcgacag cgagcaaagc tactcggcca cgctgaaaat tccgcgctgg 1140

aaaatcgccg gcttcacccc cgttttccac gtccgccaca cgcgcgtgca cagcaacgct 1200

ggctggctgg ccggctggcg caaaaacgaa gcggggatac gcttggagcg gtttttctga 1260

<210> 338

<211> 419

<212> PRT

<213> N. bacilliformis SLAM 4

<400> 338

Met Pro Cys Leu Leu Pro Leu Thr Val Ile Cys Ser Arg Leu Ala Asp

1 5 10 15

Ser Leu Ile Phe Ala Gly Val Ser Ser Ala Trp Ala Glu Ala Ala Arg

20 25 30

Leu Leu Ala Ala Tyr Arg Ala Thr Asp Gly His Asp Glu Asn Leu Ala

35 40 45

Ala Phe Thr Glu Ala Ser Ile Ala Arg Leu Asn Gly Asp Tyr Ala Gly

50 55 60

Ala Leu Arg Gln Tyr Ala Asp Leu Leu Ala Arg Gln Pro Asp Phe Ala

65 70 75 80

Arg Ala Arg Leu Asp Tyr Ala Lys Thr Leu Phe Asp Asp Lys Gln Thr

85 90 95

Arg Glu Ala Gln Ala Gln Phe Ala Arg Leu Gln Gln Glu Glu Leu Pro

100 105 110

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

115 120 125

Arg Gly Ala Trp His Gly Ser Leu Ala Val Gly Gly Val Arg Asn Ser

130 135 140

Asn Val Arg Glu Thr Thr Gly Glu Thr Tyr Cys Phe Asp Pro Tyr Gly

145 150 155 160

Leu Thr Cys Ala Leu Thr Ala Ala Pro Glu Ala Ala Glu Gly Phe Thr

165 170 175

Tyr Glu Ala Ser Ala Glu Lys His Arg Ala Leu Ala Gly His His Gly

180 185 190

Leu Phe Ala Arg Ala Thr Leu Tyr Gly Thr Arg Tyr Lys His Phe Pro

195 200 205

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

210 215 220

Ser Ala Lys Asn Thr Trp Ser Ala Ala Pro Val Ala Glu Trp Gly Arg

225 230 235 240

Ala Asp Ser Ser Leu Leu Tyr Arg Ser Ala Gly Leu Arg Gly Glu Trp

245 250 255

Gln His Asp Phe Ser Glu Arg Thr Ala Leu Ser Ala Glu Ala Glu Tyr

260 265 270

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

275 280 285

Phe Ser Leu Tyr Ala Thr Leu Met His Ala Pro Ser Asp Ala Trp Met

290 295 300

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

305 310 315 320

Thr Gly Tyr Leu Thr His Gly Phe Gln Ala Gly Ala Gln Tyr Arg Arg

325 330 335

Gly Asp Ala Phe Ser Leu Arg Pro His Ala Ala Leu Arg Tyr Arg Arg

340 345 350

Tyr Gly Gly Phe Asn Pro Trp Ile Gln Val Arg Arg Ser Asp Ser Glu

355 360 365

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

370 375 380

Phe Thr Pro Val Phe His Val Arg His Thr Arg Val His Ser Asn Ala

385 390 395 400

Gly Trp Leu Ala Gly Trp Arg Lys Asn Glu Ala Gly Ile Arg Leu Glu

405 410 415

Arg Phe Phe

<210> 339

<211> 1524

<212> DNA

<213> N. bacilliformis SLAM 5

<400> 339

atgttcccga aaaaaaccgt cccgctgctc cccttgctgt ttttcaccct ctcctccgcg 60

cccgcccttg ccgacgaccc ctccgccaaa atccaaacca cccccgaatc cggcctgctg 120

cgcggccttg ccgacgattt ggaaagccgc cgcgaacaga tcgaaaccaa cagcggcctg 180

cgcaaaaaaa aaaacgccgc cgcgcaggag gaaagcgaag acatccccga tttggacgac 240

gaagatttga aaaaacatcc cgagctggcc aaccgcgtgt taaacgccgc catgctctcc 300

gaagactggg acacactgga acacgtttcc ggcttctacc acgacatccc cggccacgac 360

cccgtgctgg acgcctatgt gcgcggcgcg cttttgcgcg cgcagggcag gccgggcaag 420

gccgcgaagg tgtaccgcga catcttgcgt caacatcccg atttgagcta tgtccgcctc 480

gatttggcgg gcatgctgtt tgaaaaccgc gcctacaaag acgcgaccaa agagtttgaa 540

caggccaaac gcgaagacat cgaacccgaa gcggcggcgc aggccgacgc ctatctggcg 600

gcggtgaaac aggccgaccc atggcagatc aggctgcgcg gcggctggca atacggcaac 660

aacaccaaca acgccacctc caacgactac ttcctctggc cgtttgccgt agtcggcagc 720

ataacctact actacaaact gccgcgcgac cccgaaagcc tgccacagcg gcagcggcat 780

cagctacggc gcgcaaatcg gcaaagacac caacctcgca ggcaaccaca acatcggttt 840

caacctcgaa gccgaaggcg tgcgctaccc gcactagcgc gacgacgacg aattttccct 900

ctccctagac gcaggctaca aataccgcac gctcaacaac accttcgccc tcacaccccg 960

ctcgtttccg cctcatggct cggcggccgc caatacagcc gcaacaccgg cgcaaacgcc 1020

tcgttttccc gctgggcaac cccccgcctg caactctccg gcgcgtacac cttcatccgc 1080

aaaaaatacc gcgacgaacg ctacgccggc tacaacgccg cgctcaacgg cctctccgcc 1140

tccgccgtct acgcgccctc accccaaact ggttcgcctt cggcggcctc ggcgtgcagc 1200

gcgaaaaaac cgacgataaa gaagaaacct ccacccgccg cttcgccaac ctcggcacac 1260

tctaccgttt cgccaacggc accaacatcc gcatcggcgg ccgctacgtc tcccgcaaat 1320

tcgcccgccc cgccgccctc tacggcggca tcacccgcag cgactgcgaa acctacgccg 1380

acgcttcggt gtggaaagaa aaatggctgc ccggcggcat caccccctaa gctggaattc 1440

tcctacctca aagtcagaag caacatctac gccttcccgc gcaacaaaaa acagatctcc 1500

ttcacgctgg aaaaagagtt ttga 1524

<210> 340

<211> 507

<212> PRT

<213> N. bacilliformis SLAM 5

<400> 340

Met Phe Pro Lys Lys Thr Val Pro Leu Leu Pro Leu Leu Phe Phe Thr
1 5 10 15

Leu Ser Ser Ala Pro Ala Leu Ala Asp Asp Pro Ser Ala Lys Ile Gln
20 25 30

Thr Thr Pro Glu Ser Gly Leu Leu Arg Gly Leu Ala Asp Asp Leu Glu
35 40 45

Ser Arg Arg Glu Gln Ile Glu Thr Asn Ser Gly Leu Arg Lys Lys Lys
50 55 60

Asn Ala Ala Ala Gln Glu Glu Ser Glu Asp Ile Pro Asp Leu Asp Asp
65 70 75 80

Glu Asp Leu Lys Lys His Pro Glu Leu Ala Asn Arg Val Leu Asn Ala
85 90 95

Ala Met Leu Ser Glu Asp Trp Asp Thr Leu Glu His Val Ser Gly Phe
100 105 110

Tyr His Asp Ile Pro Gly His Asp Pro Val Leu Asp Ala Tyr Val Arg
115 120 125

Gly Ala Leu Leu Arg Ala Gln Gly Arg Pro Gly Lys Ala Ala Lys Val
130 135 140

Tyr Arg Asp Ile Leu Arg Gln His Pro Asp Leu Ser Tyr Val Arg Leu
145 150 155 160

Asp Leu Ala Gly Met Leu Phe Glu Asn Arg Ala Tyr Lys Asp Ala Thr
165 170 175

Lys Glu Phe Glu Gln Ala Lys Arg Glu Asp Ile Glu Pro Glu Ala Ala
180 185 190

Ala Gln Ala Asp Ala Tyr Leu Ala Ala Val Lys Gln Ala Asp Pro Trp

195 200 205

Gln Ile Arg Leu Arg Gly Gly Trp Gln Tyr Gly Asn Asn Thr Asn Asn

210 215 220

Ala Thr Ser Asn Asp Tyr Phe Leu Trp Pro Phe Ala Val Val Gly Ser

225 230 235 240

Ile Thr Tyr Tyr Tyr Lys Leu Pro Arg Asp Pro Glu Ser Leu Pro Gln

245 250 255

Arg Gln Arg His Gln Leu Arg Arg Ala Asn Arg Gln Arg His Gln Pro

260 265 270

Arg Arg Gln Pro Gln His Arg Phe Gln Pro Arg Ser Arg Arg Arg Ala

275 280 285

Leu Pro Ala Leu Ala Arg Arg Arg Arg Ile Phe Pro Leu Pro Arg Arg

290 295 300

Arg Leu Gln Ile Pro His Ala Gln Gln His Leu Arg Pro His Thr Pro

305 310 315 320

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

325 330 335

Gly Ala Asn Ala Ser Phe Ser Arg Trp Ala Thr Pro Arg Leu Gln Leu

340 345 350

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

355 360 365

Ala Gly Tyr Asn Ala Ala Leu Asn Gly Leu Ser Ala Ser Ala Val Tyr

370 375 380

Ala Pro Ser Pro Gln Thr Gly Ser Pro Ser Ala Ala Ser Ala Cys Ser

385 390 395 400

Ala Lys Lys Pro Thr Ile Lys Lys Lys Pro Pro Pro Ala Ala Ser Pro

405 410 415

Thr Ser Ala His Ser Thr Val Ser Pro Thr Ala Pro Thr Ser Ala Ser

420 425 430

Ala Ala Ala Thr Ser Pro Ala Asn Ser Pro Ala Pro Pro Pro Ser Thr

435 440 445

Ala Ala Ser Pro Ala Ala Thr Ala Lys Pro Thr Pro Thr Leu Arg Cys
450 455 460

Gly Lys Lys Asn Gly Cys Pro Ala Ala Ser Pro Pro Lys Leu Glu Phe
465 470 475 480

Ser Tyr Leu Lys Val Arg Ser Asn Ile Tyr Ala Phe Pro Arg Asn Lys
485 490 495

Lys Gln Ile Ser Phe Thr Leu Glu Lys Glu Phe
500 505

<210> 341

<211> 1434

<212> DNA

<213> N. cinerea SLAM 1

<400> 341

atgactgcac aaaacagatg ggtattgcta ctgtctttgt tggcaacagc ggcatacgcc 60

gaagaaatac cgcacggacc tgatttgaga aacaagcccg agttcaagat ccatgaagtg 120

gaagttaaac ccgtcaacag ggaaaagata tcggaacagg tacaggaaaa agggaaagtt 180

ttgcagattg acggagaaac cctgctgaaa aatcccgaat tactgtcccg agccatgtat 240

tccgcagtgg tttcaaacaa tattgccggt atccgagtta ttttgccgat ttacctaaaa 300

caggcgcagc aggataagat gctggcactt tatgcacaag ggattctggc gcaggcagac 360

ggcagggtga aagaagcggt ttcctattac cgccggctga ttgccgtcca gcccgatgcg 420

cctgccgtcc gtctgcgcct tgccgccgca ttgtttgaag acaaacaaaa cgaggcggcg 480

gcagaccagt tcgaccgtct gaaaacagaa gacctgccgc ctcagcttat ggaacaagtc 540

gaattgtacc gcaaggcatt gcgtgatcgg gatgcgtgga aattcaacgg cggattcagc 600

gttacccaag agcggaatat caaccaggcc ccgaaacagc aggaatatgg acaatttacg 660

ctaccgaaac aggtgaacgg tacggcagtc aactatcaga tcggcgcgga gaaaaaatgg 720

tcgttgaaag acggatggta tgcgacggcg ggcggcgatt tgttcggcag gatttatccg 780

gacaacacga gatttaacga catgacggcg cgcgtatcta ccggtgcagg ctattcggat 840

cagcgtaaag atatagggct gacggtattc cacgaacgcc ggacctacgg caacgatgcc 900

tattcttatg ccaacggcgc gagggtaagt ttcgactatt ggctggcgca gaaactgcag 960

atgcttaccg ccgtggaaac aggttatctg aaaaatatac ggtatgaccg ttccaacaac 1020

aaaaacctta tgttgagcca ttccttgatt tactatccca atgcgcggca atattggatg 1080

ggcggtttgg atctttaccg cgagcgcaac cccgccgacc ggggcgacaa tttcaaccgt 1140

tacggcatgc gttttgcttg ggggcaggag tggggcggca gcggtttgtc ctcgctgctt 1200

cgggtcggtg tggcgcaaag gcgttatgaa aaacccagct tcttcagcag ttttaaaggg 1260
gaaaggcgca gggataggga actggatact tcgttgagcc tttggcaccg tgcgttgcat 1320
attaaaggca tcacaccgcg cctgaccttg tcgcaccgtg aaacatggag taacgatgtg 1380
atgaatgaat acgaaaaaaa cagagcgttt attgagttta acaaaacgtt ctga 1434

<210> 342
<211> 477
<212> PRT
<213> N. cinerea SLAM 1
<400> 342

Met Thr Ala Gln Asn Arg Trp Val Leu Leu Leu Ser Leu Leu Ala Thr
1 5 10 15

Ala Ala Tyr Ala Glu Glu Ile Pro His Gly Pro Asp Leu Arg Asn Lys
20 25 30
Pro Glu Phe Lys Ile His Glu Val Glu Val Lys Pro Val Asn Arg Glu
35 40 45
Lys Ile Ser Glu Gln Val Gln Glu Lys Gly Lys Val Leu Gln Ile Asp
50 55 60
Gly Glu Thr Leu Leu Lys Asn Pro Glu Leu Leu Ser Arg Ala Met Tyr
65 70 75 80

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

Leu Arg Leu Ala Ala Ala Leu Phe Glu Asp Lys Gln Asn Glu Ala Ala
145 150 155 160
Ala Asp Gln Phe Asp Arg Leu Lys Thr Glu Asp Leu Pro Pro Gln Leu

165 170 175

Met Glu Gln Val Glu Leu Tyr Arg Lys Ala Leu Arg Asp Arg Asp Ala

180 185 190

Trp Lys Phe Asn Gly Gly Phe Ser Val Thr Gln Glu Arg Asn Ile Asn

195 200 205

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

210 215 220

Val Asn Gly Thr Ala Val Asn Tyr Gln Ile Gly Ala Glu Lys Lys Trp

225 230 235 240

Ser Leu Lys Asp Gly Trp Tyr Ala Thr Ala Gly Gly Asp Leu Phe Gly

245 250 255

Arg Ile Tyr Pro Asp Asn Thr Arg Phe Asn Asp Met Thr Ala Arg Val

260 265 270

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

275 280 285

Val Phe His Glu Arg Arg Thr Tyr Gly Asn Asp Ala Tyr Ser Tyr Ala

290 295 300

Asn Gly Ala Arg Val Ser Phe Asp Tyr Trp Leu Ala Gln Lys Leu Gln

305 310 315 320

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

325 330 335

Arg Ser Asn Asn Lys Asn Leu Met Leu Ser His Ser Leu Ile Tyr Tyr

340 345 350

Pro Asn Ala Arg Gln Tyr Trp Met Gly Gly Leu Asp Leu Tyr Arg Glu

355 360 365

Arg Asn Pro Ala Asp Arg Gly Asp Asn Phe Asn Arg Tyr Gly Met Arg

370 375 380

Phe Ala Trp Gly Gln Glu Trp Gly Gly Ser Gly Leu Ser Ser Leu Leu

385 390 395 400

Arg Val Gly Val Ala Gln Arg Arg Tyr Glu Lys Pro Ser Phe Phe Ser

405 410 415

Ser Phe Lys Gly Glu Arg Arg Arg Asp Arg Glu Leu Asp Thr Ser Leu
420 425 430

Ser Leu Trp His Arg Ala Leu His Ile Lys Gly Ile Thr Pro Arg Leu
435 440 445

Thr Leu Ser His Arg Glu Thr Trp Ser Asn Asp Val Met Asn Glu Tyr
450 455 460

Glu Lys Asn Arg Ala Phe Ile Glu Phe Asn Lys Thr Phe
465 470 475

<210> 343

<211> 1413

<212> DNA

<213> N. cinerea SLAM 2

<400> 343

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gaaaacctgc ccgatcctgc gcctgccgcg ccgctttcag acggcctttc gccgcaagac 180

ggtttggaag cgcaaatcaa tcatgcggtt ttccgccgcg actggcaagc tttgccgccg 240

ctgctggcgc gttaccgcaa tctgcccgca cgcgaccaaa cgctttacga ttatgcgctg 300

ggcgcgttgc gccgcgccca gttgcgccat aaggaagcaa tcgcgttgta tcgcggcatt 360

gtcgggcggc atcccgattt ggcctatccg cgttttgact tgggcgtgat gctgtttgaa 420

gaccggcaat accgcgccgc cgaagccgag ctgcaacacg ccctgcctga tttgtcaccc 480

gaaatgcaga acattgccgg ccgatatttg gctgccgtcc gcgaggccga aagctggcag 540

cccgatgtct cactgcaata cgaggccacg gacaatgtga acaatgccgc cgacgcgcgt 600

tttatcgaaa tcgacggcaa aagatggcag aaaacggctg acagcctgcc gcagcgggca 660

cacggcctgc gctacggcgc gtctgtgtcg cgtgaaaaaa atctcggcgg acaccattat 720

gcctacgcca aactgggcgg cgacggtgtc gcttattggg acaaccatga tttcgacgag 780

cagagcctga acattgccgc aggctataaa aaccattcgg cggcgcgctc gttcggcctt 840

gtgccgtttg ccgaaaccaa ttggctgggc ggcagccgct acaaccgcgc cgatggggtg 900

caggccgatt tttcccgccg tttcggtgca aaatggcgcg tgatgctgaa tgcgggatat 960

gtccgcaaac actatcggga gccgcatatt gcagagcgct acaacggcaa aatgccgctg 1020

gcgggagtaa cgctgatgta tgccgcgcca aagggctggc tgttttacgg aggagcagac 1080

tggtcgcacg aaatgaccaa agaaacggag caggcatccg tgcgcaaggg catacgcttc 1140

ggcgcggtga aagcgtttga gaacggattc ggcatccgca ccaacctgcg ctacgcccgt 1200

cgtacctttg atgcgccgga tagcctggtt taccgcttga cccgtaagga ccatgaatat 1260

caggcaaatg tctctatttg gcacaataaa atttcatgga aaggcttggt gccgcatttg 1320

aatttccgtt atctgaaaat cgacagcaat atgagcggct tctattcccg caagagtatg 1380

cagacattcg tcagcgtgga gaagcagttt tga 1413

<210> 344

<211> 470

<212> PRT

<213> N. cinerea SLAM 2

<400> 344

Met Asn Lys Leu Ser Leu Leu Leu Leu Pro Phe Pro Leu Ala Ala Leu

1 5 10 15

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

20 25 30

Arg Glu Ala Ala Gln Met Pro Ser Glu Asn Leu Pro Asp Pro Ala Pro

35 40 45

Ala Ala Pro Leu Ser Asp Gly Leu Ser Pro Gln Asp Gly Leu Glu Ala

50 55 60

Gln Ile Asn His Ala Val Phe Arg Arg Asp Trp Gln Ala Leu Pro Pro

65 70 75 80

Leu Leu Ala Arg Tyr Arg Asn Leu Pro Ala Arg Asp Gln Thr Leu Tyr

85 90 95

Asp Tyr Ala Leu Gly Ala Leu Arg Arg Ala Gln Leu Arg His Lys Glu

100 105 110

Ala Ile Ala Leu Tyr Arg Gly Ile Val Gly Arg His Pro Asp Leu Ala

115 120 125

Tyr Pro Arg Phe Asp Leu Gly Val Met Leu Phe Glu Asp Arg Gln Tyr

130 135 140

Arg Ala Ala Glu Ala Glu Leu Gln His Ala Leu Pro Asp Leu Ser Pro

145 150 155 160

Glu Met Gln Asn Ile Ala Gly Arg Tyr Leu Ala Ala Val Arg Glu Ala
165 170 175
Glu Ser Trp Gln Pro Asp Val Ser Leu Gln Tyr Glu Ala Thr Asp Asn
180 185 190
Val Asn Asn Ala Ala Asp Ala Arg Phe Ile Glu Ile Asp Gly Lys Arg

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

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

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

385 390 395 400
Arg Thr Phe Asp Ala Pro Asp Ser Leu Val Tyr Arg Leu Thr Arg Lys

405 410 415

Asp His Glu Tyr Gln Ala Asn Val Ser Ile Trp His Asn Lys Ile Ser

420 425 430

Trp Lys Gly Leu Val Pro His Leu Asn Phe Arg Tyr Leu Lys Ile Asp

435 440 445

Ser Asn Met Ser Gly Phe Tyr Ser Arg Lys Ser Met Gln Thr Phe Val

450 455 460

Ser Val Glu Lys Gln Phe

465 470

<210> 345

<211> 1506

<212> DNA

<213> N. cinerea SLAM 3

<400> 345

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gctcttgcac atgccgatgg tcctgccgac gaacgccgcc gcctgcttga cgagggcagc 120

cgacaaacgc agcaataccg cgaaagcagt tggctggaca cggaacaggc acgcggggaa 180

gtgggggaaa acgacggcta catcatgata gacggtacag tctaccaagt tggtgatacg 240

gcggaagaac tggaaagcgc gatttaccac gccctcaata cgcggcagtg gcacaaggtg 300

cggcagttcg ctgcccgcta cgccaaactg ccccggcaca aacccgcgct gattcatttg 360

gccgatgcgc tgcaaaaacg ggacgaaggg gatttccgcg cggcggggaa cagttttcag 420

acggccttgg aagccgaacc cgacaacccc cgcctgctgc tcgaagcggg gcggttttat 480

gccgaagaca accaaaaacaa agagtcagcc gccgcgtttg agaaagttct gaaaacggat 540

attcctgcag aaacccgcta catcgtggaa aactacctgt ccgaactggg caaacgccgc 600

cgctggcacg gccaaatcag cctcggctat ggttacaaca gcaatgtaaa ccaaggcaac 660

ggcatcaacc aatgcgtgtg ggaaatcgcg ggcatgtgcc tgatggagcg caccctacct 720

gcgccaacgg attcgacctt ctcatcctat agcgcgaccg ccgaaaaaac cgtcccgctc 780

aaagggcatc acggcgtaca ggtgcgcggt gtactgtacg gcaaccgcta cacggaaaaa 840

gacaaagatt cggcggccat gccggattac ggctatcgca acggttcgct gtacgcggga 900

tacgcctatg ccgacgcacg ctcctccttt tccctgctgc cttatttcga atacgacttc 960

cgcaaccgcc acacccacta ccgcgcatgg ggtgcggatg ccgactggtc gcgcatactt 1020

tccccgcgct ggcgcatcaa cgcccgtgcc ggagcaaaaa agactggata cggcggacaa 1080

agcaaaactt attttgccga tttcaaacaa tacgaactcg gcgcgggggc ggaattttct 1140

atcacgccga aaagcggcct gtttgtaaat ttcgatgccg cacgcaaagc ctatcccgaa 1200
aaatcttctt ccagcaaaga atatacggct cggctgggtg cgtataggct tttttcgggc 1260
ggtacttatt taaacgccgt cctgctctac cgccgcagcc tgtatgacgc ggcaagtttc 1320
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ccgcaatgga atatcaaagg cgtatatccc gaactgcgtt tcaggcgaac aatcgcacac 1440
agcaacgcgg tgtattaccg ctaccgccaa aacgaatggc tgttgggttt taaatatcgg 1500
ttttga 1506

<210> 346
<211> 501
<212> PRT
<213> N. cinerea SLAM 3
<400> 346

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

Ala Glu Pro Asp Asn Pro Arg Leu Leu Leu Glu Ala Gly Arg Phe Tyr
145 150 155 160
Ala Glu Asp Asn Gln Asn Lys Glu Ser Ala Ala Ala Phe Glu Lys Val
165 170 175
Leu Lys Thr Asp Ile Pro Ala Glu Thr Arg Tyr Ile Val Glu Asn Tyr

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

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

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

370 375 380
Ser Gly Leu Phe Val Asn Phe Asp Ala Ala Arg Lys Ala Tyr Pro Glu

385 390 395 400

Lys Ser Ser Ser Ser Lys Glu Tyr Thr Ala Arg Leu Gly Ala Tyr Arg

405 410 415

Leu Phe Ser Gly Gly Thr Tyr Leu Asn Ala Val Leu Leu Tyr Arg Arg

420 425 430

Ser Leu Tyr Asp Ala Ala Ser Phe Ile Ser Asp Asn Lys Arg Arg Ser

435 440 445

Asp Lys Gln Tyr Ile Met Met Ala Ala Ala Gly Phe Pro Gln Trp Asn

450 455 460

Ile Lys Gly Val Tyr Pro Glu Leu Arg Phe Arg Arg Thr Ile Ala His

465 470 475 480

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

485 490 495

Phe Lys Tyr Arg Phe

500

<210

> 347

<211> 1482

<212> DNA

<213> N. cinerea SLAM 4

<400> 347

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caggtgcagc aaaaacaatg gttggatatt ttgtctggag aagaaaggtc gtctgaaaag 120

gatgaaaatg ttgctaaacc gaatgtaatc ggagatgagt ttttagcggc aaacccgcgt 180

attcttgaga gcgcgctgat tcaagcactt aacggcaata gcgcggattt ggtttttttcg 240

cttgccgccc tttaccgcaa acagcccaac cataatccaa agctgattgc acgtgccgat 300

gctttgctgg caaagttgaa agggcggact tccgaagcgg tcgagcgtta tcgtaccctt 360

tatgaatccg acgtttcaga cgaccgcata ttgttggatt tggcggcggc agagtttcag 420

gattatcgtt tgagcgaggc ggcagcgcat ttccatcatg ccgcgcaacg cgatataccc 480

gcccccgttt tggaaaacgt caaacgtttt caagaagccg tcaagcggca gacagaatgg 540

aaatggtccg gcggaatcag ccccgtgcat aataacaatg ccaacaacgc tgctccgcgt 600

tattgcatcg aaacaagggg gcaaaccgca tgcagtgtta ccttacctgt cagtgccaac 660

ggcttgaatt acgaattgaa cacagaaaaa ctcaccccgt tgtacgggca tcacgctgtc 720

aaattccgcg ccaacctcag cggcacaagc tatttttttcg accggaaatc ggcttacgac 780

gatgcgtttg gcagggctta tttgggctgg cagcgcaagg acggcaaaca aaccgtcagc 840

gttttaccgt tttatcaggc acagttggcg ggcagcagcg aatttgacgg caaaaaagaa 900

aacaaccgcc gcgccgtgcc ttatatgctg gcacacgggg tcggcattca ggcttcatat 960

acggtcaggt tcggacggga tatgcagttt tacagttcgt tggaacgata tcggcggtac 1020

cacagggaga atgcccgtgc ggaacgtaat gatggttggc aggacagtct gtatgtgtcg 1080

ttagcgcggc gtttcggaaa ttcggcaact gtgtttggcg gctggcagtt tgcacggttt 1140

gttccggaac gcggaatagt gcgtggcgcg gttaacaatg cggcgtacaa ccgtaacagt 1200

atcaatgttg gctgggtacg gcaatggcag gaattgggtg gtttgaacag tcggattgcc 1260

gtgtcttatg cccgccgcaa ttataagggt atggccgcat tcgctaccga ggcgcagcgt 1320

aaccgtgaat ggaacgtatc gcttggattg agtcacgacc gtttgtccta caagggtatt 1380

gtaccgacgc taacgtacag tttcggtaaa acgagcagca atatgcggta tgcagaacgc 1440

tggaatagcc agatattgtt cggggcggat tggcggtttt aa 1482

<210> 348

<211> 493

<212> PRT

<213> N. cinerea SLAM 4

<400> 348

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

1 5 10 15

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

20 25 30

Gly Glu Glu Arg Ser Ser Glu Lys Asp Glu Asn Val Ala Lys Pro Asn

35 40 45

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

50 55 60

Ala Leu Ile Gln Ala Leu Asn Gly Asn Ser Ala Asp Leu Val Phe Ser

65 70 75 80

Leu Ala Ala Leu Tyr Arg Lys Gln Pro Asn His Asn Pro Lys Leu Ile

85 90 95

Ala Arg Ala Asp Ala Leu Leu Ala Lys Leu Lys Gly Arg Thr Ser Glu

100 105 110

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

115 120 125

Arg Ile Leu Leu Asp Leu Ala Ala Ala Glu Phe Gln Asp Tyr Arg Leu

130 135 140

Ser Glu Ala Ala Ala His Phe His His Ala Ala Gln Arg Asp Ile Pro

145 150 155 160

Ala Pro Val Leu Glu Asn Val Lys Arg Phe Gln Glu Ala Val Lys Arg

165 170 175

Gln Thr Glu Trp Lys Trp Ser Gly Gly Ile Ser Pro Val His Asn Asn

180 185 190

Asn Ala Asn Asn Ala Ala Pro Arg Tyr Cys Ile Glu Thr Arg Gly Gln

195 200 205

Thr Ala Cys Ser Val Thr Leu Pro Val Ser Ala Asn Gly Leu Asn Tyr

210 215 220

Glu Leu Asn Thr Glu Lys Leu Thr Pro Leu Tyr Gly His His Ala Val

225 230 235 240

Lys Phe Arg Ala Asn Leu Ser Gly Thr Ser Tyr Phe Phe Asp Arg Lys

245 250 255

Ser Ala Tyr Asp Asp Ala Phe Gly Arg Ala Tyr Leu Gly Trp Gln Arg

260 265 270

Lys Asp Gly Lys Gln Thr Val Ser Val Leu Pro Phe Tyr Gln Ala Gln

275 280 285

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

290 295 300

Ala Val Pro Tyr Met Leu Ala His Gly Val Gly Ile Gln Ala Ser Tyr

305 310 315 320

Thr Val Arg Phe Gly Arg Asp Met Gln Phe Tyr Ser Ser Leu Glu Arg

325 330 335

Tyr Arg Arg Tyr His Arg Glu Asn Ala Arg Ala Glu Arg Asn Asp Gly

340 345 350

Trp Gln Asp Ser Leu Tyr Val Ser Leu Ala Arg Arg Phe Gly Asn Ser
355 360 365
Ala Thr Val Phe Gly Gly Trp Gln Phe Ala Arg Phe Val Pro Glu Arg
370 375 380
Gly Ile Val Arg Gly Ala Val Asn Asn Ala Ala Tyr Asn Arg Asn Ser

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

450 455 460
Thr Tyr Ser Phe Gly Lys Thr Ser Ser Asn Met Arg Tyr Ala Glu Arg
465 470 475 480
Trp Asn Ser Gln Ile Leu Phe Gly Ala Asp Trp Arg Phe
485 490

<210> 349
<211> 1494
<212> DNA
<213> N. elongata SLAM 1
<400> 349

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tccgacgatg ccgcagacga acgccgccgc ctgctggacg aaagcggccg ccaaacgcag 120

caataccgcg aaagcggttg gctggacacg gaacaggcac gcgggaaagt gggagaaaac 180
gacggctaca tcatgataga cggtacagtc taccaagtcg gcgatacggc ggaagagctg 240
gaaagcgcga tttaccacgc cctcaacgcg cggcagtggc acaaggtgcg gcagttcgcc 300
gcccgctacg ccaaactgcc gcagcacaag cccgcgctga ttcatttggc cgatgcgctg 360
caaaaacggg atgaagggga tttccgcgcg gcggggaata gttttcagac ggccttggaa 420
gtcgaatccg acaacccgcg cctgctgctc gaagcggggc ggttttatgc cgaagacaac 480

caaaacaaag agtccgccgc cacgtttgag aaagttctga aaatggatat tcccgcagaa 540

acccgcccca tcgtggaaaa ctacctgtcc gaactgggca aacgccgccg ccggcacggc 600

caaatcagcc tcggttacgg ctacaacaac aatgtaaacc aaggcaacgg catcagccaa 660

tgcgtgtggg aaatcgcggg catgtgcctg atggagcgca ccctgcccgc gccaacggat 720

tcgaccttct cgtcctatag cgcgaccgcc gaaaaaaccg tcccgctcaa agggcatcac 780

ggcgtacagg tgcgcggcgt gctgtacggc aaccgctaca cggaaaaaga caaagattcg 840

gcagccatgc cggattacgg ctatcacaac ggttcgttgt acgcgggata cgcctatgcc 900

gacgcacgct cctccttttc cctgctgccc tatttcgaat acgacttccg caaccgccac 960

atccactacc gcgcatgggg tgcggatgcc gactggtcgc gcacactctc cccgcgctgg 1020

cgtgtcaatg cccgtgccgg cgcgaaaaag accggatacg gcggacaaag caaaacttat 1080

tttgccgatt tcaaacaata cgaactgggc gcgggggcgg aattttccat cacgccgaaa 1140

agcggcctgc ttgccaactt cgatgccgcc cgcaaagcct atcccgaaaa atcctcttcc 1200

agcaaagaat atacggcacg gctgggtgcg tataggcttt tttcgggcgg tacttattta 1260

aacgccatcc tgctctaccg ccgcagcctg tatgacgcgg caagtttcgt cagcgacaac 1320

aggcggcggc gcgacaagca atacatcatg atggctgcgg cgggttttcc gcaatggaat 1380

atcaaaggcg tataccccga actgcgcttc cgccgcacca tcgcccgcag caacgcggtg 1440

tattaccgct accgccaaaa cgaatggctg ttgagcttga agtatcggtt ttga 1494

<210> 350

<211> 497

<212> PRT

<213> N. elongata SLAM 1

<400> 350

Met Thr His Arg Leu Cys Leu Leu Phe Leu Pro Leu Cys Thr Val Cys
1 5 10 15

Leu Ala Ala Pro Ser Asp Asp Ala Ala Asp Glu Arg Arg Arg Leu Leu
20 25 30

Asp Glu Ser Gly Arg Gln Thr Gln Gln Tyr Arg Glu Ser Gly Trp Leu
35 40 45

Asp Thr Glu Gln Ala Arg Gly Lys Val Gly Glu Asn Asp Gly Tyr Ile
50 55 60

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

65 70 75 80

Glu Ser Ala Ile Tyr His Ala Leu Asn Ala Arg Gln Trp His Lys Val

85 90 95

Arg Gln Phe Ala Ala Arg Tyr Ala Lys Leu Pro Gln His Lys Pro Ala

100 105 110

Leu Ile His Leu Ala Asp Ala Leu Gln Lys Arg Asp Glu Gly Asp Phe

115 120 125

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

130 135 140

Asn Pro Arg Leu Leu Leu Glu Ala Gly Arg Phe Tyr Ala Glu Asp Asn

145 150 155 160

Gln Asn Lys Glu Ser Ala Ala Thr Phe Glu Lys Val Leu Lys Met Asp

165 170 175

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

180 185 190

Gly Lys Arg Arg Arg Arg His Gly Gln Ile Ser Leu Gly Tyr Gly Tyr

195 200 205

Asn Asn Asn Val Asn Gln Gly Asn Gly Ile Ser Gln Cys Val Trp Glu

210 215 220

Ile Ala Gly Met Cys Leu Met Glu Arg Thr Leu Pro Ala Pro Thr Asp

225 230 235 240

Ser Thr Phe Ser Ser Tyr Ser Ala Thr Ala Glu Lys Thr Val Pro Leu

245 250 255

Lys Gly His His Gly Val Gln Val Arg Gly Val Leu Tyr Gly Asn Arg

260 265 270

Tyr Thr Glu Lys Asp Lys Asp Ser Ala Ala Met Pro Asp Tyr Gly Tyr

275 280 285

His Asn Gly Ser Leu Tyr Ala Gly Tyr Ala Tyr Ala Asp Ala Arg Ser

290 295 300

Ser Phe Ser Leu Leu Pro Tyr Phe Glu Tyr Asp Phe Arg Asn Arg His

305 310 315 320

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

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

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

485 490 495
Phe

<210> 351
<211> 1404
<212> DNA
<213> N. elongata SLAM 2
<400> 351
atgaaaatag cctccctgct cctgctgctt ttacccttcc acgccgtatc cgaaaccgtg 60
cacgttcccg caccggtttc cttcgaccga ctgccggaaa cacccatcag ctccgagccg 120
ccgccccaac ccgcaccgcc cgccgccgtc ctttccgacg acaacggcag caccctggaa 180

gcgcaaatta gccgcgcact gaccgaacaa gactggccgc gcctgacaaa actgctgcaa 240

aaataccaaa ccctgcccgc gcgcgacccc atcctccacg actacgcact cggcgcactc 300

cgccgcaccc aactccgtca cgatgaagcc gtcgcactgt atcgcggcat cttggcgcaa 360

cagcccgact tggcctatcc gcgttttgat ttgggtgtca tgctgtttga aaacaaacaa 420

taccgcgaag cggctgcgga actgcaacgt gccaaacccg gcctgcagcc cgacatgcaa 480

acactggccg accgttatct ggcagccatc aaaaaagaac aaggctggca gcccgaaatt 540

tccctgcaat acgccgctac cgacaatgta aacaacgctt ccgaagccga aatcatcgaa 600

tgggacggca ggcaatggcg gaaaaccgcc gacagcctgc cccaaagcgc gcacggtatc 660

cgctacggct tgggcgtatc gcgcgaaatc aacttgggcg gccgccactt cgccgcaggc 720

cgtctgaacg gcgacggcgt acattattgg ggccgccgcg aatacaacga gcagagcatc 780

caccttgccg caggctacaa aaaccgctcc gtaacgcgct cgttcggcat cctgcccttt 840

atcgaataca accggctggg cggcgaacct tacaaccgag tattcggcgc acaggccgac 900

ttttcaggcc gtctgaacga caaatggcgc atcgcgctca acgcgggcca tatctggaaa 960

cgctatcgcg aagaacgcac ggcggcacgt tacgacggcc acatgccgtc ggcgggcgca 1020

accctgatat acgccgcacc gaaaaactgg ctgctgtccg gcggtgcaga ctggtcgcac 1080

gacatcacgc gcgaagcgga acaggcttcc gtgcgcaaag gcgttcggct gggcgtattc 1140

aaaaacctttt cagacggcct cggcctgcgc accaacctgc gctactcccg ccgtgttttc 1200

gacgcgcccg gcacgctggt ttaccgcttc gtgcgcaaag accgcgaata tcaggccggc 1260

gcatccgtct ggcacgaaaa attgtcgtgg aaaggcttgg tgccgcgcct gaacctgcaa 1320

tacctgaaag tggacagcaa tatgggcggc ttctattcgc gacggaatat gcaatggttt 1380

gtcagcgtgg agaaacagtt ttaa 1404

<210> 352

<211> 467

<212> PRT

<213> N. elongata SLAM 2

<400> 352

Met Lys Ile Ala Ser Leu Leu Leu Leu Leu Leu Pro Phe His Ala Val

1 5 10 15

Ser Glu Thr Val His Val Pro Ala Pro Val Ser Phe Asp Arg Leu Pro

20 25 30

Glu Thr Pro Ile Ser Ser Glu Pro Pro Pro Gln Pro Ala Pro Pro Ala

35 40 45

Ala Val Leu Ser Asp Asp Asn Gly Ser Thr Leu Glu Ala Gln Ile Ser

50 55 60

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

65 70 75 80

Lys Tyr Gln Thr Leu Pro Ala Arg Asp Pro Ile Leu His Asp Tyr Ala

85 90 95

Leu Gly Ala Leu Arg Arg Thr Gln Leu Arg His Asp Glu Ala Val Ala

100 105 110

Leu Tyr Arg Gly Ile Leu Ala Gln Gln Pro Asp Leu Ala Tyr Pro Arg

115 120 125

Phe Asp Leu Gly Val Met Leu Phe Glu Asn Lys Gln Tyr Arg Glu Ala

130 135 140

Ala Ala Glu Leu Gln Arg Ala Lys Pro Gly Leu Gln Pro Asp Met Gln

145 150 155 160

Thr Leu Ala Asp Arg Tyr Leu Ala Ala Ile Lys Lys Glu Gln Gly Trp

165 170 175

Gln Pro Glu Ile Ser Leu Gln Tyr Ala Ala Thr Asp Asn Val Asn Asn

180 185 190

Ala Ser Glu Ala Glu Ile Ile Glu Trp Asp Gly Arg Gln Trp Arg Lys

195 200 205

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

210 215 220

Gly Val Ser Arg Glu Ile Asn Leu Gly Gly Arg His Phe Ala Ala Gly

225 230 235 240

Arg Leu Asn Gly Asp Gly Val His Tyr Trp Gly Arg Arg Glu Tyr Asn

245 250 255

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

260 265 270

Arg Ser Phe Gly Ile Leu Pro Phe Ile Glu Tyr Asn Arg Leu Gly Gly

275 280 285

Glu Pro Tyr Asn Arg Val Phe Gly Ala Gln Ala Asp Phe Ser Gly Arg

290 295 300

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

305 310 315 320

Arg Tyr Arg Glu Glu Arg Thr Ala Ala Arg Tyr Asp Gly His Met Pro

325 330 335

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

340 345 350

Ser Gly Gly Ala Asp Trp Ser His Asp Ile Thr Arg Glu Ala Glu Gln

355 360 365

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

370 375 380

Asp Gly Leu Gly Leu Arg Thr Asn Leu Arg Tyr Ser Arg Arg Val Phe

385 390 395 400

Asp Ala Pro Gly Thr Leu Val Tyr Arg Phe Val Arg Lys Asp Arg Glu

405 410 415

Tyr Gln Ala Gly Ala Ser Val Trp His Glu Lys Leu Ser Trp Lys Gly

420 425 430

Leu Val Pro Arg Leu Asn Leu Gln Tyr Leu Lys Val Asp Ser Asn Met

435 440 445

Gly Gly Phe Tyr Ser Arg Arg Asn Met Gln Trp Phe Val Ser Val Glu

450 455 460

Lys Gln Phe

465

<210> 353

<211> 1557

<212> DNA

<213> N. flavescens SLAM 1

<400> 353

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gataacatcc caaacattgc catgaaaaaa cgtctgctcc tcctcgccat ccttcccctt 120

tcccttcacg ccgccgatgt accgcctgat gtaaaacccg agcttcaagt caacactgcc 180

gaaccccaac aacccgaaac gcacaacatc cctgccgagc agacaaacag gccgtctgaa 240

aaaatcatca acgtcgatgc cgacaccctg cttgccaata ccgaattact ggcacgcgcc 300

atgtattccg ccgtcgtcgc ccataatatc cccggcatca aagccgtttt gcccatttac 360

gaacaatggc ctgaacacga ccgcgccatg gcacgctatg ccaaaggttt gcttgcccaa 420

tccgaaggga gagctgccga agccatcggc cattaccgcc gctttatcgc cgagcagccc 480

gatgcctccg ccgtccgctg gcagcttgcg accgccttgt ttgaagacaa acaaaacgaa 540

gccgcagccg accagttcga caaactgcaa accgaatccc tcccgcctgc cttgcaagaa 600

cgcatcgaaa cataccgcaa aaccctgcgc gaacgcgact catggcaatt caatgccggc 660

ttgaacatca cacgcgaaca aaacatcaac caagcccccg gccaacgccg tctgggcaac 720

cacctgagcg atgaacaatg ccgcgccgag cgccttatcc atcctaacga cgactgcttc 780

cgaggctgga cattccccga acccatcgat gccaccgcca tccactatca aatcggcgca 840

gaaaaaaaat ggtcgctgcc acacggcttc tatgccacgg caggcgcaga ccattacggc 900

aaaatctacc ccaaacacac caactacaac gacctcacca cacgcttctc ggcaggcatc 960

ggctatgccg accagcgcag cgatatcggc ataaccccgt tccacgaacg ccgcttctac 1020

ggcaacgacc cctacaccta caccaacggc gcacgcctcc actacaacca ttggtggcaa 1080

ccaaagctgc aaaccctcag cgcatttgaa gcaggccgtc tgaaaaacag ccgccgcgag 1140

cattccaaca ataccagcca actactcagc aactccatcg tgtactaccg caacgcgcgc 1200

caatactggg tagccggtat cgacctctac cgcgaacgca accgcgacga caaaagcgac 1260

agcttcaacc gctatgccct gcgcaccaca tggggacaag aatggcccaa aggcctctct 1320

accgtcctac gcctcagcgc cgcccaacgc cgttaccaag gccccagcct cttcagcaac 1380

gaacaaaacc gccgcgacaa agaagcctcc gcctccctga gcgtatggca ccgcgccctc 1440

catttcaaag gcatcacccc gcgcctgacc attgcccaca acaaaacatg gagcaacgac 1500

aagttctacg aatatggcaa aaccaaaatg tttgtcgaat tgagcaaaac gttctga 1557

<210> 354

<211> 518

<212> PRT

<213> N. flavescens SLAM 1

<400> 354

Met Ala Leu Gly Leu Gln Asn Phe Arg Leu Lys Thr Leu Tyr Asn Leu

1 5 10 15

Thr Thr Tyr Thr Asp Asn Ile Pro Asn Ile Ala Met Lys Lys Arg Leu

20 25 30

Leu Leu Leu Ala Ile Leu Pro Leu Ser Leu His Ala Ala Asp Val Pro

35 40 45

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

50 55 60

Pro Glu Thr His Asn Ile Pro Ala Glu Gln Thr Asn Arg Pro Ser Glu

65 70 75 80

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

85 90 95

Leu Ala Arg Ala Met Tyr Ser Ala Val Val Ala His Asn Ile Pro Gly

100 105 110

Ile Lys Ala Val Leu Pro Ile Tyr Glu Gln Trp Pro Glu His Asp Arg

115 120 125

Ala Met Ala Arg Tyr Ala Lys Gly Leu Leu Ala Gln Ser Glu Gly Arg

130 135 140

Ala Ala Glu Ala Ile Gly His Tyr Arg Arg Phe Ile Ala Glu Gln Pro

145 150 155 160

Asp Ala Ser Ala Val Arg Trp Gln Leu Ala Thr Ala Leu Phe Glu Asp

165 170 175

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

180 185 190

Ser Leu Pro Pro Ala Leu Gln Glu Arg Ile Glu Thr Tyr Arg Lys Thr

195 200 205

Leu Arg Glu Arg Asp Ser Trp Gln Phe Asn Ala Gly Leu Asn Ile Thr

210 215 220

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

225 230 235 240

His Leu Ser Asp Glu Gln Cys Arg Ala Glu Arg Leu Ile His Pro Asn

245 250 255

Asp Asp Cys Phe Arg Gly Trp Thr Phe Pro Glu Pro Ile Asp Ala Thr

260 265 270

Ala Ile His Tyr Gln Ile Gly Ala Glu Lys Lys Trp Ser Leu Pro His
275 280 285
Gly Phe Tyr Ala Thr Ala Gly Ala Asp His Tyr Gly Lys Ile Tyr Pro
290 295 300
Lys His Thr Asn Tyr Asn Asp Leu Thr Thr Arg Phe Ser Ala Gly Ile

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

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

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

500 505 510
Glu Leu Ser Lys Thr Phe

515

<210> 355

<211> 1470

<212> DNA

<213> N. flavescens SLAM 2

<400> 355

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gatgttgccg tgcctgtcga accgattaac gtcggtaatc ggattgcgat gccgtctgaa 120

gggggaaacc ttgctccttt accgcttgtt gaggatattg ccgtgcctgt cgagccgatt 180

aatgtcatgc cgtctgaagc ttctaaaagt gcggcaggcg gcgatgttcg agacgatcgg 240

ataggaatgc agattaatcg ggcgttgttg gcgcgggact gggcggcact gaaacgcctg 300

ttggtccaat atgccgaaca gccgcaatat gatacggtgc tgtaccgtta tgccctcggc 360

gcgttatacc gcagcgagat gcggcagggc gaggcggccg atctataccg tgagttgttg 420

tcggaaaggc ctgaccttgt ttatccacgt tttgatttgg gtgtgatgct gtttgaagac 480

aaacaatacc gtgaggcatt ggttcagttg cgccgggtcg gggaggcgtt gccgcccgat 540

atgcggcagc ttgcacgaaa atatatccgt caggcagaag cggtgcaggc gtggcatcct 600

tcgttcagta tgaactatga acaaacagat aatgtaaaca atgcttcccc ttcacgggac 660

atcatcctca acggccggaa atggacaaaa tcggaagaca gcctgcccaa acgcgccaac 720

gggataaggt acgaactggg tattgaccgg atgtttaaca ttgcaggtaa tcactttgcc 780

cgcttaggca tcagcggttc cggtgtgcat tattggaatg cccgggattt tagcgaacag 840

gcgtttcatg ccgaagtagg ctaccgttat cggaatagcc gtctagagtg gggattccgg 900

ccctttgtcg aacaaaaccg gctgggcaat aaccgttata cggcaaatac gggtattgcg 960

ttggattaca gccgccgtct gaatgaaaaa tggcacagca cccaatctct ccagtatggc 1020

cgcaaacaat accatgacga atatttggca aaacgttaca acagcaaaac gatttcagtc 1080

agcagtacgt tcagctatta cgctatgccg gcttggcagt tgtacggagg tattagcggt 1140

atgtttgata atactgtgga gaaagagcag gcttcacggc gttatggtgt aagtttgggt 1200

acggtgaaaa tattagacgg cggtctcgga ctgaagttgg gtgcaggtta cacgaaacgg 1260

atatttaaag cccctgcaac attaatttac aattttaccc ggcgcgatga tgagtatcgg 1320

ataaacgcgg ctttatggca taaaaaactg tcgtggaaag gatttacacc ccaaataaat 1380

ttccgttaca acaagatcaa cagtaatatg cccgcctttt attcgcgcag cggcaaggaa 1440

tggtttgtca gtatagaaaa aacgtattga 1470

<210> 356

<211> 489

<212> PRT

<213> N. flavescens SLAM 2

<400> 356

Met Lys Pro Arg Asn Leu Phe Phe Ala Gly Cys Leu Leu Thr Ser Ala
1 5 10 15
Val Phe Ala Glu Asp Val Ala Val Pro Val Glu Pro Ile Asn Val Gly
20 25 30
Asn Arg Ile Ala Met Pro Ser Glu Gly Gly Asn Leu Ala Pro Leu Pro
35 40 45
Leu Val Glu Asp Ile Ala Val Pro Val Glu Pro Ile Asn Val Met Pro
50 55 60

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

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

Glu Ala Val Gln Ala Trp His Pro Ser Phe Ser Met Asn Tyr Glu Gln
195 200 205
Thr Asp Asn Val Asn Asn Ala Ser Pro Ser Arg Asp Ile Ile Leu Asn

210 215 220

Gly Arg Lys Trp Thr Lys Ser Glu Asp Ser Leu Pro Lys Arg Ala Asn
225 230 235 240
Gly Ile Arg Tyr Glu Leu Gly Ile Asp Arg Met Phe Asn Ile Ala Gly
245 250 255

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

Leu Asp Tyr Ser Arg Arg Leu Asn Glu Lys Trp His Ser Thr Gln Ser
325 330 335
Leu Gln Tyr Gly Arg Lys Gln Tyr His Asp Glu Tyr Leu Ala Lys Arg
340 345 350
Tyr Asn Ser Lys Thr Ile Ser Val Ser Ser Thr Phe Ser Tyr Tyr Ala
355 360 365
Met Pro Ala Trp Gln Leu Tyr Gly Gly Ile Ser Gly Met Phe Asp Asn
370 375 380

Thr Val Glu Lys Glu Gln Ala Ser Arg Arg Tyr Gly Val Ser Leu Gly
385 390 395 400
Thr Val Lys Ile Leu Asp Gly Gly Leu Gly Leu Lys Leu Gly Ala Gly
405 410 415
Tyr Thr Lys Arg Ile Phe Lys Ala Pro Ala Thr Leu Ile Tyr Asn Phe
420 425 430
Thr Arg Arg Asp Asp Glu Tyr Arg Ile Asn Ala Ala Leu Trp His Lys
435 440 445

Lys Leu Ser Trp Lys Gly Phe Thr Pro Gln Ile Asn Phe Arg Tyr Asn
450 455 460

Lys Ile Asn Ser Asn Met Pro Ala Phe Tyr Ser Arg Ser Gly Lys Glu

465 470 475 480

Trp Phe Val Ser Ile Glu Lys Thr Tyr

485

<210> 357

<211> 1461

<212> DNA

<213> N. flavescens SLAM 3

<400> 357

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gcctttgctg aatttcccga aggtgttgtc cggctggatg cgccttctca ggatgctgcc 120

gtacaagtgc agcaaaaaca atggctggat attttgtccg aagaagaaag gtcgtctgaa 180

aagaatgaga atgtcggcga accgactgtg gtcggcgatg atttttagc ggcaaacccg 240

cgtattcttg aggacgcgct gattcaagca ctcaacggca atagcgcaga tctggtttcc 300

tcgcttgtcg ccctttaccg caaacagccc aaccacaatc ccaaactgat tgcgcgtgcc 360

gatgctttgc tggcaaagtt gaaaggacgg acttccgaag cggtcgaacg ttatcgtacc 420

ctttatgaat ccgacgtttc agacgaccgc atattgttgg atttggcggc aacagagttt 480

caggattatc gtttgggcga ggcggcggcg catttccgcc atgccgcgca acgcgatata 540

cctgcccccg ttttggagaa tgtcaaacgt tttcaagaag ccgtcaaacg gcagacagaa 600

tggaaatggt ctggcggaat cagccccgtg cataacaata atgccaacaa cgctgctccg 660

cgttattgca tcgaaacaag ggggcaaacc gcatgcagcg ttactttgcc cgtcagtgcc 720

aacggcttga attacgaatt gaacaccgaa aaactcaccc cactgtacgg gcatcacgcc 780

gtcaaattcc gcgccaacct tagcggaacg agctattttt tcgaccgtca atcggcttac 840

gacgatgcgt tcggcagggc ttatttggga tggcagcgca aggatggcaa acaaaccatc 900

agcgttttac cgttttatca ggcacagttg gcaggcagca gcgagtttga cagcaaaaaa 960

gaaaataacc gtcgcgccgc gccgtatatg ctggcacacg gggttggcgt acagctttcg 1020

catatggtcc atctcggcaa cgcgacacaa ctttattact cgctggaacg atatcgccaa 1080

aactatcggg aaactgatcg tgcactgcgc aacgatgggt ggcacgacag tgcttatctt 1140

tccctagcgc gccgtttcgg cagtacgacc ctgttcggcg gttggcaata caaccgcttt 1200

gttcctgaaa acaaaaacat acgcaatgcc gtcaacaatg cggcctacca ccgcaacggt 1260

ttcaatatag gttggataca gcaatggcag gttttaggcg ggcttaacag cagacttacc 1320

gctttaccgc ttcatttgcc aaccgtcgct ataaaggcat tatggcattc ggtacggagt 1380

cgcaacgcaa ccgggagcgc tccctctcta tcagccttag tcacaacaaa ttatcttata 1440

aaggcattac ccctactttg a 1461

<210> 358

<211> 486

<212> PRT

<213> N. flavescens SLAM 3

<400> 358

Met Leu Lys Ile Lys Gln Lys Leu Val Ser Ala Ser Leu Cys Cys Leu
1 5 10 15

Leu Pro Ser Ala Ala Phe Ala Glu Phe Pro Glu Gly Val Val Arg Leu
20 25 30

Asp Ala Pro Ser Gln Asp Ala Ala Val Gln Val Gln Gln Lys Gln Trp
35 40 45

Leu Asp Ile Leu Ser Glu Glu Glu Arg Ser Ser Glu Lys Asn Glu Asn
50 55 60

Val Gly Glu Pro Thr Val Val Gly Asp Asp Phe Leu Ala Ala Asn Pro
65 70 75 80

Arg Ile Leu Glu Asp Ala Leu Ile Gln Ala Leu Asn Gly Asn Ser Ala
85 90 95

Asp Leu Val Ser Ser Leu Val Ala Leu Tyr Arg Lys Gln Pro Asn His
100 105 110

Asn Pro Lys Leu Ile Ala Arg Ala Asp Ala Leu Leu Ala Lys Leu Lys
115 120 125

Gly Arg Thr Ser Glu Ala Val Glu Arg Tyr Arg Thr Leu Tyr Glu Ser
130 135 140

Asp Val Ser Asp Asp Arg Ile Leu Leu Asp Leu Ala Ala Thr Glu Phe
145 150 155 160

Gln Asp Tyr Arg Leu Gly Glu Ala Ala Ala His Phe Arg His Ala Ala
165 170 175

Gln Arg Asp Ile Pro Ala Pro Val Leu Glu Asn Val Lys Arg Phe Gln

180 185 190

Glu Ala Val Lys Arg Gln Thr Glu Trp Lys Trp Ser Gly Gly Ile Ser

195 200 205

Pro Val His Asn Asn Asn Ala Asn Asn Ala Ala Pro Arg Tyr Cys Ile

210 215 220

Glu Thr Arg Gly Gln Thr Ala Cys Ser Val Thr Leu Pro Val Ser Ala

225 230 235 240

Asn Gly Leu Asn Tyr Glu Leu Asn Thr Glu Lys Leu Thr Pro Leu Tyr

245 250 255

Gly His His Ala Val Lys Phe Arg Ala Asn Leu Ser Gly Thr Ser Tyr

260 265 270

Phe Phe Asp Arg Gln Ser Ala Tyr Asp Asp Ala Phe Gly Arg Ala Tyr

275 280 285

Leu Gly Trp Gln Arg Lys Asp Gly Lys Gln Thr Ile Ser Val Leu Pro

290 295 300

Phe Tyr Gln Ala Gln Leu Ala Gly Ser Ser Glu Phe Asp Ser Lys Lys

305 310 315 320

Glu Asn Asn Arg Arg Ala Ala Pro Tyr Met Leu Ala His Gly Val Gly

325 330 335

Val Gln Leu Ser His Met Val His Leu Gly Asn Ala Thr Gln Leu Tyr

340 345 350

Tyr Ser Leu Glu Arg Tyr Arg Gln Asn Tyr Arg Glu Thr Asp Arg Ala

355 360 365

Leu Arg Asn Asp Gly Trp His Asp Ser Ala Tyr Leu Ser Leu Ala Arg

370 375 380

Arg Phe Gly Ser Thr Thr Leu Phe Gly Gly Trp Gln Tyr Asn Arg Phe

385 390 395 400

Val Pro Glu Asn Lys Asn Ile Arg Asn Ala Val Asn Asn Ala Ala Tyr

405 410 415

His Arg Asn Gly Phe Asn Ile Gly Trp Ile Gln Gln Trp Gln Val Leu

420 425 430

Gly Gly Leu Asn Ser Arg Leu Thr Ala Leu Pro Leu His Leu Pro Thr
435 440 445

Val Ala Ile Lys Ala Leu Trp His Ser Val Arg Ser Arg Asn Ala Thr
450 455 460

Gly Ser Ala Pro Ser Leu Ser Ala Leu Val Thr Thr Asn Tyr Leu Ile
465 470 475 480

Lys Ala Leu Pro Leu Leu
485

<210> 359

<211> 1470

<212> DNA

<213> N. gonorrhoeae SLAM 1

<400> 359

atggttattt tttattttta tttttgtggg aagacattta tgcctgcacg aaacagatgg 60

atgctgctgc ctttattggc aagcgcggca tacgccgaag aaacaccgtg cgaaccggat 120

ttgagaagcc gtcccgagtt caggcttcat gaagcggagg tcaaaccgat cgacagggag 180

aaggtaccgg ggcaggtgcg ggaaaaagga aaagttttgc aggttgacgg cgaaaccctg 240

ctgaaaaatc ccgaattgtt gtcgcgtgcc atgtattccg cagtggtctc aaacaatatt 300

gccggtatcc gcgtgatttt gccgatttac ctacaacagg cgcggcagga taagatgttg 360

gcactttatg cacaagggat tttggcgcag gcagagggca gggtgaagga ggcggtttcc 420

cattaccggg aattgattgc cgcccaaccc gacgcgcccg ccgtccgtat gcgtttggcg 480

gcggcattgt ttgaagacag gcagaacgag gcggcggcag accagttcga ccgcctgaaa 540

acagaagatc tgccgccgca gcttatggag caggtcgagc tgtaccgcaa ggcattgcgc 600

gaacgcgatg cgtggaaggt aaacggcggt ttcagcgtta cccgcgaaca caatatcaac 660

caagccccga aacagcagca gtacggcaat tggactttcc cgaaacaggt ggacggcacg 720

gcagtcaatt accggttcgg cgcggagaaa aaatggtcgc tgaaaaacgg ctggtacacg 780

acggcgggcg gcgacgtgtc cggcagggtt tatccgggga ataagaaatt caacgatatg 840

acggcaggtg tttccggcgg catcggtttt gccgaccggc gtaaagatgt cgggctggca 900

gtgttccacg aacgccgcac ctacggcaac gacgcttatt cttacgccaa cggcgcacgc 960

ctttatttca accgttggca aaccccgaga tggcaaacgc tgtcttcggc ggagtggggg 1020

cgtttgaaga atacgcgccg ggcgcgttcc gacaataccc atttgcaaat ttccaattcg 1080

ctggtgtttt accggaatgc gcgccaatat tggacgggcg gtttggattt ttaccgcgag 1140

cgcaaccccg ccgaccgtgg cgacaatttc aaccgttacg gcctgcgctt tgcctggggg 1200

caggaatggg gcggcagcgg cctgtcttcg ctgttccgcc tcggcgtggc gaaacggcat 1260

tatgaaaaac ccggcttctt cagcagtttt aaaggggaaa ggcgcaggga taaagaatcg 1320

gacacatcct tgagcctttg gcaccgggca ttgcatttca aaggcatcac gccgcgcctg 1380

acgctgtcgc accgcgaaac gtggagcaac gatgtgttta acgaatacga gaaaaacagg 1440

gcgtttgtcg agtttaacaa aacgttctga 1470

<210> 360

<211> 489

<212> PRT

<213> N. gonorrhoeae SLAM 1

<400> 360

Met Val Ile Phe Tyr Phe Tyr Phe Cys Gly Lys Thr Phe Met Pro Ala

1 5 10 15

Arg Asn Arg Trp Met Leu Leu Pro Leu Leu Ala Ser Ala Ala Tyr Ala

20 25 30

Glu Glu Thr Pro Cys Glu Pro Asp Leu Arg Ser Arg Pro Glu Phe Arg

35 40 45

Leu His Glu Ala Glu Val Lys Pro Ile Asp Arg Glu Lys Val Pro Gly

50 55 60

Gln Val Arg Glu Lys Gly Lys Val Leu Gln Val Asp Gly Glu Thr Leu

65 70 75 80

Leu Lys Asn Pro Glu Leu Leu Ser Arg Ala Met Tyr Ser Ala Val Val

85 90 95

Ser Asn Asn Ile Ala Gly Ile Arg Val Ile Leu Pro Ile Tyr Leu Gln

100 105 110

Gln Ala Arg Gln Asp Lys Met Leu Ala Leu Tyr Ala Gln Gly Ile Leu

115 120 125

Ala Gln Ala Glu Gly Arg Val Lys Glu Ala Val Ser His Tyr Arg Glu

130 135 140

Leu Ile Ala Ala Gln Pro Asp Ala Pro Ala Val Arg Met Arg Leu Ala

145 150 155 160

Ala Ala Leu Phe Glu Asp Arg Gln Asn Glu Ala Ala Ala Asp Gln Phe
165 170 175
Asp Arg Leu Lys Thr Glu Asp Leu Pro Pro Gln Leu Met Glu Gln Val
180 185 190
Glu Leu Tyr Arg Lys Ala Leu Arg Glu Arg Asp Ala Trp Lys Val Asn

195 200 205
Gly Gly Phe Ser Val Thr Arg Glu His Asn Ile Asn Gln Ala Pro Lys
210 215 220
Gln Gln Gln Tyr Gly Asn Trp Thr Phe Pro Lys Gln Val Asp Gly Thr
225 230 235 240
Ala Val Asn Tyr Arg Phe Gly Ala Glu Lys Lys Trp Ser Leu Lys Asn
245 250 255
Gly Trp Tyr Thr Thr Ala Gly Gly Asp Val Ser Gly Arg Val Tyr Pro

260 265 270
Gly Asn Lys Lys Phe Asn Asp Met Thr Ala Gly Val Ser Gly Gly Ile
275 280 285
Gly Phe Ala Asp Arg Arg Lys Asp Val Gly Leu Ala Val Phe His Glu
290 295 300
Arg Arg Thr Tyr Gly Asn Asp Ala Tyr Ser Tyr Ala Asn Gly Ala Arg
305 310 315 320
Leu Tyr Phe Asn Arg Trp Gln Thr Pro Arg Trp Gln Thr Leu Ser Ser

325 330 335
Ala Glu Trp Gly Arg Leu Lys Asn Thr Arg Arg Ala Arg Ser Asp Asn
340 345 350
Thr His Leu Gln Ile Ser Asn Ser Leu Val Phe Tyr Arg Asn Ala Arg
355 360 365
Gln Tyr Trp Thr Gly Gly Leu Asp Phe Tyr Arg Glu Arg Asn Pro Ala
370 375 380
Asp Arg Gly Asp Asn Phe Asn Arg Tyr Gly Leu Arg Phe Ala Trp Gly

385 390 395 400
Gln Glu Trp Gly Gly Ser Gly Leu Ser Ser Leu Phe Arg Leu Gly Val

405 410 415

Ala Lys Arg His Tyr Glu Lys Pro Gly Phe Phe Ser Ser Phe Lys Gly

420 425 430

Glu Arg Arg Arg Asp Lys Glu Ser Asp Thr Ser Leu Ser Leu Trp His

435 440 445

Arg Ala Leu His Phe Lys Gly Ile Thr Pro Arg Leu Thr Leu Ser His

450 455 460

Arg Glu Thr Trp Ser Asn Asp Val Phe Asn Glu Tyr Glu Lys Asn Arg

465 470 475 480

Ala Phe Val Glu Phe Asn Lys Thr Phe

485

<210> 361

<211> 1614

<212> DNA

<213> N. gonorrhoeae SLAM 2

<400> 361

atgcgccgcg tccgccgcgc gtggggcttg cggcgtttct gccgccgccg tccggcggtg 60

ttttttaagg aaggcaaatt gaaggatagt gtgtatcggg tatgccggct gtgtgccgcg 120

ctgtgtgttt ggggtgcggt cggcgcgtat gccgccggct tgcccgacgt tcgggacgat 180

gcggcggcgt tgcgcgccca gcgtgcggct gcggagggtt gggcgggaat gccgccggaa 240

ggggattctg ccgcaaacgg cggttcgcgc gtaatcgacg gggatttcct gctgtcgcgc 300

ccgcagttgt tggaacacgt tttgcgcgac gcgctcaacg gcaatcaggc ggatttgatc 360

gcttcgttgg cggatttgta tgccaagctg ccggattatg atgcggtgtt gtacggcagg 420

gcgcgggctt tgctggcgaa attggcggga aggccggcgg aggcggtggc gcgctatcgg 480

gcgttgcaca gggataatgc ggcagacgag cgggttttgc tggatttggc ggcggcggag 540

tttgacgatt tccggctgaa gtcggcaggg ctgcattttg cggaggcggc aaaattggat 600

ttgccggcgc cggttttgga aaatgtgggg cgtttccgga aaaaaacgga ggggctgacg 660

ggctggcatt tttcgggcgg catcagccct tctgtgaaca aaaacgccaa caatgccgcg 720

ccgcaatact gcctgcaggg cggcggcagc cggatatgca gcgttaccgg acctgtccgt 780

gcggcagggt tggattatga ggccgggggcg gaaaagctga ctgcgctggc ggacaaccat 840

tatctgctgt tccgcgccaa tgtcgggggc acaagctatt atttcagccg caaatcggct 900

tatgacgatg ctttcggcag ggcttatttg ggctggcagt ataaaaatgc gcggcagacg 960

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cagttggcgc attcttaccg cctgagccgc cggtcgcagc tttcggtgtc gctggaacgt 1140
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agccggattg ccgcgtctta cgcccaccgc aactacaaag gcattgcggc attttcgacg 1440
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tacaaaggca tcgtgccgac gttgaactac cgcttcggta agacggaaag caatgtgccg 1560
tatgcaaaac gccgcaacag cgaggtgttt gtgtcggcgg attggcggtt ttga 1614

<210> 362
<211> 537
<212> PRT
<213> N. gonorrhoeae SLAM 2
<400> 362

Met Arg Arg Val Arg Arg Ala Trp Gly Leu Arg Arg Phe Cys Arg Arg
1 5 10 15

Arg Pro Ala Val Phe Phe Lys Glu Gly Lys Leu Lys Asp Ser Val Tyr
20 25 30
Arg Val Cys Arg Leu Cys Ala Ala Leu Cys Val Trp Gly Ala Val Gly
35 40 45
Ala Tyr Ala Ala Gly Leu Pro Asp Val Arg Asp Asp Ala Ala Ala Leu
50 55 60
Arg Ala Gln Arg Ala Ala Ala Glu Gly Trp Ala Gly Met Pro Pro Glu
65 70 75 80

Gly Asp Ser Ala Ala Asn Gly Gly Ser Arg Val Ile Asp Gly Asp Phe
85 90 95
Leu Leu Ser Arg Pro Gln Leu Leu Glu His Val Leu Arg Asp Ala Leu
100 105 110

Asn Gly Asn Gln Ala Asp Leu Ile Ala Ser Leu Ala Asp Leu Tyr Ala
115 120 125
Lys Leu Pro Asp Tyr Asp Ala Val Leu Tyr Gly Arg Ala Arg Ala Leu
130 135 140

Leu Ala Lys Leu Ala Gly Arg Pro Ala Glu Ala Val Ala Arg Tyr Arg
145 150 155 160
Ala Leu His Arg Asp Asn Ala Ala Asp Glu Arg Val Leu Leu Asp Leu
165 170 175
Ala Ala Ala Glu Phe Asp Asp Phe Arg Leu Lys Ser Ala Gly Leu His
180 185 190
Phe Ala Glu Ala Ala Lys Leu Asp Leu Pro Ala Pro Val Leu Glu Asn
195 200 205

Val Gly Arg Phe Arg Lys Lys Thr Glu Gly Leu Thr Gly Trp His Phe
210 215 220
Ser Gly Gly Ile Ser Pro Ser Val Asn Lys Asn Ala Asn Asn Ala Ala
225 230 235 240
Pro Gln Tyr Cys Leu Gln Gly Gly Gly Ser Arg Ile Cys Ser Val Thr
245 250 255
Gly Pro Val Arg Ala Ala Gly Leu Asp Tyr Glu Ala Gly Ala Glu Lys
260 265 270

Leu Thr Ala Leu Ala Asp Asn His Tyr Leu Leu Phe Arg Ala Asn Val
275 280 285
Gly Gly Thr Ser Tyr Tyr Phe Ser Arg Lys Ser Ala Tyr Asp Asp Ala
290 295 300
Phe Gly Arg Ala Tyr Leu Gly Trp Gln Tyr Lys Asn Ala Arg Gln Thr
305 310 315 320
Val Gly Val Leu Pro Phe Tyr Gln Ala Gln Leu Ser Gly Ser Asp Gly
325 330 335

Phe Asp Ala Lys Thr Lys Pro Pro Ala Asp Arg Arg Leu Ala Pro Tyr
340 345 350
Met Leu Ala His Gly Ala Gly Val Gln Leu Ala His Ser Tyr Arg Leu

355 360 365

Ser Arg Arg Ser Gln Leu Ser Val Ser Leu Glu Arg Tyr Arg Gln Arg

370 375 380

Tyr Arg Glu Gln Gly Arg Ala Glu Arg Asn Asp Gly Trp Gln Asp Gly

385 390 395 400

Leu Tyr Val Ser Leu Ala Arg Arg Leu Gly Gly Ser Ala Thr Val Phe

405 410 415

Gly Gly Trp Gln Phe Ala Arg Phe Val Pro Lys Arg Glu Thr Val Gly

420 425 430

Gly Ala Val Asn Asn Ala Ala Tyr Arg Arg Asn Ala Val His Ile Gly

435 440 445

Trp Ala Gln Glu Trp Gly Gly Thr Gly Gly Leu Asn Ser Arg Ile Ala

450 455 460

Ala Ser Tyr Ala His Arg Asn Tyr Lys Gly Ile Ala Ala Phe Ser Thr

465 470 475 480

Glu Ala Gln Arg Asn Arg Glu Trp Asn Val Ser Leu Ala Leu Ser His

485 490 495

Asp Lys Leu Ser Tyr Lys Gly Ile Val Pro Thr Leu Asn Tyr Arg Phe

500 505 510

Gly Lys Thr Glu Ser Asn Val Pro Tyr Ala Lys Arg Arg Asn Ser Glu

515 520 525

Val Phe Val Ser Ala Asp Trp Arg Phe

530 535

<210> 363

<211> 1494

<212> DNA

<213> N. gonorrhoeae SLAM 3

<400> 363

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tccaacgatg ccgccgacga acgccgccgc ctgctggacg agggcagccg ccaaacgcag 120

caataccgcg aaagcggttg gctggacacg gaacaggcac gcggggaagt agaggaaaac 180

gacggctata tttcgatagg cggcgaaatc taccaagtcg gcgatacggc ggaagaactg 240

gaaagcgcaa tttaccacgc cctcaatgcg cggcagtggc acaaggtgcg gcagttcgcc 300

gcccgctacg ccaaactgcc ccggcacaag cccgcgctga ttcatttggc cgatgcgctg 360
caaaaacggg acgaagggga tttccgcgcg gcggggaaca gttttcagac ggccttggaa 420
gccgaacccg acaacccgcg cctgctgctc gaagcggggc ggttttatgc cgaagacaac 480
caaaacaaag agtctgccgc cgcgtttgag aaagttctga aaacggacat tcccgcagaa 540
acccgcccca tcgtggaaaa ctacctgtcc gaactgggca aacgccgccg ctggcacggc 600
caaatcagcc tcggctacgg ctataacagc aatgtaaacc aaggcaacgg catcaaccaa 660
tgcgtgtggg aaattgcggg catgtgcctg atggagcgca ccctgcccgc gccaacggat 720

tcgaccttct catcctatag cgcgaccgcc gaaaaaaccg tcccgctcaa agggaatcac 780
ggcgtacagg tgcgcggtgt actgtacggc aaccgctaca cggaaaaaga caaagattcg 840
gcggctatgc cggattacgg ctatcgcaac ggttcgctgt acgcgggata cgcctatgcc 900
gacgcacgct cctccttttc cctgctgcct tatttcgaat acgatttccg caaccgccac 960
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cgcattaact cacatgccgg agcaaaaaag accggatacg gcggacaaag caaaacttat 1080
tttgccgatt tcaaacaata cgaactcggc gcgggggcgg aattttccat cacgctgaaa 1140

agcggcctgc ttgtaaattt cgatgccgca cgcaaagcct atcccgaaaa atcctcttcc 1200
agcaaagaat atacggctcg gctgggcgcg tataggcttt tttcgggcgg tacttattta 1260
aacgccgtcc tgctctaccg ccgcagcctg tatgacgcgg caagtttcgt cagcgataac 1320
aaacggcggc gcgacaagca atacatcatg atggctgcgg cgggttttcc gcaatggaat 1380
atcaaaggcg tatatcccga actgcgtttc aggcgaacaa tcgcacacag caacgcggtg 1440
tattaccgct accgccaaaa cgaatggctg ttgggtttta aatatcggtt ttga 1494

<210> 364
<211> 497
<212> PRT
<213> N. gonorrhoeae SLAM 3

<400> 364

Met Thr His Arg Leu Cys Leu Leu Phe Leu Pro Leu Cys Thr Val Cys
1 5 10 15
Leu Ala Ala Pro Ser Asn Asp Ala Ala Asp Glu Arg Arg Arg Leu Leu
20 25 30
Asp Glu Gly Ser Arg Gln Thr Gln Gln Tyr Arg Glu Ser Gly Trp Leu

```
        35                  40                  45
Asp Thr Glu Gln Ala Arg Gly Glu Val Glu Glu Asn Asp Gly Tyr Ile
    50                  55                  60

Ser Ile Gly Gly Glu Ile Tyr Gln Val Gly Asp Thr Ala Glu Glu Leu
65                  70                  75                  80
Glu Ser Ala Ile Tyr His Ala Leu Asn Ala Arg Gln Trp His Lys Val
                85                  90                  95
Arg Gln Phe Ala Ala Arg Tyr Ala Lys Leu Pro Arg His Lys Pro Ala
            100                 105                 110
Leu Ile His Leu Ala Asp Ala Leu Gln Lys Arg Asp Glu Gly Asp Phe
        115                 120                 125

Arg Ala Ala Gly Asn Ser Phe Gln Thr Ala Leu Glu Ala Glu Pro Asp
    130                 135                 140
Asn Pro Arg Leu Leu Leu Glu Ala Gly Arg Phe Tyr Ala Glu Asp Asn
145                 150                 155                 160
Gln Asn Lys Glu Ser Ala Ala Ala Phe Glu Lys Val Leu Lys Thr Asp
                165                 170                 175
Ile Pro Ala Glu Thr Arg Pro Ile Val Glu Asn Tyr Leu Ser Glu Leu
            180                 185                 190

Gly Lys Arg Arg Arg Trp His Gly Gln Ile Ser Leu Gly Tyr Gly Tyr
        195                 200                 205
Asn Ser Asn Val Asn Gln Gly Asn Gly Ile Asn Gln Cys Val Trp Glu
    210                 215                 220
Ile Ala Gly Met Cys Leu Met Glu Arg Thr Leu Pro Ala Pro Thr Asp
225                 230                 235                 240
Ser Thr Phe Ser Ser Tyr Ser Ala Thr Ala Glu Lys Thr Val Pro Leu
                245                 250                 255

Lys Gly Asn His Gly Val Gln Val Arg Gly Val Leu Tyr Gly Asn Arg
            260                 265                 270
Tyr Thr Glu Lys Asp Lys Asp Ser Ala Ala Met Pro Asp Tyr Gly Tyr
        275                 280                 285
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Arg Asn Gly Ser Leu Tyr Ala Gly Tyr Ala Tyr Ala Asp Ala Arg Ser
290 295 300
Ser Phe Ser Leu Leu Pro Tyr Phe Glu Tyr Asp Phe Arg Asn Arg His
305 310 315 320

Thr His Tyr Arg Ala Trp Gly Ala Asp Ala Asp Trp Ser Arg Thr Leu
325 330 335
Ser Pro His Trp Arg Ile Asn Ser His Ala Gly Ala Lys Lys Thr Gly
340 345 350
Tyr Gly Gly Gln Ser Lys Thr Tyr Phe Ala Asp Phe Lys Gln Tyr Glu
355 360 365
Leu Gly Ala Gly Ala Glu Phe Ser Ile Thr Leu Lys Ser Gly Leu Leu
370 375 380

Val Asn Phe Asp Ala Ala Arg Lys Ala Tyr Pro Glu Lys Ser Ser Ser
385 390 395 400
Ser Lys Glu Tyr Thr Ala Arg Leu Gly Ala Tyr Arg Leu Phe Ser Gly
405 410 415
Gly Thr Tyr Leu Asn Ala Val Leu Leu Tyr Arg Arg Ser Leu Tyr Asp
420 425 430
Ala Ala Ser Phe Val Ser Asp Asn Lys Arg Arg Arg Asp Lys Gln Tyr
435 440 445

Ile Met Met Ala Ala Ala Gly Phe Pro Gln Trp Asn Ile Lys Gly Val
450 455 460
Tyr Pro Glu Leu Arg Phe Arg Arg Thr Ile Ala His Ser Asn Ala Val
465 470 475 480
Tyr Tyr Arg Tyr Arg Gln Asn Glu Trp Leu Leu Gly Phe Lys Tyr Arg
485 490 495
Phe

<210> 365
<211> 1416
<212> DNA
<213> N. indicus SLAM 1

<400> 365

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ttcagcgtaa gggtttcgag tttgcgcagt ctgttcttgg ccgctctcat gtgcctcgga 120

gcgatcaccg gccccgctgt ctcggcgccg gcggccgaag gaggcagcac ggctatcgtt 180

tccagtgcgc aggcagtcgc cacggtgcgc agtctcgtcg atgcaggtcg cttcgaggag 240

gcgcgcggct tcattgcccg gtggaatgcg ggcagccgca gtcactccat gcgcgttgcg 300

ttcgttgaag gtttgattgc tgcgcgttcc ggcaggcacg ctcaggctgc ggccatcttc 360

cgggaaatat tggctgtcga cccacagaac gatgtggcgc gcatagagct cgcccgctcg 420

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cggccactgc ggttccgcgg ttatctgtcg cttctcccct caaccaacat caaccggggt 600

acggacaacg agaccgtggc cttcggtccc atcgacctgc ggatcaatcc ggacgcgcga 660

cgcaagtccg gtatcggcct tctgctcggt ggcgagatga tttaccagaa gccgctcagc 720

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tatctgggcg gtcaggcccg catccaggac gatctcgttt cggatgcccg cgatggctat 1020

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catgaggtcg agctgcgtct gaccaaagac ttctag 1416

<210> 366

<211> 471

<212> PRT

<213> N. indicus SLAM 1

<400> 366

Met Ile Ser Gly Ser Met His Glu Lys Ala Cys Ala Pro Ser Arg Glu

1 5 10 15

Gly Thr Gly Leu Phe Ser Val Arg Val Ser Ser Leu Arg Ser Leu Phe

20 25 30

Leu Ala Ala Leu Met Cys Leu Gly Ala Ile Thr Gly Pro Ala Val Ser

35 40 45

Ala Pro Ala Ala Glu Gly Gly Ser Thr Ala Ile Val Ser Ser Ala Gln

50 55 60

Ala Val Ala Thr Val Arg Ser Leu Val Asp Ala Gly Arg Phe Glu Glu

65 70 75 80

Ala Arg Gly Phe Ile Ala Arg Trp Asn Ala Gly Ser Arg Ser His Ser

85 90 95

Met Arg Val Ala Phe Val Glu Gly Leu Ile Ala Ala Arg Ser Gly Arg

100 105 110

His Ala Gln Ala Ala Ala Ile Phe Arg Glu Ile Leu Ala Val Asp Pro

115 120 125

Gln Asn Asp Val Ala Arg Ile Glu Leu Ala Arg Ser Leu Ala Ala Leu

130 135 140

Asn Asp Ala Asp Gly Val Arg Ala Gln Ala Glu Leu Leu Arg Ala Ser

145 150 155 160

Gly Ile Asp Asp Arg Leu Gly Gly Ala Ile Thr Arg Leu Ala Asp Leu

165 170 175

Val Asp Ala Gly Arg Pro Leu Arg Phe Arg Gly Tyr Leu Ser Leu Leu

180 185 190

Pro Ser Thr Asn Ile Asn Arg Gly Thr Asp Asn Glu Thr Val Ala Phe

195 200 205

Gly Pro Ile Asp Leu Arg Ile Asn Pro Asp Ala Arg Arg Lys Ser Gly

210 215 220

Ile Gly Leu Leu Leu Gly Gly Glu Met Ile Tyr Gln Lys Pro Leu Ser

225 230 235 240

Pro Thr Arg Arg Leu Ile Ser Val Thr Ser Ala Thr Gly Arg Phe Tyr

245 250 255

Pro Lys Leu Pro Ser Ala Ser Ser Leu Gln Val Asp Gly Ala Leu Gly
260 265 270
Val Glu Gln Arg Ile Gly Ser Thr Arg Ala Met Val Ala Leu Thr Gly
275 280 285
Ser Ile Val Val Thr Pro Asp Ala Val Thr Thr Val Gln Thr Gly Ile

290 295 300
Arg Gly Glu Leu Ser Gly Arg Phe Ala Ala Ala Pro Arg Trp Phe Trp
305 310 315 320
Tyr Leu Gly Gly Gln Ala Arg Ile Gln Asp Asp Leu Val Ser Asp Ala
325 330 335
Arg Asp Gly Tyr Val Ala Asn Leu Gly Phe Asn Leu Asp Arg Met Phe
340 345 350
Ala Thr Gly His Phe Ile Arg Phe Gly Val Arg Gly Glu Leu Ala Arg

355 360 365
Leu Arg Glu Gly Arg Phe Ser Tyr Asp Glu Ala Gly Leu Leu Val Gly
370 375 380
Tyr Ala Arg Pro Leu Pro Leu Gly Ile Asn Val Phe Ala Gln Ala Ala
385 390 395 400
Leu Ser Trp Arg Asp Tyr His Gly Leu Tyr Pro Gly Leu Asp Glu Gly
405 410 415
Gln Ser Asp Ile Arg Phe Thr Gly Asp Ile Ile Ala Thr Lys Arg Asp

420 425 430
Leu His Ile Ala Gly Phe Ala Pro Gln Leu Gln Tyr Arg Phe Glu Arg
435 440 445
Val Ser Ser Asn Ala Ala Phe Glu Asp Tyr Thr Arg His Glu Val Glu
450 455 460
Leu Arg Leu Thr Lys Asp Phe
465 470

<210> 367

<211> 1488

<212> DNA

<213> N. lacisaponensis SLAM 1

<400> 367

atgtttaatc tacacataac acgctggcag gtgggtggtt tatggactgt cttgttgctg 60

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gatcagcagg ctgaaacgct ggagcggcgc ttactggctg atgaagacta tcagcctgcc 180

gggcagccac agctgattat tgaaggccgc gcgtatcctg ttggggataa tgttgatgat 240

ctcgggcgag cactctatgt ggcgctacag caacgtcagt ggtctgcggt ggtgtatttt 300

ctgcagcgct atgccgcact ggaggatgct gatccgatgc tgttggcctt cgcacaaggc 360

tccctggctc gggtgcaggg tgatttacgc ggtgccgaag cattttccg acaattgctg 420

cttttgcaac cgggcttcct gccagggcag ctggagttgg cgcgggtgtt gttcgaaaat 480

cataagaacc ctgaagccta tcaatcattt gagcagattg cggcacagtt ggacccgctc 540

gatgagcgtc agacgggtgt acgccgtact gtacagaatt ttttgcaggc gttggatcag 600

cgccatgcct ggcaaggatc ggtggctttt ggacctatct ggaatgacaa cctgaatcag 660

tcatcgggta gccgtacctg tctgctggag cttaacggtc agtgttatta cgaacgtaaa 720

gtgccggatg cgctggctgc gaccggtgtg gattatgagt ttagcctgaa tcgtcagttc 780

agcttgtcag ggcatcatgg catgtatgtg cgtgcgctct ggtatgggca atcctatgac 840

gaaacgcgtg agtataatga gagtacgttg aatctgcagt caggctatcg ttatcaggat 900

cagcgtcacc agtttcgact ggcacctgtc gttgaattga ccgctcaggg tgacaaagtg 960

ctgcatgatg cctggggtgt gcatgccgaa tggatgtatc acctgaatcc ccggcgtgtt 1020

tttaagctgg agggtagttc acggcagttg cgctatcagg atgaccggtt tgatcgttac 1080

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caaccgggct tgcgtctggg tatggctggc gctttgaatc agcatctgca cacaacgtta 1260

ttgttgtcgc atcgcgagcg gcggcatcag gcatttagtg ctgtgctggg tgaaagacgc 1320

agtgatgatg agcagagtgt aacactgata ctgcgtgcac caacattgca ggttgccggt 1380

tttgaacccg tgctaacgct tcgccaccga aaaattcgca gcaatgtcga ctggctttac 1440

agccatgacc gtaatcaggt gagcctgaag ctggaacgac gcttctga 1488

<210> 368

<211> 495

<212> PRT

<213> N. lacisaponensis SLAM 1

<400> 368

Met Phe Asn Leu His Ile Thr Arg Trp Gln Val Gly Gly Leu Trp Thr
1 5 10 15
Val Leu Leu Leu Leu Ala Met Pro Leu Ala Ala Gln Asp Ala Asp Val

20 25 30
Gln Leu Arg Leu Gln Gln Ser Leu Asp Gln Gln Ala Glu Thr Leu Glu
35 40 45
Arg Arg Leu Leu Ala Asp Glu Asp Tyr Gln Pro Ala Gly Gln Pro Gln
50 55 60
Leu Ile Ile Glu Gly Arg Ala Tyr Pro Val Gly Asp Asn Val Asp Asp
65 70 75 80
Leu Gly Arg Ala Leu Tyr Val Ala Leu Gln Gln Arg Gln Trp Ser Ala

85 90 95
Val Val Tyr Phe Leu Gln Arg Tyr Ala Ala Leu Glu Asp Ala Asp Pro
100 105 110
Met Leu Leu Ala Phe Ala Gln Gly Ser Leu Ala Arg Val Gln Gly Asp
115 120 125
Leu Arg Gly Ala Glu Ala Phe Phe Arg Gln Leu Leu Leu Leu Gln Pro
130 135 140
Gly Phe Leu Pro Gly Gln Leu Glu Leu Ala Arg Val Leu Phe Glu Asn

145 150 155 160
His Lys Asn Pro Glu Ala Tyr Gln Ser Phe Glu Gln Ile Ala Ala Gln
165 170 175
Leu Asp Pro Leu Asp Glu Arg Gln Thr Gly Val Arg Arg Thr Val Gln
180 185 190
Asn Phe Leu Gln Ala Leu Asp Gln Arg His Ala Trp Gln Gly Ser Val
195 200 205
Ala Phe Gly Pro Ile Trp Asn Asp Asn Leu Asn Gln Ser Ser Gly Ser

210 215 220
Arg Thr Cys Leu Leu Glu Leu Asn Gly Gln Cys Tyr Tyr Glu Arg Lys
225 230 235 240
Val Pro Asp Ala Leu Ala Ala Thr Gly Val Asp Tyr Glu Phe Ser Leu

245 250 255

Asn Arg Gln Phe Ser Leu Ser Gly His His Gly Met Tyr Val Arg Ala

260 265 270

Leu Trp Tyr Gly Gln Ser Tyr Asp Glu Thr Arg Glu Tyr Asn Glu Ser

275 280 285

Thr Leu Asn Leu Gln Ser Gly Tyr Arg Tyr Gln Asp Gln Arg His Gln

290 295 300

Phe Arg Leu Ala Pro Val Val Glu Leu Thr Ala Gln Gly Asp Lys Val

305 310 315 320

Leu His Asp Ala Trp Gly Val His Ala Glu Trp Met Tyr His Leu Asn

325 330 335

Pro Arg Arg Val Phe Lys Leu Glu Gly Ser Ser Arg Gln Leu Arg Tyr

340 345 350

Gln Asp Asp Arg Phe Asp Arg Tyr Asn Gly Pro Ser His Ala Val His

355 360 365

Ala Thr Val Trp Gln Val Leu Pro Asn Asn Trp Thr Ala Phe Thr Gly

370 375 380

Leu Asp Trp Gln Tyr Arg Asp Ala Glu Asp Glu Thr Leu Ala Tyr Gln

385 390 395 400

Gln Pro Gly Leu Arg Leu Gly Met Ala Gly Ala Leu Asn Gln His Leu

405 410 415

His Thr Thr Leu Leu Leu Ser His Arg Glu Arg Arg His Gln Ala Phe

420 425 430

Ser Ala Val Leu Gly Glu Arg Arg Ser Asp Asp Glu Gln Ser Val Thr

435 440 445

Leu Ile Leu Arg Ala Pro Thr Leu Gln Val Ala Gly Phe Glu Pro Val

450 455 460

Leu Thr Leu Arg His Arg Lys Ile Arg Ser Asn Val Asp Trp Leu Tyr

465 470 475 480

Ser His Asp Arg Asn Gln Val Ser Leu Lys Leu Glu Arg Arg Phe

485 490 495

<210> 369

<211> 1467

<212> DNA

<213> N. lactamica SLAM 1

<400> 369

atggttattt tttatttttg tgggaagaca tttatgcctg cacgaaacag atggatgctg 60

ctgctgcctt tattggcaag cgcggcatat gccgaagaaa caccgcgcga accggatttg 120

agaagccgtc ccgagttcag gcttcatgaa gcggaggtca aaccaatcga cagggagaag 180

gtaccggggc aggtgcggga aaaaggaaaa gttttgcaga ttgacggaga aaccctgctg 240

aaaaatcccg aattgctgtc ccgcgcgatg tattccgcag tggtctcaaa caatattgcc 300

ggtatccgcg ttattttgcc gatttaccta caacaggcgc agcaggataa gatgttggca 360

ctttatgcac aagggatttt ggcgcaggca gacggtaggg tgaaagaagc gatttcccat 420

taccgggaat tgattgccgc ccaacccgac gcgcccgccg tccgtatgcg tttggcggcg 480

gcattgtttg aagacaggca gaacgaggcg gcggcagacc agttcgaccg cctgaaggcg 540

gaaaacctgc cgccgcagct tatggagcag gtcgagctgt accgcaaggc attgcgcgaa 600

cgcgatgcgt ggaaggtaaa cggcggcttc agcgtcaccc gcgaacacaa tatcaaccaa 660

gccccgaaac ggcagcagta cggcaaatgg actttcccga aacaggtgga cggcacggcg 720

gtcaattacc ggctcggcgc ggagaaaaaa tggtcgctga aaaacggctg gtacacgacg 780

gggggggggcg acgtgtccgg cagggtttat ccggggaata agaaattcaa cgatatgacg 840

gcaggtgttt ccggcggcat cggttttgcc gaccggcgta aagatgtcgg gctggcagtg 900

ttccacgaac gccgcaccta cggcaacgac gcttattctt acaccaacgg cgcacgcctt 960

tatttcaacc gttggcaaac cccgaaatgg caaacgttgt cttcggcgga gtgggggcgt 1020

ttgaagaata cgcgccgggc gcgttccgac aatacccatt tgcaaatttc caattcgctg 1080

gtgttttacc ggaatgcgcg ccaatattgg acgggcggtt tggattttta ccgcgagcgc 1140

aaccccgccg accgtggcga caatttcaac cgttacggcc tgcgctttgc ctggggacag 1200

gaatggggcg gcagcggcct gtcttcgctg ttgcgcctcg gcgcggcgaa acggcattat 1260

gaaaaacccg gctttttcag cggttttaaa ggggaaaggc gcagggataa agaattggac 1320

acatccttga gcctttggca ccgggcattg catttcaaag gcatcacgcc gcgcctgacg 1380

ctgtcgcacc gcgaaacgtg gagtaacgat gtgttcaacg aatacgagaa aaatcgggcg 1440

tttgtcgagt ttaacaaaac gttctga 1467

<210> 370

<211> 488

<212> PRT

<213> N. lactamica SLAM 1

<400> 370

Met Val Ile Phe Tyr Phe Cys Gly Lys Thr Phe Met Pro Ala Arg Asn
1 5 10 15

Arg Trp Met Leu Leu Leu Pro Leu Leu Ala Ser Ala Ala Tyr Ala Glu
20 25 30

Glu Thr Pro Arg Glu Pro Asp Leu Arg Ser Arg Pro Glu Phe Arg Leu
35 40 45

His Glu Ala Glu Val Lys Pro Ile Asp Arg Glu Lys Val Pro Gly Gln
50 55 60

Val Arg Glu Lys Gly Lys Val Leu Gln Ile Asp Gly Glu Thr Leu Leu
65 70 75 80

Lys Asn Pro Glu Leu Leu Ser Arg Ala Met Tyr Ser Ala Val Val Ser
85 90 95

Asn Asn Ile Ala Gly Ile Arg Val Ile Leu Pro Ile Tyr Leu Gln Gln
100 105 110

Ala Gln Gln Asp Lys Met Leu Ala Leu Tyr Ala Gln Gly Ile Leu Ala
115 120 125

Gln Ala Asp Gly Arg Val Lys Glu Ala Ile Ser His Tyr Arg Glu Leu
130 135 140

Ile Ala Ala Gln Pro Asp Ala Pro Ala Val Arg Met Arg Leu Ala Ala
145 150 155 160

Ala Leu Phe Glu Asp Arg Gln Asn Glu Ala Ala Ala Asp Gln Phe Asp
165 170 175

Arg Leu Lys Ala Glu Asn Leu Pro Pro Gln Leu Met Glu Gln Val Glu
180 185 190

Leu Tyr Arg Lys Ala Leu Arg Glu Arg Asp Ala Trp Lys Val Asn Gly
195 200 205

Gly Phe Ser Val Thr Arg Glu His Asn Ile Asn Gln Ala Pro Lys Arg
210 215 220

Gln Gln Tyr Gly Lys Trp Thr Phe Pro Lys Gln Val Asp Gly Thr Ala
225 230 235 240
Val Asn Tyr Arg Leu Gly Ala Glu Lys Lys Trp Ser Leu Lys Asn Gly

245 250 255
Trp Tyr Thr Thr Gly Gly Gly Asp Val Ser Gly Arg Val Tyr Pro Gly
260 265 270
Asn Lys Lys Phe Asn Asp Met Thr Ala Gly Val Ser Gly Gly Ile Gly
275 280 285
Phe Ala Asp Arg Arg Lys Asp Val Gly Leu Ala Val Phe His Glu Arg
290 295 300
Arg Thr Tyr Gly Asn Asp Ala Tyr Ser Tyr Thr Asn Gly Ala Arg Leu

305 310 315 320
Tyr Phe Asn Arg Trp Gln Thr Pro Lys Trp Gln Thr Leu Ser Ser Ala
325 330 335
Glu Trp Gly Arg Leu Lys Asn Thr Arg Arg Ala Arg Ser Asp Asn Thr
340 345 350
His Leu Gln Ile Ser Asn Ser Leu Val Phe Tyr Arg Asn Ala Arg Gln
355 360 365
Tyr Trp Thr Gly Gly Leu Asp Phe Tyr Arg Glu Arg Asn Pro Ala Asp

370 375 380
Arg Gly Asp Asn Phe Asn Arg Tyr Gly Leu Arg Phe Ala Trp Gly Gln
385 390 395 400
Glu Trp Gly Gly Ser Gly Leu Ser Ser Leu Leu Arg Leu Gly Ala Ala
405 410 415
Lys Arg His Tyr Glu Lys Pro Gly Phe Phe Ser Gly Phe Lys Gly Glu
420 425 430
Arg Arg Arg Asp Lys Glu Leu Asp Thr Ser Leu Ser Leu Trp His Arg

435 440 445
Ala Leu His Phe Lys Gly Ile Thr Pro Arg Leu Thr Leu Ser His Arg
450 455 460
Glu Thr Trp Ser Asn Asp Val Phe Asn Glu Tyr Glu Lys Asn Arg Ala

465 470 475 480

Phe Val Glu Phe Asn Lys Thr Phe

485

<210> 371

<211> 1518

<212> DNA

<213> N. lactamica SLAM 2

<400> 371

atgttgtatt tcagatacgg ttttttggtt gtttggtgtg cggcaggtgt ttctgccgcc 60

tatggggcgg atgcgcccgc gattttggat gacaaggcat tgttgcaggt gcagcggtcg 120

gtgtcggata agtgggcgga atcggattgg aaagttgaaa atgatgctcc gcgcgtggtt 180

gacggggatt ttttgttggc gcatccgaaa atgttggaac atagtttgcg cgacgcgctc 240

aacggcaatc aggcggattt aatcgcttcg ttggcggatt tgtatgccaa gctgccggat 300

tatgacgcgg ttttgtacgg cagggcgcgg gctttgctgg cgaaattggc gggaaggccg 360

gcggaggcgg tggcgcggta tcgggaactg cacggggaaa atgcggcaga cgagcggatt 420

ttgctggatt tggcggcggc ggagtttgac gatttccgac tgaagtcggc agaaaggcat 480

tttgcggagg cggcaaaatt ggatttgccg gcgccggttt tggaaaatgt ggggcgtttt 540

cggaaaaaaa cggaggggct gacgggctgg cgtttttcgg gcggtatcag cccggcggtc 600

aatagaaatg ccaataatgc cgcgccgcag tattgccagc aaaacggagg ccggcagata 660

tgcagtgtca gccgggcgga gcgagcggca gggttgaatt atgaaatcga ggcggaaaaa 720

ctgacggcgt tggcggataa tcattatttg ttgttccgtt ccaatatcgg cggcacgagc 780

tattatttca gtaaaaaatc agcttatgat gacgggttcg gcagggcgta tttgggttgg 840

cagtataaaa atgcacggca gacggcgggg attttgccgt tttatcaggt gcagttgtcg 900

ggcagcgacg gctttgatgc gaaaacaaaa cgggtaaaca accgccgcct gccgccgtat 960

atgctggcgc acggagtcgg cgtgcagctg tcccatactt accgcccaaa cccgggatgg 1020

caattttcgg tcgcgctgga acattaccgc caacgctatc gcgaacagga tagggcggaa 1080

tacaataacg gtcggcagga cgggttttat gtttcgtcgg caaaacgttt gggcgaatcg 1140

gcaactgtgt tcggcggctg gcagtttgtg cggtttgtgc cgaaacgcga aacggtgggc 1200

ggcgcggtca ataatgccgc ctaccggcgc aacggtgttt atgccggctg ggcgcaggag 1260

tggcggcagt tgggcggttt gaacagtcgg gtttccgcgt cttatgcccg ccgcaactat 1320

aagggcgttg cggctttctc gacagaggcg caacgcaacc gcgaatggaa tgtctcgctg 1380

gctttgagcc acgacaagtt gtcgtacaaa ggtatcgtac cggcgttgaa ttatcgtttc 1440

ggcaggacgg aaagtaatgt gccgtatgcg aaacgccgca acagcgaggt gtttgtgtcg 1500

gcggattggc ggttttga 1518

<210> 372

<211> 505

<212> PRT

<213> N. lactamica SLAM 2

<400> 372

Met Leu Tyr Phe Arg Tyr Gly Phe Leu Val Val Trp Cys Ala Ala Gly
1 5 10 15

Val Ser Ala Ala Tyr Gly Ala Asp Ala Pro Ala Ile Leu Asp Asp Lys
20 25 30

Ala Leu Leu Gln Val Gln Arg Ser Val Ser Asp Lys Trp Ala Glu Ser
35 40 45

Asp Trp Lys Val Glu Asn Asp Ala Pro Arg Val Val Asp Gly Asp Phe
50 55 60

Leu Leu Ala His Pro Lys Met Leu Glu His Ser Leu Arg Asp Ala Leu
65 70 75 80

Asn Gly Asn Gln Ala Asp Leu Ile Ala Ser Leu Ala Asp Leu Tyr Ala
85 90 95

Lys Leu Pro Asp Tyr Asp Ala Val Leu Tyr Gly Arg Ala Arg Ala Leu
100 105 110

Leu Ala Lys Leu Ala Gly Arg Pro Ala Glu Ala Val Ala Arg Tyr Arg
115 120 125

Glu Leu His Gly Glu Asn Ala Ala Asp Glu Arg Ile Leu Leu Asp Leu
130 135 140

Ala Ala Ala Glu Phe Asp Asp Phe Arg Leu Lys Ser Ala Glu Arg His
145 150 155 160

Phe Ala Glu Ala Ala Lys Leu Asp Leu Pro Ala Pro Val Leu Glu Asn
165 170 175

Val Gly Arg Phe Arg Lys Lys Thr Glu Gly Leu Thr Gly Trp Arg Phe
180 185 190

Ser Gly Gly Ile Ser Pro Ala Val Asn Arg Asn Ala Asn Asn Ala Ala
195 200 205

Pro Gln Tyr Cys Gln Gln Asn Gly Gly Arg Gln Ile Cys Ser Val Ser
210 215 220
Arg Ala Glu Arg Ala Ala Gly Leu Asn Tyr Glu Ile Glu Ala Glu Lys
225 230 235 240
Leu Thr Ala Leu Ala Asp Asn His Tyr Leu Leu Phe Arg Ser Asn Ile
245 250 255
Gly Gly Thr Ser Tyr Tyr Phe Ser Lys Lys Ser Ala Tyr Asp Asp Gly
260 265 270

Phe Gly Arg Ala Tyr Leu Gly Trp Gln Tyr Lys Asn Ala Arg Gln Thr
275 280 285
Ala Gly Ile Leu Pro Phe Tyr Gln Val Gln Leu Ser Gly Ser Asp Gly
290 295 300
Phe Asp Ala Lys Thr Lys Arg Val Asn Asn Arg Arg Leu Pro Pro Tyr
305 310 315 320
Met Leu Ala His Gly Val Gly Val Gln Leu Ser His Thr Tyr Arg Pro
325 330 335

Asn Pro Gly Trp Gln Phe Ser Val Ala Leu Glu His Tyr Arg Gln Arg
340 345 350
Tyr Arg Glu Gln Asp Arg Ala Glu Tyr Asn Asn Gly Arg Gln Asp Gly
355 360 365
Phe Tyr Val Ser Ser Ala Lys Arg Leu Gly Glu Ser Ala Thr Val Phe
370 375 380
Gly Gly Trp Gln Phe Val Arg Phe Val Pro Lys Arg Glu Thr Val Gly
385 390 395 400

Gly Ala Val Asn Asn Ala Ala Tyr Arg Arg Asn Gly Val Tyr Ala Gly
405 410 415
Trp Ala Gln Glu Trp Arg Gln Leu Gly Gly Leu Asn Ser Arg Val Ser
420 425 430
Ala Ser Tyr Ala Arg Arg Asn Tyr Lys Gly Val Ala Ala Phe Ser Thr

435 440 445

Glu Ala Gln Arg Asn Arg Glu Trp Asn Val Ser Leu Ala Leu Ser His

450 455 460

Asp Lys Leu Ser Tyr Lys Gly Ile Val Pro Ala Leu Asn Tyr Arg Phe

465 470 475 480

Gly Arg Thr Glu Ser Asn Val Pro Tyr Ala Lys Arg Arg Asn Ser Glu

485 490 495

Val Phe Val Ser Ala Asp Trp Arg Phe

500 505

<210> 373

<211> 1224

<212> DNA

<213> N. lactamica SLAM 3

<400> 373

atgcagatta accgggcgtt gttggcgcgg gattgggcgg cactgaaacg cctgttggcc 60

caatatgccg aacaaccgca atatgatgcg gtgctgtacc gttatgccct cggcgcgtta 120

taccgcagcg agatgcggca gggcgaggcg gccgatctat accgtgagtt gttgtcagaa 180

aggcctgacc ttgtttatcc ccgttttgat ttgggcgtga tgctgtttga agacaaacaa 240

tatcgtgagg cattggttca gttgcaccgg gtcgaggagg cgttgcctcc cgatatgcgg 300

cagcttgcac gggaatatat ccgtcaggtg gaagcggtgc aggcgtggca tccttcgttc 360

aatatgaatt acgaacaaac agataatgta aacaatgctt ccccttcgcg ggacatcgtc 420

ctcaacggcc ggaaatggac aagatcagaa gacagcctgc ccaaacgcgc caacgggata 480

aggtacgaac tgggtattga ccggatgttt aacattgcag gcaatcactt tgcccgctta 540

ggcatcagcg gttccggtgt gcattattgg aatgcccggg attttagcga acaggcgttt 600

catgccgaag gaggctaccg ttatcggaat agccgtctag agtggggatt ccggcccttt 660

gtcgaacaaa accggctggg caataaccgt tatactgcaa atatgggtat tgcgttggat 720

tacagtcgcc gtctgaatga aaaatggcgc agcaaccaat ctttccagta cggccgcaaa 780

caataccata acgaatattt ggcaaaacgt tacaacagta aaacgatttc agtcagcagt 840

acgttcggct attacgctat gccggcttgg cagttgtacg gaggtattag cggtatgttt 900

gataatactg tggagaaaga gcaggcttca cggcgttatg gtgtaagttt gggtacggtg 960

aaaatattag acggcggtct tggactgaag ttgggtatag gttacacgaa acggatattt 1020

aaagcccctg caacattaat ttacaatttt acccggcgtg atgatgaata tcggatgagt 1080

gcggctttat ggcataaaaa actgtcgtgg aaaggattta caccccaaat aaatttccgt 1140

tacaacaaga tcaacagcaa tatgcccgcc ttttattcgc gcagcggcaa ggaatggttt 1200

gtcagtatag aaaaaacgta ttga 1224

<210> 374

<211> 500

<212> PRT

<213> N. lactamica SLAM 3

<400> 374

Met Ala Leu Leu Gly Ile Leu Phe Glu Phe Val Met Lys Leu Met Lys

1 5 10 15

Ser Lys Asn Ile Phe Phe Met Gly Tyr Leu Ile Ala Ser Ala Val Phe

20 25 30

Ala Glu Asp Ile Gly Val Pro Val Glu Pro Ile Asn Val Gly Ser Arg

35 40 45

Ala Ala Met Pro Ser Glu Gly Glu Ser Leu Ala Leu Leu Pro Phe Ala

50 55 60

Glu Asp Val Pro Pro Val Arg Asp Ala Met Pro Ser Glu Val Pro Lys

65 70 75 80

Ser Ala Ala Gly Gly Asp Val Arg Asp Asp Arg Ile Gly Met Gln Ile

85 90 95

Asn Arg Ala Leu Leu Ala Arg Asp Trp Ala Ala Leu Lys Arg Leu Leu

100 105 110

Ala Gln Tyr Ala Glu Gln Pro Gln Tyr Asp Ala Val Leu Tyr Arg Tyr

115 120 125

Ala Leu Gly Ala Leu Tyr Arg Ser Glu Met Arg Gln Gly Glu Ala Ala

130 135 140

Asp Leu Tyr Arg Glu Leu Leu Ser Glu Arg Pro Asp Leu Val Tyr Pro

145 150 155 160

Arg Phe Asp Leu Gly Val Met Leu Phe Glu Asp Lys Gln Tyr Arg Glu

165 170 175

Ala Leu Val Gln Leu His Arg Val Glu Glu Ala Leu Pro Pro Asp Met

180 185 190

Arg Gln Leu Ala Arg Glu Tyr Ile Arg Gln Val Glu Ala Val Gln Ala

195 200 205

Trp His Pro Ser Phe Asn Met Asn Tyr Glu Gln Thr Asp Asn Val Asn

210 215 220

Asn Ala Ser Pro Ser Arg Asp Ile Val Leu Asn Gly Arg Lys Trp Thr

225 230 235 240

Arg Ser Glu Asp Ser Leu Pro Lys Arg Ala Asn Gly Ile Arg Tyr Glu

245 250 255

Leu Gly Ile Asp Arg Met Phe Asn Ile Ala Gly Asn His Phe Ala Arg

260 265 270

Leu Gly Ile Ser Gly Ser Gly Val His Tyr Trp Asn Ala Arg Asp Phe

275 280 285

Ser Glu Gln Ala Phe His Ala Glu Gly Gly Tyr Arg Tyr Arg Asn Ser

290 295 300

Arg Leu Glu Trp Gly Phe Arg Pro Phe Val Glu Gln Asn Arg Leu Gly

305 310 315 320

Asn Asn Arg Tyr Thr Ala Asn Met Gly Ile Ala Leu Asp Tyr Ser Arg

325 330 335

Arg Leu Asn Glu Lys Trp Arg Ser Asn Gln Ser Phe Gln Tyr Gly Arg

340 345 350

Lys Gln Tyr His Asn Glu Tyr Leu Ala Lys Arg Tyr Asn Ser Lys Thr

355 360 365

Ile Ser Val Ser Ser Thr Phe Gly Tyr Tyr Ala Met Pro Ala Trp Gln

370 375 380

Leu Tyr Gly Gly Ile Ser Gly Met Phe Asp Asn Thr Val Glu Lys Glu

385 390 395 400

Gln Ala Ser Arg Arg Tyr Gly Val Ser Leu Gly Thr Val Lys Ile Leu

405 410 415

Asp Gly Gly Leu Gly Leu Lys Leu Gly Ile Gly Tyr Thr Lys Arg Ile

420 425 430

Phe Lys Ala Pro Ala Thr Leu Ile Tyr Asn Phe Thr Arg Arg Asp Asp

435 440 445

Glu Tyr Arg Met Ser Ala Ala Leu Trp His Lys Lys Leu Ser Trp Lys

450 455 460

Gly Phe Thr Pro Gln Ile Asn Phe Arg Tyr Asn Lys Ile Asn Ser Asn

465 470 475 480

Met Pro Ala Phe Tyr Ser Arg Ser Gly Lys Glu Trp Phe Val Ser Ile

485 490 495

Glu Lys Thr Tyr

500

<210> 375

<211> 1305

<212> DNA

<213> N. lactamica SLAM 4

<400> 375

gtgccgtctg aaacccttgc agccggagaa tccgccgaag ccgtttcaga cggcaatgcc 60

tctcttgcgg gtttggaaga gcagatcaac cgcgccgtca tcgcccgcga ttgggatacg 120

ctgcaaacgc tgctggaaag ctatcgcgcc ctgccggatt tcaatccggt tctgcacgat 180

tacgcgctgg gcggtttgcg ccgcagccag ttgcgccata acgaggcggt ggctttgtat 240

cgcggcattt tggcgcaaca gcccgatttg gcgtatccgc gtttcgattt gagcgtaatg 300

ctgtttgaaa acaaacagta ccgcgaggca aaggcagaat tggagcgggc gaaacccgat 360

ttgcagccgc cgatgcagca gcttgccgac cgctatcttg ccgccataga caaggctcaa 420

ggctggaagc ccgatgtgtc gctgcaatac gagcaaacgg acaatgtgaa caacgcttcg 480

tccgaaaaaa cgattgaatt tgcaggaaaa agctggacaa aaaccgccga cagcctgccg 540

caaaaggcac acggtttgcg ctacggcttg ggcgtgtcgc gcgaaatcaa tgcgggcggg 600

catcatttcc tctacggcgg catcagcggc ggcggcgtgc attattggga taacaaagat 660

ttcagcgaac agagcctgcg cctgtcgttc ggctataaaa accgttcggt aacgcgctcg 720

ttcggcatcg tgccgtttgt cgagcaaaac ctcttaggcg gcagccgata caatttcgtc 780

ggcggcttca atgccgattt ctcccaacgc ttgagcgaac gctggcggct gacgctgaac 840

gcgggcaata tgtggaagcg ttatcaggaa gaccgcaccg ccgcccgata cgacagccat 900

atgtcgctgg tgggcgcgac gctgatgtat tccgcgccga aagactggct gctttacggc 960

ggtgcggact ggtcgcacga catgacgaaa gaggcggaac aggcttccgt ccgcaagggt 1020

ttgcgtgtcg gcgcggtcaa aacgttcgac ggcggcctgg gtctgcgggc aaacctgcgc 1080

tatacccgca ggacttttga cgcacccggg accattgtgt accgcttccc gcgcaaagac 1140

cacgaatatc aggcaaacct gtcgttgtgg cacgacaaaa tctcttggaa gggatttacg 1200

ccgcaactca atttccgcta tctgaaaatc gacagcaata tgaaaagttt ttacacacgc 1260

aaaaacatgc agattttcat gagcgtggaa aaggatttca aataa 1305

<210> 376

<211> 433

<212> PRT

<213> N. lactamica SLAM 4

<400> 376

Met Pro Ser Glu Thr Leu Ala Ala Gly Glu Ser Ala Glu Ala Val Ser

1 5 10 15

Asp Gly Asn Ala Ser Leu Ala Gly Leu Glu Glu Gln Ile Asn Arg Ala

20 25 30

Val Ile Ala Arg Asp Trp Asp Thr Leu Gln Thr Leu Leu Glu Ser Tyr

35 40 45

Arg Ala Leu Pro Asp Phe Asn Pro Val Leu His Asp Tyr Ala Leu Gly

50 55 60

Gly Leu Arg Arg Ser Gln Leu Arg His Asn Glu Ala Val Ala Leu Tyr

65 70 75 80

Arg Gly Ile Leu Ala Gln Gln Pro Asp Leu Ala Tyr Pro Arg Phe Asp

85 90 95

Leu Ser Val Met Leu Phe Glu Asn Lys Gln Tyr Arg Glu Ala Lys Ala

100 105 110

Glu Leu Glu Arg Ala Lys Pro Asp Leu Gln Pro Pro Met Gln Gln Leu

115 120 125

Ala Asp Arg Tyr Leu Ala Ala Ile Asp Lys Ala Gln Gly Trp Lys Pro

130 135 140

Asp Val Ser Leu Gln Tyr Glu Gln Thr Asp Asn Val Asn Asn Ala Ser

145 150 155 160

Ser Glu Lys Thr Ile Glu Phe Ala Gly Lys Ser Trp Thr Lys Thr Ala

165 170 175

Asp Ser Leu Pro Gln Lys Ala His Gly Leu Arg Tyr Gly Leu Gly Val

180 185 190

Ser Arg Glu Ile Asn Ala Gly Gly His His Phe Leu Tyr Gly Gly Ile

195 200 205

Ser Gly Gly Gly Val His Tyr Trp Asp Asn Lys Asp Phe Ser Glu Gln

210 215 220

Ser Leu Arg Leu Ser Phe Gly Tyr Lys Asn Arg Ser Val Thr Arg Ser

225 230 235 240

Phe Gly Ile Val Pro Phe Val Glu Gln Asn Leu Leu Gly Gly Ser Arg

245 250 255

Tyr Asn Phe Val Gly Gly Phe Asn Ala Asp Phe Ser Gln Arg Leu Ser

260 265 270

Glu Arg Trp Arg Leu Thr Leu Asn Ala Gly Asn Met Trp Lys Arg Tyr

275 280 285

Gln Glu Asp Arg Thr Ala Ala Arg Tyr Asp Ser His Met Ser Leu Val

290 295 300

Gly Ala Thr Leu Met Tyr Ser Ala Pro Lys Asp Trp Leu Leu Tyr Gly

305 310 315 320

Gly Ala Asp Trp Ser His Asp Met Thr Lys Glu Ala Glu Gln Ala Ser

325 330 335

Val Arg Lys Gly Leu Arg Val Gly Ala Val Lys Thr Phe Asp Gly Gly

340 345 350

Leu Gly Leu Arg Ala Asn Leu Arg Tyr Thr Arg Arg Thr Phe Asp Ala

355 360 365

Pro Gly Thr Ile Val Tyr Arg Phe Pro Arg Lys Asp His Glu Tyr Gln

370 375 380

Ala Asn Leu Ser Leu Trp His Asp Lys Ile Ser Trp Lys Gly Phe Thr

385 390 395 400

Pro Gln Leu Asn Phe Arg Tyr Leu Lys Ile Asp Ser Asn Met Lys Ser

405 410 415

Phe Tyr Thr Arg Lys Asn Met Gln Ile Phe Met Ser Val Glu Lys Asp

420 425 430

Phe

<210> 377

<211> 1515

<212> DNA

<213> N. macacae SLAM 1

<400> 377

atgcccgaaa gcaccaaaat gcccgatatg gtttcgcctc aaataaaaaa cgcagattca 60

tgcatcattg caacccaaac gtcttacgaa atcatgaaaa cactcttact cctctccctg 120

ctcgccgtgt ccgcagcgga agccgccgac gtgccgtccg agcctcaaaa ccagcctgcc 180

cccgagttgc aggtcaaaac ggcagaacct gcccccgtcg aagaagcagc ggccaagcct 240

gctgccgaaa cgtcgtctga aaaagtcgtc aacgtcgatg ccaaaaccct gctcgacaat 300

ccccaattgc tttcccgcgc catgtattcc gccgttgttt cacgcaacat cgcgggcatc 360

aaagtcgtcc tgccgattta cgaacaatgg ccgggacacg ataaaaacat ggcactctac 420

gcgcacggat tggttgccca agacgaaggc aaaatgaaag aagccatcgg gtattaccgt 480

caatttatcg ccgaaaaccc cgatgccccc gtcgtccgct ggcagcttgc caccgctttg 540

tttgaagaca agcaaaacga agccgccgcc gaccagttcg acaaactcaa aacagaagcc 600

aacctgcccg agccgctcgt caaaggcatc gaatcctacc gcaaagcatt gcgcgagcgc 660

gattcgtgga aattcaatgc cggcttgagc gttacccgcg aacaaaacat caaccaagcc 720

cccagccgcc gcacatacgg caactggacc ttccccgagc ctatcgacgc caccgccatc 780

aactaccaac tcggcgcaga gaaaaaatgg tcgctgccca aaggctggta cgttacggca 840

ggcgcggaca attacggcaa aatttatccc gaacaaacca agtataacga cgtaaccacc 900

cgcttttcag taggcgcagg ctacgccgac caacgcaacg acatcggctt gaccccgttc 960

cacgaacgcc gcttctacgg caacgacccg tatacctact ccagcggtgc gcgcctgcac 1020

atcaaccgct ggtggcagcc taagctgcaa accttgagtg ccgttgaaat gggtcgtctg 1080

aaaaacaccc gccgcgccaa atccgacagc aacaaccgcc tgttgagcaa ttccgtcgtc 1140

tattaccgaa acgcccgcca atactgggtc ggcggtttcg acatctatca ggaacgcaat 1200

aaagaagaca aatcggacag cttcgaccgt tacagcctcc gtaccgcatg ggggcaggaa 1260

tggggcaaag ggctgtcgac tatgttgcgg ctgagtgcgg cacaacgccg ttatcaaacg 1320

cccagccttt tgagcggtca ggaaaaccgc cgcgataaag aagcggatat ttcgctcgcc 1380

gtgtggcacc gcgctttcca cttcaaaggc atcaccccgc gcctgaccgt tgcccaccac 1440

aaaacatgga gcaacgacaa atactacgaa tacggcaaaa ccagaatgtt tgtcgaattc 1500

agcaaaacgt tctga 1515

<210> 378

<211> 504

<212> PRT

<213> N. macacae SLAM 1

<400> 378

Met Pro Glu Ser Thr Lys Met Pro Asp Met Val Ser Pro Gln Ile Lys

1 5 10 15

Asn Ala Asp Ser Cys Ile Ile Ala Thr Gln Thr Ser Tyr Glu Ile Met

20 25 30

Lys Thr Leu Leu Leu Leu Ser Leu Leu Ala Val Ser Ala Ala Glu Ala

35 40 45

Ala Asp Val Pro Ser Glu Pro Gln Asn Gln Pro Ala Pro Glu Leu Gln

50 55 60

Val Lys Thr Ala Glu Pro Ala Pro Val Glu Glu Ala Ala Ala Lys Pro

65 70 75 80

Ala Ala Glu Thr Ser Ser Glu Lys Val Val Asn Val Asp Ala Lys Thr

85 90 95

Leu Leu Asp Asn Pro Gln Leu Leu Ser Arg Ala Met Tyr Ser Ala Val

100 105 110

Val Ser Arg Asn Ile Ala Gly Ile Lys Val Val Leu Pro Ile Tyr Glu

115 120 125

Gln Trp Pro Gly His Asp Lys Asn Met Ala Leu Tyr Ala His Gly Leu

130 135 140

Val Ala Gln Asp Glu Gly Lys Met Lys Glu Ala Ile Gly Tyr Tyr Arg

145 150 155 160

Gln Phe Ile Ala Glu Asn Pro Asp Ala Pro Val Val Arg Trp Gln Leu

165 170 175

Ala Thr Ala Leu Phe Glu Asp Lys Gln Asn Glu Ala Ala Ala Asp Gln

180 185 190

Phe Asp Lys Leu Lys Thr Glu Ala Asn Leu Pro Glu Pro Leu Val Lys

195 200 205

Gly Ile Glu Ser Tyr Arg Lys Ala Leu Arg Glu Arg Asp Ser Trp Lys

210 215 220

Phe Asn Ala Gly Leu Ser Val Thr Arg Glu Gln Asn Ile Asn Gln Ala

225 230 235 240

Pro Ser Arg Arg Thr Tyr Gly Asn Trp Thr Phe Pro Glu Pro Ile Asp

245 250 255

Ala Thr Ala Ile Asn Tyr Gln Leu Gly Ala Glu Lys Lys Trp Ser Leu

260 265 270

Pro Lys Gly Trp Tyr Val Thr Ala Gly Ala Asp Asn Tyr Gly Lys Ile

275 280 285

Tyr Pro Glu Gln Thr Lys Tyr Asn Asp Val Thr Thr Arg Phe Ser Val

290 295 300

Gly Ala Gly Tyr Ala Asp Gln Arg Asn Asp Ile Gly Leu Thr Pro Phe

305 310 315 320

His Glu Arg Arg Phe Tyr Gly Asn Asp Pro Tyr Thr Tyr Ser Ser Gly

325 330 335

Ala Arg Leu His Ile Asn Arg Trp Trp Gln Pro Lys Leu Gln Thr Leu

340 345 350

Ser Ala Val Glu Met Gly Arg Leu Lys Asn Thr Arg Arg Ala Lys Ser

355 360 365

Asp Ser Asn Asn Arg Leu Leu Ser Asn Ser Val Val Tyr Tyr Arg Asn

370 375 380

Ala Arg Gln Tyr Trp Val Gly Gly Phe Asp Ile Tyr Gln Glu Arg Asn

385 390 395 400

Lys Glu Asp Lys Ser Asp Ser Phe Asp Arg Tyr Ser Leu Arg Thr Ala

405 410 415

Trp Gly Gln Glu Trp Gly Lys Gly Leu Ser Thr Met Leu Arg Leu Ser

420 425 430

Ala Ala Gln Arg Arg Tyr Gln Thr Pro Ser Leu Leu Ser Gly Gln Glu

435 440 445

Asn Arg Arg Asp Lys Glu Ala Asp Ile Ser Leu Ala Val Trp His Arg

450 455 460

Ala Phe His Phe Lys Gly Ile Thr Pro Arg Leu Thr Val Ala His His

465 470 475 480

Lys Thr Trp Ser Asn Asp Lys Tyr Tyr Glu Tyr Gly Lys Thr Arg Met

485 490 495

Phe Val Glu Phe Ser Lys Thr Phe

500

<210> 379

<211> 1440

<212> DNA

<213> N. macacae SLAM 2

<400> 379

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cgttctgact tttcagacga ccgtaccgcg caacgtctgt ggcaggacac ccgccaaacc 120

atgcaggaac aggaacaaaa agtgcgcgaa taccgcctcg acattcccgc cgaacacatc 180

gggcagacag ccgaaaccga ccccgaagcc gaccaaggcg aagccctgtt taacgccgtc 240

aaccgcagcg actggcaaac cgtgcgcccg ctgcttgagc gttataccca gcaaaccgaa 300

tacgaccccg acatcgccct ctttgcccgc gcctcgctcg cccgcggcga aggcagatgg 360

aaagccgcca aacaagacta cgaaaccctg ctgcaacgcc atcccgactt cacgcgcgga 420

cggctcgatt acgcccgcct gctctttgaa ggtcgtctga accgcgaagc cacttccgaa 480

tttatgcgcc tgcaaaacga agacctgccc gaagccgtca aagaaaacat cggccatttt 540

cgcgactctc taaaccaacg ccaaagctgg cagggcagcc tttccgtcgg cgccgtctac 600

aacagcaaca tcaacgaagc cagcggcaaa gtgtggtgta aaaccgaaat cgacggcgaa 660

tgctgggaag aattttcagg cgaccaaccc atttccgcca acggcatcaa atacgaagcc 720

gccgccgtcc gccgctggca gattaaagga caccacggca tcgccgcccg cgcgctcggc 780

tacggacgtt tctaccacga ccataaagac ttcaacgaac acacgctcaa cctcagcgca 840

ggctaccagt ttgaaaacca ccgccacacc ttcgccctcg ccccgctcgt cgaatggaac 900

ggcagcggcg gcaaaaccct caaccgcgcc tacggcgtgc gcagcgagtg gaacctcgac 960

aaaggcagtt ggacgtggaa caccgaagcc gagtggaaac acctctccta ttccgacaaa 1020

acccgcctgc tcgacggcag cctcttctcc gtttacaaca ccctgtccta cttcccgcgc 1080

aacgacctca tgctctacgg cggcatagac tggcagcagc gcaaagccaa agagccggtg 1140

gacagctacc gcctcatctc cgcacggctg ggcgcggcaa aaatgtttga agccggtttc 1200

gacgcctccg cctccgccac cttcggcatc cgcagccacc gcgaagaaaa cgccgtactc 1260

gaacaacgcc gccgcgacaa agaacagacc taccgcctca gcataggcgc ggaccgctgg 1320

aaattcgccg gcatgaagcc cgtcctcagc tacaaacacc gccgcgtcca cggcaacacc 1380

gactggctgt acagctataa gcaaaacgaa gtcggtctgt cgctggtcaa atcgttctaa 1440

<210> 380

<211> 479

<212> PRT

<213> N. macacae SLAM 2

<400> 380

Met Tyr Lys Pro Ser Ala Cys Leu Ile Leu Phe Leu Ala Ala Pro Val
1 5 10 15

Leu Ala Ala Pro Arg Ser Asp Phe Ser Asp Asp Arg Thr Ala Gln Arg
20 25 30

Leu Trp Gln Asp Thr Arg Gln Thr Met Gln Glu Gln Glu Gln Lys Val
35 40 45

Arg Glu Tyr Arg Leu Asp Ile Pro Ala Glu His Ile Gly Gln Thr Ala
50 55 60

Glu Thr Asp Pro Glu Ala Asp Gln Gly Glu Ala Leu Phe Asn Ala Val
65 70 75 80

Asn Arg Ser Asp Trp Gln Thr Val Arg Pro Leu Leu Glu Arg Tyr Thr
85 90 95

Gln Gln Thr Glu Tyr Asp Pro Asp Ile Ala Leu Phe Ala Arg Ala Ser
100 105 110

Leu Ala Arg Gly Glu Gly Arg Trp Lys Ala Ala Lys Gln Asp Tyr Glu
115 120 125

Thr Leu Leu Gln Arg His Pro Asp Phe Thr Arg Gly Arg Leu Asp Tyr
130 135 140

Ala Arg Leu Leu Phe Glu Gly Arg Leu Asn Arg Glu Ala Thr Ser Glu

145 150 155 160

Phe Met Arg Leu Gln Asn Glu Asp Leu Pro Glu Ala Val Lys Glu Asn

165 170 175

Ile Gly His Phe Arg Asp Ser Leu Asn Gln Arg Gln Ser Trp Gln Gly

180 185 190

Ser Leu Ser Val Gly Ala Val Tyr Asn Ser Asn Ile Asn Glu Ala Ser

195 200 205

Gly Lys Val Trp Cys Lys Thr Glu Ile Asp Gly Glu Cys Trp Glu Glu

210 215 220

Phe Ser Gly Asp Gln Pro Ile Ser Ala Asn Gly Ile Lys Tyr Glu Ala

225 230 235 240

Ala Ala Val Arg Arg Trp Gln Ile Lys Gly His His Gly Ile Ala Ala

245 250 255

Arg Ala Leu Gly Tyr Gly Arg Phe Tyr His Asp His Lys Asp Phe Asn

260 265 270

Glu His Thr Leu Asn Leu Ser Ala Gly Tyr Gln Phe Glu Asn His Arg

275 280 285

His Thr Phe Ala Leu Ala Pro Leu Val Glu Trp Asn Gly Ser Gly Gly

290 295 300

Lys Thr Leu Asn Arg Ala Tyr Gly Val Arg Ser Glu Trp Asn Leu Asp

305 310 315 320

Lys Gly Ser Trp Thr Trp Asn Thr Glu Ala Glu Trp Lys His Leu Ser

325 330 335

Tyr Ser Asp Lys Thr Arg Leu Leu Asp Gly Ser Leu Phe Ser Val Tyr

340 345 350

Asn Thr Leu Ser Tyr Phe Pro Arg Asn Asp Leu Met Leu Tyr Gly Gly

355 360 365

Ile Asp Trp Gln Gln Arg Lys Ala Lys Glu Pro Val Asp Ser Tyr Arg

370 375 380

Leu Ile Ser Ala Arg Leu Gly Ala Ala Lys Met Phe Glu Ala Gly Phe

385 390 395 400

Asp Ala Ser Ala Ser Ala Thr Phe Gly Ile Arg Ser His Arg Glu Glu

405 410 415

Asn Ala Val Leu Glu Gln Arg Arg Arg Asp Lys Glu Gln Thr Tyr Arg

420 425 430

Leu Ser Ile Gly Ala Asp Arg Trp Lys Phe Ala Gly Met Lys Pro Val

435 440 445

Leu Ser Tyr Lys His Arg Arg Val His Gly Asn Thr Asp Trp Leu Tyr

450 455 460

Ser Tyr Lys Gln Asn Glu Val Gly Leu Ser Leu Val Lys Ser Phe

465 470 475

<210> 381

<211> 1467

<212> DNA

<213> N. macacae SLAM 3

<400> 381

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gacagggaag accgcttcat gcagctcaaa cagggaacgg aactccgccg cgcgcagcag 120

gaaaggaacg aagcggacaa tacggcgatt gagttcggcg cgggagaagt gcaggacggc 180

gaagatttgg cgttgtcgct gatgaaggcg gtcaacgcgc aaaacgaaga ggaaacggcg 240

cggctgttgg acatttaccg ccgtcaggat gattccgacc ccgatatagt gctgtttgcc 300

gaggccaatc aggcggtgtt ccgcgacgat ttgaaggccg cgctggcgaa ataccgcgag 360

ctttaccgta aaaatcccga atttctgcgc ggccgcctgg atttggcgcg gctgctgttt 420

atagacaaac aaaacaaaga atcggcggca ttgttcgacg gcatcgatat tcctgaagtg 480

cccgccgtca atgagaaaat caaagtgttt gccgacgctt tgaagaaacg cgatgcgtgg 540

agcggttcgg tttcgttcgg cgcgggttac gacaccaact taaaccaatc gtcgggcgcg 600

acggttgtcc gcaatcagac aagctgcggt ttcgattcga acgggcaacc gattctggac 660

ggcgacggaa tgctgtcctg ccgcaacgaa cggcttgacg cctacgcgcc cgatgcgttg 720

aaaaaccgga tgtgggtata tgaagccaac ttaagcagac gcatttcgct caacggccac 780

cacggcctgc aactgggcgg ctacgcatgg ggccggctct atcccggcaa caaggaatac 840

ggcgaacaca atatcaacgt cagccccgct tacagttttc agagcaaaga ccattccttc 900

agtatcggcc cgcaggtgca atacgaatgg tcgggcggca aactgcgcga cagcagcgcc 960

ggcatcagca cggcatacag ccgcaccttt tccgaccaag cctcgctggg cgtgcagctt 1020

gatcacaaat acgaccgcta ccgcggcgaa ttaaaacatt tcaacggccc gcagacgctt 1080

ctgttcacca ccgccatcta cgccctgccg aaagactggc tggtattcgg cggctacgac 1140

tacctgcgca aaaacagccg cgaaaaagtg gattcctacc gccggcacgg cctgcgcgcg 1200

ggtgtcaaca aacgtttcga atccggcatc gacgccacct ttcaggcaat ctggcgtaaa 1260

acagcatatc aggactacca tgcctggctg gaaacccgcc gccatgattc cgaacgcacc 1320

tatcagttgg acatcaaatt tgaccgtccg tccttccgcg gcatcacgcc cgttttcagc 1380

atcaaacaca ccgacaacaa aagctcgtcc tggctgaacc gctacaaacg caacgaattt 1440

accgtcaaag cagaatacaa gttttaa 1467

<210> 382

<211> 488

<212> PRT

<213> N. macacae SLAM 3

<400> 382

Met Lys Arg Leu Leu Ile Leu Pro Val Phe Leu Ser Leu Leu Pro His
1 5 10 15

Ala Phe Ala Asp Asp Arg Glu Asp Arg Phe Met Gln Leu Lys Gln Gly
20 25 30

Thr Glu Leu Arg Arg Ala Gln Gln Glu Arg Asn Glu Ala Asp Asn Thr
35 40 45

Ala Ile Glu Phe Gly Ala Gly Glu Val Gln Asp Gly Glu Asp Leu Ala
50 55 60

Leu Ser Leu Met Lys Ala Val Asn Ala Gln Asn Glu Glu Glu Thr Ala
65 70 75 80

Arg Leu Leu Asp Ile Tyr Arg Arg Gln Asp Asp Ser Asp Pro Asp Ile
85 90 95

Val Leu Phe Ala Glu Ala Asn Gln Ala Val Phe Arg Asp Asp Leu Lys
100 105 110

Ala Ala Leu Ala Lys Tyr Arg Glu Leu Tyr Arg Lys Asn Pro Glu Phe
115 120 125

Leu Arg Gly Arg Leu Asp Leu Ala Arg Leu Leu Phe Ile Asp Lys Gln

130 135 140

Asn Lys Glu Ser Ala Ala Leu Phe Asp Gly Ile Asp Ile Pro Glu Val
145 150 155 160
Pro Ala Val Asn Glu Lys Ile Lys Val Phe Ala Asp Ala Leu Lys Lys
165 170 175
Arg Asp Ala Trp Ser Gly Ser Val Ser Phe Gly Ala Gly Tyr Asp Thr
180 185 190
Asn Leu Asn Gln Ser Ser Gly Ala Thr Val Val Arg Asn Gln Thr Ser
195 200 205

Cys Gly Phe Asp Ser Asn Gly Gln Pro Ile Leu Asp Gly Asp Gly Met
210 215 220
Leu Ser Cys Arg Asn Glu Arg Leu Asp Ala Tyr Ala Pro Asp Ala Leu
225 230 235 240
Lys Asn Arg Met Trp Val Tyr Glu Ala Asn Leu Ser Arg Arg Ile Ser
245 250 255
Leu Asn Gly His His Gly Leu Gln Leu Gly Gly Tyr Ala Trp Gly Arg
260 265 270

Leu Tyr Pro Gly Asn Lys Glu Tyr Gly Glu His Asn Ile Asn Val Ser
275 280 285
Pro Ala Tyr Ser Phe Gln Ser Lys Asp His Ser Phe Ser Ile Gly Pro
290 295 300
Gln Val Gln Tyr Glu Trp Ser Gly Gly Lys Leu Arg Asp Ser Ser Ala
305 310 315 320
Gly Ile Ser Thr Ala Tyr Ser Arg Thr Phe Ser Asp Gln Ala Ser Leu
325 330 335

Gly Val Gln Leu Asp His Lys Tyr Asp Arg Tyr Arg Gly Glu Leu Lys
340 345 350
His Phe Asn Gly Pro Gln Thr Leu Leu Phe Thr Thr Ala Ile Tyr Ala
355 360 365
Leu Pro Lys Asp Trp Leu Val Phe Gly Gly Tyr Asp Tyr Leu Arg Lys
370 375 380

Asn Ser Arg Glu Lys Val Asp Ser Tyr Arg Arg His Gly Leu Arg Ala
385 390 395 400

Gly Val Asn Lys Arg Phe Glu Ser Gly Ile Asp Ala Thr Phe Gln Ala
405 410 415
Ile Trp Arg Lys Thr Ala Tyr Gln Asp Tyr His Ala Trp Leu Glu Thr
420 425 430
Arg Arg His Asp Ser Glu Arg Thr Tyr Gln Leu Asp Ile Lys Phe Asp
435 440 445
Arg Pro Ser Phe Arg Gly Ile Thr Pro Val Phe Ser Ile Lys His Thr
450 455 460

Asp Asn Lys Ser Ser Ser Trp Leu Asn Arg Tyr Lys Arg Asn Glu Phe
465 470 475 480
Thr Val Lys Ala Glu Tyr Lys Phe
485

<210> 383
<211> 1476
<212> DNA
<213> N. macacae SLAM 4
<400> 383
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ggctggctgg acgacggcac acccgcaggc gatatcgaaa acgacgacgc atacatccgc 180
atcggcggtc agatttacac cgtaggcaac aataccgaag agctggaaag cgcgatttat 240

catgccatta acgaacatca atggaaaaag gctgaacgct tcgccacgcg ctacgccgcc 300
ctgcccggcc acaatcccgc cctgcccaaa ttggtactcg gtttgaaaca acgcgccgaa 360
ggacgcctcg ccgaagcctt acggaacctg caagcagcag aagcactcga ccccgccaac 420
ccgcgcatcc tgctcgaaac cgcgcgcctt tataccgaag acaaccaaaa ccgcgaagcc 480
cgaagcgcat tcgtccgcgc ccaaaccgcc gacattcccg aagaaacccg cgccctgatc 540
ggacaatacc tcggcgaaat cgacaaacgc agccgctggc acggacaaat cggcatcgct 600
tacggctaca acagcaacat caaccaatcc gacggctccg tccgctgcat cctgccgctt 660

gacggccaat gcctcgccta ccaaaacctg cccgacccca tccgttcccc cgtatggaat 720

tacagcctga gcgcaggcaa aatcaccccc gtcaaaggac accacagcct caaaaccaac 780

ctcctcgcct acggcacgca ctaccgccgc aaagacacag acgccgcctt gtccgactac 840

ggcagccaaa ccggcacact gtctgccggt tacgaatacg ccgacgccca aagccgccta 900

tcgctgatgc ccgtttacga acacgaacgg cgcaaccgcc acacctacta caacgcctac 960

ggcgccgaag cctcgtggac gcataccatc aacccaaaat ggcaggtcaa cgccgactgg 1020

tcgggcaaac gctaccgcca cagcggcacc gcgaaaacct acgccgccga ctacaccgaa 1080

taccgcacag gcttaggcgc agaatacgcc ctgaccccga aaaccggcgt gttcgcaggc 1140

tccgactaca cccgccgcac atacaacggc ggcacatccg accaccgcga atacaccctc 1200

cgcacaggct tatacaccct gtttgacaac ggcacctacc tcaacgccct cgtcatgaaa 1260

cggcgcaacc tctacgaccg cgcaggcatc gccgcagacg gacaaagacg cagcgaccgc 1320

caaaccgtct ggctcgccgc cgcaggcttc agacaatggc acatcggcgg cttctacccc 1380

gaactgcgct tcaaacacac caccgtcaaa agcaattccg tgttctaccg ctaccgccaa 1440

aacgaaatca tgttgggcgt gaagaaacag ttttga 1476

<210> 384

<211> 491

<212> PRT

<213> N. macacae SLAM 4

<400> 384

Met Asn Lys Ser Cys Leu Leu Leu Leu Ala Leu Leu Pro Leu Ser Ala

1 5 10 15

His Ala Asp Ser Asp Asp Leu Arg Arg Leu Ser Glu Glu Asn Gly Arg

20 25 30

Val Gln Gln Gln Tyr Arg Glu Ser Gly Trp Leu Asp Asp Gly Thr Pro

35 40 45

Ala Gly Asp Ile Glu Asn Asp Asp Ala Tyr Ile Arg Ile Gly Gly Gln

50 55 60

Ile Tyr Thr Val Gly Asn Asn Thr Glu Glu Leu Glu Ser Ala Ile Tyr

65 70 75 80

His Ala Ile Asn Glu His Gln Trp Lys Lys Ala Glu Arg Phe Ala Thr

85 90 95

Arg Tyr Ala Ala Leu Pro Gly His Asn Pro Ala Leu Pro Lys Leu Val

100 105 110

Leu Gly Leu Lys Gln Arg Ala Glu Gly Arg Leu Ala Glu Ala Leu Arg

115 120 125

Asn Leu Gln Ala Ala Glu Ala Leu Asp Pro Ala Asn Pro Arg Ile Leu

130 135 140

Leu Glu Thr Ala Arg Leu Tyr Thr Glu Asp Asn Gln Asn Arg Glu Ala

145 150 155 160

Arg Ser Ala Phe Val Arg Ala Gln Thr Ala Asp Ile Pro Glu Glu Thr

165 170 175

Arg Ala Leu Ile Gly Gln Tyr Leu Gly Glu Ile Asp Lys Arg Ser Arg

180 185 190

Trp His Gly Gln Ile Gly Ile Ala Tyr Gly Tyr Asn Ser Asn Ile Asn

195 200 205

Gln Ser Asp Gly Ser Val Arg Cys Ile Leu Pro Leu Asp Gly Gln Cys

210 215 220

Leu Ala Tyr Gln Asn Leu Pro Asp Pro Ile Arg Ser Pro Val Trp Asn

225 230 235 240

Tyr Ser Leu Ser Ala Gly Lys Ile Thr Pro Val Lys Gly His His Ser

245 250 255

Leu Lys Thr Asn Leu Leu Ala Tyr Gly Thr His Tyr Arg Arg Lys Asp

260 265 270

Thr Asp Ala Ala Leu Ser Asp Tyr Gly Ser Gln Thr Gly Thr Leu Ser

275 280 285

Ala Gly Tyr Glu Tyr Ala Asp Ala Gln Ser Arg Leu Ser Leu Met Pro

290 295 300

Val Tyr Glu His Glu Arg Arg Asn Arg His Thr Tyr Tyr Asn Ala Tyr

305 310 315 320

Gly Ala Glu Ala Ser Trp Thr His Thr Ile Asn Pro Lys Trp Gln Val

325 330 335

Asn Ala Asp Trp Ser Gly Lys Arg Tyr Arg His Ser Gly Thr Ala Lys

340 345 350

Thr Tyr Ala Ala Asp Tyr Thr Glu Tyr Arg Thr Gly Leu Gly Ala Glu

355 360 365

Tyr Ala Leu Thr Pro Lys Thr Gly Val Phe Ala Gly Ser Asp Tyr Thr

370 375 380

Arg Arg Thr Tyr Asn Gly Gly Thr Ser Asp His Arg Glu Tyr Thr Leu

385 390 395 400

Arg Thr Gly Leu Tyr Thr Leu Phe Asp Asn Gly Thr Tyr Leu Asn Ala

405 410 415

Leu Val Met Lys Arg Arg Asn Leu Tyr Asp Arg Ala Gly Ile Ala Ala

420 425 430

Asp Gly Gln Arg Arg Ser Asp Arg Gln Thr Val Trp Leu Ala Ala Ala

435 440 445

Gly Phe Arg Gln Trp His Ile Gly Gly Phe Tyr Pro Glu Leu Arg Phe

450 455 460

Lys His Thr Thr Val Lys Ser Asn Ser Val Phe Tyr Arg Tyr Arg Gln

465 470 475 480

Asn Glu Ile Met Leu Gly Val Lys Lys Gln Phe

485 490

<210> 385

<211> 1467

<212> DNA

<213> N. meningitidis SLAM 1

<400> 385

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ctgctgcctt tattggcaag cgcggcatat gccgaagaaa caccgcgcga accggatttg 120

agaagccgtc ccgagttcag gcttcatgaa gcggaggtca aaccgatcga cagggagaag 180

gtgccggggc aggtgcggga aaaaggaaaa gttttgcaga ttgacggcga aaccctgctg 240

aaaaatcccg aattgttgtc ccgcgcgatg tattccgcag tggtctcaaa caatattgcc 300

ggtatccgcg ttattttgcc gatttaccta caacaggcgc agcaggataa gatgttggca 360

ctttatgcac aagggatttt ggcgcaggca gacggtaggg tgaaggaggc gatttcccat 420

taccgggaat tgattgccgc ccaacccgac gcgcccgccg tccgtatgcg tttggcggca 480

gcattgtttg aaaacaggca gaacgaggcg gcggcagacc agttcgaccg cctgaaggcg 540

gaaaacctgc cgccgcagct gatggagcag gtcgagctgt accgcaaggc attgcgcgaa 600

cgcgatgcgt ggaaggtaaa tggcggcttc agcgtcaccc gcgaacacaa tatcaaccaa 660

gccccgaaac ggcagcagta cggcaaatgg actttcccga aacaggtgga cggcacggcg 720

gtcaattacc ggctcggcgc ggagaaaaaa tggtcgctga aaaacggctg gtacacgacg 780

gcgggcggcg acgtgtccgg cagggtttat ccggggaata agaaattcaa cgatatgacg 840

gcaggcgttt ccggcggcat cggttttgcc gaccggcgca aagatgccgg gctggcagtg 900

ttccacgaac gccgcaccta cggcaacgac gcttattctt acaccaacgg cgcacgcctt 960

tatttcaacc gttggcaaac cccgaaatgg caaacgttgt cttcggcgga gtgggggcgt 1020

ttgaagaata cgcgccgggc gcgttccgac aatacccatt tgcaaatttc caattcgctg 1080

gtgttttacc ggaatgcgcg ccaatattgg atgggcggtt tggattttta ccgcgagcgc 1140

aaccccgccg accggggcga caatttcaac cgttacggcc tgcgctttgc ctgggggcag 1200

gaatggggcg gcagcggcct gtcttcgctg ttgcgcctcg gcgcggcgaa acggcattat 1260

gaaaaacccg gctttttcag cggttttaaa ggggaaaggc gcagggataa agaattgaac 1320

acatccttga gcctttggca ccgggcattg catttcaaag gcatcacgcc gcgcctgacg 1380

ttgtcgcacc gcgaaacgcg gagtaacgat gtgttcaacg aatacgagaa aaatcgggcg 1440

tttgtcgagt ttaataaaac gttctga 1467

<210> 386

<211> 488

<212> PRT

<213> N. meningitidis SLAM 1

<400> 386

Met Val Ile Phe Tyr Phe Cys Gly Lys Thr Phe Met Pro Ala Arg Asn

1 5 10 15

Arg Trp Met Leu Leu Leu Pro Leu Leu Ala Ser Ala Ala Tyr Ala Glu

20 25 30

Glu Thr Pro Arg Glu Pro Asp Leu Arg Ser Arg Pro Glu Phe Arg Leu

35 40 45

His Glu Ala Glu Val Lys Pro Ile Asp Arg Glu Lys Val Pro Gly Gln

50 55 60

Val Arg Glu Lys Gly Lys Val Leu Gln Ile Asp Gly Glu Thr Leu Leu

65 70 75 80

Lys Asn Pro Glu Leu Leu Ser Arg Ala Met Tyr Ser Ala Val Val Ser

85 90 95

Asn Asn Ile Ala Gly Ile Arg Val Ile Leu Pro Ile Tyr Leu Gln Gln

100 105 110

Ala Gln Gln Asp Lys Met Leu Ala Leu Tyr Ala Gln Gly Ile Leu Ala

115 120 125

Gln Ala Asp Gly Arg Val Lys Glu Ala Ile Ser His Tyr Arg Glu Leu

130 135 140

Ile Ala Ala Gln Pro Asp Ala Pro Ala Val Arg Met Arg Leu Ala Ala

145 150 155 160

Ala Leu Phe Glu Asn Arg Gln Asn Glu Ala Ala Ala Asp Gln Phe Asp

165 170 175

Arg Leu Lys Ala Glu Asn Leu Pro Pro Gln Leu Met Glu Gln Val Glu

180 185 190

Leu Tyr Arg Lys Ala Leu Arg Glu Arg Asp Ala Trp Lys Val Asn Gly

195 200 205

Gly Phe Ser Val Thr Arg Glu His Asn Ile Asn Gln Ala Pro Lys Arg

210 215 220

Gln Gln Tyr Gly Lys Trp Thr Phe Pro Lys Gln Val Asp Gly Thr Ala

225 230 235 240

Val Asn Tyr Arg Leu Gly Ala Glu Lys Lys Trp Ser Leu Lys Asn Gly

245 250 255

Trp Tyr Thr Thr Ala Gly Gly Asp Val Ser Gly Arg Val Tyr Pro Gly

260 265 270

Asn Lys Lys Phe Asn Asp Met Thr Ala Gly Val Ser Gly Gly Ile Gly

275 280 285

Phe Ala Asp Arg Arg Lys Asp Ala Gly Leu Ala Val Phe His Glu Arg

290 295 300

Arg Thr Tyr Gly Asn Asp Ala Tyr Ser Tyr Thr Asn Gly Ala Arg Leu

305 310 315 320

Tyr Phe Asn Arg Trp Gln Thr Pro Lys Trp Gln Thr Leu Ser Ser Ala

325 330 335

Glu Trp Gly Arg Leu Lys Asn Thr Arg Arg Ala Arg Ser Asp Asn Thr

340 345 350

His Leu Gln Ile Ser Asn Ser Leu Val Phe Tyr Arg Asn Ala Arg Gln

355 360 365

Tyr Trp Met Gly Gly Leu Asp Phe Tyr Arg Glu Arg Asn Pro Ala Asp

370 375 380

Arg Gly Asp Asn Phe Asn Arg Tyr Gly Leu Arg Phe Ala Trp Gly Gln

385 390 395 400

Glu Trp Gly Gly Ser Gly Leu Ser Ser Leu Leu Arg Leu Gly Ala Ala

405 410 415

Lys Arg His Tyr Glu Lys Pro Gly Phe Phe Ser Gly Phe Lys Gly Glu

420 425 430

Arg Arg Arg Asp Lys Glu Leu Asn Thr Ser Leu Ser Leu Trp His Arg

435 440 445

Ala Leu His Phe Lys Gly Ile Thr Pro Arg Leu Thr Leu Ser His Arg

450 455 460

Glu Thr Arg Ser Asn Asp Val Phe Asn Glu Tyr Glu Lys Asn Arg Ala

465 470 475 480

Phe Val Glu Phe Asn Lys Thr Phe

485

<210> 387

<211> 1518

<212> DNA

<213> N. meningitidis SLAM 2

<400> 387

atgttgtatt tcagatacgg ctttttggtt gtttggtgtg cggcaggtgt ttctgccgcc 60

tatggggcgg atgcgcccgc gattttggat gacaaggcat tgttgcaggt gcagcggtcg 120

gtgtcggata agtgggcgga atcagattgg aaagttgaaa atgatgcccc gcgcgtggtt 180

gacggggatt ttttgttggc gcatccgaaa atgttggaac atagtttgcg cgacgcgctc 240

aacggcaatc aggcggattt aatcgcttcg ttggcggatt tgtatgccaa gctgccggat 300

tatgacgcgg ttttgtacgg cagggcgcgg gctttgctgg cgaaattggc gggaaggccg 360

gcggaggcgg tggcgcggta tcgggaactg cacggggaaa atgcggcaga cgagcggatt 420

ttgctggatt tggcggcggc ggagtttgac gatttccggc tgaagtcggc agaaaggcat 480

tttgcggagg cggcaaaatt ggatttgccg gcaccggttt tggaaaatgt ggggcgtttt 540

cggaaaaaaa cggaggggct gacgggctgg cgtttttcgg gcggcatcag tccggcggtc 600

aatagaaatg ccaataatgc cgcgccgcaa tattgccggc aaaacggagg ccggcagata 660

tgcagtgtca gccgggcgga gcgggcggca gggttgaatt atgaaatcga ggcggaaaag 720

ctgacgccgt tggcagataa tcattatttg ttgttccgtt ccaatatcgg cggcacgagc 780

tattatttca gtaaaaaatc agcttatgat gacgggttcg gcagggcgta tttgggttgg 840

cagtataaaa atgcacggca gacggcgggg attttgccgt tttatcaggt gcagttgtcg 900

ggcagcgacg gctttgatgc gaaaacaaaa cgggtaaaca accgccgcct gccgccgtat 960

atgctggcgc acggagtcgg cgtgcagctg tcccatactt accgcccaaa cccgggatgg 1020

caattttcgg tcgcgctgga acattaccgc caacgctacc gcgaacagga tagggcggaa 1080

tacaataacg gcaggcagga cgggttttat gtttcgtcgg caaaacgttt gggcgaatcg 1140

gcaactgtgt tcggcggctg gcagtttgtg cggtttgtgc cgaaacgcga aacggtgggc 1200

ggcgcggtca ataatgccgc ctaccggcgc aacggtgttt atgccggttg ggcgcaggag 1260

tggcggcagt tgggcggttt gaacagtcgg gtttccgcgt cttatgcccg ccgcaactat 1320

aagggcattg cggctttctc gacagaggcg caacgcaacc gcgaatggaa tgtctcgctg 1380

gctttgagcc acgacaagtt gtcgtacaaa ggtatcgtgc cggcgttgaa ttatcgtttc 1440

ggcaggacgg aaagtaatgt gccgtatgcg aaacgccgca acagcgaggt gtttgtgtcg 1500

gcggattggc ggttttga 1518

<210> 388

<211> 505

<212> PRT

<213> N. meningitidis SLAM 3

<400> 388

Met Leu Tyr Phe Arg Tyr Gly Phe Leu Val Val Trp Cys Ala Ala Gly

1 5 10 15

Val Ser Ala Ala Tyr Gly Ala Asp Ala Pro Ala Ile Leu Asp Asp Lys

20 25 30

Ala Leu Leu Gln Val Gln Arg Ser Val Ser Asp Lys Trp Ala Glu Ser

35 40 45

Asp Trp Lys Val Glu Asn Asp Ala Pro Arg Val Val Asp Gly Asp Phe
50 55 60
Leu Leu Ala His Pro Lys Met Leu Glu His Ser Leu Arg Asp Ala Leu
65 70 75 80
Asn Gly Asn Gln Ala Asp Leu Ile Ala Ser Leu Ala Asp Leu Tyr Ala
85 90 95
Lys Leu Pro Asp Tyr Asp Ala Val Leu Tyr Gly Arg Ala Arg Ala Leu
100 105 110

Leu Ala Lys Leu Ala Gly Arg Pro Ala Glu Ala Val Ala Arg Tyr Arg
115 120 125
Glu Leu His Gly Glu Asn Ala Ala Asp Glu Arg Ile Leu Leu Asp Leu
130 135 140
Ala Ala Ala Glu Phe Asp Asp Phe Arg Leu Lys Ser Ala Glu Arg His
145 150 155 160
Phe Ala Glu Ala Ala Lys Leu Asp Leu Pro Ala Pro Val Leu Glu Asn
165 170 175

Val Gly Arg Phe Arg Lys Lys Thr Glu Gly Leu Thr Gly Trp Arg Phe
180 185 190
Ser Gly Gly Ile Ser Pro Ala Val Asn Arg Asn Ala Asn Asn Ala Ala
195 200 205
Pro Gln Tyr Cys Arg Gln Asn Gly Gly Arg Gln Ile Cys Ser Val Ser
210 215 220
Arg Ala Glu Arg Ala Ala Gly Leu Asn Tyr Glu Ile Glu Ala Glu Lys
225 230 235 240

Leu Thr Pro Leu Ala Asp Asn His Tyr Leu Leu Phe Arg Ser Asn Ile
245 250 255
Gly Gly Thr Ser Tyr Tyr Phe Ser Lys Lys Ser Ala Tyr Asp Asp Gly
260 265 270
Phe Gly Arg Ala Tyr Leu Gly Trp Gln Tyr Lys Asn Ala Arg Gln Thr
275 280 285

Ala Gly Ile Leu Pro Phe Tyr Gln Val Gln Leu Ser Gly Ser Asp Gly
290 295 300

Phe Asp Ala Lys Thr Lys Arg Val Asn Asn Arg Arg Leu Pro Pro Tyr
305 310 315 320
Met Leu Ala His Gly Val Gly Val Gln Leu Ser His Thr Tyr Arg Pro
325 330 335
Asn Pro Gly Trp Gln Phe Ser Val Ala Leu Glu His Tyr Arg Gln Arg
340 345 350
Tyr Arg Glu Gln Asp Arg Ala Glu Tyr Asn Asn Gly Arg Gln Asp Gly
355 360 365

Phe Tyr Val Ser Ser Ala Lys Arg Leu Gly Glu Ser Ala Thr Val Phe
370 375 380
Gly Gly Trp Gln Phe Val Arg Phe Val Pro Lys Arg Glu Thr Val Gly
385 390 395 400
Gly Ala Val Asn Asn Ala Ala Tyr Arg Arg Asn Gly Val Tyr Ala Gly
405 410 415
Trp Ala Gln Glu Trp Arg Gln Leu Gly Gly Leu Asn Ser Arg Val Ser
420 425 430

Ala Ser Tyr Ala Arg Arg Asn Tyr Lys Gly Ile Ala Ala Phe Ser Thr
435 440 445
Glu Ala Gln Arg Asn Arg Glu Trp Asn Val Ser Leu Ala Leu Ser His
450 455 460
Asp Lys Leu Ser Tyr Lys Gly Ile Val Pro Ala Leu Asn Tyr Arg Phe
465 470 475 480
Gly Arg Thr Glu Ser Asn Val Pro Tyr Ala Lys Arg Arg Asn Ser Glu
485 490 495

Val Phe Val Ser Ala Asp Trp Arg Phe
500 505

<210> 389
<211> 1422
<212> DNA

<213> N. mucosa SLAM 1

<400> 389

atgaaaacac tcttactcct ctccctgctc gccatgtccg cagcagaagc cgtcgacgtg 60

tcgtccgaga ctcaaaacca gcctgctccc gagttgcagg tcaaaacggc agaaccagac 120

cctgttgaag aagaaacggt caaacctgcc gccgagacgt cgtctgaaaa agttgtcaac 180

gtcgatgcca aaaccctgct cgacaatccc caattacttt cccgtgccat gtattccgcc 240

gttgtttcgc gcaatatcgc gggcatcaag gttgtcctgc cgatttacga acaatggcag 300

ggacacgata aaaacatggc gctctacgca cgcggattgg ttgcccaaaa cgacggcaaa 360

atgaaagaag ccatcgggta ttaccgtcaa tttatcgccg aaaccccga tgcccccgtc 420

gtccgctggc agcttgcaac cgctttgttt gaagacaagc aaaacgaagc cgccgccgac 480

cagttcgaca agctcaaaac agaacccaat ctgcccgagc cgttcgtcaa aggcatcgag 540

tcttaccgca aagcattgcg cgagcgcgat tcgtggaaat tcaacgccgg cttgagcgtg 600

acccgcgaac aaaatatcaa ccaagccccc agccgccgca catacggcaa ctggactttc 660

cccgagccta tcgacgctac cgccatcaac taccaactcg gcgcagagaa aaaatggtcg 720

ctgcccaaag gctggtacgc cacggcaggc gcggataatt acggcaaaat ttatcctgaa 780

cgcaccaagt ataacgacgt gaccacccgc ttctcagtgg gcgcaggcta cgccgaccag 840

cgcaacgaca tcggcttgac cccgttccac gaacgccgct tctacggcaa cgacccgtac 900

acctactcta gcggcgcgcg cctgcacatc aaccgctggt ggcagcccaa gctgcaaacc 960

ctgagcgccg ttgaaatggg tcgtctgaaa aacacccgcc gcgcccgttc caataataac 1020

aaccgccttc tgagcaattc cgtcgtctat taccgaaacg cccgccaata ctgggtcggt 1080

ggcttcgata tttatcagga acgcaataaa gaagataaga ccgacaactt cgaccgttac 1140

agccttcgta ccgcatgggg gcaggagtgg ggcaaaggat tgtccaccat gttgcggctg 1200

agtgcggcgc aacgccatta tcaaacgcct agtcttttga gcggtcagga aaaccgtcgc 1260

gataaagaag cggatatttc gctcgccgtg tggcaccgcg ctttccattt caaaggcatc 1320

accccgcgcc tgaccgtcgc ccatcacaaa acatggagca acgacaaata taatgaatac 1380

ggcaaaacca gaatgtttgt cgagttcagc aaaacgttct ga 1422

<210> 390

<211> 473

<212> PRT

<213> N. mucosa SLAM 1

<400> 390

Met Lys Thr Leu Leu Leu Leu Ser Leu Leu Ala Met Ser Ala Ala Glu

1 5 10 15

Ala Val Asp Val Ser Ser Glu Thr Gln Asn Gln Pro Ala Pro Glu Leu

20 25 30

Gln Val Lys Thr Ala Glu Pro Asp Pro Val Glu Glu Glu Thr Val Lys

35 40 45

Pro Ala Ala Glu Thr Ser Ser Glu Lys Val Val Asn Val Asp Ala Lys

50 55 60

Thr Leu Leu Asp Asn Pro Gln Leu Leu Ser Arg Ala Met Tyr Ser Ala

65 70 75 80

Val Val Ser Arg Asn Ile Ala Gly Ile Lys Val Val Leu Pro Ile Tyr

85 90 95

Glu Gln Trp Gln Gly His Asp Lys Asn Met Ala Leu Tyr Ala Arg Gly

100 105 110

Leu Val Ala Gln Asn Asp Gly Lys Met Lys Glu Ala Ile Gly Tyr Tyr

115 120 125

Arg Gln Phe Ile Ala Glu Thr Pro Asp Ala Pro Val Val Arg Trp Gln

130 135 140

Leu Ala Thr Ala Leu Phe Glu Asp Lys Gln Asn Glu Ala Ala Ala Asp

145 150 155 160

Gln Phe Asp Lys Leu Lys Thr Glu Pro Asn Leu Pro Glu Pro Phe Val

165 170 175

Lys Gly Ile Glu Ser Tyr Arg Lys Ala Leu Arg Glu Arg Asp Ser Trp

180 185 190

Lys Phe Asn Ala Gly Leu Ser Val Thr Arg Glu Gln Asn Ile Asn Gln

195 200 205

Ala Pro Ser Arg Arg Thr Tyr Gly Asn Trp Thr Phe Pro Glu Pro Ile

210 215 220

Asp Ala Thr Ala Ile Asn Tyr Gln Leu Gly Ala Glu Lys Lys Trp Ser

225 230 235 240

Leu Pro Lys Gly Trp Tyr Ala Thr Ala Gly Ala Asp Asn Tyr Gly Lys

245 250 255

Ile Tyr Pro Glu Arg Thr Lys Tyr Asn Asp Val Thr Thr Arg Phe Ser

260 265 270

Val Gly Ala Gly Tyr Ala Asp Gln Arg Asn Asp Ile Gly Leu Thr Pro

275 280 285

Phe His Glu Arg Arg Phe Tyr Gly Asn Asp Pro Tyr Thr Tyr Ser Ser

290 295 300

Gly Ala Arg Leu His Ile Asn Arg Trp Trp Gln Pro Lys Leu Gln Thr

305 310 315 320

Leu Ser Ala Val Glu Met Gly Arg Leu Lys Asn Thr Arg Arg Ala Arg

325 330 335

Ser Asn Asn Asn Asn Arg Leu Leu Ser Asn Ser Val Val Tyr Tyr Arg

340 345 350

Asn Ala Arg Gln Tyr Trp Val Gly Gly Phe Asp Ile Tyr Gln Glu Arg

355 360 365

Asn Lys Glu Asp Lys Thr Asp Asn Phe Asp Arg Tyr Ser Leu Arg Thr

370 375 380

Ala Trp Gly Gln Glu Trp Gly Lys Gly Leu Ser Thr Met Leu Arg Leu

385 390 395 400

Ser Ala Ala Gln Arg His Tyr Gln Thr Pro Ser Leu Leu Ser Gly Gln

405 410 415

Glu Asn Arg Arg Asp Lys Glu Ala Asp Ile Ser Leu Ala Val Trp His

420 425 430

Arg Ala Phe His Phe Lys Gly Ile Thr Pro Arg Leu Thr Val Ala His

435 440 445

His Lys Thr Trp Ser Asn Asp Lys Tyr Asn Glu Tyr Gly Lys Thr Arg

450 455 460

Met Phe Val Glu Phe Ser Lys Thr Phe

465 470

<210> 391

<211> 1440

<212> DNA

<213> N. mucosa SLAM 2

<400> 391

atgtacaaac cgtctgcctg ccttatcctc tttctcgccg cgcccgtcct tgccgcgccc 60

cgttctgact tttcagacga ccgtaccgcg caacgcctgt ggcaggacac ccgccaaacc 120

atgcaggaac aggaacaaaa agtgcgcgaa taccgcctcg acattccctc cgaaaacatc 180

gggcagacag ccgaaaccga tcccgaagcc gaccaaggcg aagccctgtt caacgccgtc 240

aaccacagcg actggcagac cgtgcgtccg ctgctcgagc gttatacaca gcaaaccgaa 300

tacgaccccg acatcgccct ctttgcccgc gcctcgctcg cccgcggcga aggcaggtgg 360

aaagccgcca aacaagacta cgaaaccctg ctgcaacgcc atcccgactt cacgcgcgga 420

cggctcgatt acacccgcct gctctttgaa ggtcgtctga accgcgaagc cacttccgaa 480

tttatgcgcc ttcaaaacga agacctgccc gaagccgtca aagaaaacat cggacatttc 540

cgcgactctc taaaccaacg ccaaagctgg cagggtagcc tttccgtcgg cgccgtccac 600

aacagcaaca tcaacgaagc cagcggcaaa acgtggtgta aaaccgaaat cgacggcgaa 660

tgctgggaag aattttcagg cgacaaaccc atttccgcca acggcatcaa atacgaagcc 720

gccgccgtcc gccgctggca gattaaggga caccacggca tcgccgcccg cgcgctcggc 780

tacggccgct tctaccgcga ccataaagac ttcaacgaac acacgctcaa cctcagcgca 840

ggttatcagt ttgaaaacca ccgccacacc ttcgcccttg ccccgctcgt cgaatggaac 900

ggcagcggcg gcaaaaccct caaccgcgcc tacggcgtgc gcagcgagtg gaacctcgac 960

aaaggcagct ggacttggaa caccgaagcc gagtggaaac acctctccta ttccgacaaa 1020

acccgcctgc ttgacggcaa cctcatctcc gtttacaaca ccctgtccta cttcccgcgc 1080

aacgacctca tgctctacgg cggcatagac tggcagcagc gcaaagccaa agaaccggtg 1140

gacagctacc gcctcatctc cgcacggctg ggcgcggcaa aaatgtttga agccggcttc 1200

gatgcctccg cctccgccac cttcggcatc cgcagccacc gcgaagaaaa cgccgtactc 1260

gaacaacgcc gccgcgacaa agagcaaacc taccgcctca gcataggcgc ggaccgctgg 1320

aaattcgccg gcctcaagcc cgtcctcagt tacaaacacc gccgcgtcca cggcaacacc 1380

gactggctgt acagctacaa acaaaacgaa gtcggtctgt cgctggtcaa atcgttctaa 1440

<210> 392

<211> 479

<212> PRT

<213> N. mucosa SLAM 2

<400> 392

Met Tyr Lys Pro Ser Ala Cys Leu Ile Leu Phe Leu Ala Ala Pro Val
1 5 10 15
Leu Ala Ala Pro Arg Ser Asp Phe Ser Asp Asp Arg Thr Ala Gln Arg
20 25 30
Leu Trp Gln Asp Thr Arg Gln Thr Met Gln Glu Gln Glu Gln Lys Val
35 40 45
Arg Glu Tyr Arg Leu Asp Ile Pro Ser Glu Asn Ile Gly Gln Thr Ala
50 55 60

Glu Thr Asp Pro Glu Ala Asp Gln Gly Glu Ala Leu Phe Asn Ala Val
65 70 75 80
Asn His Ser Asp Trp Gln Thr Val Arg Pro Leu Leu Glu Arg Tyr Thr
85 90 95
Gln Gln Thr Glu Tyr Asp Pro Asp Ile Ala Leu Phe Ala Arg Ala Ser
100 105 110
Leu Ala Arg Gly Glu Gly Arg Trp Lys Ala Ala Lys Gln Asp Tyr Glu
115 120 125

Thr Leu Leu Gln Arg His Pro Asp Phe Thr Arg Gly Arg Leu Asp Tyr
130 135 140
Thr Arg Leu Leu Phe Glu Gly Arg Leu Asn Arg Glu Ala Thr Ser Glu
145 150 155 160
Phe Met Arg Leu Gln Asn Glu Asp Leu Pro Glu Ala Val Lys Glu Asn
165 170 175
Ile Gly His Phe Arg Asp Ser Leu Asn Gln Arg Gln Ser Trp Gln Gly
180 185 190

Ser Leu Ser Val Gly Ala Val His Asn Ser Asn Ile Asn Glu Ala Ser
195 200 205
Gly Lys Thr Trp Cys Lys Thr Glu Ile Asp Gly Glu Cys Trp Glu Glu
210 215 220
Phe Ser Gly Asp Lys Pro Ile Ser Ala Asn Gly Ile Lys Tyr Glu Ala
225 230 235 240
Ala Ala Val Arg Arg Trp Gln Ile Lys Gly His His Gly Ile Ala Ala

245 250 255

Arg Ala Leu Gly Tyr Gly Arg Phe Tyr Arg Asp His Lys Asp Phe Asn
260 265 270
Glu His Thr Leu Asn Leu Ser Ala Gly Tyr Gln Phe Glu Asn His Arg
275 280 285
His Thr Phe Ala Leu Ala Pro Leu Val Glu Trp Asn Gly Ser Gly Gly
290 295 300
Lys Thr Leu Asn Arg Ala Tyr Gly Val Arg Ser Glu Trp Asn Leu Asp
305 310 315 320

Lys Gly Ser Trp Thr Trp Asn Thr Glu Ala Glu Trp Lys His Leu Ser
325 330 335
Tyr Ser Asp Lys Thr Arg Leu Leu Asp Gly Asn Leu Ile Ser Val Tyr
340 345 350
Asn Thr Leu Ser Tyr Phe Pro Arg Asn Asp Leu Met Leu Tyr Gly Gly
355 360 365
Ile Asp Trp Gln Gln Arg Lys Ala Lys Glu Pro Val Asp Ser Tyr Arg
370 375 380

Leu Ile Ser Ala Arg Leu Gly Ala Ala Lys Met Phe Glu Ala Gly Phe
385 390 395 400
Asp Ala Ser Ala Ser Ala Thr Phe Gly Ile Arg Ser His Arg Glu Glu
405 410 415
Asn Ala Val Leu Glu Gln Arg Arg Arg Asp Lys Glu Gln Thr Tyr Arg
420 425 430
Leu Ser Ile Gly Ala Asp Arg Trp Lys Phe Ala Gly Leu Lys Pro Val
435 440 445

Leu Ser Tyr Lys His Arg Arg Val His Gly Asn Thr Asp Trp Leu Tyr
450 455 460
Ser Tyr Lys Gln Asn Glu Val Gly Leu Ser Leu Val Lys Ser Phe
465 470 475
<210> 393
<211> 1422

<212> DNA

<213> N. mucosa SLAM 3

<400> 393

atgaataaaa atcacctagt cttactgatg ctctctttcc caatagccgc ccttgccgat 60

acacccgttg tccgtgtacc tgcgcctgta ttttttgaca agcaaccgaa cagcgataca 120

ccctcaaaag attttaccga cgacaaacct gcagaacaga ggctttcaga cgacctttct 180

gccgattcct cattggaagc acagatcaac cgcgcattaa tcggacggga ctggaagacg 240

ctggaaggct tgttggcgca atataaagcc gcgcccgacc gggatgccgt tttatacgat 300

tatgctttag gcgccttgcg gcgcagtcag ttgcggcatg gtgaggctgt atcgctctat 360

cgcggcattt tggcgaaaca tccggatttg gcgtatccgc gtttcgattt gggcgtaatg 420

atgtttgaaa acaaacagta ccatgaggca aaagctgaat tgaaacgggc aaaaccggat 480

ttgcagccgc ccatgcagca acttgccgac cgctatcttg cttccattga atcggcgcaa 540

agctggcagc ccgatgtttc actgcaatac gagcagaccg ataatgtgaa caatgcctca 600

tccgagcacg ttatagaatg gaacggcaga cgctggaata aaaccgctga gagcctgccg 660

caaaaggcac atggtatccg ctatggcgca ggcgtatcgc gcgaaattaa tgcgggtggg 720

catcatttcg tttacggcag cctgagcggc gacggtgtat attattggga taatcaggat 780

tttaacgagc aaagcctacg cttggcggcg ggttataaaa accgttcggc ggtgcaatct 840

ttcggggttg taccgtttgc cgagcaaaac tggctgggtg gcaaacgcta taatcgcgaa 900

accggtatcc ataccgattt ttcacgtcgt ctgaacgaaa aatggcggct ctcgctcaat 960

gcaggctata tcaaaaaata ctatcggaac agcgattcgg cagcgcgtta caacagccat 1020

atgccgctgg cgggggcaac gctagcatac tctgcgccga aaaactggct gctctacggc 1080

ggcgcagact ggtcgcacga catgaccaaa gaagcggagc aggcatctgt gcgcaagggc 1140

atacgcttcg gcgcggcgaa agcgtttgag aacggattcg gcatccgcac caacctgcgc 1200

tacgcccgcc gtacctttga tgcgccggga agcctggtgt accgtctgac ccgtaaagac 1260

catgaatatc aagcaaatgc ctctatttgg cacaataaaa tttcatggaa aggcttggtg 1320

ccgcatttga atttccgtta tctgaaaatc gacagcaata tgagcggctt ctattcccgc 1380

aagagtatgc agacattcgt cagcgtggag aaacagtttt ga 1422

<210> 394

<211> 473

<212> PRT

<213> N. mucosa SLAM 3

<400> 394

Met Asn Lys Asn His Leu Val Leu Leu Met Leu Ser Phe Pro Ile Ala
1 5 10 15
Ala Leu Ala Asp Thr Pro Val Val Arg Val Pro Ala Pro Val Phe Phe
20 25 30
Asp Lys Gln Pro Asn Ser Asp Thr Pro Ser Lys Asp Phe Thr Asp Asp
35 40 45
Lys Pro Ala Glu Gln Arg Leu Ser Asp Asp Leu Ser Ala Asp Ser Ser

50 55 60
Leu Glu Ala Gln Ile Asn Arg Ala Leu Ile Gly Arg Asp Trp Lys Thr
65 70 75 80
Leu Glu Gly Leu Leu Ala Gln Tyr Lys Ala Ala Pro Asp Arg Asp Ala
85 90 95
Val Leu Tyr Asp Tyr Ala Leu Gly Ala Leu Arg Arg Ser Gln Leu Arg
100 105 110
His Gly Glu Ala Val Ser Leu Tyr Arg Gly Ile Leu Ala Lys His Pro

115 120 125
Asp Leu Ala Tyr Pro Arg Phe Asp Leu Gly Val Met Met Phe Glu Asn
130 135 140
Lys Gln Tyr His Glu Ala Lys Ala Glu Leu Lys Arg Ala Lys Pro Asp
145 150 155 160
Leu Gln Pro Pro Met Gln Gln Leu Ala Asp Arg Tyr Leu Ala Ser Ile
165 170 175
Glu Ser Ala Gln Ser Trp Gln Pro Asp Val Ser Leu Gln Tyr Glu Gln

180 185 190
Thr Asp Asn Val Asn Asn Ala Ser Ser Glu His Val Ile Glu Trp Asn
195 200 205
Gly Arg Arg Trp Asn Lys Thr Ala Glu Ser Leu Pro Gln Lys Ala His
210 215 220
Gly Ile Arg Tyr Gly Ala Gly Val Ser Arg Glu Ile Asn Ala Gly Gly
225 230 235 240

His His Phe Val Tyr Gly Ser Leu Ser Gly Asp Gly Val Tyr Tyr Trp

245 250 255

Asp Asn Gln Asp Phe Asn Glu Gln Ser Leu Arg Leu Ala Ala Gly Tyr

260 265 270

Lys Asn Arg Ser Ala Val Gln Ser Phe Gly Val Val Pro Phe Ala Glu

275 280 285

Gln Asn Trp Leu Gly Gly Lys Arg Tyr Asn Arg Glu Thr Gly Ile His

290 295 300

Thr Asp Phe Ser Arg Arg Leu Asn Glu Lys Trp Arg Leu Ser Leu Asn

305 310 315 320

Ala Gly Tyr Ile Lys Lys Tyr Tyr Arg Asn Ser Asp Ser Ala Ala Arg

325 330 335

Tyr Asn Ser His Met Pro Leu Ala Gly Ala Thr Leu Ala Tyr Ser Ala

340 345 350

Pro Lys Asn Trp Leu Leu Tyr Gly Gly Ala Asp Trp Ser His Asp Met

355 360 365

Thr Lys Glu Ala Glu Gln Ala Ser Val Arg Lys Gly Ile Arg Phe Gly

370 375 380

Ala Ala Lys Ala Phe Glu Asn Gly Phe Gly Ile Arg Thr Asn Leu Arg

385 390 395 400

Tyr Ala Arg Arg Thr Phe Asp Ala Pro Gly Ser Leu Val Tyr Arg Leu

405 410 415

Thr Arg Lys Asp His Glu Tyr Gln Ala Asn Ala Ser Ile Trp His Asn

420 425 430

Lys Ile Ser Trp Lys Gly Leu Val Pro His Leu Asn Phe Arg Tyr Leu

435 440 445

Lys Ile Asp Ser Asn Met Ser Gly Phe Tyr Ser Arg Lys Ser Met Gln

450 455 460

Thr Phe Val Ser Val Glu Lys Gln Phe

465 470

<210> 395

<211> 1542

<212> DNA

<213> N. mucosa SLAM 4

<400> 395

atgttaagaa taaaacaaaa aatggtttcg gcatctttat gttgcctgtt gccttccgca 60

gtcttggctg aattgcccga aggtggtgtc cggcaggatg caccttctca ggatgctgcc 120

gtacaagtgc agcaaaaaca atggctggat attttgtccg aagaagaaag gtcgtctgaa 180

aagaatgaga atgtcggcga accggctgta gtcggcgatg atttttttagc ggcaaacccg 240

cgtattcttg aggacgcgct gattcaagca cttaacggca atagcgcaga tttggtttct 300

tcgcttgccg cactttaccg taaacagccc aaccacaatc ccaagctgat tgcacgtgcc 360

gatgctttac tggcaaagtt gaaagggcgg acttccgaag cggtcgaacg ttatcgtacc 420

ctttatgaat ccgacgtttc agacgaccgc atattgttgg atttggcggc ggcagagttt 480

caggattatc gtttgggcga ggcggcggcg catttccgcc atgccgcgca acgcgatata 540

cctgcccccg ttttggaaaa cgtcaaacgt tttcaagaag ctgtcaagcg gcagacagaa 600

tggaaatggt ctggtggaat cagtcccgta catagcgata acgccaacaa cgctgctccg 660

cgttattgca tcgaaacaag ggggcaaacc gcatgcagcg ttactgtgcc cgtcagtgcc 720

aacggcttga attacgaatt gaacaccgaa aaactcaccc cgctgtacgg gcatcacgcc 780

gtcaaattcc gcgccaacct cagcggaacg agctattttt tcgaccacca atcggcttac 840

gacgatgcgt tcggcagggc ttatttgggc tggcagcgca aggacggtaa acaaaccgtc 900

agcgttttac cgttttatca ggcacagttg gcaggcagca gcgagtttga cagcaaaaaa 960

gaaaacaacc gccgtgccgc gccttatatg ctggcacacg ggattggcgt acagctttcg 1020

catatggtca atctcggcaa cgcgacacaa ctttattact cgctggaacg ctatcgccaa 1080

aactatcggg aaactgatcg tgcgctgcgc aacgacggtt ggcacgacag tacctatctc 1140

tccctagcgc gccgtttcgg cagaacgacc ctgttcggtg gttggcaata caaccgcttt 1200

gttcctgaaa acaaaaacat acgcaatgcc gtcaacaatg ccgcctaccg ccgcagcggg 1260

ttcaatatag gctggataca gcaatggccg tttttgggcg ggctgaacag ccgcctgacc 1320

gcttcatttg ccaaccgccg ctataaaggc attatggcat tcggtacaga gtcgcaacgt 1380

aaccgcgagc actcactctc cgtcagcctt agtcatgaca aattgtccta caaaggtatc 1440

acgccgacct tgaattacgg atacagccgt atccgcagca atgcccctta tgcacgacgc 1500

agcagccgtc aatggtcgtt gggagctgaa tggaattttt aa 1542

<210> 396

<211> 513

<212> PRT

<213> N. mucosa SLAM 4

<400> 396

Met Leu Arg Ile Lys Gln Lys Met Val Ser Ala Ser Leu Cys Cys Leu
1 5 10 15

Leu Pro Ser Ala Val Leu Ala Glu Leu Pro Glu Gly Gly Val Arg Gln
20 25 30

Asp Ala Pro Ser Gln Asp Ala Ala Val Gln Val Gln Gln Lys Gln Trp
35 40 45

Leu Asp Ile Leu Ser Glu Glu Glu Arg Ser Ser Glu Lys Asn Glu Asn
50 55 60

Val Gly Glu Pro Ala Val Val Gly Asp Asp Phe Leu Ala Ala Asn Pro
65 70 75 80

Arg Ile Leu Glu Asp Ala Leu Ile Gln Ala Leu Asn Gly Asn Ser Ala
85 90 95

Asp Leu Val Ser Ser Leu Ala Ala Leu Tyr Arg Lys Gln Pro Asn His
100 105 110

Asn Pro Lys Leu Ile Ala Arg Ala Asp Ala Leu Leu Ala Lys Leu Lys
115 120 125

Gly Arg Thr Ser Glu Ala Val Glu Arg Tyr Arg Thr Leu Tyr Glu Ser
130 135 140

Asp Val Ser Asp Asp Arg Ile Leu Leu Asp Leu Ala Ala Ala Glu Phe
145 150 155 160

Gln Asp Tyr Arg Leu Gly Glu Ala Ala Ala His Phe Arg His Ala Ala
165 170 175

Gln Arg Asp Ile Pro Ala Pro Val Leu Glu Asn Val Lys Arg Phe Gln
180 185 190

Glu Ala Val Lys Arg Gln Thr Glu Trp Lys Trp Ser Gly Gly Ile Ser
195 200 205

Pro Val His Ser Asp Asn Ala Asn Asn Ala Ala Pro Arg Tyr Cys Ile
210 215 220

Glu Thr Arg Gly Gln Thr Ala Cys Ser Val Thr Val Pro Val Ser Ala

225 230 235 240

Asn Gly Leu Asn Tyr Glu Leu Asn Thr Glu Lys Leu Thr Pro Leu Tyr

245 250 255

Gly His His Ala Val Lys Phe Arg Ala Asn Leu Ser Gly Thr Ser Tyr

260 265 270

Phe Phe Asp His Gln Ser Ala Tyr Asp Asp Ala Phe Gly Arg Ala Tyr

275 280 285

Leu Gly Trp Gln Arg Lys Asp Gly Lys Gln Thr Val Ser Val Leu Pro

290 295 300

Phe Tyr Gln Ala Gln Leu Ala Gly Ser Ser Glu Phe Asp Ser Lys Lys

305 310 315 320

Glu Asn Asn Arg Arg Ala Ala Pro Tyr Met Leu Ala His Gly Ile Gly

325 330 335

Val Gln Leu Ser His Met Val Asn Leu Gly Asn Ala Thr Gln Leu Tyr

340 345 350

Tyr Ser Leu Glu Arg Tyr Arg Gln Asn Tyr Arg Glu Thr Asp Arg Ala

355 360 365

Leu Arg Asn Asp Gly Trp His Asp Ser Thr Tyr Leu Ser Leu Ala Arg

370 375 380

Arg Phe Gly Arg Thr Thr Leu Phe Gly Gly Trp Gln Tyr Asn Arg Phe

385 390 395 400

Val Pro Glu Asn Lys Asn Ile Arg Asn Ala Val Asn Asn Ala Ala Tyr

405 410 415

Arg Arg Ser Gly Phe Asn Ile Gly Trp Ile Gln Gln Trp Pro Phe Leu

420 425 430

Gly Gly Leu Asn Ser Arg Leu Thr Ala Ser Phe Ala Asn Arg Arg Tyr

435 440 445

Lys Gly Ile Met Ala Phe Gly Thr Glu Ser Gln Arg Asn Arg Glu His

450 455 460

Ser Leu Ser Val Ser Leu Ser His Asp Lys Leu Ser Tyr Lys Gly Ile

465 470 475 480

Thr Pro Thr Leu Asn Tyr Gly Tyr Ser Arg Ile Arg Ser Asn Ala Pro

485 490 495

Tyr Ala Arg Arg Ser Ser Arg Gln Trp Ser Leu Gly Ala Glu Trp Asn

500 505 510

Phe

<210> 397

<211> 1335

<212> DNA

<213> N. nitrogenifigens SLAM 1

<400> 397

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cccccgttca cgccaccctc cccgacgacc gggacgcttc agctttcacc tgtgcagatg 120

ttcgattttg ccgaggcggc gtcaaaacga ggtgactatg acaccgccga acgagccctg 180

cgtgcactga tcggcaatcc gggcatcgac atccgttgcg aggcgcgctt tcgtctcgct 240

cgcctgctcg ccggtccctt ccatcgtcgg accgaagcgg ctttgctctt gcgacggata 300

cttgatgaaa agcccaatgc cgcaccggtg cggctcgaac tggcacgcct cgaagctgaa 360

atgggccgga ccggcgcggc cgggcgcgaa ttgcgcgccg cgcaagcgat cggccttccc 420

gccgacatcg cccgcatggt gcgtttctat caacaggcgc tcgaggcgca gcgccccatg 480

agcggcagca tcgaactcgc gctggccccc gacagcaacg tcaatcgcgc gaccacggcg 540

tcaaccatgg gcaccgtcat tggcgatttc acgctcagcc gggacgcgcg cgcaacttcg 600

ggcatggggc tggtcgtccg gacacaggcg ttcgcacgac tgcggatgac gccgcgcctg 660

tccctgctcg cgcgcctgtc cggcagcgcc agtctctatc gcgaccccgg tttcgacgac 720

gaagtggtcg ccccgcagat cggccccgaa tggagcctgg gcgacgatcg cgtcagcctg 780

agcggtggcg cggcactgcg ctggtacggc gggcgaagtt ataccaccgc cacgactgcc 840

gcgatcgact ggcaacatcg gctgggcaag cgcgggctgc tgcgggtgag cgccaaccac 900

gcctttgtcg acaatcaccg caacgctctg gaaaccggtt cggcctgggg cggcacggca 960

ggtctcgacc gcgcgttctc ggcccgcttt ggcgggggtc tttcgctctt cggcaatcgc 1020

caggataccc gcgatcccgg ctatgccacg accagcttcg gcttcagccc ctatgtcttt 1080

cgcgaaatag gccgggcgac cgtgacggct acgctgtcct acagccacct tgccgccgat 1140

gcccgcattg ccttgttcaa cgatcgccga cgcgatcagg cctatggcct gaaccttgcc 1200

gcgacattgc gccaaattcg catcggttcc ttgtcaccgc tcctgcgttt gcggctagaa 1260

cggaacgcat caaccgtcca actctatgat tataaaagag tcgccggaga agtgggaata 1320

gcctccgcat tctga 1335

<210> 398

<211> 444

<212> PRT

<213> N. nitrogenifigens SLAM 1

<400> 398

Met Pro Val Leu Ile Leu Ala Leu Ala Pro Thr Leu Met Ala Val Ser
1 5 10 15

Thr Pro Ala Leu Pro Pro Phe Thr Pro Pro Ser Pro Thr Thr Gly Thr
20 25 30

Leu Gln Leu Ser Pro Val Gln Met Phe Asp Phe Ala Glu Ala Ala Ser
35 40 45

Lys Arg Gly Asp Tyr Asp Thr Ala Glu Arg Ala Leu Arg Ala Leu Ile
50 55 60

Gly Asn Pro Gly Ile Asp Ile Arg Cys Glu Ala Arg Phe Arg Leu Ala
65 70 75 80

Arg Leu Leu Ala Gly Pro Phe His Arg Arg Thr Glu Ala Ala Leu Leu
85 90 95

Leu Arg Arg Ile Leu Asp Glu Lys Pro Asn Ala Ala Pro Val Arg Leu
100 105 110

Glu Leu Ala Arg Leu Glu Ala Glu Met Gly Arg Thr Gly Ala Ala Gly
115 120 125

Arg Glu Leu Arg Ala Ala Gln Ala Ile Gly Leu Pro Ala Asp Ile Ala
130 135 140

Arg Met Val Arg Phe Tyr Gln Gln Ala Leu Glu Ala Gln Arg Pro Met
145 150 155 160

Ser Gly Ser Ile Glu Leu Ala Leu Ala Pro Asp Ser Asn Val Asn Arg
165 170 175

Ala Thr Thr Ala Ser Thr Met Gly Thr Val Ile Gly Asp Phe Thr Leu

180 185 190

Ser Arg Asp Ala Arg Ala Thr Ser Gly Met Gly Leu Val Val Arg Thr
195 200 205

Gln Ala Phe Ala Arg Leu Arg Met Thr Pro Arg Leu Ser Leu Leu Ala
210 215 220

Arg Leu Ser Gly Ser Ala Ser Leu Tyr Arg Asp Pro Gly Phe Asp Asp
225 230 235 240

Glu Val Val Ala Pro Gln Ile Gly Pro Glu Trp Ser Leu Gly Asp Asp
245 250 255

Arg Val Ser Leu Ser Gly Gly Ala Ala Leu Arg Trp Tyr Gly Gly Arg
260 265 270

Ser Tyr Thr Thr Ala Thr Thr Ala Ala Ile Asp Trp Gln His Arg Leu
275 280 285

Gly Lys Arg Gly Leu Leu Arg Val Ser Ala Asn His Ala Phe Val Asp
290 295 300

Asn His Arg Asn Ala Leu Glu Thr Gly Ser Ala Trp Gly Gly Thr Ala
305 310 315 320

Gly Leu Asp Arg Ala Phe Ser Ala Arg Phe Gly Gly Gly Leu Ser Leu
325 330 335

Phe Gly Asn Arg Gln Asp Thr Arg Asp Pro Gly Tyr Ala Thr Thr Ser
340 345 350

Phe Gly Phe Ser Pro Tyr Val Phe Arg Glu Ile Gly Arg Ala Thr Val
355 360 365

Thr Ala Thr Leu Ser Tyr Ser His Leu Ala Ala Asp Ala Arg Ile Ala
370 375 380

Leu Phe Asn Asp Arg Arg Arg Asp Gln Ala Tyr Gly Leu Asn Leu Ala
385 390 395 400

Ala Thr Leu Arg Gln Ile Arg Ile Gly Ser Leu Ser Pro Leu Leu Arg
405 410 415

Leu Arg Leu Glu Arg Asn Ala Ser Thr Val Gln Leu Tyr Asp Tyr Lys
420 425 430

Arg Val Ala Gly Glu Val Gly Ile Ala Ser Ala Phe

435 440

<210> 399

<

211> 1341

<212> DNA

<213> N. pentaromativorans SLAM 1

<400> 399

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gcacatgatg gcaattcgaa cggtcctgaa cttcgggaga ccaggctcga acacctttct 120

gccgacgatg tgctggcgct ggccggaaaa ctgatcgacg cgggccggta cgaggaagcg 180

caagtcttgc tggaccggct ggcggcggac ggtgcgggag gcgtcgagcg cgcctttctt 240

gatggaatgc tggcacttgc gcgcaaggat tacccgcagg ctgaacgatt gctccgcaag 300

atactcgaag gcgaccccag cctggttcgg gtgaggcttg aacttgcccg gaccctcttt 360

ctcgcaaaga aggacgagca ggccgactac cagttccgcc tcgccatcgc cgagcacccg 420

cccgagacgg tgattgccaa tatcgcccgc ttccgcgaag caatccgtgc gcggcgggct 480

tggcgcttca atgtcaacat cgggatcgcg ccggacacca acatcaactc ggccaccaac 540

aaggagcagg tcgatatctt cggcttgcca ttcaagcttg acgacaatgc gagggcgcgt 600

tcggggatcg gcatggtcgc aggtggtgat gcatcggtgc gtctgtggcg cttcagcaag 660

gtaccggtct atctcggcgc ctatggccgt gtccttcgct acaaggacca tgacttcgac 720

gacatctatg tcggcgggga ggctggcccc gagtttcgcc tttcgggcgg gcgtctcaga 780

gccacggcca ctgctttcca gcgctggtac ggaggcaagg acctcgtcac cagtcttggc 840

ggcaggctca attacgacaa ggtgatcggc ggcaagttgg gtattgatgc cagccttgcc 900

tttcgccgcg acaactatgc ccggcgccgc gatctggatg cttgggctat cgaggcgacc 960

ctctccgcca acagggcgat atcactatct gcgataggct tcgcctatac cactgtccgg 1020

cgcagcattg ctcacgagcc gggctattcg aactggaacg cgaggattgg cggcggcgtg 1080

ctcaaggaga tcggctgggg cctgcgcccg caactgggca tcgaggtcgg ccgacagatc 1140

aacgacgaga ggctcggggt cttcggcagg acgcgccgcg actggtcgct gcaggccagc 1200

gccagcatct acaagcgcga ctggaacatt gccggcttcg ccccatccgt caaagtcaca 1260

tggagccgca cctactccac cattgccttc tatgaccaga agcgcctgcg cacagagttc 1320

gggctcacca aggcattctg a 1341

<210> 400

<211> 446

<212> PRT

<213> N. pentaromativorans SLAM 1

<400> 400

Met Phe Gly Pro Val Leu Val Tyr Ala Ala Thr Leu Ala Ala Pro Ala
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Thr Ser Ala Ala Ala His Asp Gly Asn Ser Asn Gly Pro Glu Leu Arg

20 25 30
Glu Thr Arg Leu Glu His Leu Ser Ala Asp Asp Val Leu Ala Leu Ala
35 40 45
Gly Lys Leu Ile Asp Ala Gly Arg Tyr Glu Glu Ala Gln Val Leu Leu
50 55 60
Asp Arg Leu Ala Ala Asp Gly Ala Gly Gly Val Glu Arg Ala Phe Leu
65 70 75 80
Asp Gly Met Leu Ala Leu Ala Arg Lys Asp Tyr Pro Gln Ala Glu Arg

85 90 95
Leu Leu Arg Lys Ile Leu Glu Gly Asp Pro Ser Leu Val Arg Val Arg
100 105 110
Leu Glu Leu Ala Arg Thr Leu Phe Leu Ala Lys Lys Asp Glu Gln Ala
115 120 125
Asp Tyr Gln Phe Arg Leu Ala Ile Ala Glu His Pro Pro Glu Thr Val
130 135 140
Ile Ala Asn Ile Ala Arg Phe Arg Glu Ala Ile Arg Ala Arg Arg Ala

145 150 155 160
Trp Arg Phe Asn Val Asn Ile Gly Ile Ala Pro Asp Thr Asn Ile Asn
165 170 175
Ser Ala Thr Asn Lys Glu Gln Val Asp Ile Phe Gly Leu Pro Phe Lys
180 185 190
Leu Asp Asp Asn Ala Arg Ala Arg Ser Gly Ile Gly Met Val Ala Gly
195 200 205
Gly Asp Ala Ser Val Arg Leu Trp Arg Phe Ser Lys Val Pro Val Tyr

210 215 220

Leu Gly Ala Tyr Gly Arg Val Leu Arg Tyr Lys Asp His Asp Phe Asp

225 230 235 240

Asp Ile Tyr Val Gly Gly Glu Ala Gly Pro Glu Phe Arg Leu Ser Gly

245 250 255

Gly Arg Leu Arg Ala Thr Ala Thr Ala Phe Gln Arg Trp Tyr Gly Gly

260 265 270

Lys Asp Leu Val Thr Ser Leu Gly Gly Arg Leu Asn Tyr Asp Lys Val

275 280 285

Ile Gly Gly Lys Leu Gly Ile Asp Ala Ser Leu Ala Phe Arg Arg Asp

290 295 300

Asn Tyr Ala Arg Arg Arg Asp Leu Asp Ala Trp Ala Ile Glu Ala Thr

305 310 315 320

Leu Ser Ala Asn Arg Ala Ile Ser Leu Ser Ala Ile Gly Phe Ala Tyr

325 330 335

Thr Thr Val Arg Arg Ser Ile Ala His Glu Pro Gly Tyr Ser Asn Trp

340 345 350

Asn Ala Arg Ile Gly Gly Gly Val Leu Lys Glu Ile Gly Trp Gly Leu

355 360 365

Arg Pro Gln Leu Gly Ile Glu Val Gly Arg Gln Ile Asn Asp Glu Arg

370 375 380

Leu Gly Val Phe Gly Arg Thr Arg Arg Asp Trp Ser Leu Gln Ala Ser

385 390 395 400

Ala Ser Ile Tyr Lys Arg Asp Trp Asn Ile Ala Gly Phe Ala Pro Ser

405 410 415

Val Lys Val Thr Trp Ser Arg Thr Tyr Ser Thr Ile Ala Phe Tyr Asp

420 425 430

Gln Lys Arg Leu Arg Thr Glu Phe Gly Leu Thr Lys Ala Phe

435 440 445

<210> 401

<211> 1305

<212> DNA

<213> N. pentaromativorans SLAM 2

<400> 401

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tcgaccgatg cagaagacgc accggtcgtc ggccttgaag cccttgtcga acaattgctt 120

cgggagggtc ggaccgagga ggccgcaagc atcctggaac aatttgcaaa ggacgatctc 180

cacaaggtcc gcatgcagtt cctgaaaggc atggtcgcgc ttacccgccg cgattaccgc 240

gaagcgatca accggttccg cgtgatcctg atcgatcatc ccgacgctgt tcgcgtgcgc 300

ctcgaattgg cgcgcgcctt cttcatggac aaggattacg ccaatgccga cagacagttc 360

agactgactc gcgccgggaa gctgccccgc gacgttctcg ccaatatcga cgcctatctc 420

ttcgcgatcc gacagtccaa ggaatggtcc tacagcgtca acctgtcgct ggcgcccgac 480

accaatatca atgccggccc gactgcgcgc gaagtgacac tctacggcct gcctttcgaa 540

ctctccgacg atgcccgaca tcgcagcgga attggcctcg ctgcggactt gagcgtcgaa 600

tgggcacctc ggattgcccg taatgcgcgc ctgcgcatgg ggttcaacgg ccagcgccgc 660

gaatattccg ggtcacgctt cgacgacatg accctgggaa cctacatcgg gccacgcttc 720

gtcagccgta agtgggacat ctccttgctg ggtacgggct tccagcgctg gtatgcaggt 780

tcaccctacg cgcgatccgc cggcacacgc gtggatgcaa cccactacct ctcaccgacc 840

ttcgtgctat cggccagtgc ttcggcccag tggctggacc accagcgcgt gccggcaatg 900

agcggtccga tcctgtcgtt tggtgtgagc gcctttcatc cgcttaattc gtcgagcgcg 960

ctcacggcca agatcggaat caaccggcaa gatgccagag acgcagccta ttcaaactgg 1020

agcggctatg ccgcgctggg ttattatcgc gatctgccgg cgggattctc gatatacatt 1080

gaaccctcac tggcattcgc ccgctacgac aaggctgtcc cggcgatcgg cttgaagcgt 1140

tcggacagaa ccttgtcggg ccaggtgacc ttgctcaacc ggcacatcgt cctgtcacgc 1200

ttcacaccgc gcctgtccta cactttcacg aagcaggaca gcaacgtccc gctctaccgc 1260

ttcacacgca gtcgtatcga gataggcctg acaacgaact tctga 1305

<210> 402

<211> 434

<212> PRT

<213> N. pentaromativorans SLAM 2

<400> 402

Met Ala Ser Ser Glu Ala Ala Ala Asn Glu Pro Ala Pro Val Ala Met

1 5 10 15

Asn Ala Arg Pro Ser Thr Asp Ala Glu Asp Ala Pro Val Val Gly Leu
20 25 30
Glu Ala Leu Val Glu Gln Leu Leu Arg Glu Gly Arg Thr Glu Glu Ala
35 40 45
Ala Ser Ile Leu Glu Gln Phe Ala Lys Asp Asp Leu His Lys Val Arg
50 55 60

Met Gln Phe Leu Lys Gly Met Val Ala Leu Thr Arg Arg Asp Tyr Arg
65 70 75 80
Glu Ala Ile Asn Arg Phe Arg Val Ile Leu Ile Asp His Pro Asp Ala
85 90 95
Val Arg Val Arg Leu Glu Leu Ala Arg Ala Phe Phe Met Asp Lys Asp
100 105 110
Tyr Ala Asn Ala Asp Arg Gln Phe Arg Leu Thr Arg Ala Gly Lys Leu
115 120 125

Pro Arg Asp Val Leu Ala Asn Ile Asp Ala Tyr Leu Phe Ala Ile Arg
130 135 140
Gln Ser Lys Glu Trp Ser Tyr Ser Val Asn Leu Ser Leu Ala Pro Asp
145 150 155 160
Thr Asn Ile Asn Ala Gly Pro Thr Ala Arg Glu Val Thr Leu Tyr Gly
165 170 175
Leu Pro Phe Glu Leu Ser Asp Asp Ala Arg His Arg Ser Gly Ile Gly
180 185 190

Leu Ala Ala Asp Leu Ser Val Glu Trp Ala Pro Arg Ile Ala Arg Asn
195 200 205
Ala Arg Leu Arg Met Gly Phe Asn Gly Gln Arg Arg Glu Tyr Ser Gly
210 215 220
Ser Arg Phe Asp Asp Met Thr Leu Gly Thr Tyr Ile Gly Pro Arg Phe
225 230 235 240
Val Ser Arg Lys Trp Asp Ile Ser Leu Leu Gly Thr Gly Phe Gln Arg
245 250 255

Trp Tyr Ala Gly Ser Pro Tyr Ala Arg Ser Ala Gly Thr Arg Val Asp

260 265 270

Ala Thr His Tyr Leu Ser Pro Thr Phe Val Leu Ser Ala Ser Ala Ser

275 280 285

Ala Gln Trp Leu Asp His Gln Arg Val Pro Ala Met Ser Gly Pro Ile

290 295 300

Leu Ser Phe Gly Val Ser Ala Phe His Pro Leu Asn Ser Ser Ser Ala

305 310 315 320

Leu Thr Ala Lys Ile Gly Ile Asn Arg Gln Asp Ala Arg Asp Ala Ala

325 330 335

Tyr Ser Asn Trp Ser Gly Tyr Ala Ala Leu Gly Tyr Tyr Arg Asp Leu

340 345 350

Pro Ala Gly Phe Ser Ile Tyr Ile Glu Pro Ser Leu Ala Phe Ala Arg

355 360 365

Tyr Asp Lys Ala Val Pro Ala Ile Gly Leu Lys Arg Ser Asp Arg Thr

370 375 380

Leu Ser Gly Gln Val Thr Leu Leu Asn Arg His Ile Val Leu Ser Arg

385 390 395 400

Phe Thr Pro Arg Leu Ser Tyr Thr Phe Thr Lys Gln Asp Ser Asn Val

405 410 415

Pro Leu Tyr Arg Phe Thr Arg Ser Arg Ile Glu Ile Gly Leu Thr Thr

420 425 430

Asn Phe

<210> 403

<211> 1383

<212> DNA

<213> N. polysaccharea SLAM 1

<400> 403

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atgctgctgc tgcctttatt ggcaagcgcg gcatatgccg aagaaacacc gcgcgaaccg 120

gatttgagaa gccgtcccga gttcaggctt catgaagcgg aggtcaaacc gatcgacagg 180

gagaaggtac cggggcaggt gcgggaaaaa ggaaaagttt tgcagattga cggagaaacc 240

ctgctgaaaa gtcccgaatt gctgtcccgc gcgatgtatt ccgcagtggt cgcaaacaat 300

attgccggta tccgcgttat tttgccgatt tacctacaac aggcgcagca ggataagatg 360

ctggcacttt atgcacaagg gattttggcg caggcagacg gcagggtaaa ggaggcggtt 420

tcccattacc gggaactgat tgccgcccaa cccgacgcgc ccgccgtccg tatgcgtttg 480

gcggcggcat tgtttgaaga caggcagaac gaggcggcgg cagaccagtt cgaccgcctg 540

aaaacggaaa acctgccgcc gcagcttatg gaacaagtcg aactgtaccg caaggcattg 600

cgcgaacgcg atgcgtggaa ggtaaacggc ggtttcagcg ttacccgcga acacaatatc 660

aaccaagctc cgaaacagca gcagtacggc agatggactt tcccgaaaca ggtggacggc 720

acggcggtca attaccggct cggcgcggag aaaaaatggt cgctgaaaaa cggttggtac 780

acgacggcgg gcggagacgt gtccggcagg gcttatccgg ggaacaagaa attcaacgat 840

atgacggcag gcgtttccgg cggcatcggt tttgccgatc ggcgtaaaga tgtcgggctg 900

gcagtgttcc acgaacgccg cacctacggc aacgacgctt attcttacgc caacggcgcg 960

cgcctttatt tcaaccgttg gcaaaccccg aaatgggtgt tttaccggaa cgcgcgccaa 1020

tattggacgg gcggtttgga tttttaccac gagcgcaacc ccgccgaccg aggcgacaat 1080

tttaatcgtt acggcctgcg ctttgcctgg gggcaggaat ggggcggcag cggcctgtct 1140

tcgctgttgc gcctcggcgc ggcgaaacgg cattatgaaa aacccggctt tttcagcggt 1200

tttaaagggg aaaggcgcag ggacagggaa ttggacacat ccttgagcct ttggcaccgg 1260

gcattgcatt ttaaaggcat cacgccgcgc ctgaccttgt cgcaccgcga aacgtggagt 1320

aatgatgtgt ttaacgaata tgagaaaaac cgggtgtttg tcgagtttaa caaaacgttc 1380

tga 1383

<210> 404

<211> 460

<212> PRT

<213> N. polysaccharea SLAM 1

<400> 404

Met Val Ile Phe Tyr Phe Tyr Phe Cys Gly Lys Thr Phe Met Pro Ala

1 5 10 15

Arg Asn Arg Trp Met Leu Leu Leu Pro Leu Leu Ala Ser Ala Ala Tyr

20 25 30

Ala Glu Glu Thr Pro Arg Glu Pro Asp Leu Arg Ser Arg Pro Glu Phe

35 40 45

Arg Leu His Glu Ala Glu Val Lys Pro Ile Asp Arg Glu Lys Val Pro

50 55 60

Gly Gln Val Arg Glu Lys Gly Lys Val Leu Gln Ile Asp Gly Glu Thr

65 70 75 80

Leu Leu Lys Ser Pro Glu Leu Leu Ser Arg Ala Met Tyr Ser Ala Val

85 90 95

Val Ala Asn Asn Ile Ala Gly Ile Arg Val Ile Leu Pro Ile Tyr Leu

100 105 110

Gln Gln Ala Gln Gln Asp Lys Met Leu Ala Leu Tyr Ala Gln Gly Ile

115 120 125

Leu Ala Gln Ala Asp Gly Arg Val Lys Glu Ala Val Ser His Tyr Arg

130 135 140

Glu Leu Ile Ala Ala Gln Pro Asp Ala Pro Ala Val Arg Met Arg Leu

145 150 155 160

Ala Ala Ala Leu Phe Glu Asp Arg Gln Asn Glu Ala Ala Ala Asp Gln

165 170 175

Phe Asp Arg Leu Lys Thr Glu Asn Leu Pro Pro Gln Leu Met Glu Gln

180 185 190

Val Glu Leu Tyr Arg Lys Ala Leu Arg Glu Arg Asp Ala Trp Lys Val

195 200 205

Asn Gly Gly Phe Ser Val Thr Arg Glu His Asn Ile Asn Gln Ala Pro

210 215 220

Lys Gln Gln Gln Tyr Gly Arg Trp Thr Phe Pro Lys Gln Val Asp Gly

225 230 235 240

Thr Ala Val Asn Tyr Arg Leu Gly Ala Glu Lys Lys Trp Ser Leu Lys

245 250 255

Asn Gly Trp Tyr Thr Thr Ala Gly Gly Asp Val Ser Gly Arg Ala Tyr

260 265 270

Pro Gly Asn Lys Lys Phe Asn Asp Met Thr Ala Gly Val Ser Gly Gly

275 280 285

Ile Gly Phe Ala Asp Arg Arg Lys Asp Val Gly Leu Ala Val Phe His

290 295 300

Glu Arg Arg Thr Tyr Gly Asn Asp Ala Tyr Ser Tyr Ala Asn Gly Ala

305 310 315 320

Arg Leu Tyr Phe Asn Arg Trp Gln Thr Pro Lys Trp Met Phe Tyr Arg

325 330 335

Asn Ala Arg Gln Tyr Trp Thr Gly Gly Leu Asp Phe Tyr His Glu Arg

340 345 350

Asn Pro Ala Asp Arg Gly Asp Asn Phe Asn Arg Tyr Gly Leu Arg Phe

355 360 365

Ala Trp Gly Gln Glu Trp Gly Gly Ser Gly Leu Ser Ser Leu Leu Arg

370 375 380

Leu Gly Ala Ala Lys Arg His Tyr Glu Lys Pro Gly Phe Phe Ser Gly

385 390 395 400

Phe Lys Gly Glu Arg Arg Arg Asp Arg Glu Leu Asp Thr Ser Leu Ser

405 410 415

Leu Trp His Arg Ala Leu His Phe Lys Gly Ile Thr Pro Arg Leu Thr

420 425 430

Leu Ser His Arg Glu Thr Trp Ser Asn Asp Val Phe Asn Glu Tyr Glu

435 440 445

Lys Asn Arg Val Phe Val Glu Phe Asn Lys Thr Phe

450 455 460

<210> 405

<211> 1518

<212> DNA

<213> N. polysaccharea SLAM 2

<400> 405

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gacggggatt ttttgttggc gcatccgaaa atgttggaac atagtttgcg cgacgcgctc 240

aacggcaatc aggcggattt aatcgcttcg ttggcggatt tgtatgccaa gctgccggat 300

tatgatgcag ttttgtacgg cagggcgcgg gctttgctgg cgaaattggc gggaaggtcg 360

gcggaggcgg tggtgcggta tcggaagctg cacggggaaa atgcggcaga cgagcggatt 420

ttgctggatt tggcggcggc ggagtttgac gatttccggc tgaagtcggc agaaaggcat 480

tttgccgagg cggaaaaatt ggatttgccg ccgccggttt tggaaaatgt ggggcgtttt 540

cggaaaaaag cggaggggct gacgggctgg cgtttttcgg gcggtatcag cccagcggtc 600

aatcaaaacg ccaataatgc cgcgccgcaa tattgccggc aagacggagg cagtcagata 660

tgcagtgtca gccgggcgga gcgggcggca gggttgaatt atgaaatcga ggcggaaaaa 720

ctgacggcgt tggcggataa tcattatttg ttgttccgtt ccaatatcgg cggcacgagc 780

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cagtataaaa atgcacggca gacggcgggg attttgccgt tttatcaggt gcagttgtcg 900

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tacaataacg gtcggcagga cgggttttat gtttcgtcgg caaaacgttt gggcgaatcg 1140

gcaactgtgt tcggcggctg gcagtttgtg cggtttgtgc cgaaacgcga aacggtgggc 1200

ggcgcggtca ataatgccgc ctaccggcgc aacggtgttt atgccggctg ggcgcaggag 1260

tggcggcagt tgggcggttt gaacagtcgg gtttccgcgt cttatgcccg ccgcaactat 1320

aagggcgttg cggctttctc gacagaggcg caacgcaacc gcgaatggaa tgtctcgctg 1380

gctttgagcc acgacaagtt gtcgtacaaa ggtatcgtgc cggcgttaaa ttatcgtttc 1440

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gcggattggc ggttttga 1518

<210> 406

<211> 505

<212> PRT

<213> N. polysaccharea SLAM 2

<400> 406

Met Leu Tyr Phe Arg Tyr Gly Phe Leu Val Val Trp Cys Ala Ala Gly

1 5 10 15

Val Ser Ala Ala Tyr Gly Ala Asp Ala Pro Ala Ile Leu Asp Asp Lys

20 25 30

Ala Leu Leu Gln Val Gln Arg Ser Val Ser Asp Lys Trp Ala Glu Ser

35 40 45

Asp Trp Lys Val Glu Asn Asp Ala Pro Arg Val Val Asp Gly Asp Phe

50 55 60

Leu Leu Ala His Pro Lys Met Leu Glu His Ser Leu Arg Asp Ala Leu

65 70 75 80

Asn Gly Asn Gln Ala Asp Leu Ile Ala Ser Leu Ala Asp Leu Tyr Ala

85 90 95

Lys Leu Pro Asp Tyr Asp Ala Val Leu Tyr Gly Arg Ala Arg Ala Leu

100 105 110

Leu Ala Lys Leu Ala Gly Arg Ser Ala Glu Ala Val Val Arg Tyr Arg

115 120 125

Lys Leu His Gly Glu Asn Ala Ala Asp Glu Arg Ile Leu Leu Asp Leu

130 135 140

Ala Ala Ala Glu Phe Asp Asp Phe Arg Leu Lys Ser Ala Glu Arg His

145 150 155 160

Phe Ala Glu Ala Glu Lys Leu Asp Leu Pro Pro Pro Val Leu Glu Asn

165 170 175

Val Gly Arg Phe Arg Lys Lys Ala Glu Gly Leu Thr Gly Trp Arg Phe

180 185 190

Ser Gly Gly Ile Ser Pro Ala Val Asn Gln Asn Ala Asn Asn Ala Ala

195 200 205

Pro Gln Tyr Cys Arg Gln Asp Gly Gly Ser Gln Ile Cys Ser Val Ser

210 215 220

Arg Ala Glu Arg Ala Ala Gly Leu Asn Tyr Glu Ile Glu Ala Glu Lys

225 230 235 240

Leu Thr Ala Leu Ala Asp Asn His Tyr Leu Leu Phe Arg Ser Asn Ile

245 250 255

Gly Gly Thr Ser Tyr Tyr Phe Ser Lys Lys Ser Ala Tyr Asp Asp Gly

260 265 270

Phe Gly Arg Ala Tyr Leu Gly Trp Gln Tyr Lys Asn Ala Arg Gln Thr

275 280 285

Ala Gly Ile Leu Pro Phe Tyr Gln Val Gln Leu Ser Gly Ser Asp Gly

290 295 300

Phe Asp Ala Lys Thr Lys Arg Val Asn Asn Arg Arg Leu Pro Pro Tyr

305 310 315 320

Met Leu Ala His Gly Val Gly Val Gln Leu Ser His Thr Tyr Arg Pro

325 330 335

Asn Pro Gly Trp Gln Phe Ser Val Ala Leu Glu His Tyr Arg Gln Cys

340 345 350

Tyr Arg Glu Gln Asp Arg Ala Glu Tyr Asn Asn Gly Arg Gln Asp Gly

355 360 365

Phe Tyr Val Ser Ser Ala Lys Arg Leu Gly Glu Ser Ala Thr Val Phe

370 375 380

Gly Gly Trp Gln Phe Val Arg Phe Val Pro Lys Arg Glu Thr Val Gly

385 390 395 400

Gly Ala Val Asn Asn Ala Ala Tyr Arg Arg Asn Gly Val Tyr Ala Gly

405 410 415

Trp Ala Gln Glu Trp Arg Gln Leu Gly Gly Leu Asn Ser Arg Val Ser

420 425 430

Ala Ser Tyr Ala Arg Arg Asn Tyr Lys Gly Val Ala Ala Phe Ser Thr

435 440 445

Glu Ala Gln Arg Asn Arg Glu Trp Asn Val Ser Leu Ala Leu Ser His

450 455 460

Asp Lys Leu Ser Tyr Lys Gly Ile Val Pro Ala Leu Asn Tyr Arg Phe

465 470 475 480

Gly Arg Thr Glu Ser Asn Val Pro Tyr Ala Lys Arg Arg Asn Ser Glu

485 490 495

Val Phe Val Ser Ala Asp Trp Arg Phe

500 505

<210> 407

<211> 1668

<212> DNA

<213> N. polysaccharea SLAM 3

<400> 407

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gtgcctgccg aaaggcttga aaggtctggc gaaacagaaa tgccggttct gccgcttgct 180

tcctatgccc catcttttga cgaacagatc gacaatgcct tccgcctgtt acagcgtgcc 240

gcgccgaagc gggctgccgc gcctgttgtt gctcctgccg gagagtcgga agagaccgaa 300

atcaagcctg tggcaacaca taagaagttt tccaacgagg cggctttcgg tacgggtgcg 360

tccgtgccgt ctgaaaccct tgcagccgga gaagccgccg aagccgtttc agacggcaat 420

gcctctcttg cgggtttgga agagcagatc aaccgcgccg tcgtcgcccg tgattgggac 480

acgctgcaaa cgctgctgga aagctaccgc gccctgccgg atttcaatcc ggttctgcac 540

gattacgcgc tgggcggttt gcgccgcagc cagttgcgcc ataacgaggc ggtggctttg 600

tatcgcggca ttttggcgca acagcccgat ttggcgtatc cgcgtttcga tttgggcgtg 660

atgctgtttg aaaacaaaca gtaccgcgag gcgaaggcgg aattggatcg ggcgaaaccc 720

gatttgcagc cgccgatgca gcagcttgcc gaccgctatc ttgccgccat agacaaggct 780

caaggctgga agcccgatgt gtcgctgcaa tacgaacaaa cggacaatgt gaacaacgct 840

tcatccgaaa aaacgattga atttgcaggc agaagctgga cgaaaaccgc cgacagcctg 900

ccgcaaaagg cacacggttt gcgctacggc ttgggcgtgt cgcgcgaaat caatgcgggc 960

gggcatcatt tcctctacgg cgacatcagc ggcggcggcg tgcactattg ggataacaaa 1020

gatttcagcg aacagagcct gcgcctgtcg ctcggctata aaaaccgttc agtaacgcgc 1080

tcgttcggca tcgtgccgtt tatcgagcaa aacctcttag gcggcagccg atacaatttc 1140

gtcggcggct tcaatgccga tttctcccaa cgcttgagcg aacgctggcg gttgacgctg 1200

aacgcgggca atatgtggaa gcgttatcag gaagaccgca ccgccgcccg atacgacagc 1260

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cgctataccc gcaggacgtt tgacgcaccc gggaccattg tgtaccgctt cccgcgcaaa 1500

gaccgcgaat atcaggcaaa cctgtcgttg tggcacgaca aaatctcttg gaagggattt 1560

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cgcaaaaaca cgcagatttt catgagtgtg gaaaaggatt tcaaataa 1668

<210> 408

<211> 555

<212> PRT

<213> N. polysaccharea SLAM 3

<400> 408

Met Lys Lys Phe Ala Leu Leu Leu Leu Ser Val Pro Thr Ala Ala Val

1 5 10 15

Ser Glu Thr Pro Val Leu Pro Ile Pro Val Ser Lys Gln Val Phe Val

20 25 30

Asp Gly Lys Phe Asp Asp Arg Ile Val Pro Ala Glu Arg Leu Glu Arg

35 40 45

Ser Gly Glu Thr Glu Met Pro Val Leu Pro Leu Ala Ser Tyr Ala Pro

50 55 60

Ser Phe Asp Glu Gln Ile Asp Asn Ala Phe Arg Leu Leu Gln Arg Ala

65 70 75 80

Ala Pro Lys Arg Ala Ala Ala Pro Val Val Ala Pro Ala Gly Glu Ser

85 90 95

Glu Glu Thr Glu Ile Lys Pro Val Ala Thr His Lys Lys Phe Ser Asn

100 105 110

Glu Ala Ala Phe Gly Thr Gly Ala Ser Val Pro Ser Glu Thr Leu Ala

115 120 125

Ala Gly Glu Ala Ala Glu Ala Val Ser Asp Gly Asn Ala Ser Leu Ala

130 135 140

Gly Leu Glu Glu Gln Ile Asn Arg Ala Val Val Ala Arg Asp Trp Asp

145 150 155 160

Thr Leu Gln Thr Leu Leu Glu Ser Tyr Arg Ala Leu Pro Asp Phe Asn

165 170 175

Pro Val Leu His Asp Tyr Ala Leu Gly Gly Leu Arg Arg Ser Gln Leu

180 185 190

Arg His Asn Glu Ala Val Ala Leu Tyr Arg Gly Ile Leu Ala Gln Gln

195 200 205

Pro Asp Leu Ala Tyr Pro Arg Phe Asp Leu Gly Val Met Leu Phe Glu

210 215 220

Asn Lys Gln Tyr Arg Glu Ala Lys Ala Glu Leu Asp Arg Ala Lys Pro

225 230 235 240

Asp Leu Gln Pro Pro Met Gln Gln Leu Ala Asp Arg Tyr Leu Ala Ala

245 250 255

Ile Asp Lys Ala Gln Gly Trp Lys Pro Asp Val Ser Leu Gln Tyr Glu

260 265 270

Gln Thr Asp Asn Val Asn Asn Ala Ser Ser Glu Lys Thr Ile Glu Phe

275 280 285

Ala Gly Arg Ser Trp Thr Lys Thr Ala Asp Ser Leu Pro Gln Lys Ala

290 295 300

His Gly Leu Arg Tyr Gly Leu Gly Val Ser Arg Glu Ile Asn Ala Gly

305 310 315 320

Gly His His Phe Leu Tyr Gly Asp Ile Ser Gly Gly Gly Val His Tyr

325 330 335

Trp Asp Asn Lys Asp Phe Ser Glu Gln Ser Leu Arg Leu Ser Leu Gly

340 345 350

Tyr Lys Asn Arg Ser Val Thr Arg Ser Phe Gly Ile Val Pro Phe Ile

355 360 365

Glu Gln Asn Leu Leu Gly Gly Ser Arg Tyr Asn Phe Val Gly Gly Phe

370 375 380

Asn Ala Asp Phe Ser Gln Arg Leu Ser Glu Arg Trp Arg Leu Thr Leu

385 390 395 400

Asn Ala Gly Asn Met Trp Lys Arg Tyr Gln Glu Asp Arg Thr Ala Ala

405 410 415

Arg Tyr Asp Ser His Met Pro Leu Ala Gly Ala Thr Leu Met Tyr Ser

420 425 430

Ala Pro Lys Asp Trp Leu Leu Tyr Gly Gly Ala Asp Trp Ser His Asp

435 440 445

Leu Thr Lys Glu Ala Glu Gln Ala Ser Ile Arg Lys Gly Leu Arg Val

450 455 460

Gly Ala Val Lys Thr Phe Asp Gly Gly Leu Gly Leu Arg Ala Asn Leu

465 470 475 480

Arg Tyr Thr Arg Arg Thr Phe Asp Ala Pro Gly Thr Ile Val Tyr Arg

485 490 495

Phe Pro Arg Lys Asp Arg Glu Tyr Gln Ala Asn Leu Ser Leu Trp His

500 505 510

Asp Lys Ile Ser Trp Lys Gly Phe Thr Pro Gln Leu Asn Phe Arg Tyr

515 520 525

Leu Lys Ile Asp Ser Asn Met Lys Ser Phe Tyr Thr Arg Lys Asn Thr

530 535 540

Gln Ile Phe Met Ser Val Glu Lys Asp Phe Lys

545 550 555

<210> 409

<211> 1518

<212> DNA

<213> N. resinovorum SLAM 1

<400> 409

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accaggctgc gccttgatca ggagttgcag gggcaggagc gcaagacaga gtcccggctt 180

ctcgaagatg ccgacgcgct ggacgggccc ccgacgtcgc tggaaatcga cggcaagact 240

tacgcggtcg gcgataatgt cgatgagatg ggacaggccc tctatattgc gatccggcgc 300

cgcatatgga gcgaggctcg ccgttttctg acggcctatg agggatacac agatcgtgat 360

cccaaactcg tgcttttcgc caagggcgcg cttgcgcgcc aggatcgcaa gctgggtgaa 420

gccgaacggc attatcgtgc actggtggag ctcgaccccg atctcatgtc gggccaacta 480

gaactggcgc gggtcttgtt cgaaaaccgc aaggaccgtg aagcgcagga cgccttccgg 540

caggtgcgcg aacgcctggt tgtcgatggc gacagatcga cgggggtggt ccgtaccgta 600

gacgcctttc tcctggcgtt gagacagcgg cggggctggc aaggcaatat cgccataggc 660

cccagctaca gcaccaatct caatcaatcg tccgaaagct acacctgcct gctggcgacc 720

agcgacggca cttgcctgtt cgaccggcag ttgcccgatg cggtaaaggc catggggatc 780

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gcgcgcttcc ccggtttcgc tttcgccggg ctgacgcctg aggttgtgtt ccagcacaat 1440

cgcgtcgaaa gcaacatcga ctggctctat tcctacaagc gcaccaccgc cagcgtgagg 1500

ctgagccgtg cgttctag 1518

<210> 410

<211> 505

<212> PRT

<213> N. resinovorum SLAM 1

<400> 410

Met Pro Ile Leu Asn Phe Ala Ile Ala Ser Arg Cys Arg Thr Gly Leu

1 5 10 15

Thr Thr Leu Leu Cys Ala Ala Ala Pro Cys Val Ser Val Pro Val Leu

20 25 30

Ala Gln Ser Thr Ala Glu Gln Asp Thr Arg Leu Arg Leu Asp Gln Glu

35 40 45

Leu Gln Gly Gln Glu Arg Lys Thr Glu Ser Arg Leu Leu Glu Asp Ala

50 55 60

Asp Ala Leu Asp Gly Pro Pro Thr Ser Leu Glu Ile Asp Gly Lys Thr

65 70 75 80

Tyr Ala Val Gly Asp Asn Val Asp Glu Met Gly Gln Ala Leu Tyr Ile

85 90 95

Ala Ile Arg Arg Arg Ile Trp Ser Glu Ala Arg Arg Phe Leu Thr Ala

100 105 110

Tyr Glu Gly Tyr Thr Asp Arg Asp Pro Lys Leu Val Leu Phe Ala Lys

115 120 125

Gly Ala Leu Ala Arg Gln Asp Arg Lys Leu Gly Glu Ala Glu Arg His

130 135 140

Tyr Arg Ala Leu Val Glu Leu Asp Pro Asp Leu Met Ser Gly Gln Leu

145 150 155 160

Glu Leu Ala Arg Val Leu Phe Glu Asn Arg Lys Asp Arg Glu Ala Gln

165 170 175

Asp Ala Phe Arg Gln Val Arg Glu Arg Leu Val Val Asp Gly Asp Arg

180 185 190

Ser Thr Gly Val Val Arg Thr Val Asp Ala Phe Leu Leu Ala Leu Arg

195 200 205

Gln Arg Arg Gly Trp Gln Gly Asn Ile Ala Ile Gly Pro Ser Tyr Ser

210 215 220

Thr Asn Leu Asn Gln Ser Ser Glu Ser Tyr Thr Cys Leu Leu Ala Thr

225 230 235 240

Ser Asp Gly Thr Cys Leu Phe Asp Arg Gln Leu Pro Asp Ala Val Lys

245 250 255

Ala Met Gly Ile Ser Phe Glu Gly Ser Leu Asn Arg Ser Ile Pro Ile

260 265 270

Ser Gly His His Gly Leu Arg Ala Arg Ala Leu Leu Phe Gly Asp Val

275 280 285

Tyr Pro Ser Glu His Glu Tyr Ser Gln Ala Ser Leu Ile Met Arg Leu

290 295 300

Gly Tyr Gln Tyr Gln Ser Ala Arg Asp Thr Phe Ser Leu Ser Pro Ser

305 310 315 320

Phe Asp Ile Gly Thr Leu Gly Ser Ser Val Leu Tyr Asp Ala Trp Gly

325 330 335

Ala Asn Ala Glu Trp Gln His Thr Leu Ser Arg Lys Val Leu Leu Arg

340 345 350

Leu Glu Gly Asn Tyr Arg Asp Tyr Arg Tyr Arg Gln Arg Gly Phe Ser

355 360 365

Ser Gln Asp Gly Pro Leu Ile Asp Thr Ser Leu Thr Ala Trp Tyr Thr

370 375 380

Pro Ala Pro Gly Trp Thr Val Phe Gly Gly Pro Asp Leu Ala Val Lys
385 390 395 400
Asp Thr Pro Ala Ala Thr Asn Ala Tyr Arg Gln Trp Gly Gly Arg Leu

405 410 415
Gly Ile Gly Arg Thr Leu Gly Lys Ser Ala Ser Leu Leu Leu Leu Gly
420 425 430
Ser Tyr Arg His Arg Asp Asn Arg Ala Tyr Ser Ala Val Phe Ala Ala
435 440 445
Lys Arg Ser Asp Asp Gln Phe Asn Ala Thr Ala Ile Ala Arg Phe Pro
450 455 460
Gly Phe Ala Phe Ala Gly Leu Thr Pro Glu Val Val Phe Gln His Asn

465 470 475 480
Arg Val Glu Ser Asn Ile Asp Trp Leu Tyr Ser Tyr Lys Arg Thr Thr
485 490 495
Ala Ser Val Arg Leu Ser Arg Ala Phe
500 505

<210> 411
<211> 1407
<212> DNA
<213> N. rosorum SLAM 1
<400> 411
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caactgaagc atcagtacaa atggaatcag cgctggcaat cagcactgaa ttttaatcat 960

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cattttgaag ggaagcatta tctttatggc tatccacgtc aggatcggga atatcagtca 1260

ttgatctcaa tctggcatga aaaaataagc tggaagggaa tcttgccgaa actgaatttc 1320

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<210> 412

<211> 468

<212> PRT

<213> N. rosorum SLAM 1

<400> 412

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1 5 10 15

Ala Ala Asn Val Pro Ile Gln Asn Arg Asp Pro Ile Ser Phe Glu Gln

20 25 30

Ser Ala Val Asp Ile Lys Gln Phe Ser Ser Met Ala Phe Asp Asp Asn

35 40 45

Thr Lys Lys Asp Ile Ser Pro Val Leu Thr Val Ser Asp Thr Asn Gln

50 55 60

Gln Ile Asn Gln Ala Ile Leu Leu Lys Gln Trp Asp Val Leu Ala Ala

65 70 75 80

Leu Leu Ser Asp Tyr Pro Asp Gln Ala Gln Phe Asp Pro Ile Leu Tyr

85 90 95

His Tyr Ala Ala Ala Ala Leu Ser Tyr Ala Lys Gly Gln His Gly Asp

100 105 110

Ala Ile Tyr His Tyr Glu Gln Val Leu Ser Leu Asp Pro Ser Leu Thr

115 120 125

Tyr Ser Arg Phe Asp Leu Ala Leu Ile Leu Phe Glu Asp Lys Gln Phe

130 135 140

Asp Ala Ala Arg Gln Gln Phe Gln Leu Ala Tyr Gly Arg Leu Asp Pro

145 150 155 160

Gln Met Arg Thr Val Thr Gln Ser Tyr Leu Gln Ala Ile Asp Glu Ala

165 170 175

Gln Ser Trp Arg Thr Asp Phe Tyr Leu Gln Tyr Thr Gln Thr Ser Asn

180 185 190

Val Asn Asn Val Ser Pro Ser Arg Val Val Asn Ile Asn Gly Arg Gln

195 200 205

Phe Ile Lys Ser Glu Asp Ser Leu Pro Gln Ser Ala His Gly Phe Asn

210 215 220

Tyr Gly Met Asp Ile Glu Arg Asp Ile Asn Leu His Gly His His Phe

225 230 235 240

Leu Ser Ser Ala Val Lys Phe Gly Gly Val Tyr Tyr Trp Asp Asn Gln

245 250 255

Glu Tyr Asn Glu Gln Thr Leu His Phe Ala Leu Gly Tyr Arg Tyr Lys

260 265 270

Asn Ala Arg Gln Thr Phe Gly Val Leu Pro Phe Ala Glu Gln Asn Trp

275 280 285

Phe Gly His Ser Arg Tyr Asn Lys Gln Phe Gly Val Gln Leu Lys His

290 295 300

Gln Tyr Lys Trp Asn Gln Arg Trp Gln Ser Ala Leu Asn Phe Asn His

305 310 315 320

Tyr Tyr Lys Arg Tyr Arg Asp Glu Leu Thr Ala Trp Arg Tyr Asn Ser

325 330 335

Trp Gln Asn Glu Ala Thr Gly Leu Leu Phe Trp Gln Pro Thr Gly His

340 345 350

Trp Arg Leu Phe Gly Gly Leu Glu Leu Asn Arg Glu Asn Thr Lys Glu

355 360 365

Lys Ala Leu Ser Ser His Lys Ile Gly Gly Ile Gly Gly Leu Val Tyr

370 375 380

Gln Ala Pro Leu Trp Gly Gly Met Met Thr Leu Arg Tyr Ser Glu Arg

385 390 395 400

His Phe Glu Gly Lys His Tyr Leu Tyr Gly Tyr Pro Arg Gln Asp Arg

405 410 415

Glu Tyr Gln Ser Leu Ile Ser Ile Trp His Glu Lys Ile Ser Trp Lys

420 425 430

Gly Ile Leu Pro Lys Leu Asn Phe Lys Trp Gln Lys Ile Asp Ser Asn

435 440 445

Ile Pro Asp Phe Tyr Ser Arg Thr Asn Lys Ser Met Phe Ile Thr Leu

450 455 460

Glu Lys Arg Phe

465

<210> 413

<211> 1494

<212> DNA

<213> N. rosorum SLAM 2

<400> 413

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gcccttcagc tctggcagca gcataagcaa gccagccggc agcaacaacg agaaagccgg 180

gttgatcagc cgatcgccga agccgcacac gaaatgatct ttgacggcca atcgatcacg 240

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cagcgctatc gcgagctgct gcgggcggat ccgaccttta tccgcgctca gctcgatctg 480

gcgcgcgtgc tgttcgaaaa taaaaaaacg cgggaatcca ccgcactttt tgagaatctg 540

gcaaggctgg atctgccggc tgaagtccgt gacagcgtcg acggctatcg tcaggcatta 600

agcctgcggg aaaaatggca gctgtctttc gctctgggct atcagtacgc caccaatatc 660

aaccagtctt cccgacgcag cctgtgcgcg ctgtatctgg gcgagatctg ttccgcccga 720

ttcacttcgc ccgacgccat aaatgcgcag ggctggcgct atgatctcag tgtacggaag 780

caaaccgctt tatccggtca tcacgggata atattttatc tcaacagcta cggttatttt 840

tatccccatg ccaaggatta tgccgaagat aacagcaaag tttatgtcgg ttatcagtac 900

caaaatcagc acaccgaact gacccttgcg ccgttgttcg aatataaccg gctgggcaac 960

cgcacttatt cgcgggcatg gggcgtacag cttgccttaa gccggcaaat ggccgcccgc 1020

cattggctga atttgcagtt cgaacagaaa aaactgcgct tttccccgca ctataatgcg 1080

ctgcgtcatg cggatcagag cgcgctgtat gccacttggt attatgccgc cggcgcacaa 1140

accactttat tcggcgggct ggactggcaa tatcggcaca cccgatatca cgacgacaac 1200

tttcatatgt acggcgttcg tttaggcctt aaccggcaat ttgatttcgg gctggacgcc 1260

accctgctgg cgttattgcg ccgttatgat tatcaaggtt tcaacgcggc actcaaccga 1320

acccgacacg ataaacagca ggtttatctg gcgatcctta aaatgccgtc gtggcaattt 1380

tacggcgcaa cgccgagcct gttgctgaaa cgcaccgaca accgcagtaa cgtggattgg 1440

ctgtatgctt ataaacagaa tgaaattcaa ctgaatatcg aatggcaatt ttaa 1494

<210> 414

<211> 480

<212> PRT

<213> N. rosorum SLAM 2

<400> 414

Met Leu Leu Leu Leu Leu Pro Ala Tyr Thr Ala Gln Tyr Ala Ala Ala
1 5 10 15

Gln Val Gln Asn Asn His Asp Ala Leu Gln Leu Trp Gln Gln His Lys
20 25 30

Gln Ala Ser Arg Gln Gln Gln Arg Glu Ser Arg Val Asp Gln Pro Ile
35 40 45

Ala Glu Ala Ala His Glu Met Ile Phe Asp Gly Gln Ser Ile Thr Ile
50 55 60

Asp Asn Thr Ala Glu Ala Val Gly Gln Ala Leu Phe Ile Ala Leu Asn
65 70 75 80

Gln Gln Leu Trp Asp Tyr Ala Gln Thr Phe Leu Arg His Tyr Lys Thr
85 90 95

Phe Asp Asp His Asn Leu Glu Leu Val Leu Phe Ala Glu Ala Ala Leu
100 105 110

Ala Arg Gln His Gly Asp Leu Asn Arg Ala Glu Gln Arg Tyr Arg Glu
115 120 125
Leu Leu Arg Ala Asp Pro Thr Phe Ile Arg Ala Gln Leu Asp Leu Ala
130 135 140
Arg Val Leu Phe Glu Asn Lys Lys Thr Arg Glu Ser Thr Ala Leu Phe
145 150 155 160
Glu Asn Leu Ala Arg Leu Asp Leu Pro Ala Glu Val Arg Asp Ser Val
165 170 175

Asp Gly Tyr Arg Gln Ala Leu Ser Leu Arg Glu Lys Trp Gln Leu Ser
180 185 190
Phe Ala Leu Gly Tyr Gln Tyr Ala Thr Asn Ile Asn Gln Ser Ser Arg
195 200 205
Arg Ser Leu Cys Ala Leu Tyr Leu Gly Glu Ile Cys Ser Ala Arg Phe
210 215 220
Thr Ser Pro Asp Ala Ile Asn Ala Gln Gly Trp Arg Tyr Asp Leu Ser
225 230 235 240

Val Arg Lys Gln Thr Ala Leu Ser Gly His His Gly Ile Ile Phe Tyr
245 250 255
Leu Asn Ser Tyr Gly Tyr Phe Tyr Pro His Ala Lys Asp Tyr Ala Glu
260 265 270
Asp Asn Ser Lys Val Tyr Val Gly Tyr Gln Tyr Gln Asn Gln His Thr
275 280 285
Glu Leu Thr Leu Ala Pro Leu Phe Glu Tyr Asn Arg Leu Gly Asn Arg
290 295 300

Thr Tyr Ser Arg Ala Trp Gly Val Gln Leu Ala Leu Ser Arg Gln Met
305 310 315 320
Ala Ala Arg His Trp Leu Asn Leu Gln Phe Glu Gln Lys Lys Leu Arg
325 330 335
Phe Ser Pro His Tyr Asn Ala Leu Arg His Ala Asp Gln Ser Ala Leu

340 345 350

Tyr Ala Thr Trp Tyr Tyr Ala Ala Gly Ala Gln Thr Thr Leu Phe Gly

355 360 365

Gly Leu Asp Trp Gln Tyr Arg His Thr Arg Tyr His Asp Asp Asn Phe

370 375 380

His Met Tyr Gly Val Arg Leu Gly Leu Asn Arg Gln Phe Asp Phe Gly

385 390 395 400

Leu Asp Ala Thr Leu Leu Ala Leu Leu Arg Arg Tyr Asp Tyr Gln Gly

405 410 415

Phe Asn Ala Ala Leu Asn Arg Thr Arg His Asp Lys Gln Gln Val Tyr

420 425 430

Leu Ala Ile Leu Lys Met Pro Ser Trp Gln Phe Tyr Gly Ala Thr Pro

435 440 445

Ser Leu Leu Leu Lys Arg Thr Asp Asn Arg Ser Asn Val Asp Trp Leu

450 455 460

Tyr Ala Tyr Lys Gln Asn Glu Ile Gln Leu Asn Ile Glu Trp Gln Phe

465 470 475 480

<210> 415

<211> 1443

<212> DNA

<213> N. shayeganii SLAM 1

<400> 415

atgtctttac accttccccg cctatccctg ttcggctgta tctgcctgct ccccgccctg 60

ctgtacgccc aaacgccgcc ggccctgcct aggccgcaac cggaaacccg tttcgacatc 120

agccccgaaa tccgttccga cgcaccgcct gccgcacaca ctacaggtag cccggaccct 180

caacagccgc tcaacatcag ccccgaagag ctgctgcaaa accctgagtt gctgcatcgc 240

gccctgcagt cttccgtact gctcaacaac ctcgaaggcg tgcgtctgct gctgccgctc 300

taccgccagc tgcccccgcc gcacgaagaa atgctgctgg tgctggccga tgccatgatc 360

gcccgtgcag atggaaaata caatcaagcc gttaccgcct accgccgggc cctttcgctg 420

gagccggata tgcccgccgt gcgcctgtcg ctggcgcaat ccctgtttga aaaccacgaa 480

aacgaagccg cccgcgacca attcacccgc ctgcgcgccg acggacaact gccgcccgaa 540

atccgccaac tggtcgacca ttacctcacc gccctcgatc aacgcaacac ttggtctttc 600

tacggcagcc tccactatct gcgcgacggc aacatcaaca atgcccccgc caaccgcacc 660

ttccgcaccg ccaacggcga attcaccttc cccgaacccg aatccgcaga aggcctggcc 720

taccgcctcg gcggcgcacg cgactggctg ctgggcggcc attggtcgct gcgtaccgct 780

gccgacgctt ccggcaaatg gtattggaac aaccgcccat acgatgacgc ctcagcccgc 840

ctgaccgttg gcggcgccta caaaaccgcc cgcgccgaag ccgccctgct gccctatttc 900

gaacgccgct ggttcggcaa ccgcgcctat ttgcgcgaag ccggcctgcg cgccgaatgg 960

cgctactggc tcgcacccgg ccaccagctt ctgctggccg gcgaatgggg gcagcagcag 1020

cacgaccgcc gcacctttct cgacggcccc aaccgcaatg tttccgccac ttggctgtat 1080

attcaaaacc cgcgccaata ctggattttg ggcacagact acgcccgcaa gagcgcccgc 1140

gaccgcagcg acacctatca gcgcaacagc ctgcgtgccg gctggaccag ggaatggtcg 1200

tacggcctct ccaccgccct cacggccgaa gccggcttgc gccgatacga cggcccggat 1260

ttcctcaaca tccgccgaga agacaaagaa tacgccgcca gcctgtctgt ctggcaccgc 1320

cgcgtccact tctggggcat cacccccgc ttggtgggca cctggcaaaa gagcgacagc 1380

aaccacccgc tttaccgttt ccaaaaaagc aatctgttta tccaaatcgg caaaaccttt 1440

tag 1443

<210> 416

<211> 480

<212> PRT

<213> N. shayeganii SLAM 1

<400> 416

Met Ser Leu His Leu Pro Arg Leu Ser Leu Phe Gly Cys Ile Cys Leu
1 5 10 15

Leu Pro Ala Leu Leu Tyr Ala Gln Thr Pro Pro Ala Leu Pro Arg Pro
20 25 30

Gln Pro Glu Thr Arg Phe Asp Ile Ser Pro Glu Ile Arg Ser Asp Ala
35 40 45

Pro Pro Ala Ala His Thr Thr Gly Ser Pro Asp Pro Gln Gln Pro Leu
50 55 60

Asn Ile Ser Pro Glu Glu Leu Leu Gln Asn Pro Glu Leu Leu His Arg
65 70 75 80

Ala Leu Gln Ser Ser Val Leu Leu Asn Asn Leu Glu Gly Val Arg Leu

85 90 95

Leu Leu Pro Leu Tyr Arg Gln Leu Pro Pro Pro His Glu Glu Met Leu
100 105 110
Leu Val Leu Ala Asp Ala Met Ile Ala Arg Ala Asp Gly Lys Tyr Asn
115 120 125
Gln Ala Val Thr Ala Tyr Arg Arg Ala Leu Ser Leu Glu Pro Asp Met
130 135 140
Pro Ala Val Arg Leu Ser Leu Ala Gln Ser Leu Phe Glu Asn His Glu
145 150 155 160

Asn Glu Ala Ala Arg Asp Gln Phe Thr Arg Leu Arg Ala Asp Gly Gln
165 170 175
Leu Pro Pro Glu Ile Arg Gln Leu Val Asp His Tyr Leu Thr Ala Leu
180 185 190
Asp Gln Arg Asn Thr Trp Ser Phe Tyr Gly Ser Leu His Tyr Leu Arg
195 200 205
Asp Gly Asn Ile Asn Asn Ala Pro Ala Asn Arg Thr Phe Arg Thr Ala
210 215 220

Asn Gly Glu Phe Thr Phe Pro Glu Pro Glu Ser Ala Glu Gly Leu Ala
225 230 235 240
Tyr Arg Leu Gly Gly Ala Arg Asp Trp Leu Leu Gly Gly His Trp Ser
245 250 255
Leu Arg Thr Ala Ala Asp Ala Ser Gly Lys Trp Tyr Trp Asn Asn Arg
260 265 270
Pro Tyr Asp Asp Ala Ser Ala Arg Leu Thr Val Gly Gly Ala Tyr Lys
275 280 285

Thr Ala Arg Ala Glu Ala Ala Leu Leu Pro Tyr Phe Glu Arg Arg Trp
290 295 300
Phe Gly Asn Arg Ala Tyr Leu Arg Glu Ala Gly Leu Arg Ala Glu Trp
305 310 315 320
Arg Tyr Trp Leu Ala Pro Gly His Gln Leu Leu Leu Ala Gly Glu Trp
325 330 335

Gly Gln Gln Gln His Asp Arg Arg Thr Phe Leu Asp Gly Pro Asn Arg
340 345 350

Asn Val Ser Ala Thr Trp Leu Tyr Ile Gln Asn Pro Arg Gln Tyr Trp
355 360 365
Ile Leu Gly Thr Asp Tyr Ala Arg Lys Ser Ala Arg Asp Arg Ser Asp
370 375 380
Thr Tyr Gln Arg Asn Ser Leu Arg Ala Gly Trp Thr Arg Glu Trp Ser
385 390 395 400
Tyr Gly Leu Ser Thr Ala Leu Thr Ala Glu Ala Gly Leu Arg Arg Tyr
405 410 415

Asp Gly Pro Asp Phe Leu Asn Ile Arg Arg Glu Asp Lys Glu Tyr Ala
420 425 430
Ala Ser Leu Ser Val Trp His Arg Arg Val His Phe Trp Gly Ile Thr
435 440 445
Pro Arg Leu Val Gly Thr Trp Gln Lys Ser Asp Ser Asn His Pro Leu
450 455 460
Tyr Arg Phe Gln Lys Ser Asn Leu Phe Ile Gln Ile Gly Lys Thr Phe
465 470 475 480

<210> 417
<211> 1488
<212> DNA
<213> N. shayeganii SLAM 2
<400> 417
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gctgccgagg aaatccccgt attgagggcg gccgatttgg cccgctaccc gcaactgctg 180
acggaaatga tcgagtcggc gctggaccgg caacaccccg agctgttaaa cgagctgctg 240
ccggtctatg ccgccaccgt cagcgccgac gactatctac tccgacgcgc caccggcatg 300
gcggcgcgct tccgcagaga ctacgccgaa gcgattgccg tctaccaaca actggcgaca 360

gaaagaccgg cggatgtgcg agtgcgcttg gacttggcgg ccatgctggc cgaagacaag 420
caatggccgg aagcggaaaa gctgtttgca gaggtcaggc ggcaggaggg actgccgccc 480

caagtgggcg aaaacgtcca acactatctg aatgccgccg aataccggcg gcgttggcag 540

tgggacggcg gcgtttcgcc cgcattcaac gacaacatca ataatgcggc gagagagcat 600

tgcagcatca tcggctgcag ccgcgagcgc tcggaaaatg ccgccggcct ggcatacagc 660

atccgcgtca gccggcaagt gcccttggcc ggccaccaca atttgttttt cgaagcgcgc 720

gcagacggcc aaacccatta ttggagcaat aaatcggcct acgattgggg gcagggccgc 780

atcggtttgg gttggctgta tcaagatgcg cggcaagatt tgctgctcag tccgttttac 840

caaatcgatt tgagtggcag cgacaattgg ggcggcagca agccgcaaca gacacaaacc 900

ttcaatatgg atacttgggc gcacggctac ggcatcaggg cgcaatacca gcggcaactg 960

tctgcacgct ggcaagcctc gcttgccgcc gacatcaccc gccgccatta ccgccatgca 1020

ccgcaagcgg agcagcaaaa cggatggtac agcggccaga gtgccggcat ccactggcaa 1080

gccggcgccc gcgatgggct ttatggcggc atatttttca atcaagcctt ccccgagcaa 1140

cgcaccattc agggccgcgc caataatacg gcctaccgcc gctacggcct gcaagccggt 1200

tggatacacg actgggcttg gctgggcggt ctctccaccc gcgtttccgc ctctgtcgcc 1260

caacggcggt ttaaaggaga gtcgctcaac gtgaccgcgc aaggctttcc tttgcagcag 1320

cggcgcgacc gcgaatatca atatggtctc gcggtatggc atcgcgcttg gacaatctgg 1380

ggcatgacgc cgaagctgaa tctgtcgcgg caggaaatcc gcagcagcca cacttgggca 1440

cagcgtaaaa acagccaagt ctttatcgaa ctggaacggc ggttttaa 1488

<210> 418

<211> 495

<212> PRT

<213> N. shayeganii SLAM 2

<400> 418

Met Asn Lys Met Thr His Thr His Ser Ile Met Leu Gly Ala Leu Met

1 5 10 15

Ala Leu Leu Val Pro Ile Ser Ala Ala Ala Pro Thr Asp Ala Ala Ala

20 25 30

Pro Val Pro Asn Ala Asn Glu Thr Ala Ala Glu Glu Ile Pro Val Leu

35 40 45

Arg Ala Ala Asp Leu Ala Arg Tyr Pro Gln Leu Leu Thr Glu Met Ile

50 55 60

Glu Ser Ala Leu Asp Arg Gln His Pro Glu Leu Leu Asn Glu Leu Leu

65 70 75 80

Pro Val Tyr Ala Ala Thr Val Ser Ala Asp Asp Tyr Leu Leu Arg Arg

85 90 95

Ala Thr Gly Met Ala Ala Arg Phe Arg Arg Asp Tyr Ala Glu Ala Ile

100 105 110

Ala Val Tyr Gln Gln Leu Ala Thr Glu Arg Pro Ala Asp Val Arg Val

115 120 125

Arg Leu Asp Leu Ala Ala Met Leu Ala Glu Asp Lys Gln Trp Pro Glu

130 135 140

Ala Glu Lys Leu Phe Ala Glu Val Arg Arg Gln Glu Gly Leu Pro Pro

145 150 155 160

Gln Val Gly Glu Asn Val Gln His Tyr Leu Asn Ala Ala Glu Tyr Arg

165 170 175

Arg Arg Trp Gln Trp Asp Gly Gly Val Ser Pro Ala Phe Asn Asp Asn

180 185 190

Ile Asn Asn Ala Ala Arg Glu His Cys Ser Ile Ile Gly Cys Ser Arg

195 200 205

Glu Arg Ser Glu Asn Ala Ala Gly Leu Ala Tyr Ser Ile Arg Val Ser

210 215 220

Arg Gln Val Pro Leu Ala Gly His His Asn Leu Phe Phe Glu Ala Arg

225 230 235 240

Ala Asp Gly Gln Thr His Tyr Trp Ser Asn Lys Ser Ala Tyr Asp Trp

245 250 255

Gly Gln Gly Arg Ile Gly Leu Gly Trp Leu Tyr Gln Asp Ala Arg Gln

260 265 270

Asp Leu Leu Leu Ser Pro Phe Tyr Gln Ile Asp Leu Ser Gly Ser Asp

275 280 285

Asn Trp Gly Gly Ser Lys Pro Gln Gln Thr Gln Thr Phe Asn Met Asp

290 295 300

Thr Trp Ala His Gly Tyr Gly Ile Arg Ala Gln Tyr Gln Arg Gln Leu

305 310 315 320

Ser Ala Arg Trp Gln Ala Ser Leu Ala Ala Asp Ile Thr Arg Arg His

325 330 335

Tyr Arg His Ala Pro Gln Ala Glu Gln Gln Asn Gly Trp Tyr Ser Gly

340 345 350

Gln Ser Ala Gly Ile His Trp Gln Ala Gly Ala Arg Asp Gly Leu Tyr

355 360 365

Gly Gly Ile Phe Phe Asn Gln Ala Phe Pro Glu Gln Arg Thr Ile Gln

370 375 380

Gly Arg Ala Asn Asn Thr Ala Tyr Arg Arg Tyr Gly Leu Gln Ala Gly

385 390 395 400

Trp Ile His Asp Trp Ala Trp Leu Gly Gly Leu Ser Thr Arg Val Ser

405 410 415

Ala Ser Val Ala Gln Arg Arg Phe Lys Gly Glu Ser Leu Asn Val Thr

420 425 430

Ala Gln Gly Phe Pro Leu Gln Gln Arg Arg Asp Arg Glu Tyr Gln Tyr

435 440 445

Gly Leu Ala Val Trp His Arg Ala Trp Thr Ile Trp Gly Met Thr Pro

450 455 460

Lys Leu Asn Leu Ser Arg Gln Glu Ile Arg Ser Ser His Thr Trp Ala

465 470 475 480

Gln Arg Lys Asn Ser Gln Val Phe Ile Glu Leu Glu Arg Arg Phe

485 490 495

<210> 419

<211> 1515

<212> DNA

<213> N. sicca SLAM 1

<400> 419

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tgcgccattg caacccaaac gtcttacgaa atcatgaaaa cactcttact cctctccctg 120

ctcgccgtgt ccgcagcaga agccgccgac gtgccgtccg agcctcaaaa ccagcctgcc 180

cccgagttgc aggtcaaaac ggcagaacct gcccccgtcg aagaagcagc ggccaagcct 240

gctgccgaaa cgtcgtctga aaaagtcgtc aacgtcgatg ccaaaaccct gctcgacaat 300

ccccaattgc tttcccgcgc catgtattcc gccgttgtgt cgcgcaacat cgcgggcatc 360

aaagtcgtcc tgccgattta cgaacaatgg ccgggacacg ataaaaacat ggcgctctac 420

gcgcacggat tggttgccca agatgaaggc aaaatgaaag aagccatcgg gtattaccgt 480

caatttatcg ccgaaaaccc caatgccccc gtcgtccgct ggcagcttgc caccgctttg 540

tttgaagaca agcaaaacga agccgccgcc gaccagttcg acaaactcaa aacagaagcc 600

aacctgcccg agccgctcgt caaaggcatc gaatcctacc gcaaagcatt gcgcgagcgc 660

gattcgtgga aattcaatgc cggcttgagc gttacccgcg aacaaaacat caaccaagcg 720

cccagccgcc gcacatacgg caactggacc ttccccgagc ctatcgacgc taccgccatc 780

aactaccaac tcggcgcaga gaaaaaatgg tcgctgccca aaggctggta cgttacggca 840

ggcgcggaca attacggcaa aatttatccc gaacaaacca agtataacga cgtgaccacc 900

cgcttttcgg taggcgcagg ctacgccgac cagcgcaacg acatcggctt gaccccgttc 960

cacgaacgcc gcttctacgg caacgacccg tatacctact ccagcggtgc gcgcctgcac 1020

atcaaccgct ggtggcagcc taagctgcaa accttgagcg ccgttgaaat gggtcgtctg 1080

aaaaacaccc gccgcgcccg ttccgacagc aacaaccgcc tgttgagcaa ttccgtcgtc 1140

tattaccgaa acgcccgcca atactgggtc ggcggtttcg acatttatca ggaacgcaat 1200

aaagaagaca aatcggacag cttcgaccgt tacagcctcc gtaccgcatg ggggcaggaa 1260

tggggcaaag ggctgtccac catgttgcgg ctgagtgcgg cacaacgccg ttatcaaacg 1320

cccagccttt tgagcggtca ggaaaaccgc cgcgataaag aagcggatat ttctctcgcc 1380

gtgtggcacc gcgctttcca cttcaaaggc atcaccccgc gcctgaccgt cgcccaccac 1440

aaaacgtgga gcaacgacaa atactacgaa tacggcaaaa ccagaatgtt tgtcgaattc 1500

agcaaaacgt tctga 1515

<210> 420

<211> 504

<212> PRT

<213> N. sicca SLAM 2

<400> 420

Met Pro Glu Ser Thr Gln Met Leu Asp Met Val Ser Pro Gln Ile Lys

1 5 10 15

Asn Ala Asp Ser Cys Ala Ile Ala Thr Gln Thr Ser Tyr Glu Ile Met

20 25 30

Lys Thr Leu Leu Leu Leu Ser Leu Leu Ala Val Ser Ala Ala Glu Ala
35 40 45
Ala Asp Val Pro Ser Glu Pro Gln Asn Gln Pro Ala Pro Glu Leu Gln
50 55 60
Val Lys Thr Ala Glu Pro Ala Pro Val Glu Glu Ala Ala Ala Lys Pro
65 70 75 80
Ala Ala Glu Thr Ser Ser Glu Lys Val Val Asn Val Asp Ala Lys Thr
85 90 95

Leu Leu Asp Asn Pro Gln Leu Leu Ser Arg Ala Met Tyr Ser Ala Val
100 105 110
Val Ser Arg Asn Ile Ala Gly Ile Lys Val Val Leu Pro Ile Tyr Glu
115 120 125
Gln Trp Pro Gly His Asp Lys Asn Met Ala Leu Tyr Ala His Gly Leu
130 135 140
Val Ala Gln Asp Glu Gly Lys Met Lys Glu Ala Ile Gly Tyr Tyr Arg
145 150 155 160

Gln Phe Ile Ala Glu Asn Pro Asn Ala Pro Val Val Arg Trp Gln Leu
165 170 175
Ala Thr Ala Leu Phe Glu Asp Lys Gln Asn Glu Ala Ala Ala Asp Gln
180 185 190
Phe Asp Lys Leu Lys Thr Glu Ala Asn Leu Pro Glu Pro Leu Val Lys
195 200 205
Gly Ile Glu Ser Tyr Arg Lys Ala Leu Arg Glu Arg Asp Ser Trp Lys
210 215 220

Phe Asn Ala Gly Leu Ser Val Thr Arg Glu Gln Asn Ile Asn Gln Ala
225 230 235 240
Pro Ser Arg Arg Thr Tyr Gly Asn Trp Thr Phe Pro Glu Pro Ile Asp
245 250 255
Ala Thr Ala Ile Asn Tyr Gln Leu Gly Ala Glu Lys Lys Trp Ser Leu
260 265 270
Pro Lys Gly Trp Tyr Val Thr Ala Gly Ala Asp Asn Tyr Gly Lys Ile

275 280 285

Tyr Pro Glu Gln Thr Lys Tyr Asn Asp Val Thr Thr Arg Phe Ser Val
290 295 300
Gly Ala Gly Tyr Ala Asp Gln Arg Asn Asp Ile Gly Leu Thr Pro Phe
305 310 315 320
His Glu Arg Arg Phe Tyr Gly Asn Asp Pro Tyr Thr Tyr Ser Ser Gly
325 330 335
Ala Arg Leu His Ile Asn Arg Trp Trp Gln Pro Lys Leu Gln Thr Leu
340 345 350

Ser Ala Val Glu Met Gly Arg Leu Lys Asn Thr Arg Arg Ala Arg Ser
355 360 365
Asp Ser Asn Asn Arg Leu Leu Ser Asn Ser Val Val Tyr Tyr Arg Asn
370 375 380
Ala Arg Gln Tyr Trp Val Gly Gly Phe Asp Ile Tyr Gln Glu Arg Asn
385 390 395 400
Lys Glu Asp Lys Ser Asp Ser Phe Asp Arg Tyr Ser Leu Arg Thr Ala
405 410 415

Trp Gly Gln Glu Trp Gly Lys Gly Leu Ser Thr Met Leu Arg Leu Ser
420 425 430
Ala Ala Gln Arg Arg Tyr Gln Thr Pro Ser Leu Leu Ser Gly Gln Glu
435 440 445
Asn Arg Arg Asp Lys Glu Ala Asp Ile Ser Leu Ala Val Trp His Arg
450 455 460
Ala Phe His Phe Lys Gly Ile Thr Pro Arg Leu Thr Val Ala His His
465 470 475 480

Lys Thr Trp Ser Asn Asp Lys Tyr Tyr Glu Tyr Gly Lys Thr Arg Met
485 490 495
Phe Val Glu Phe Ser Lys Thr Phe
500

<210> 421
<211> 1464

<212> DNA

<213> N. sicca SLAM 2

<400> 421

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gaaacaattg ctaaccctga aactgaagcc gatcgccaaa tggaaaggat acaagaaatg 120

gccattccta aaccaccgga ggtaggcacc tccctttga atggtgtcaa ggcttctttg 180

aatgagcata ctcagacatt gacattagat gatctagcca aacaaccaga gctggccgaa 240

cctttgttaa atcaagcatt gcaagcgcga aactatattg ctgcagagca actcttgcct 300

atatatcgta aatggaatgg gtatgaccca attttattgg attatgcgca aggcgcaatt 360

tggcgttcgc aaggaaagca taaaaaagcc attacacttt accgtaatat ccttgttcga 420

catcctaatc ttgttgccgt ccgtctagac ttggctgcta tgctttatga ggataagcaa 480

acccgtaatt cacaacatga atttaatgct gccaaaaagc aaggtttacc agaagatgtc 540

cttcctacta ttgcccttta tgaaaacgct atggggcaaa ataaatggca attttcaggc 600

agtctgagtt acacccaaga caacaatatc aacaacgttt cagctgagcg tgaaatccat 660

cttcctcaat ttgataactt ggcttttgaa aaaaattctg actatctgcc acaaaaaggg 720

catggtttta cctacgccct atccgttgat cgcgatatca atctcaaagg caaccattat 780

ttcgctcttt caggcgatgt cgacggcgtc agctattggg ataatcatga ttatgatgat 840

caaacggcaa aagtcagtct aggttataaa aataaaagtt ttaaaacaga tagttttgtt 900

atgccatttt tagaaaagcg tcgctacgga aatcatcctt attacacgcg tacaggtgta 960

gatttaggtg cttcacgttg gataaaacca aatttacgcc tatctgccaa cggaaccttt 1020

gcacaaaaag attatgccta taccaaacaa caagggaaag attatcagat tggatttggg 1080

acgacctacc tgatgaatga taaaacctat ttcttaggag gtttgagtta tgcgcgtgac 1140

aaagttgaaa atttcgcagg cagcagctcc aaacggatag gaggttactt aggttggggg 1200

caaatttggg gtgaaaattt caatagtcgc cttatcatca atcactacaa tgaacgcttt 1260

gatggaaaac attacgtctt taccgaccgt catcgtacag ataatgtcgt ggttaccaat 1320

ttaagcctct ggcacaataa acttagtttt ctaggaatta cgccgagatt aaattggcga 1380

tatacaaaca ataacagcaa tattaacgaa cttcatagtt atactaaaaa tcgcgtattt 1440

atagattttg agaaaacgtt ttga 1464

<210> 422

<211> 487

<212> PRT

<213> N. sicca SLAM 2

<400> 422

Met Lys Ser Asn Gln Phe Ile Phe Ile Ala Gly Ile Leu Phe Pro Ile
1 5 10 15

Met Val Thr Ala Glu Thr Ile Ala Asn Pro Glu Thr Glu Ala Asp Arg
20 25 30

Gln Met Glu Arg Ile Gln Glu Met Ala Ile Pro Lys Pro Pro Glu Val
35 40 45

Gly Thr Ser Leu Leu Asn Gly Val Lys Ala Ser Leu Asn Glu His Thr

50 55 60

Gln Thr Leu Thr Leu Asp Asp Leu Ala Lys Gln Pro Glu Leu Ala Glu
65 70 75 80

Pro Leu Leu Asn Gln Ala Leu Gln Ala Arg Asn Tyr Ile Ala Ala Glu
85 90 95

Gln Leu Leu Pro Ile Tyr Arg Lys Trp Asn Gly Tyr Asp Pro Ile Leu
100 105 110

Leu Asp Tyr Ala Gln Gly Ala Ile Trp Arg Ser Gln Gly Lys His Lys

115 120 125

Lys Ala Ile Thr Leu Tyr Arg Asn Ile Leu Val Arg His Pro Asn Leu
130 135 140

Val Ala Val Arg Leu Asp Leu Ala Ala Met Leu Tyr Glu Asp Lys Gln
145 150 155 160

Thr Arg Asn Ser Gln His Glu Phe Asn Ala Ala Lys Lys Gln Gly Leu
165 170 175

Pro Glu Asp Val Leu Pro Thr Ile Ala Leu Tyr Glu Asn Ala Met Gly

180 185 190

Gln Asn Lys Trp Gln Phe Ser Gly Ser Leu Ser Tyr Thr Gln Asp Asn
195 200 205

Asn Ile Asn Asn Val Ser Ala Glu Arg Glu Ile His Leu Pro Gln Phe
210 215 220

Asp Asn Leu Ala Phe Glu Lys Asn Ser Asp Tyr Leu Pro Gln Lys Gly
225 230 235 240

His Gly Phe Thr Tyr Ala Leu Ser Val Asp Arg Asp Ile Asn Leu Lys

245 250 255

Gly Asn His Tyr Phe Ala Leu Ser Gly Asp Val Asp Gly Val Ser Tyr

260 265 270

Trp Asp Asn His Asp Tyr Asp Asp Gln Thr Ala Lys Val Ser Leu Gly

275 280 285

Tyr Lys Asn Lys Ser Phe Lys Thr Asp Ser Phe Val Met Pro Phe Leu

290 295 300

Glu Lys Arg Arg Tyr Gly Asn His Pro Tyr Tyr Thr Arg Thr Gly Val

305 310 315 320

Asp Leu Gly Ala Ser Arg Trp Ile Lys Pro Asn Leu Arg Leu Ser Ala

325 330 335

Asn Gly Thr Phe Ala Gln Lys Asp Tyr Ala Tyr Thr Lys Gln Gln Gly

340 345 350

Lys Asp Tyr Gln Ile Gly Phe Gly Thr Thr Tyr Leu Met Asn Asp Lys

355 360 365

Thr Tyr Phe Leu Gly Gly Leu Ser Tyr Ala Arg Asp Lys Val Glu Asn

370 375 380

Phe Ala Gly Ser Ser Ser Lys Arg Ile Gly Gly Tyr Leu Gly Trp Gly

385 390 395 400

Gln Ile Trp Gly Glu Asn Phe Asn Ser Arg Leu Ile Ile Asn His Tyr

405 410 415

Asn Glu Arg Phe Asp Gly Lys His Tyr Val Phe Thr Asp Arg His Arg

420 425 430

Thr Asp Asn Val Val Val Thr Asn Leu Ser Leu Trp His Asn Lys Leu

435 440 445

Ser Phe Leu Gly Ile Thr Pro Arg Leu Asn Trp Arg Tyr Thr Asn Asn

450 455 460

Asn Ser Asn Ile Asn Glu Leu His Ser Tyr Thr Lys Asn Arg Val Phe

465 470 475 480

Ile Asp Phe Glu Lys Thr Phe

485

<210> 423

<211> 1440

<212> DNA

<213> N. sicca SLAM 3

<400> 423

atgtacaaac cgtctgcctg ccttatcctc tttctcgccg cccccgtcct tgccgcgcca 60

cgttctgact tttcagacga ccgtaccgcg caacgcctgt ggcaggatac ccgccaaacc 120

atgcaggaac aggaacaaaa agtgcgcgaa taccgcctcg acattcccgc cgaaaacatc 180

gggcagacag ccgaaaccga ccccgaagcc gaccaaggcg aagccttgtt taacgccgtc 240

aaccgcagcg actggcaaac cgtgcgcccg ctgctcgagc gttataccca gcaaaccgaa 300

tacgaccccg acatcgccct ctttgcccgc gcctcgctcg cccgtggcga aggcaggtgg 360

aaagatgcca aacaagacta cgaaaccctg ctgcaacgcc atcccgactt cacgcgcgga 420

cggctcgatt acgcccgcct gctctttgaa ggtcgtctga accgcgaagc cacttccgaa 480

tttatgcgcc tgcaaaacga agacctgccc gaagccgtca aagaaaacat cggccatttc 540

cgcgattcct taaaccaacg ccaaagctgg cagggcagcc tttccgtcgg cgccgtccac 600

aacagcaaca tcaacgaagc cagcggcaaa gtgtggtgta aaaccgaaat cgacggcgaa 660

tgctgggaag aattttccgg cgacctgccc atttccgcca acggcatcaa atacgaagcc 720

gccgccgtcc gccgctggca gattaaagga caccacggca tcgccgcccg cgcgctcggc 780

tacagccgct tctaccgcga ccataaagac ttcaacgaac acacgctcaa cctcagcgca 840

ggctaccagt ttgaaaacca ccgccacacc ttcgccctcg ccccgctcgt cgaatggaac 900

ggcagcggcg gcaaaaccct caaccgcgcc tacggcgtgc gcagcgagtg gaacctcgac 960

aaaggcagct ggacgtggaa caccgaagcc gagtggaaac acctctccta ttccgacaaa 1020

acccgcctgc tcgacggcag cctcttctcc gtttacaaca ccctgtccta cttcccgcgc 1080

aacgacctca tgctctacgg cggcatagac tggcagcagc gcaaagccaa agaacccgtg 1140

gacagctacc gcctcatctc cgcacggctg ggcgcagcaa aaatgtttga agccggcttc 1200

gacgcctccg cctccgccac cttcggcatc cgcagccacc gcgaagaaaa cgccgtactc 1260

gaacaacgcc gccgcgacaa agaacaaacc taccgcctca gcataggcgc ggaccgctgg 1320

aaattcgccg gcctcaagcc cgtcctcagc tacaaacacc gccgcgtcaa aggcaacacc 1380

gactggctat acagctacaa acaaaacgaa gtcggtctgt cgctggtgaa atcgttctaa 1440

<210> 424

<211> 479

<212> PRT

<213> N. sicca SLAM 3

<400> 424

Met Tyr Lys Pro Ser Ala Cys Leu Ile Leu Phe Leu Ala Ala Pro Val
1 5 10 15

Leu Ala Ala Pro Arg Ser Asp Phe Ser Asp Asp Arg Thr Ala Gln Arg
20 25 30

Leu Trp Gln Asp Thr Arg Gln Thr Met Gln Glu Gln Glu Gln Lys Val
35 40 45

Arg Glu Tyr Arg Leu Asp Ile Pro Ala Glu Asn Ile Gly Gln Thr Ala
50 55 60

Glu Thr Asp Pro Glu Ala Asp Gln Gly Glu Ala Leu Phe Asn Ala Val
65 70 75 80

Asn Arg Ser Asp Trp Gln Thr Val Arg Pro Leu Leu Glu Arg Tyr Thr
85 90 95

Gln Gln Thr Glu Tyr Asp Pro Asp Ile Ala Leu Phe Ala Arg Ala Ser
100 105 110

Leu Ala Arg Gly Glu Gly Arg Trp Lys Asp Ala Lys Gln Asp Tyr Glu
115 120 125

Thr Leu Leu Gln Arg His Pro Asp Phe Thr Arg Gly Arg Leu Asp Tyr
130 135 140

Ala Arg Leu Leu Phe Glu Gly Arg Leu Asn Arg Glu Ala Thr Ser Glu
145 150 155 160

Phe Met Arg Leu Gln Asn Glu Asp Leu Pro Glu Ala Val Lys Glu Asn
165 170 175

Ile Gly His Phe Arg Asp Ser Leu Asn Gln Arg Gln Ser Trp Gln Gly
180 185 190

Ser Leu Ser Val Gly Ala Val His Asn Ser Asn Ile Asn Glu Ala Ser
195 200 205

Gly Lys Val Trp Cys Lys Thr Glu Ile Asp Gly Glu Cys Trp Glu Glu
210 215 220

Phe Ser Gly Asp Leu Pro Ile Ser Ala Asn Gly Ile Lys Tyr Glu Ala

225 230 235 240

Ala Ala Val Arg Arg Trp Gln Ile Lys Gly His His Gly Ile Ala Ala

245 250 255

Arg Ala Leu Gly Tyr Ser Arg Phe Tyr Arg Asp His Lys Asp Phe Asn

260 265 270

Glu His Thr Leu Asn Leu Ser Ala Gly Tyr Gln Phe Glu Asn His Arg

275 280 285

His Thr Phe Ala Leu Ala Pro Leu Val Glu Trp Asn Gly Ser Gly Gly

290 295 300

Lys Thr Leu Asn Arg Ala Tyr Gly Val Arg Ser Glu Trp Asn Leu Asp

305 310 315 320

Lys Gly Ser Trp Thr Trp Asn Thr Glu Ala Glu Trp Lys His Leu Ser

325 330 335

Tyr Ser Asp Lys Thr Arg Leu Leu Asp Gly Ser Leu Phe Ser Val Tyr

340 345 350

Asn Thr Leu Ser Tyr Phe Pro Arg Asn Asp Leu Met Leu Tyr Gly Gly

355 360 365

Ile Asp Trp Gln Gln Arg Lys Ala Lys Glu Pro Val Asp Ser Tyr Arg

370 375 380

Leu Ile Ser Ala Arg Leu Gly Ala Ala Lys Met Phe Glu Ala Gly Phe

385 390 395 400

Asp Ala Ser Ala Ser Ala Thr Phe Gly Ile Arg Ser His Arg Glu Glu

405 410 415

Asn Ala Val Leu Glu Gln Arg Arg Arg Asp Lys Glu Gln Thr Tyr Arg

420 425 430

Leu Ser Ile Gly Ala Asp Arg Trp Lys Phe Ala Gly Leu Lys Pro Val

435 440 445

Leu Ser Tyr Lys His Arg Arg Val Lys Gly Asn Thr Asp Trp Leu Tyr

450 455 460

Ser Tyr Lys Gln Asn Glu Val Gly Leu Ser Leu Val Lys Ser Phe

465 470 475

<210> 425

<211> 1476

<212> DNA

<213> N. sicca SLAM 4

<400> 425

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gacgacctgc gccgcctgtc cgaagaaaac gggcgcgtgc agcagcaata tcgggaaagc 120

gactggctgg acggcggcac acccgcaggc gacatcgaaa acgacgacgc atacatccgc 180

atcggcggtc agatttacac cgtaggcaac aataccgaag agctggaaag cgcgatttat 240

catgccatta acgaacgcca atggaaaaag gctgaacgct tcgccacgcg ctacgccgcc 300

ctgcccgacc acaatcccgc cctgcccaaa ttggtgctcg gtttaaaaca acgcgccgaa 360

ggacgcctcg ccgaagcctt gcgaaacctg caatcggcag aagcactcga ccccgccaac 420

ccgcgcatcc tgctcgaaac cgcgcgcctt tataccgaag acaatcaaaa ccgcgaagcc 480

cgaagcgcat tcgcccgcgc ccaagccgcc gatattcccg aagaaacccg cgccctgatc 540

ggacaatacc tcggcgaaat cgacaaacgc agccgctggc acggacaaat cggcatcgct 600

tacggctaca acagcaacat caaccaatcc gacggctccg tccgctgcat cctgccgctt 660

gacggccaat gcctcgccta ccaaaacctg cccgacccca tccgttcccc cgtatggaat 720

tacagcctga gcgcaggcaa aatcaccccc gtcaaaggac accacagcct caaaaccaac 780

ctcctcgcct acggcacgca ctaccgccgc aaagacacag acaccgccct gtccgactac 840

ggcagccaaa caggcacact gtccgccggt tacgaatacg ccgacgcaca aagccgcctc 900

tcgatgatgc ccgtttacga acacgaacgg cgcaaccgcc acacctacta caacgcctac 960

ggcgccgaaa cctcgtggac gcataccatc aaccccaaat ggcaggtcaa cgccgactgg 1020

tcgggcaaac gctaccgcca cagcggcacc gcgaaaacct acgccgccga ctacaccgaa 1080

taccgcacag gcttaggcgc agaatacgcc ctgaccccga aaaccggcgt gttcgcaggc 1140

tccgactaca cccgccgcac atacaacggc ggcacatccg accaccgcga atacaccctc 1200

cgcacaggct tatacaccct gtttgacaac ggcacctacc tcaacgccct cgtcatgaaa 1260

cggcgcaacc tctacgaccg cgcaggcatc gccgcagacg gacaaagacg cagcgaccgc 1320

caaaccgtct ggctcgccgc cgcaggcttc agacaatggc acatcggcgg cttctacccc 1380

gaactgcgct tcaaacacac caccgtcaaa agcaattccg tgttctaccg ctaccgccaa 1440

aacgaaatca tgctgggcgt gaaaaaacag ttttga 1476

<210> 426

<211> 491

<212> PRT

<213> N. sicca SLAM 4

<400> 426

Met Asn Lys Ser Cys Leu Leu Leu Leu Ala Leu Leu Pro Leu Ser Ala
1 5 10 15

His Ala Asp Ser Asp Asp Leu Arg Arg Leu Ser Glu Glu Asn Gly Arg
20 25 30

Val Gln Gln Gln Tyr Arg Glu Ser Asp Trp Leu Asp Gly Gly Thr Pro
35 40 45

Ala Gly Asp Ile Glu Asn Asp Asp Ala Tyr Ile Arg Ile Gly Gly Gln
50 55 60

Ile Tyr Thr Val Gly Asn Asn Thr Glu Glu Leu Glu Ser Ala Ile Tyr
65 70 75 80

His Ala Ile Asn Glu Arg Gln Trp Lys Lys Ala Glu Arg Phe Ala Thr
85 90 95

Arg Tyr Ala Ala Leu Pro Asp His Asn Pro Ala Leu Pro Lys Leu Val
100 105 110

Leu Gly Leu Lys Gln Arg Ala Glu Gly Arg Leu Ala Glu Ala Leu Arg
115 120 125

Asn Leu Gln Ser Ala Glu Ala Leu Asp Pro Ala Asn Pro Arg Ile Leu
130 135 140

Leu Glu Thr Ala Arg Leu Tyr Thr Glu Asp Asn Gln Asn Arg Glu Ala
145 150 155 160

Arg Ser Ala Phe Ala Arg Ala Gln Ala Ala Asp Ile Pro Glu Glu Thr
165 170 175

Arg Ala Leu Ile Gly Gln Tyr Leu Gly Glu Ile Asp Lys Arg Ser Arg
180 185 190

Trp His Gly Gln Ile Gly Ile Ala Tyr Gly Tyr Asn Ser Asn Ile Asn
195 200 205

Gln Ser Asp Gly Ser Val Arg Cys Ile Leu Pro Leu Asp Gly Gln Cys
210 215 220
Leu Ala Tyr Gln Asn Leu Pro Asp Pro Ile Arg Ser Pro Val Trp Asn
225 230 235 240
Tyr Ser Leu Ser Ala Gly Lys Ile Thr Pro Val Lys Gly His His Ser
245 250 255
Leu Lys Thr Asn Leu Leu Ala Tyr Gly Thr His Tyr Arg Arg Lys Asp
260 265 270

Thr Asp Thr Ala Leu Ser Asp Tyr Gly Ser Gln Thr Gly Thr Leu Ser
275 280 285
Ala Gly Tyr Glu Tyr Ala Asp Ala Gln Ser Arg Leu Ser Met Met Pro
290 295 300
Val Tyr Glu His Glu Arg Arg Asn Arg His Thr Tyr Tyr Asn Ala Tyr
305 310 315 320
Gly Ala Glu Thr Ser Trp Thr His Thr Ile Asn Pro Lys Trp Gln Val
325 330 335

Asn Ala Asp Trp Ser Gly Lys Arg Tyr Arg His Ser Gly Thr Ala Lys
340 345 350
Thr Tyr Ala Ala Asp Tyr Thr Glu Tyr Arg Thr Gly Leu Gly Ala Glu
355 360 365
Tyr Ala Leu Thr Pro Lys Thr Gly Val Phe Ala Gly Ser Asp Tyr Thr
370 375 380
Arg Arg Thr Tyr Asn Gly Gly Thr Ser Asp His Arg Glu Tyr Thr Leu
385 390 395 400

Arg Thr Gly Leu Tyr Thr Leu Phe Asp Asn Gly Thr Tyr Leu Asn Ala
405 410 415
Leu Val Met Lys Arg Arg Asn Leu Tyr Asp Arg Ala Gly Ile Ala Ala
420 425 430
Asp Gly Gln Arg Arg Ser Asp Arg Gln Thr Val Trp Leu Ala Ala Ala
435 440 445
Gly Phe Arg Gln Trp His Ile Gly Gly Phe Tyr Pro Glu Leu Arg Phe

450 455 460

Lys His Thr Thr Val Lys Ser Asn Ser Val Phe Tyr Arg Tyr Arg Gln
465 470 475 480
Asn Glu Ile Met Leu Gly Val Lys Lys Gln Phe
485 490

<210> 427

<211> 1557

<212> DNA

<213> N. subflava SLAM 1

<400> 427

atggcactcg gtttgcaaaa tttccgactc aaaacattgt acaatctgcc cacttatacc 60

gataacatcc ccaacattgc catgaaaaaa cgtctgctcc tcctcgccat cctgcccctt 120

tcccttacg ccgccgatgt gccgcccaac gtaaaacccg agcttcaagt caacactgcc 180

gaaccccaac agcccgaagc gcacaatatc cctgccgaac agacaaacag gccgtctgaa 240

aaaatcatcg acgtcgatgc cgacaccctg cttgccaaca ccgaattact ggcacgcgcc 300

atgtattccg ccgtcgtcgc ccacaatatc cccggcatca aagccgtttt gcccatttac 360

gaacaatggc ccgaacacga ccgtgccatg gcacgctatg ccaaaggttt gcttgcccaa 420

tccgaagggc gcgccgccga agccgtcggc cattaccgcc gctttatcgc cgagcagccc 480

gatgcctccg ccgtccgctg gcagcttgca accgccttgt ttgaagacaa acaaaacgaa 540

gccgcggccg accagttcga caaactgcaa accgaatccc tcccgcctgc cttgcaagaa 600

cgcatcgaaa cctaccgcaa agccctgcgc gaacgcgact tatggcaatt caacgccggc 660

ctgaacatca cgcgcgaaca aaacatcaac caagccccca gccaacgccg tctgggcaac 720

cacctgagcg acgaacaatg ccgcgccgtg cgccttgtct atcccgacga cgactgcttc 780

cgaggctgga cattccccga acccatcgat gccaccgccg tccattacca aatcggtgca 840

gaaaaaaaat ggtcgttgcc acgtggcttc tatgtcacgg caggcgcaga ccattacggc 900

aaaatctacc ccaaacacac caactacaac gacctcacca cacgcttctc ggcaggccta 960

ggctatgccg accagcgcag cgatatcggc attaccccgt tccacgaacg ccgcttctac 1020

ggcaacgacc cctacaccta caccaacggc gcacgcctcc actacaacca ttggtggcaa 1080

cccaagctac aaaccctcag cgcatttgaa gcaggccgtc tgaaaaacag ccgccgcgaa 1140

cattccgaca acaccagcca actgctcagc aactccatcg tgtactaccg caacgcgcgc 1200

caatactggg tagccggtat cgacctctac cgcgaacgca accgcgacga caaaagcgac 1260

agcttcaacc gctacgccct gcgcaccaca tggggacaag aatggcccaa aggcctctcc 1320

accgtcctac gcctcagcgc cgcccaacgc cgttaccaag cccccggctt cttcagtaac 1380

gaacaaaacc gccgcgacaa agaaacctcc gcctccctga gcgtatggca ccgcgccctc 1440

catttcaaag gcatcacccc gcgcctgacc attgcccaca acaaaacatg gagcaacgac 1500

aagttctacg aatacggcaa aaccaaaatg tttgtcgaat tgagcaaaac gttctga 1557

<210> 428

<211> 518

<212> PRT

<213> N. subflava SLAM 1

<400> 428

Met Ala Leu Gly Leu Gln Asn Phe Arg Leu Lys Thr Leu Tyr Asn Leu
1 5 10 15

Pro Thr Tyr Thr Asp Asn Ile Pro Asn Ile Ala Met Lys Lys Arg Leu
20 25 30

Leu Leu Leu Ala Ile Leu Pro Leu Ser Leu Tyr Ala Ala Asp Val Pro
35 40 45

Pro Asn Val Lys Pro Glu Leu Gln Val Asn Thr Ala Glu Pro Gln Gln
50 55 60

Pro Glu Ala His Asn Ile Pro Ala Glu Gln Thr Asn Arg Pro Ser Glu
65 70 75 80

Lys Ile Ile Asp Val Asp Ala Asp Thr Leu Leu Ala Asn Thr Glu Leu
85 90 95

Leu Ala Arg Ala Met Tyr Ser Ala Val Val Ala His Asn Ile Pro Gly
100 105 110

Ile Lys Ala Val Leu Pro Ile Tyr Glu Gln Trp Pro Glu His Asp Arg
115 120 125

Ala Met Ala Arg Tyr Ala Lys Gly Leu Leu Ala Gln Ser Glu Gly Arg
130 135 140

Ala Ala Glu Ala Val Gly His Tyr Arg Arg Phe Ile Ala Glu Gln Pro
145 150 155 160

Asp Ala Ser Ala Val Arg Trp Gln Leu Ala Thr Ala Leu Phe Glu Asp

165 170 175

Lys Gln Asn Glu Ala Ala Ala Asp Gln Phe Asp Lys Leu Gln Thr Glu

180 185 190

Ser Leu Pro Pro Ala Leu Gln Glu Arg Ile Glu Thr Tyr Arg Lys Ala

195 200 205

Leu Arg Glu Arg Asp Leu Trp Gln Phe Asn Ala Gly Leu Asn Ile Thr

210 215 220

Arg Glu Gln Asn Ile Asn Gln Ala Pro Ser Gln Arg Arg Leu Gly Asn

225 230 235 240

His Leu Ser Asp Glu Gln Cys Arg Ala Val Arg Leu Val Tyr Pro Asp

245 250 255

Asp Asp Cys Phe Arg Gly Trp Thr Phe Pro Glu Pro Ile Asp Ala Thr

260 265 270

Ala Val His Tyr Gln Ile Gly Ala Glu Lys Lys Trp Ser Leu Pro Arg

275 280 285

Gly Phe Tyr Val Thr Ala Gly Ala Asp His Tyr Gly Lys Ile Tyr Pro

290 295 300

Lys His Thr Asn Tyr Asn Asp Leu Thr Thr Arg Phe Ser Ala Gly Leu

305 310 315 320

Gly Tyr Ala Asp Gln Arg Ser Asp Ile Gly Ile Thr Pro Phe His Glu

325 330 335

Arg Arg Phe Tyr Gly Asn Asp Pro Tyr Thr Tyr Thr Asn Gly Ala Arg

340 345 350

Leu His Tyr Asn His Trp Trp Gln Pro Lys Leu Gln Thr Leu Ser Ala

355 360 365

Phe Glu Ala Gly Arg Leu Lys Asn Ser Arg Arg Glu His Ser Asp Asn

370 375 380

Thr Ser Gln Leu Leu Ser Asn Ser Ile Val Tyr Tyr Arg Asn Ala Arg

385 390 395 400

Gln Tyr Trp Val Ala Gly Ile Asp Leu Tyr Arg Glu Arg Asn Arg Asp

405 410 415

Asp Lys Ser Asp Ser Phe Asn Arg Tyr Ala Leu Arg Thr Thr Trp Gly

420 425 430

Gln Glu Trp Pro Lys Gly Leu Ser Thr Val Leu Arg Leu Ser Ala Ala

435 440 445

Gln Arg Arg Tyr Gln Ala Pro Gly Phe Phe Ser Asn Glu Gln Asn Arg

450 455 460

Arg Asp Lys Glu Thr Ser Ala Ser Leu Ser Val Trp His Arg Ala Leu

465 470 475 480

His Phe Lys Gly Ile Thr Pro Arg Leu Thr Ile Ala His Asn Lys Thr

485 490 495

Trp Ser Asn Asp Lys Phe Tyr Glu Tyr Gly Lys Thr Lys Met Phe Val

500 505 510

Glu Leu Ser Lys Thr Phe

515

<210> 429

<211> 1467

<212> DNA

<213> N. subflava SLAM 2

<400> 429

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gacagggaag accgcttcat gcagctcaaa cagggaacgg aactccgccg cgctcagcag 120

gaaaggaacg aagcggacaa tacggtgatt gagttcggtg cgggagaagt gcaggacggc 180

gaagatttgg cgttgtcgct gatgaaggcg gtcaacgcgc aaaacgagga agaaacggca 240

cggctgttgg acatttaccg ccgtcaggat gattacgacc ccgatatagt gctgtttgcc 300

gaggccaatc aggcggtgtt ctgcgacgat ttgaaggccg cgctggcgaa ataccgcgag 360

ctttaccgca aaaatcccga atttctgcgc ggccgcctgg atttggcgcg gctgctgttt 420

atagacaaac aaaacaaaga atcagcggca ttgttcgacg gcatcgatat tcctgaagta 480

cccgccgtca atgagaaaat caaagtgttt gccgacgctt tgaagaaacg cgatgcgtgg 540

agcggctcgg tttcgttcgg cgcgggttat gacaccaact taaaccagtc gtcgggagcg 600

acggtcgtcc gcaatcagac aagctgcggt ttcgattcga acgggcagcc gattctggac 660

ggcgacggaa tgctgtcctg ccgcaacgaa cggcttgatg cctacgcgcc cgatgcgttg 720

aaaaaccgga tgtgggtata tgaagccaac ttaagcagac gcatttcgct caacggccac 780

cacggcctgc aactgggcgg ctacacatgg ggccggctct atcccggcaa cagagaatac 840

agcgaacaca atatcaacgt cagccccgct tacagttttc agagcaaaga ccattccttc 900

agtatcggcc cgcaggtgca atacgaatgg tctggcggca aactgcgcga cagcagcgcc 960

ggcatcagca cggcatacag ccgcaccttt tccgaccaag cctcgctggg cgtgcagctc 1020

gaccacaaat acgaccgcta ccgcggcgaa ttaaaacatt tcaacggccc acagacgctt 1080

ctgttcacca ccgccatcta cgccctgccg aaagactggc tggtattcgg cggctacgac 1140

tacctgcgca aaaacagccg cgaaaaagtg gattcctacc gtcggcacgg cctgcgcacg 1200

ggtgtcaata agcgttttga atccggcatc gacgccacct ttcaggcaat ctggcgcaaa 1260

acagcctatc aggactacca tgcctggctg gaaacccgcc gccgtgattt cgaacgcacc 1320

taccagttgg acatcaaatt cgaccgccct ttcctccgca gcttcgtacc tgtccttacc 1380

gtaaaacaca ccgaaaacaa aagctcgtcc tggctaaatc gttataaacg gaatgaattt 1440

ctaattaaaa tagaacatag gttttga 1467

<210> 430

<211> 488

<212> PRT

<213> N. subflava SLAM 2

<400> 430

Met Lys Arg Leu Leu Leu Leu Pro Phe Phe Ile Ser Leu Leu Pro His
1 5 10 15

Ala Phe Ala Asp Asp Arg Glu Asp Arg Phe Met Gln Leu Lys Gln Gly
20 25 30

Thr Glu Leu Arg Arg Ala Gln Gln Glu Arg Asn Glu Ala Asp Asn Thr
35 40 45

Val Ile Glu Phe Gly Ala Gly Glu Val Gln Asp Gly Glu Asp Leu Ala
50 55 60

Leu Ser Leu Met Lys Ala Val Asn Ala Gln Asn Glu Glu Glu Thr Ala
65 70 75 80

Arg Leu Leu Asp Ile Tyr Arg Arg Gln Asp Asp Tyr Asp Pro Asp Ile
85 90 95

Val Leu Phe Ala Glu Ala Asn Gln Ala Val Phe Cys Asp Asp Leu Lys

100 105 110

Ala Ala Leu Ala Lys Tyr Arg Glu Leu Tyr Arg Lys Asn Pro Glu Phe
115 120 125
Leu Arg Gly Arg Leu Asp Leu Ala Arg Leu Leu Phe Ile Asp Lys Gln
130 135 140
Asn Lys Glu Ser Ala Ala Leu Phe Asp Gly Ile Asp Ile Pro Glu Val
145 150 155 160
Pro Ala Val Asn Glu Lys Ile Lys Val Phe Ala Asp Ala Leu Lys Lys
165 170 175

Arg Asp Ala Trp Ser Gly Ser Val Ser Phe Gly Ala Gly Tyr Asp Thr
180 185 190
Asn Leu Asn Gln Ser Ser Gly Ala Thr Val Val Arg Asn Gln Thr Ser
195 200 205
Cys Gly Phe Asp Ser Asn Gly Gln Pro Ile Leu Asp Gly Asp Gly Met
210 215 220
Leu Ser Cys Arg Asn Glu Arg Leu Asp Ala Tyr Ala Pro Asp Ala Leu
225 230 235 240

Lys Asn Arg Met Trp Val Tyr Glu Ala Asn Leu Ser Arg Arg Ile Ser
245 250 255
Leu Asn Gly His His Gly Leu Gln Leu Gly Gly Tyr Thr Trp Gly Arg
260 265 270
Leu Tyr Pro Gly Asn Arg Glu Tyr Ser Glu His Asn Ile Asn Val Ser
275 280 285
Pro Ala Tyr Ser Phe Gln Ser Lys Asp His Ser Phe Ser Ile Gly Pro
290 295 300

Gln Val Gln Tyr Glu Trp Ser Gly Gly Lys Leu Arg Asp Ser Ser Ala
305 310 315 320
Gly Ile Ser Thr Ala Tyr Ser Arg Thr Phe Ser Asp Gln Ala Ser Leu
325 330 335
Gly Val Gln Leu Asp His Lys Tyr Asp Arg Tyr Arg Gly Glu Leu Lys
340 345 350

His Phe Asn Gly Pro Gln Thr Leu Leu Phe Thr Thr Ala Ile Tyr Ala
355 360 365

Leu Pro Lys Asp Trp Leu Val Phe Gly Gly Tyr Asp Tyr Leu Arg Lys
370 375 380
Asn Ser Arg Glu Lys Val Asp Ser Tyr Arg Arg His Gly Leu Arg Thr
385 390 395 400
Gly Val Asn Lys Arg Phe Glu Ser Gly Ile Asp Ala Thr Phe Gln Ala
405 410 415
Ile Trp Arg Lys Thr Ala Tyr Gln Asp Tyr His Ala Trp Leu Glu Thr
420 425 430

Arg Arg Arg Asp Phe Glu Arg Thr Tyr Gln Leu Asp Ile Lys Phe Asp
435 440 445
Arg Pro Phe Leu Arg Ser Phe Val Pro Val Leu Thr Val Lys His Thr
450 455 460
Glu Asn Lys Ser Ser Ser Trp Leu Asn Arg Tyr Lys Arg Asn Glu Phe
465 470 475 480
Leu Ile Lys Ile Glu His Arg Phe
485

<210> 431
<211> 1278
<212> DNA
<213> N. wadsworthii SLAM 1

<400> 431
atgaaacgtg cagtcttgtt attgagttta tttgcttcgt tttgcggagt tgtcgccgct 60
gatggcgaag tacagcccgc ttcggacttg ccttaccgcc agatagaagt tgcgccgctt 120
cccgatagcg agctgaaatc agagctggaa gccgcgcttg ccaaacaaga ttggcaaaat 180
atgcccgagt tgctgaaaca ataccgcagc cgctttctgg ctgatcaagt attcgctgat 240
tatgcagaag cccgctggcg cagcagtcaa ggcgaatata tgcaggcgca agccttatac 300
cgtcgcgtgt tggcgcaacg ccctgattgg caggaagcgc gtgcggctac aatccacaac 360
ctttctgccg cacgctccgc accgcgtgcc ggtgatttcg gcaagcgttt gcaagcatcc 420

gatgtttggc agcttcctgt caacctgagc catgtccgca ataatcaagg gtatattccg 480

cgcgatcaaa aaacactact tgccggtaac cgttatccgg acaaaaataa tgatgctttg 540

cgctacaatc tgggcgccga gcatgatttc agtctgaaag gcaatcaccg cctgaggctc 600

ggactcacca gcggcggtac gcactattgg gattattacg accgcagcac ccgttccgtc 660

cgcctggctg cgggctaccg cagcagcgca ggtaaacaaa gttggtcgtt tacaccatac 720

accgaacaaa gctggctggg cagcgaaaaa tacacactca acaccggcgc ttctgcggca 780

tacaataata aattcaatga taactggcgc gtgtcgcttt ccgcttccag tgttaaccgc 840

agttacaaca atcccgatca tgcaaaatat tatgatggca acatcaacag cgtatccggt 900

actgccgaat ggcgccccaa tagcgcatgg gcaatcagcg caggtgcgga ttatcgggcc 960

gatctcacgc gtaacgaaac acgctcgtcc gaccgaacgg tctttcgcac cggcatctcg 1020

cgccagtttg aaggcggcat taaagcaggt gcttccgttc agtatggccg gcgtgaattc 1080

agccattcgg agccgctgta cggcatcggc aggaaagaca atgaatacaa tgccagcgcc 1140

tcgctctctt accagccgcg gcgttggaaa ggcgtagcgc ctaaaatcga ttaccgctat 1200

tccaaaatcg acagcaatgt ggattcttcg tctcgtgagc aatcgcaatg gtttatgagt 1260

ttggaaaaaa aattttaa 1278

<210> 432

<211> 425

<212> PRT

<213> N. wadsworthii SLAM 1

<400> 432

Met Lys Arg Ala Val Leu Leu Leu Ser Leu Phe Ala Ser Phe Cys Gly
1 5 10 15

Val Val Ala Ala Asp Gly Glu Val Gln Pro Ala Ser Asp Leu Pro Tyr
20 25 30

Arg Gln Ile Glu Val Ala Pro Leu Pro Asp Ser Glu Leu Lys Ser Glu
35 40 45

Leu Glu Ala Ala Leu Ala Lys Gln Asp Trp Gln Asn Met Pro Glu Leu
50 55 60

Leu Lys Gln Tyr Arg Ser Arg Phe Leu Ala Asp Gln Val Phe Ala Asp
65 70 75 80

Tyr Ala Glu Ala Arg Trp Arg Ser Ser Gln Gly Glu Tyr Met Gln Ala
85 90 95

Gln Ala Leu Tyr Arg Arg Val Leu Ala Gln Arg Pro Asp Trp Gln Glu

100 105 110

Ala Arg Ala Ala Thr Ile His Asn Leu Ser Ala Ala Arg Ser Ala Pro
115 120 125
Arg Ala Gly Asp Phe Gly Lys Arg Leu Gln Ala Ser Asp Val Trp Gln
130 135 140
Leu Pro Val Asn Leu Ser His Val Arg Asn Asn Gln Gly Tyr Ile Pro
145 150 155 160
Arg Asp Gln Lys Thr Leu Leu Ala Gly Asn Arg Tyr Pro Asp Lys Asn
165 170 175

Asn Asp Ala Leu Arg Tyr Asn Leu Gly Ala Glu His Asp Phe Ser Leu
180 185 190
Lys Gly Asn His Arg Leu Arg Leu Gly Leu Thr Ser Gly Gly Thr His
195 200 205
Tyr Trp Asp Tyr Tyr Asp Arg Ser Thr Arg Ser Val Arg Leu Ala Ala
210 215 220
Gly Tyr Arg Ser Ser Ala Gly Lys Gln Ser Trp Ser Phe Thr Pro Tyr
225 230 235 240

Thr Glu Gln Ser Trp Leu Gly Ser Glu Lys Tyr Thr Leu Asn Thr Gly
245 250 255
Ala Ser Ala Ala Tyr Asn Asn Lys Phe Asn Asp Asn Trp Arg Val Ser
260 265 270
Leu Ser Ala Ser Ser Val Asn Arg Ser Tyr Asn Asn Pro Asp His Ala
275 280 285
Lys Tyr Tyr Asp Gly Asn Ile Asn Ser Val Ser Gly Thr Ala Glu Trp
290 295 300

Arg Pro Asn Ser Ala Trp Ala Ile Ser Ala Gly Ala Asp Tyr Arg Ala
305 310 315 320
Asp Leu Thr Arg Asn Glu Thr Arg Ser Ser Asp Arg Thr Val Phe Arg
325 330 335
Thr Gly Ile Ser Arg Gln Phe Glu Gly Gly Ile Lys Ala Gly Ala Ser
340 345 350

Val Gln Tyr Gly Arg Arg Glu Phe Ser His Ser Glu Pro Leu Tyr Gly
355 360 365

Ile Gly Arg Lys Asp Asn Glu Tyr Asn Ala Ser Ala Ser Leu Ser Tyr
370 375 380
Gln Pro Arg Arg Trp Lys Gly Val Ala Pro Lys Ile Asp Tyr Arg Tyr
385 390 395 400
Ser Lys Ile Asp Ser Asn Val Asp Ser Ser Ser Arg Glu Gln Ser Gln
405 410 415
Trp Phe Met Ser Leu Glu Lys Lys Phe
420 425

<210> 433
<211> 900
<212> DNA

<213> N. wadsworthii SLAM 2
<400> 433
ttggaaaatc gacaaaaatg gcaagactct gtttctagag gtttaatatg gagcagcaat 60
ataaacgaag gctcagacgg tccggagtgc ctgcatattg aagaattagg cgacatttgg 120
gagcattgtc aaaacggcga accatcggaa aaagcgcttg gcatcaatta tgaagccgcc 180
gcttcccgcc gctttcaaat cagcggacac cacggcttga acacccgcat actggcatac 240
ggcaaaatct accgaaacca tcaaaaatac aatgaacaca cgctcaatgt aagcgcaggc 300
taccaatttg ccaacgccaa gcgcacagtc actttggcgc ctttgtggga atggagcagc 360
agcggccaac atgcacaaca ccgcgcttac ggcgcccgcg cagaatggaa cgaagcccgc 420

agccgctggt cgtggaacac cgaagccgaa tggaaaaagc aggtctattt caacagcgac 480
atgaaacaca ataaccaccg cctgttttcc gtgttcaaca ctttgtcata cggcttgcgg 540
gatgatgttg taatcttcgg cggtttggac tggcagcagc gcttttccga agaaccgacc 600
gaaagctacc gccaacccgc tatccggctg ggagcggcaa aacaatttgc cggcggcttc 660
gacgcctcgc tctacaccct gctccgccac cgctcctaca aacaagaaaa tgaattctta 720
ggcaaacggc gcagggataa cgaacaaatc tacaccttaa acctcggctc cgaccgctgg 780
aaaatagccg atatgaaacc tgtattcaca ctcaaacacc gccgcgttaa tagcaatatc 840

aaatggttaa acagtttcaa acaaaatgaa atcggcattt ctctaataaa gcagttttaa 900
<210> 434

<211> 299

<212> PRT

<213> N. wadsworthii SLAM 2

<400> 434

Met Glu Asn Arg Gln Lys Trp Gln Asp Ser Val Ser Arg Gly Leu Ile
1 5 10 15

Trp Ser Ser Asn Ile Asn Glu Gly Ser Asp Gly Pro Glu Cys Leu His
20 25 30

Ile Glu Glu Leu Gly Asp Ile Trp Glu His Cys Gln Asn Gly Glu Pro
35 40 45

Ser Glu Lys Ala Leu Gly Ile Asn Tyr Glu Ala Ala Ala Ser Arg Arg
50 55 60

Phe Gln Ile Ser Gly His His Gly Leu Asn Thr Arg Ile Leu Ala Tyr
65 70 75 80

Gly Lys Ile Tyr Arg Asn His Gln Lys Tyr Asn Glu His Thr Leu Asn
85 90 95

Val Ser Ala Gly Tyr Gln Phe Ala Asn Ala Lys Arg Thr Val Thr Leu
100 105 110

Ala Pro Leu Trp Glu Trp Ser Ser Ser Gly Gln His Ala Gln His Arg
115 120 125

Ala Tyr Gly Ala Arg Ala Glu Trp Asn Glu Ala Arg Ser Arg Trp Ser
130 135 140

Trp Asn Thr Glu Ala Glu Trp Lys Lys Gln Val Tyr Phe Asn Ser Asp
145 150 155 160

Met Lys His Asn Asn His Arg Leu Phe Ser Val Phe Asn Thr Leu Ser
165 170 175

Tyr Gly Leu Arg Asp Asp Val Val Ile Phe Gly Gly Leu Asp Trp Gln
180 185 190

Gln Arg Phe Ser Glu Glu Pro Thr Glu Ser Tyr Arg Gln Pro Ala Ile
195 200 205

Arg Leu Gly Ala Ala Lys Gln Phe Ala Gly Gly Phe Asp Ala Ser Leu
210 215 220

Tyr Thr Leu Leu Arg His Arg Ser Tyr Lys Gln Glu Asn Glu Phe Leu
225 230 235 240

Gly Lys Arg Arg Arg Asp Asn Glu Gln Ile Tyr Thr Leu Asn Leu Gly
245 250 255

Ser Asp Arg Trp Lys Ile Ala Asp Met Lys Pro Val Phe Thr Leu Lys
260 265 270

His Arg Arg Val Asn Ser Asn Ile Lys Trp Leu Asn Ser Phe Lys Gln
275 280 285

Asn Glu Ile Gly Ile Ser Leu Ile Lys Gln Phe
290 295

<210> 435

<211> 1449

<212> DNA

<213> N. weaveri SLAM 1

<400> 435

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ttgcctgttt acgccgaaga tgtcaagcct cagcccaaac cggtggaacc ggaagggcat 120

tttaacgtga caactccggt taataggcct gcaaacgtac cggaaggctt ggaaaaaaag 180

cgggaacagg ccagtatcga tattagcgaa gaagagctgc ttcagcgccc ggatttgttg 240

aagcgtgcat taatttcatc agttttgttt agcaatgtgg agggcgttaa agtcctgttg 300

ccgttatata aacagcttcc cgaaaagaaa gacgaactgt taatgaagat ttcggaagcc 360

atgatcgccc gttcggaagg ggaatatgaa caggcaatcc ggcaataccg cgaagcgtta 420

cagcaaaacg gagatttgca gtttgcacgt attgctttgg ctcaagcatt gtttgagaat 480

catgcggata aaagtgcgga agcagaattt caaaaaatca agcagttgcc ggatgcaccc 540

aagcaaattg tcaatatggc cgacaactat ttgaaagctt tggacgaacg caagagctgg 600

caatttaatg tcgatgcgaa ttatgtgcgt gataacaaca tcaataatgc aacagggaag 660

aggcagatca aagacggcaa aggcacttgg actttgccga aagcagaatc cgcacaaggt 720

atcgcttaca atgtcggcgc cagtaaaaat tggcgtttgg ccgataatta tgcattaaga 780

accgagctag acggttacgg caaattttat tgggacaatc ataaatatga tgatttgacc 840

gtccgcgccg gaattggcgg tgtgtaccaa actgcacgtt tggaagcgtc tttacagcct 900

ttttttgaaa gacgttggta cggcaccgaa aaatactcca aagaaaaagg tttgcgtgcg 960

gctgcacagt attgggtaac gcccaagcat aaaatgtatg tagcggcgga agccggtgat 1020

cagcgtcatg aaagacggaa gcatctagac ggtaaaaact atacggcatc agccacttgg 1080

ctgtttgttc ccaataaccg ccaatattgg acattaggtg cggattgggc gcgcaaagaa 1140

gctaaagacc gctcggatgc ttaccgacgc agcggtgccc gagtgggttg gacgcagcag 1200

tggcagaagc atttaaccac atctatgtcg cttggatatg ccgttcgcaa ttatgaagca 1260

gcagatattt ttcaagtggt ccgtaaagac aaagaatatt ccgccagttt ggctgtttcc 1320

cataaacgtt tgagttttaa aggtgtaacg ccgaagttgg ttggcgtatg gcaaaaaacc 1380

aagagcaacc atccgtttta cggtcatgag aaaagcaatg tttatattca gttgaataaa 1440

aacttctaa 1449

<210> 436

<211> 482

<212> PRT

<213> N. weaveri SLAM 1

<400> 436

Met Phe Ser Ser Ser Leu Ile Arg Lys Ile Ala Val Ser Ala Ser Leu

1 5 10 15

Ala Val Phe Ala Leu Pro Val Tyr Ala Glu Asp Val Lys Pro Gln Pro

20 25 30

Lys Pro Val Glu Pro Glu Gly His Phe Asn Val Thr Thr Pro Val Asn

35 40 45

Arg Pro Ala Asn Val Pro Glu Gly Leu Glu Lys Lys Arg Glu Gln Ala

50 55 60

Ser Ile Asp Ile Ser Glu Glu Glu Leu Leu Gln Arg Pro Asp Leu Leu

65 70 75 80

Lys Arg Ala Leu Ile Ser Ser Val Leu Phe Ser Asn Val Glu Gly Val

85 90 95

Lys Val Leu Leu Pro Leu Tyr Lys Gln Leu Pro Glu Lys Lys Asp Glu

100 105 110

Leu Leu Met Lys Ile Ser Glu Ala Met Ile Ala Arg Ser Glu Gly Glu

115 120 125

Tyr Glu Gln Ala Ile Arg Gln Tyr Arg Glu Ala Leu Gln Gln Asn Gly

130 135 140

Asp Leu Gln Phe Ala Arg Ile Ala Leu Ala Gln Ala Leu Phe Glu Asn

145 150 155 160

His Ala Asp Lys Ser Ala Glu Ala Glu Phe Gln Lys Ile Lys Gln Leu

165 170 175

Pro Asp Ala Pro Lys Gln Ile Val Asn Met Ala Asp Asn Tyr Leu Lys

180 185 190

Ala Leu Asp Glu Arg Lys Ser Trp Gln Phe Asn Val Asp Ala Asn Tyr

195 200 205

Val Arg Asp Asn Asn Ile Asn Asn Ala Thr Gly Lys Arg Gln Ile Lys

210 215 220

Asp Gly Lys Gly Thr Trp Thr Leu Pro Lys Ala Glu Ser Ala Gln Gly

225 230 235 240

Ile Ala Tyr Asn Val Gly Ala Ser Lys Asn Trp Arg Leu Ala Asp Asn

245 250 255

Tyr Ala Leu Arg Thr Glu Leu Asp Gly Tyr Gly Lys Phe Tyr Trp Asp

260 265 270

Asn His Lys Tyr Asp Asp Leu Thr Val Arg Ala Gly Ile Gly Gly Val

275 280 285

Tyr Gln Thr Ala Arg Leu Glu Ala Ser Leu Gln Pro Phe Phe Glu Arg

290 295 300

Arg Trp Tyr Gly Thr Glu Lys Tyr Ser Lys Glu Lys Gly Leu Arg Ala

305 310 315 320

Ala Ala Gln Tyr Trp Val Thr Pro Lys His Lys Met Tyr Val Ala Ala

325 330 335

Glu Ala Gly Asp Gln Arg His Glu Arg Arg Lys His Leu Asp Gly Lys

340 345 350

Asn Tyr Thr Ala Ser Ala Thr Trp Leu Phe Val Pro Asn Asn Arg Gln

355 360 365

Tyr Trp Thr Leu Gly Ala Asp Trp Ala Arg Lys Glu Ala Lys Asp Arg

370 375 380

Ser Asp Ala Tyr Arg Arg Ser Gly Ala Arg Val Gly Trp Thr Gln Gln

385 390 395 400

Trp Gln Lys His Leu Thr Thr Ser Met Ser Leu Gly Tyr Ala Val Arg

405 410 415

Asn Tyr Glu Ala Ala Asp Ile Phe Gln Val Val Arg Lys Asp Lys Glu

420 425 430

Tyr Ser Ala Ser Leu Ala Val Ser His Lys Arg Leu Ser Phe Lys Gly

435 440 445

Val Thr Pro Lys Leu Val Gly Val Trp Gln Lys Thr Lys Ser Asn His

450 455 460

Pro Phe Tyr Gly His Glu Lys Ser Asn Val Tyr Ile Gln Leu Asn Lys

465 470 475 480

Asn Phe

<210> 437

<211> 1539

<212> DNA

<213> N. weaveri SLAM 2

<400> 437

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acgagctttg cgagtttcgc caaaatcggc aaagccggct tcactaaaac gggtttcacc 120

actgccttgt tgctgttcac atgcaccaca acggcacaaa cactcacgcc tgaacaaaaa 180

cccgaacccg tccaacccga actgcccgaa ctggcatccg atcagcccgt atggcaaccc 240

gccgaagcag cctccgcgcc catacaggat atcgacgaag ccactttgct cgcccgaccg 300

caactgctca acctgctgct ggataaaagc gtattgcgaa acgactttga cggcatcggc 360

gtattactgc ccgtttaccg caaactgccc tcaagcaacc gcgaccccat ccttttgcaa 420

ttggccgaaa gcaaactggc catgcaccaa ggccgcttcg gtgaagccgt agccgggctc 480

cgcaacctga ttgccgaaaa acccgagcta aacgtaatcc gcatgtatct ggcgattgct 540

ctcttctacg accgccaaga cctcgccgcc aaagaccaat ttaccaaact tctcgcccaa 600

tccgacctgc ccgaaccgga aaaacaagcc atcaaccgct ttctcgacga actgcggcaa 660

agccaccgct ggcaattcag cggcggagcc aactacacct acgaacccaa tatcaacaac 720

gcccccatcg tcaaacaaca aggcaatctc gacacccgat cgcaacccga aagtgcccac 780

ggcgtcagct accgtatcgg cgcagaaaaa gactgggtgc tgccgcacgg cttcaccgcc 840

aaattcagca ccgacatcca cggcaagcac tatcccgcac acaaacaata caacgatctg 900

ctggttaaca ccgccgccgg tatcggctac cgcaacgccc gttttgatgc cgaaatcatg 960

ccgttcgttt ccaaacgctg gtggcggggc ggcaaagaag aaagcggtct gaaaccgtat 1020

tccgagagct tcggcgccac cctcggcgta agtacccgac tcgaccgccg ctggcggctg 1080

aaccaatacg cccgcatcga aaaaatcaac cacgaacacc gcttccgctt cgacggcatc 1140

cgccgccaaa ccggccacac cctgatttac caatccaacc cgcgccaagc atggttcggc 1200

ggattggatt tccagcgcga aaccctacac gaccccgaca acagcaacca ccaatggaca 1260

gcatcgctgg gctggataca ggaatggccc aaaggcttca gcacccgcac ccgcgccgca 1320

tggagcaaac aaacctacca cgcccccatg ccttggccga ttcaaaaaaa ccgaaaagac 1380

cgagccttgc agctcaacct ttccgtatgg caccgcaata tccatttctg gggcattacc 1440

ccgcgcatca cttggcagca tacccgcaac aagagtaacg tgtttctcta tgattatcgc 1500

aaacagaata tgtttgtaga attttccaaa acattttaa 1539

<210> 438

<211> 512

<212> PRT

<213> N. weaveri SLAM 2

<400> 438

Met His Thr Asn Thr His Arg Ser Gly Arg Leu Lys Thr Ser Lys Ala
1 5 10 15

Gly Phe Ala Lys Thr Ser Phe Ala Ser Phe Ala Lys Ile Gly Lys Ala
20 25 30

Gly Phe Thr Lys Thr Gly Phe Thr Thr Ala Leu Leu Leu Phe Thr Cys
35 40 45

Thr Thr Thr Ala Gln Thr Leu Thr Pro Glu Gln Lys Pro Glu Pro Val
50 55 60

Gln Pro Glu Leu Pro Glu Leu Ala Ser Asp Gln Pro Val Trp Gln Pro
65 70 75 80

Ala Glu Ala Ala Ser Ala Pro Ile Gln Asp Ile Asp Glu Ala Thr Leu
85 90 95

Leu Ala Arg Pro Gln Leu Leu Asn Leu Leu Leu Asp Lys Ser Val Leu

100 105 110

Arg Asn Asp Phe Asp Gly Ile Gly Val Leu Leu Pro Val Tyr Arg Lys

115 120 125

Leu Pro Ser Ser Asn Arg Asp Pro Ile Leu Leu Gln Leu Ala Glu Ser

130 135 140

Lys Leu Ala Met His Gln Gly Arg Phe Gly Glu Ala Val Ala Gly Leu

145 150 155 160

Arg Asn Leu Ile Ala Glu Lys Pro Glu Leu Asn Val Ile Arg Met Tyr

165 170 175

Leu Ala Ile Ala Leu Phe Tyr Asp Arg Gln Asp Leu Ala Ala Lys Asp

180 185 190

Gln Phe Thr Lys Leu Leu Ala Gln Ser Asp Leu Pro Glu Pro Glu Lys

195 200 205

Gln Ala Ile Asn Arg Phe Leu Asp Glu Leu Arg Gln Ser His Arg Trp

210 215 220

Gln Phe Ser Gly Gly Ala Asn Tyr Thr Tyr Glu Pro Asn Ile Asn Asn

225 230 235 240

Ala Pro Ile Val Lys Gln Gln Gly Asn Leu Asp Thr Arg Ser Gln Pro

245 250 255

Glu Ser Ala His Gly Val Ser Tyr Arg Ile Gly Ala Glu Lys Asp Trp

260 265 270

Val Leu Pro His Gly Phe Thr Ala Lys Phe Ser Thr Asp Ile His Gly

275 280 285

Lys His Tyr Pro Ala His Lys Gln Tyr Asn Asp Leu Leu Val Asn Thr

290 295 300

Ala Ala Gly Ile Gly Tyr Arg Asn Ala Arg Phe Asp Ala Glu Ile Met

305 310 315 320

Pro Phe Val Ser Lys Arg Trp Trp Arg Gly Gly Lys Glu Glu Ser Gly

325 330 335

Leu Lys Pro Tyr Ser Glu Ser Phe Gly Ala Thr Leu Gly Val Ser Thr

340 345 350

Arg Leu Asp Arg Arg Trp Arg Leu Asn Gln Tyr Ala Arg Ile Glu Lys

355 360 365

Ile Asn His Glu His Arg Phe Arg Phe Asp Gly Ile Arg Arg Gln Thr

370 375 380

Gly His Thr Leu Ile Tyr Gln Ser Asn Pro Arg Gln Ala Trp Phe Gly

385 390 395 400

Gly Leu Asp Phe Gln Arg Glu Thr Leu His Asp Pro Asp Asn Ser Asn

405 410 415

His Gln Trp Thr Ala Ser Leu Gly Trp Ile Gln Glu Trp Pro Lys Gly

420 425 430

Phe Ser Thr Arg Thr Arg Ala Ala Trp Ser Lys Gln Thr Tyr His Ala

435 440 445

Pro Met Pro Trp Pro Ile Gln Lys Asn Arg Lys Asp Arg Ala Leu Gln

450 455 460

Leu Asn Leu Ser Val Trp His Arg Asn Ile His Phe Trp Gly Ile Thr

465 470 475 480

Pro Arg Ile Thr Trp Gln His Thr Arg Asn Lys Ser Asn Val Phe Leu

485 490 495

Tyr Asp Tyr Arg Lys Gln Asn Met Phe Val Glu Phe Ser Lys Thr Phe

500 505 510

<210> 439

<211> 1428

<212> DNA

<213> N. weaveri SLAM 3

<400> 439

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gacacggccc aacgcctgtg gcagaccacc cgtcaggcag tccaaatcca agagcggaaa 120

agtgtcgaag acaacaccct gaacaccggc atggaaagtc cgcaagcccg ccgtcaagac 180

accgcacaag aagacaacgg cgaagccctg tttatggctg tcaaccgcag cgactggccg 240

caagtccgcc gcctgctcaa ccaataccgc caacaagccc attacgatca ggacattgcc 300

ctatttgccg aagcggcact caacaaatca gacggccgca tgaaagaagc gcggcaaaaa 360

tacgaacaac tattgcaacg ccaacccgat ttcacacgag gccggctcga cttggcacgc 420

ctgctgttcg acgaccacct gaaccgcgaa tccgcagccg aatttgccaa agccaagcaa 480

gaacccctgc ccgaacccgt attaaacaat attcaagctt ttcagacggc catcgaccga 540

cgccgcagct ggcagggttc ggtcaatgtc ggcggcattt ggaacagcaa cgtcaaccaa 600

ggcagcaacg gcatccactg cacccatgaa ttcgaaggca aatgtatcgg caactattgg 660

acggccgaca aacccgaaac cgccgccggt ctcaaatacg aaaccgccgt ctcacgccac 720

tggcaagtga aagggcatca cggggtcaat gtccgcgctt tggcctacgg ccgcgtttac 780

cgcaaccacc aaaaacacaa cgaacatacc gccaacttaa gcgcaggcta ccaatttacc 840

aacgcccgcc gcaccgtcac cgccgcaccg ttatgggaat ggagtgcaga aggcaaacac 900

gcctcacacc gcgcttacgg cctacgtacc gaatgggacg aaaatctcgg caactggtct 960

tggaacactg aagccgaatg gaaaaaactc aaatacttcg atgaagaatc ggcgcacaac 1020

aacggcacgt cgctggccgt atacaacacc gtttcctaca gcccccgcgc cgactgggcc 1080

gtcttcggag gcttggattg gctgcaacgc aaaacttcag acggccaagg cgattaccgc 1140

cagccaagcc tgcgtttggg cataggcaaa caattcgagc agggttttga cgcttccgca 1200

cacgccgttt tccaacagcg cacctacaaa agcgaagacc gcattctgga aaaacgccgc 1260

cgcgaccacg aacaaaccta tattctcaac atcggcgcag aacgctggcg gtttgccggt 1320

atgaaaccta cgctgacctt caaacaccgc agggttaaca gcaatatcca atggctgtac 1380

caataccggc aaaacgaagt cggcgtttcg ctgatgaaag tgttttaa 1428

<210> 440

<211> 475

<212> PRT

<213> N. weaveri SLAM 3

<400> 440

Met Leu Lys Lys Ser Met Tyr Leu Cys Leu Thr Val Ser Leu Pro Ala
1 5 10 15

Val Ala Ala Asp Asp Thr Ala Gln Arg Leu Trp Gln Thr Thr Arg Gln
20 25 30

Ala Val Gln Ile Gln Glu Arg Lys Ser Val Glu Asp Asn Thr Leu Asn
35 40 45

Thr Gly Met Glu Ser Pro Gln Ala Arg Arg Gln Asp Thr Ala Gln Glu

50 55 60

Asp Asn Gly Glu Ala Leu Phe Met Ala Val Asn Arg Ser Asp Trp Pro
65 70 75 80
Gln Val Arg Arg Leu Leu Asn Gln Tyr Arg Gln Gln Ala His Tyr Asp
85 90 95
Gln Asp Ile Ala Leu Phe Ala Glu Ala Ala Leu Asn Lys Ser Asp Gly
100 105 110
Arg Met Lys Glu Ala Arg Gln Lys Tyr Glu Gln Leu Leu Gln Arg Gln
115 120 125

Pro Asp Phe Thr Arg Gly Arg Leu Asp Leu Ala Arg Leu Leu Phe Asp
130 135 140
Asp His Leu Asn Arg Glu Ser Ala Ala Glu Phe Ala Lys Ala Lys Gln
145 150 155 160
Glu Pro Leu Pro Glu Pro Val Leu Asn Asn Ile Gln Ala Phe Gln Thr
165 170 175
Ala Ile Asp Arg Arg Arg Ser Trp Gln Gly Ser Val Asn Val Gly Gly
180 185 190

Ile Trp Asn Ser Asn Val Asn Gln Gly Ser Asn Gly Ile His Cys Thr
195 200 205
His Glu Phe Glu Gly Lys Cys Ile Gly Asn Tyr Trp Thr Ala Asp Lys
210 215 220
Pro Glu Thr Ala Ala Gly Leu Lys Tyr Glu Thr Ala Val Ser Arg His
225 230 235 240
Trp Gln Val Lys Gly His His Gly Val Asn Val Arg Ala Leu Ala Tyr
245 250 255

Gly Arg Val Tyr Arg Asn His Gln Lys His Asn Glu His Thr Ala Asn
260 265 270
Leu Ser Ala Gly Tyr Gln Phe Thr Asn Ala Arg Arg Thr Val Thr Ala
275 280 285
Ala Pro Leu Trp Glu Trp Ser Ala Glu Gly Lys His Ala Ser His Arg
290 295 300

Ala Tyr Gly Leu Arg Thr Glu Trp Asp Glu Asn Leu Gly Asn Trp Ser
305 310 315 320

Trp Asn Thr Glu Ala Glu Trp Lys Lys Leu Lys Tyr Phe Asp Glu Glu
325 330 335
Ser Ala His Asn Asn Gly Thr Ser Leu Ala Val Tyr Asn Thr Val Ser
340 345 350
Tyr Ser Pro Arg Ala Asp Trp Ala Val Phe Gly Gly Leu Asp Trp Leu
355 360 365
Gln Arg Lys Thr Ser Asp Gly Gln Gly Asp Tyr Arg Gln Pro Ser Leu
370 375 380

Arg Leu Gly Ile Gly Lys Gln Phe Glu Gln Gly Phe Asp Ala Ser Ala
385 390 395 400
His Ala Val Phe Gln Gln Arg Thr Tyr Lys Ser Glu Asp Arg Ile Leu
405 410 415
Glu Lys Arg Arg Arg Asp His Glu Gln Thr Tyr Ile Leu Asn Ile Gly
420 425 430
Ala Glu Arg Trp Arg Phe Ala Gly Met Lys Pro Thr Leu Thr Phe Lys
435 440 445

His Arg Arg Val Asn Ser Asn Ile Gln Trp Leu Tyr Gln Tyr Arg Gln
450 455 460
Asn Glu Val Gly Val Ser Leu Met Lys Val Phe
465 470 475

<210> 441
<211> 1527
<212> DNA
<213> N. weaveri SLAM 4
<400> 441

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acgttgcaaa aacaatcgca ccaaactacc caagcgcagg aacattctgc caatcaaacc 180

actgtaccca ccattaccaa tcaagattta atccaaaatc cggaactgct gactgctcta 240

atgcaacaag ccatcgatac caagcagcaa gacttactga cctctctttc tgaagcctac 300

gccatgctgc ctgaacaaca tcaaaatcct gcgatgcggc aacaagcctc aggaacgctc 360

gcatatctga aaaaagacta taaatccgcc attaaaatct ataacaactt attacaagaa 420

atccctgaaa atccgcgaat caggttggat cttgctgcca tgcagtttga agacaagcaa 480

tggtcagaat ctctcaatca cttcaacacc gtttttttccc aaccggaaac ccctgaaaat 540

gtaaaataca atatcgcacg gtttcaaaac accataagaa ataccactgc ttggcaacta 600

aatgctggac tgacccctac ccgccaatca aacatcaacg atgctccccc gaaatactgc 660

ataagcaacc gcgtatgttc aacagaaaca cctgtttcag caacaggcct ttcctaccac 720

ttgggtataa gcaagctcat gccgctgaaa acaaaccata acttaatctt tcaaagtcat 780

atcaacggaa caagctattt cctggataaa aaatccgaat acgaccatgc tttttccaga 840

atccatctgg gctggcaatg gcaggattac cgacactctt tatcgattaa gccctttttac 900

caagcccaat ttggcggaag cgacggcttc agcagcaaac ctaaaaagtc aaagcgggtt 960

ctgccttata tgcttaacca tggaataggc gcacagattg cttacaccca tacccattcc 1020

aacaaaatgc aaagtcaata ttcattcgag cgatatgctg tagactatag agaagcaaac 1080

agagccaaat tgaataacgg tttgcaagac agctcctata catccttagc gtatcaaatc 1140

acacccgata tgctattaat cggcagctat caattcaacc gcttcattcc caaacacaga 1200

caaatccact ctaagcaaaa caacgccgct tataaccgtc atgcattcag cttgggatgg 1260

atccaacatt ggaaacatac cggcggactc gagagcagta ttttttacac ccaagccaaa 1320

cgcaattaca aaggcattgc cagcttaagc aacgaatcac aaagaaacaa agaaacaaca 1380

tggaatatca gcttaagcca caacaaactg tcttataaag gctttaaacc caaattaaac 1440

tttcaccgct acacggttaa cagtaatcaa gcatgggcaa ctcgaaaaaa taccaaccta 1500

tccgttaccg tagaaaaaaa cttttaa 1527

<210> 442

<211> 508

<212> PRT

<213> N. weaveri SLAM 4

<400> 442

Met Lys Lys Ile Leu Leu Thr Leu Ile Ile Ile Pro Met Ser Asn Leu

1 5 10 15

Thr Thr Ala Ser Ile Ile His Pro Pro Thr Asp Gln Gln Ser Glu Gln

20 25 30

Ile Gln Gln Glu Gln Trp Val Glu Thr Leu Gln Lys Gln Ser His Gln

35 40 45

Thr Thr Gln Ala Gln Glu His Ser Ala Asn Gln Thr Thr Val Pro Thr

50 55 60

Ile Thr Asn Gln Asp Leu Ile Gln Asn Pro Glu Leu Leu Thr Ala Leu

65 70 75 80

Met Gln Gln Ala Ile Asp Thr Lys Gln Gln Asp Leu Leu Thr Ser Leu

85 90 95

Ser Glu Ala Tyr Ala Met Leu Pro Glu Gln His Gln Asn Pro Ala Met

100 105 110

Arg Gln Gln Ala Ser Gly Thr Leu Ala Tyr Leu Lys Lys Asp Tyr Lys

115 120 125

Ser Ala Ile Lys Ile Tyr Asn Asn Leu Leu Gln Glu Ile Pro Glu Asn

130 135 140

Pro Arg Ile Arg Leu Asp Leu Ala Ala Met Gln Phe Glu Asp Lys Gln

145 150 155 160

Trp Ser Glu Ser Leu Asn His Phe Asn Thr Val Phe Ser Gln Pro Glu

165 170 175

Thr Pro Glu Asn Val Lys Tyr Asn Ile Ala Arg Phe Gln Asn Thr Ile

180 185 190

Arg Asn Thr Thr Ala Trp Gln Leu Asn Ala Gly Leu Thr Pro Thr Arg

195 200 205

Gln Ser Asn Ile Asn Asp Ala Pro Pro Lys Tyr Cys Ile Ser Asn Arg

210 215 220

Val Cys Ser Thr Glu Thr Pro Val Ser Ala Thr Gly Leu Ser Tyr His

225 230 235 240

Leu Gly Ile Ser Lys Leu Met Pro Leu Lys Thr Asn His Asn Leu Ile

245 250 255

Phe Gln Ser His Ile Asn Gly Thr Ser Tyr Phe Leu Asp Lys Lys Ser

260 265 270

Glu Tyr Asp His Ala Phe Ser Arg Ile His Leu Gly Trp Gln Trp Gln

275 280 285

Asp Tyr Arg His Ser Leu Ser Ile Lys Pro Phe Tyr Gln Ala Gln Phe

290 295 300

Gly Gly Ser Asp Gly Phe Ser Ser Lys Pro Lys Lys Ser Lys Arg Val

305 310 315 320

Leu Pro Tyr Met Leu Asn His Gly Ile Gly Ala Gln Ile Ala Tyr Thr

325 330 335

His Thr His Ser Asn Lys Met Gln Ser Gln Tyr Ser Phe Glu Arg Tyr

340 345 350

Ala Val Asp Tyr Arg Glu Ala Asn Arg Ala Lys Leu Asn Asn Gly Leu

355 360 365

Gln Asp Ser Ser Tyr Thr Ser Leu Ala Tyr Gln Ile Thr Pro Asp Met

370 375 380

Leu Leu Ile Gly Ser Tyr Gln Phe Asn Arg Phe Ile Pro Lys His Arg

385 390 395 400

Gln Ile His Ser Lys Gln Asn Asn Ala Ala Tyr Asn Arg His Ala Phe

405 410 415

Ser Leu Gly Trp Ile Gln His Trp Lys His Thr Gly Gly Leu Glu Ser

420 425 430

Ser Ile Phe Tyr Thr Gln Ala Lys Arg Asn Tyr Lys Gly Ile Ala Ser

435 440 445

Leu Ser Asn Glu Ser Gln Arg Asn Lys Glu Thr Thr Trp Asn Ile Ser

450 455 460

Leu Ser His Asn Lys Leu Ser Tyr Lys Gly Phe Lys Pro Lys Leu Asn

465 470 475 480

Phe His Arg Tyr Thr Val Asn Ser Asn Gln Ala Trp Ala Thr Arg Lys

485 490 495

Asn Thr Asn Leu Ser Val Thr Val Glu Lys Asn Phe

500 505

<210> 443

<211> 1515

<212> DNA

<213> Neisseria sp GTA CT1 SLAM 1

<400> 443

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tgcaccattg caacccaaac gtcttacgaa aacatgaaaa cactcttact cctctccctg 120

ctcgccgtgt ccgcagcgga agccgccgac gtgccacccg agcctcaaaa ccagcctgcc 180

cccgagttgc aggtcaaaac ggcagaacct gcccctgtcg aagaagcagc ggccaaacct 240

gccgccgaaa cgtcgtctga aaaagtcgtc aacgtcgatg ccaaaaccct gctcgacaat 300

ccccaattgc tttcccgcgc catgtattcc gccgttgtgt cgcgcaacat cgcgggcatc 360

aaagtcgtcc tgccgattta cgaacaatgg cagggacacg ataaaaacat ggcgctctac 420

gcgcacggat tggttgccca agacgaaggc aaaatgaaag aagccatcgg gtattaccgt 480

caatttatcg ctgaaaaccc cgatgccccc gtcgtccgct ggcagcttgc cactgctttg 540

tttgaagaca agcaaaacga agccgccgcc gaccagttcg acaaactcaa aacagaagcc 600

aacctgcccg agccgctcgt caaaggcatc gaatcctacc gtaaagcatt gcgcgagcgc 660

gattcgtgga aattcaacgc cggtttgagc gttacccgcg aacaaaacat caaccaagcc 720

cccagccgcc gcacatacgg caactggacc ttccctgagc ctatcgacgc caccgccatc 780

aactaccaac tcggcgcaga gaaaaaatgg tcgctgccca aaggctggta cgttacggca 840

ggcgcggaca attacggcaa aatttatccc gaacaaacca agtataacga cgtaaccacc 900

cgcttctcag taggcgcagg ctatgccgac cagcgcaacg acatcggctt gaccccgttc 960

cacgaacgcc gcttctacgg caacgacccg tacacctact ccagcggtgc gcgcctgcac 1020

atcaaccgct ggtggcagcc taagctgcaa accttgagcg ccgttgaaat gggtcgtctg 1080

aaaaacaccc gccgcgcccg ttccgacagc aacaaccgcc tgctgagcaa ttccgtcgtc 1140

tattaccgaa acgcccgcca atactgggtc ggcggttttg acatctatca ggaacgcaat 1200

aaagaagaca aatcggacag cttcgaccgt tacagcctcc gtaccgcatg ggggcaggaa 1260

tggggcaaag ggctgtccac catgttgcgg ctgagtgcgg cgcaacgccg ttatcaaacg 1320

cccagccttt tgagcggtca ggaaaaccgc cgcgataaag aagcggatat ttcgctcgcc 1380

gtgtggcacc gcgctttcca cttcaaaggc atcaccccgc gcctgaccgt cgcccaccac 1440

aaaacatgga gcaacgacaa atattacgaa tacggcaaaa ccagaatgtt tgtcgaattc 1500

agcaaaacgt tctga 1515

<210> 444

<211> 504

<212> PRT

<213> Neisseria sp GTA CT1 SLAM 1

<400> 444

Met Pro Glu Ser Thr Lys Met Pro Asp Met Val Ser Pro Gln Ile Lys
1 5 10 15

Asn Ala Asp Ser Cys Thr Ile Ala Thr Gln Thr Ser Tyr Glu Asn Met
20 25 30

Lys Thr Leu Leu Leu Leu Ser Leu Leu Ala Val Ser Ala Ala Glu Ala
35 40 45

Ala Asp Val Pro Pro Glu Pro Gln Asn Gln Pro Ala Pro Glu Leu Gln
50 55 60

Val Lys Thr Ala Glu Pro Ala Pro Val Glu Glu Ala Ala Ala Lys Pro
65 70 75 80

Ala Ala Glu Thr Ser Ser Glu Lys Val Val Asn Val Asp Ala Lys Thr
85 90 95

Leu Leu Asp Asn Pro Gln Leu Leu Ser Arg Ala Met Tyr Ser Ala Val
100 105 110

Val Ser Arg Asn Ile Ala Gly Ile Lys Val Val Leu Pro Ile Tyr Glu
115 120 125

Gln Trp Gln Gly His Asp Lys Asn Met Ala Leu Tyr Ala His Gly Leu
130 135 140

Val Ala Gln Asp Glu Gly Lys Met Lys Glu Ala Ile Gly Tyr Tyr Arg
145 150 155 160

Gln Phe Ile Ala Glu Asn Pro Asp Ala Pro Val Val Arg Trp Gln Leu
165 170 175

Ala Thr Ala Leu Phe Glu Asp Lys Gln Asn Glu Ala Ala Ala Asp Gln
180 185 190

Phe Asp Lys Leu Lys Thr Glu Ala Asn Leu Pro Glu Pro Leu Val Lys
195 200 205

Gly Ile Glu Ser Tyr Arg Lys Ala Leu Arg Glu Arg Asp Ser Trp Lys
210 215 220

Phe Asn Ala Gly Leu Ser Val Thr Arg Glu Gln Asn Ile Asn Gln Ala

225 230 235 240

Pro Ser Arg Arg Thr Tyr Gly Asn Trp Thr Phe Pro Glu Pro Ile Asp
245 250 255
Ala Thr Ala Ile Asn Tyr Gln Leu Gly Ala Glu Lys Lys Trp Ser Leu
260 265 270
Pro Lys Gly Trp Tyr Val Thr Ala Gly Ala Asp Asn Tyr Gly Lys Ile
275 280 285
Tyr Pro Glu Gln Thr Lys Tyr Asn Asp Val Thr Thr Arg Phe Ser Val
290 295 300

Gly Ala Gly Tyr Ala Asp Gln Arg Asn Asp Ile Gly Leu Thr Pro Phe
305 310 315 320
His Glu Arg Arg Phe Tyr Gly Asn Asp Pro Tyr Thr Tyr Ser Ser Gly
325 330 335
Ala Arg Leu His Ile Asn Arg Trp Trp Gln Pro Lys Leu Gln Thr Leu
340 345 350
Ser Ala Val Glu Met Gly Arg Leu Lys Asn Thr Arg Arg Ala Arg Ser
355 360 365

Asp Ser Asn Asn Arg Leu Leu Ser Asn Ser Val Val Tyr Tyr Arg Asn
370 375 380
Ala Arg Gln Tyr Trp Val Gly Gly Phe Asp Ile Tyr Gln Glu Arg Asn
385 390 395 400
Lys Glu Asp Lys Ser Asp Ser Phe Asp Arg Tyr Ser Leu Arg Thr Ala
405 410 415
Trp Gly Gln Glu Trp Gly Lys Gly Leu Ser Thr Met Leu Arg Leu Ser
420 425 430

Ala Ala Gln Arg Arg Tyr Gln Thr Pro Ser Leu Leu Ser Gly Gln Glu
435 440 445
Asn Arg Arg Asp Lys Glu Ala Asp Ile Ser Leu Ala Val Trp His Arg
450 455 460
Ala Phe His Phe Lys Gly Ile Thr Pro Arg Leu Thr Val Ala His His
465 470 475 480

Lys Thr Trp Ser Asn Asp Lys Tyr Tyr Glu Tyr Gly Lys Thr Arg Met
485 490 495

Phe Val Glu Phe Ser Lys Thr Phe
500

<210> 445

<211> 1464

<212> DNA

<213> Neisseria sp GTA CT1 SLAM 2

<400> 445

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gaaaccattg ctaaccctga aactgaagcc gatcgccaga tggaaagaat ccaagaaatg 120

gccattccta aaccaccgga ggtaggtacc tccctttga aaggtgtcaa ggcttctttg 180

aatgagcata ctcagacatt gacattagat gatctagcca aacaaccaga gctgaccgaa 240

cctttgttaa atcaagcatt gcaagcgcga aactatattg ctgcagagca gctcttgcct 300

atatatcgta aatgggatat gcatgaccct attttattgg attatgcgca aggcgcaatt 360

tggcgttcgc aaggaaagca taaaaaagcc attacacttt accgtaatat tcttgttcga 420

catcctaatc ttgtcaccgt tcgtctagac ttggctgcta tgctttatga ggataagcaa 480

acccgtaatt cacaacatga atttaatgct gccaaaaagc aaggtttgcc agaagatgtc 540

cttcctacta ttgcccttta tgaaaacgct atggggcaaa ataaatggca attttcaggc 600

agtctgagtt acacccaaga caacaatatc aacaacgttt cagctgagcg tgaaatccat 660

cttcctcaat ttgataactt ggcttttgaa aaaaattctg actatctgcc acaaaaaggg 720

catggtttta cctacgccct atccgttgat cgcgatatca atctcaaagg caaccattat 780

ttcgctcttt caggcgatgt cgacggtgtc agctattggg ataatcatga ttatgatgat 840

caaacggcaa aagtcagtct tggttataaa aataaaagtt ttaaaacaga tagttttgtt 900

atgccatttt tagaaaagcg tcgctacgga aatcatcctt attacacgcg tacaggtgta 960

gatttaggtg tttcacgttg gataaaacca aatttacgtc tatctgccaa cggaaccttt 1020

gcacaaaaag attatgccta taccaaacaa caagggaaag attatcagat tggatttggg 1080

acgacctacc tgatgaatga taaaacctat ttcttaggag gtttgagtta tgcgcgtgac 1140

aaagttgaaa atttcgcagg cagcagctcc aaacggatag gaggttactt aggttggggg 1200

caaatttggg gtgaaaattt caatagtcgc cttatcatca atcactacaa tgaacgcttt 1260

gatggaaaac attacgtctt taccgaccgt catcgtacag ataatgtcgt ggttaccaat 1320

ttaagcctct ggcacaataa actgagtttt ctagaaatta cgccgagatt aaattggcga 1380

tatacaaaca ataacagcaa tattaatgaa cttcatggtt atacaaaaaa tcgtgtattt 1440

atagattttg agaaaacgtt ttga 1464

<210> 446

<211> 487

<212> PRT

<213> Neisseria sp GTA CT1 SLAM 2

<400> 446

Met Lys Ser Asn Gln Phe Ile Phe Ile Ala Gly Ile Leu Phe Pro Ile
1 5 10 15

Met Val Thr Ala Glu Thr Ile Ala Asn Pro Glu Thr Glu Ala Asp Arg
20 25 30

Gln Met Glu Arg Ile Gln Glu Met Ala Ile Pro Lys Pro Pro Glu Val
35 40 45

Gly Thr Ser Leu Leu Lys Gly Val Lys Ala Ser Leu Asn Glu His Thr
50 55 60

Gln Thr Leu Thr Leu Asp Asp Leu Ala Lys Gln Pro Glu Leu Thr Glu
65 70 75 80

Pro Leu Leu Asn Gln Ala Leu Gln Ala Arg Asn Tyr Ile Ala Ala Glu
85 90 95

Gln Leu Leu Pro Ile Tyr Arg Lys Trp Asp Met His Asp Pro Ile Leu
100 105 110

Leu Asp Tyr Ala Gln Gly Ala Ile Trp Arg Ser Gln Gly Lys His Lys
115 120 125

Lys Ala Ile Thr Leu Tyr Arg Asn Ile Leu Val Arg His Pro Asn Leu
130 135 140

Val Thr Val Arg Leu Asp Leu Ala Ala Met Leu Tyr Glu Asp Lys Gln
145 150 155 160

Thr Arg Asn Ser Gln His Glu Phe Asn Ala Ala Lys Lys Gln Gly Leu
165 170 175

Pro Glu Asp Val Leu Pro Thr Ile Ala Leu Tyr Glu Asn Ala Met Gly

180 185 190

Gln Asn Lys Trp Gln Phe Ser Gly Ser Leu Ser Tyr Thr Gln Asp Asn
195 200 205
Asn Ile Asn Asn Val Ser Ala Glu Arg Glu Ile His Leu Pro Gln Phe
210 215 220
Asp Asn Leu Ala Phe Glu Lys Asn Ser Asp Tyr Leu Pro Gln Lys Gly
225 230 235 240
His Gly Phe Thr Tyr Ala Leu Ser Val Asp Arg Asp Ile Asn Leu Lys
245 250 255

Gly Asn His Tyr Phe Ala Leu Ser Gly Asp Val Asp Gly Val Ser Tyr
260 265 270
Trp Asp Asn His Asp Tyr Asp Asp Gln Thr Ala Lys Val Ser Leu Gly
275 280 285
Tyr Lys Asn Lys Ser Phe Lys Thr Asp Ser Phe Val Met Pro Phe Leu
290 295 300
Glu Lys Arg Arg Tyr Gly Asn His Pro Tyr Tyr Thr Arg Thr Gly Val
305 310 315 320

Asp Leu Gly Val Ser Arg Trp Ile Lys Pro Asn Leu Arg Leu Ser Ala
325 330 335
Asn Gly Thr Phe Ala Gln Lys Asp Tyr Ala Tyr Thr Lys Gln Gln Gly
340 345 350
Lys Asp Tyr Gln Ile Gly Phe Gly Thr Thr Tyr Leu Met Asn Asp Lys
355 360 365
Thr Tyr Phe Leu Gly Gly Leu Ser Tyr Ala Arg Asp Lys Val Glu Asn
370 375 380

Phe Ala Gly Ser Ser Ser Lys Arg Ile Gly Gly Tyr Leu Gly Trp Gly
385 390 395 400
Gln Ile Trp Gly Glu Asn Phe Asn Ser Arg Leu Ile Ile Asn His Tyr
405 410 415
Asn Glu Arg Phe Asp Gly Lys His Tyr Val Phe Thr Asp Arg His Arg
420 425 430

Thr Asp Asn Val Val Val Thr Asn Leu Ser Leu Trp His Asn Lys Leu
435 440 445

Ser Phe Leu Glu Ile Thr Pro Arg Leu Asn Trp Arg Tyr Thr Asn Asn
450 455 460
Asn Ser Asn Ile Asn Glu Leu His Gly Tyr Thr Lys Asn Arg Val Phe
465 470 475 480
Ile Asp Phe Glu Lys Thr Phe
485

<210> 447
<211> 1440
<212> DNA
<213> Neisseria sp GTA CT1 SLAM 3
<400> 447

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cgttctgact tttcagacga ccgtaccgcg caacgcctgt ggcaaaacac ccgccaaacc 120

atgcaggagc aggaacaaaa agtgcgcgaa taccgcctcg acattccctc cgaaaacatc 180
gggcagacag ccgaaaccga ccccgaagcc gaccaaggcg aagccctgtt taacgccgtc 240
aaccgcagcg actggcaaac cgtgcgcccg ctgcttgaac gttataccca gcaaaccgaa 300
tacgaccccg acatcgccct ctttgcccgc gcctcgctcg cccgcggcga aggcaggtgg 360
aaagatgcca aacaagacta cgaaaccctg ctgcaacgcc atcccgactt cacgcgcgga 420
cggctcgatt acgcccgcct gctctttgaa ggtcgtctga accgcgaagc cacttccgaa 480
tttatgcgcc ttcaaaacga agacctgccc gaagccgtca aagaaaacat cggccatttc 540

cgcgactctc taaaccaacg ccaaagctgg cagggcagcc tttccgtcgg cgccgtccac 600
aacagcaaca tcaacgaagc cagcggcaaa gtgtggtgta aaaccgaaat agacggcgaa 660
tgctgggaag aattttcagg cgaccagccc atttccgcca acggcatcaa atacgaagcc 720
gccgccgtcc gccgctggca gattaaagga caccacggca tcgccgcccg cgcgctcggc 780
tacggccgct tctaccgcga ccataaagac ttcaacgaac acacactcaa cctcagcgca 840
ggctatcagt ttgaaaacca ccgccacacc ttcgccctcg ccccgctcgt cgaatggaac 900
ggcagcggcg gcaaaaccct caaccgcgcc tacggcgtgc gcagcgagtg gaacctcgac 960

aaaggcagct ggacgtggaa taccgaagcc gagtggaaat acctttccta ttccgacaaa 1020
acccgcctac tcgacggcag cctcttctcc gtttacaaca ccctgtccta cttcccgcgc 1080

aacgacctca tgctctacgg cggcatagac tggcagcagc gcaaagccaa agagccggta 1140

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gaacaacgcc gccgcgacaa agaacagacc taccgcctca gcataggcgc ggaccgctgg 1320

aaattcgccg gcctcaagcc cgtcctcagc tacaaacacc gccgcgtcca cggcaacacc 1380

gactggctgt acagctacaa gcaaaacgaa gtcggtctgt cgctggtgaa atcgttctaa 1440

<210> 448

<211> 479

<212> PRT

<213> Neisseria sp GTA CT1 SLAM 3

<400> 448

Met Tyr Lys Pro Ser Ala Cys Leu Leu Leu Phe Leu Ala Ala Pro Val
1 5 10 15

Leu Ala Ala Pro Arg Ser Asp Phe Ser Asp Asp Arg Thr Ala Gln Arg
20 25 30

Leu Trp Gln Asn Thr Arg Gln Thr Met Gln Glu Gln Glu Gln Lys Val
35 40 45

Arg Glu Tyr Arg Leu Asp Ile Pro Ser Glu Asn Ile Gly Gln Thr Ala
50 55 60

Glu Thr Asp Pro Glu Ala Asp Gln Gly Glu Ala Leu Phe Asn Ala Val
65 70 75 80

Asn Arg Ser Asp Trp Gln Thr Val Arg Pro Leu Leu Glu Arg Tyr Thr
85 90 95

Gln Gln Thr Glu Tyr Asp Pro Asp Ile Ala Leu Phe Ala Arg Ala Ser
100 105 110

Leu Ala Arg Gly Glu Gly Arg Trp Lys Asp Ala Lys Gln Asp Tyr Glu
115 120 125

Thr Leu Leu Gln Arg His Pro Asp Phe Thr Arg Gly Arg Leu Asp Tyr
130 135 140

Ala Arg Leu Leu Phe Glu Gly Arg Leu Asn Arg Glu Ala Thr Ser Glu
145 150 155 160

Phe Met Arg Leu Gln Asn Glu Asp Leu Pro Glu Ala Val Lys Glu Asn

165 170 175

Ile Gly His Phe Arg Asp Ser Leu Asn Gln Arg Gln Ser Trp Gln Gly
180 185 190
Ser Leu Ser Val Gly Ala Val His Asn Ser Asn Ile Asn Glu Ala Ser
195 200 205
Gly Lys Val Trp Cys Lys Thr Glu Ile Asp Gly Glu Cys Trp Glu Glu
210 215 220
Phe Ser Gly Asp Gln Pro Ile Ser Ala Asn Gly Ile Lys Tyr Glu Ala
225 230 235 240

Ala Ala Val Arg Arg Trp Gln Ile Lys Gly His His Gly Ile Ala Ala
245 250 255
Arg Ala Leu Gly Tyr Gly Arg Phe Tyr Arg Asp His Lys Asp Phe Asn
260 265 270
Glu His Thr Leu Asn Leu Ser Ala Gly Tyr Gln Phe Glu Asn His Arg
275 280 285
His Thr Phe Ala Leu Ala Pro Leu Val Glu Trp Asn Gly Ser Gly Gly
290 295 300

Lys Thr Leu Asn Arg Ala Tyr Gly Val Arg Ser Glu Trp Asn Leu Asp
305 310 315 320
Lys Gly Ser Trp Thr Trp Asn Thr Glu Ala Glu Trp Lys Tyr Leu Ser
325 330 335
Tyr Ser Asp Lys Thr Arg Leu Leu Asp Gly Ser Leu Phe Ser Val Tyr
340 345 350
Asn Thr Leu Ser Tyr Phe Pro Arg Asn Asp Leu Met Leu Tyr Gly Gly
355 360 365

Ile Asp Trp Gln Gln Arg Lys Ala Lys Glu Pro Val Asp Ser Tyr Arg
370 375 380
Leu Ile Ser Ala Arg Leu Gly Ala Ala Lys Met Phe Glu Ala Gly Phe
385 390 395 400
Asp Ala Ser Ala Ser Ala Thr Phe Gly Ile Arg Ser His Arg Glu Glu
405 410 415

Asn Ala Val Leu Glu Gln Arg Arg Arg Asp Lys Glu Gln Thr Tyr Arg
420 425 430

Leu Ser Ile Gly Ala Asp Arg Trp Lys Phe Ala Gly Leu Lys Pro Val
435 440 445

Leu Ser Tyr Lys His Arg Arg Val His Gly Asn Thr Asp Trp Leu Tyr
450 455 460

Ser Tyr Lys Gln Asn Glu Val Gly Leu Ser Leu Val Lys Ser Phe
465 470 475

<210> 449

<211> 1467

<212> DNA

<213> Neisseria sp GTA CT1 SLAM 4

<400> 449

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gacagggaag accgcttcat gcagctcaaa cagggaacgg aactccgccg cgcgcagcag 120

gaaaggaacg aagcggacaa tacggcggtt gagttcggcg caggagaagt gcaggacggc 180

gaagatttgg cgttgtcgct gatgaaggcg gtcaacgcgc aaaacgaaga ggaaacggcg 240

cggctgttgg acatttaccg ccgtcaggat gattccgacc ccgatatagt gctgtttgcc 300

gaggctaatc aggcagtgtt ccgcgacgat ttgaaggccg cgctggcgaa ataccgcgaa 360

ctttaccgca aaaatcccga atttctgcgc ggccgcctgg atttggcgcg gctgctgttt 420

atagacaaac aaaacaaaga atcggcggca ttgttcgacg gcatcgatat tcccgaagtg 480

cccgccgtca atgagaaaat caaagtgttt gccgacgctt tgaagaaacg cgatgcgtgg 540

agcggttcgg tttcgttcgg cgcgggttac gacaccaact taaaccagtc gtcgggcgcg 600

acggttgtcc gcaatcagac aagctgcggt ttcgattcga acgggcagcc gattttggac 660

ggcgacggaa tgctgtcctg ccgcaacgaa cagcttgacg cctacgcgcc cgatgcgttg 720

aaaaaccgga tgtgggtata tgaagccaac ttaagcagac gcatatcgct caacggccac 780

cacggcctgc aactgggcgg ctacgcatgg ggtcggctct atcccggcaa caaggaatac 840

ggcgaacaca atatcaacgt cagccccgct tacagttttc agagcaaaga ccattccttc 900

agtatcggcc cgcaggtgca atacgaatgg tcgggcggca aactgcgcga tagcagtgcc 960

ggcatcagca cggcatacag ccgtaccttt tccgaccaag cctcgctggg cgtgcagctc 1020

gaccacaaat acgaccgcta ccgcggtgaa ttaaaacatt tcaacggccc gcagacgctt 1080

ctgttcacca ccgccatcta cgccctgccg aaagactggc tggtattcgg cggctacgac 1140

tacctgcgca aaaacagccg cgaaaaagtg gattcctacc gtaggcacgg tctgcgtgcg 1200

ggtgtcaaca agcgttttga atccggtatc gacgccacct ttcaggcaat ctggcgcaaa 1260

acagcctatc aggactacca tgcctggctg gaaacccgcc gccatgattt cgaacgcacc 1320

tatcagttgg acatcaaatt tgaccgtccg tcctttcgcg gcatcacgcc cgttttcagc 1380

atcaaacaca ccgacaacaa aagctcgtcc tggctgaacc gctacaaacg caacgaattt 1440

accgtcaaag cagaatacag gttttaa 1467

<210> 450

<211> 488

<212> PRT

<213> Neisseria sp GTA CT1 SLAM 4

<400> 450

Met Lys Arg Leu Leu Leu Leu Pro Phe Phe Ile Ser Leu Leu Pro His
1 5 10 15

Ala Phe Ala Asp Asp Arg Glu Asp Arg Phe Met Gln Leu Lys Gln Gly

20 25 30

Thr Glu Leu Arg Arg Ala Gln Gln Glu Arg Asn Glu Ala Asp Asn Thr
35 40 45

Ala Val Glu Phe Gly Ala Gly Glu Val Gln Asp Gly Glu Asp Leu Ala
50 55 60

Leu Ser Leu Met Lys Ala Val Asn Ala Gln Asn Glu Glu Glu Thr Ala
65 70 75 80

Arg Leu Leu Asp Ile Tyr Arg Arg Gln Asp Asp Ser Asp Pro Asp Ile

85 90 95

Val Leu Phe Ala Glu Ala Asn Gln Ala Val Phe Arg Asp Asp Leu Lys
100 105 110

Ala Ala Leu Ala Lys Tyr Arg Glu Leu Tyr Arg Lys Asn Pro Glu Phe
115 120 125

Leu Arg Gly Arg Leu Asp Leu Ala Arg Leu Leu Phe Ile Asp Lys Gln
130 135 140

Asn Lys Glu Ser Ala Ala Leu Phe Asp Gly Ile Asp Ile Pro Glu Val

145 150 155 160

Pro Ala Val Asn Glu Lys Ile Lys Val Phe Ala Asp Ala Leu Lys Lys

165 170 175

Arg Asp Ala Trp Ser Gly Ser Val Ser Phe Gly Ala Gly Tyr Asp Thr

180 185 190

Asn Leu Asn Gln Ser Ser Gly Ala Thr Val Val Arg Asn Gln Thr Ser

195 200 205

Cys Gly Phe Asp Ser Asn Gly Gln Pro Ile Leu Asp Gly Asp Gly Met

210 215 220

Leu Ser Cys Arg Asn Glu Gln Leu Asp Ala Tyr Ala Pro Asp Ala Leu

225 230 235 240

Lys Asn Arg Met Trp Val Tyr Glu Ala Asn Leu Ser Arg Arg Ile Ser

245 250 255

Leu Asn Gly His His Gly Leu Gln Leu Gly Gly Tyr Ala Trp Gly Arg

260 265 270

Leu Tyr Pro Gly Asn Lys Glu Tyr Gly Glu His Asn Ile Asn Val Ser

275 280 285

Pro Ala Tyr Ser Phe Gln Ser Lys Asp His Ser Phe Ser Ile Gly Pro

290 295 300

Gln Val Gln Tyr Glu Trp Ser Gly Gly Lys Leu Arg Asp Ser Ser Ala

305 310 315 320

Gly Ile Ser Thr Ala Tyr Ser Arg Thr Phe Ser Asp Gln Ala Ser Leu

325 330 335

Gly Val Gln Leu Asp His Lys Tyr Asp Arg Tyr Arg Gly Glu Leu Lys

340 345 350

His Phe Asn Gly Pro Gln Thr Leu Leu Phe Thr Thr Ala Ile Tyr Ala

355 360 365

Leu Pro Lys Asp Trp Leu Val Phe Gly Gly Tyr Asp Tyr Leu Arg Lys

370 375 380

Asn Ser Arg Glu Lys Val Asp Ser Tyr Arg Arg His Gly Leu Arg Ala

385 390 395 400

Gly Val Asn Lys Arg Phe Glu Ser Gly Ile Asp Ala Thr Phe Gln Ala

405 410 415

Ile Trp Arg Lys Thr Ala Tyr Gln Asp Tyr His Ala Trp Leu Glu Thr

420 425 430

Arg Arg His Asp Phe Glu Arg Thr Tyr Gln Leu Asp Ile Lys Phe Asp

435 440 445

Arg Pro Ser Phe Arg Gly Ile Thr Pro Val Phe Ser Ile Lys His Thr

450 455 460

Asp Asn Lys Ser Ser Ser Trp Leu Asn Arg Tyr Lys Arg Asn Glu Phe

465 470 475 480

Thr Val Lys Ala Glu Tyr Arg Phe

485

<210> 451

<211> 1476

<212> DNA

<213> Neisseria sp GTA CT1 SLAM 5

<400> 451

atgaacaaat cctgcctcct cctgctcgcc ctgctgcccc tgtccgccca cgcagacagt 60

gacgacctgc gccgcctgtc cgaagaaaac gggcgcgtgc agcagcaata tcgggaaagc 120

ggctggctgg acggcggcac acccgcaggc gacatcgaaa acgacgacgc atacatccgt 180

atcggcggtc agatttacac cgtaggcaac aataccgaag agctggaaag cgcgatttat 240

catgccatta acgaacgtca atggaaaaag gcagaacgct tcgccacgcg ctacgccgcc 300

ctgcccggcc acaatcccgc cctacccaaa ttggtactcg gtttaaaaca acgcgccgaa 360

ggacgcctcg ccgaagcctt acggaacctg caagcggcag aagcactcga ccccgccaac 420

ccgcgcatcc tgctcgaaac cgcgcgcctt tataccgaag acaaccaaaa ccgcgaagcc 480

cgaagcgcat tcgcccgcgc ccaagccgcc gacatcccag aagaaacccg cgccctgatc 540

ggacaatacc tcggcgaaat cgacaaacgc agccgctggc acggacaaat cggcatcgct 600

tacggctaca acagcaacat caaccaatcc gacggctccg tccgctgcat tctgccgctt 660

gacggccaat gcctcgccta ccaaaacctg cccgacccca tccgttcccc cgtatggaat 720

tacagcctga gcgcaggcaa aatcaccccc attaaaggac accacagcct caaaaccaac 780

ctcctcgcct acggcacgca ctaccgccgc aaagacacag acgccgccct gtccgactac 840

ggcagccaaa caggcacact gtctgccggt tacgaatacg ccgacgcaca aagccgcttc 900

tcgctgatgc ccgtttacga acacgaacgg cgcaaccgcc acacctacta caacgcctac 960

ggcgccgaaa cctcgtggac gcataccatc aaccccaaat ggcaggtcaa cgccgactgg 1020

tcgggcaaac gctaccgcca cagcggcacc gcgaaaacct acgccgccga ctacaccgaa 1080

taccgcacag gcttaggcgc agaatacgcc ctgaccccga aaaccggcgt gttcgcaggc 1140

tccgactaca cccgccgcac atacaacggc ggcacatccg accaccgcga atacaccctc 1200

cgcacaggct tatacaccct gtttgacaac ggcacctacc tcaacgccct cgttatgaaa 1260

cggcgcaacc tctacgaccg cgcaggcatc gccgcagacg gacaaagacg cagcgaccgc 1320

caaaccgtct ggctcgccgc cgcaggcttc agacaatggc acatcggcgg cttctacccc 1380

gaactgcgct tcaaacacac caccgtcaaa agcaattccg tgttctaccg ctaccgccaa 1440

aacgaaatca tgctgggcgt gaagaaacag ttttga 1476

<210> 452

<211> 491

<212> PRT

<213> Neisseria sp GTA CT1 SLAM 5

<400> 452

Met Asn Lys Ser Cys Leu Leu Leu Leu Ala Leu Leu Pro Leu Ser Ala

1 5 10 15

His Ala Asp Ser Asp Asp Leu Arg Arg Leu Ser Glu Glu Asn Gly Arg

20 25 30

Val Gln Gln Gln Tyr Arg Glu Ser Gly Trp Leu Asp Gly Gly Thr Pro

35 40 45

Ala Gly Asp Ile Glu Asn Asp Asp Ala Tyr Ile Arg Ile Gly Gly Gln

50 55 60

Ile Tyr Thr Val Gly Asn Asn Thr Glu Glu Leu Glu Ser Ala Ile Tyr

65 70 75 80

His Ala Ile Asn Glu Arg Gln Trp Lys Lys Ala Glu Arg Phe Ala Thr

85 90 95

Arg Tyr Ala Ala Leu Pro Gly His Asn Pro Ala Leu Pro Lys Leu Val

100 105 110

Leu Gly Leu Lys Gln Arg Ala Glu Gly Arg Leu Ala Glu Ala Leu Arg

```
        115                 120                 125
Asn Leu Gln Ala Ala Glu Ala Leu Asp Pro Ala Asn Pro Arg Ile Leu
    130                 135                 140
Leu Glu Thr Ala Arg Leu Tyr Thr Glu Asp Asn Gln Asn Arg Glu Ala
145                 150                 155                 160
Arg Ser Ala Phe Ala Arg Ala Gln Ala Ala Asp Ile Pro Glu Glu Thr
                165                 170                 175
Arg Ala Leu Ile Gly Gln Tyr Leu Gly Glu Ile Asp Lys Arg Ser Arg

            180                 185                 190
Trp His Gly Gln Ile Gly Ile Ala Tyr Gly Tyr Asn Ser Asn Ile Asn
        195                 200                 205
Gln Ser Asp Gly Ser Val Arg Cys Ile Leu Pro Leu Asp Gly Gln Cys
    210                 215                 220
Leu Ala Tyr Gln Asn Leu Pro Asp Pro Ile Arg Ser Pro Val Trp Asn
225                 230                 235                 240
Tyr Ser Leu Ser Ala Gly Lys Ile Thr Pro Ile Lys Gly His His Ser

                245                 250                 255
Leu Lys Thr Asn Leu Leu Ala Tyr Gly Thr His Tyr Arg Arg Lys Asp
            260                 265                 270
Thr Asp Ala Ala Leu Ser Asp Tyr Gly Ser Gln Thr Gly Thr Leu Ser
        275                 280                 285
Ala Gly Tyr Glu Tyr Ala Asp Ala Gln Ser Arg Phe Ser Leu Met Pro
    290                 295                 300
Val Tyr Glu His Glu Arg Arg Asn Arg His Thr Tyr Tyr Asn Ala Tyr

305                 310                 315                 320
Gly Ala Glu Thr Ser Trp Thr His Thr Ile Asn Pro Lys Trp Gln Val
                325                 330                 335
Asn Ala Asp Trp Ser Gly Lys Arg Tyr Arg His Ser Gly Thr Ala Lys
            340                 345                 350
Thr Tyr Ala Ala Asp Tyr Thr Glu Tyr Arg Thr Gly Leu Gly Ala Glu
        355                 360                 365
```

Tyr Ala Leu Thr Pro Lys Thr Gly Val Phe Ala Gly Ser Asp Tyr Thr

370 375 380

Arg Arg Thr Tyr Asn Gly Gly Thr Ser Asp His Arg Glu Tyr Thr Leu

385 390 395 400

Arg Thr Gly Leu Tyr Thr Leu Phe Asp Asn Gly Thr Tyr Leu Asn Ala

405 410 415

Leu Val Met Lys Arg Arg Asn Leu Tyr Asp Arg Ala Gly Ile Ala Ala

420 425 430

Asp Gly Gln Arg Arg Ser Asp Arg Gln Thr Val Trp Leu Ala Ala Ala

435 440 445

Gly Phe Arg Gln Trp His Ile Gly Gly Phe Tyr Pro Glu Leu Arg Phe

450 455 460

Lys His Thr Thr Val Lys Ser Asn Ser Val Phe Tyr Arg Tyr Arg Gln

465 470 475 480

Asn Glu Ile Met Leu Gly Val Lys Lys Gln Phe

485 490

<210> 453

<211> 1416

<212> DNA

<213> Neisseria sp. oral taxon 014 SLAM 1

<400

> 453

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atccaagaaa tggccattcc taaaccaccg gaggtaggca cctccctttt gaatggtgtc 120

aaggcttctt tgaatgagca tactcaaaca ttgacattag atgatctagc caaacaacca 180

gagctggccg aacctttgtt aaatcaagca ttgcaagcgc gaaactatat tgctgcagag 240

cagctcttgc ctatatatcg taaatgggat gggtatgacc caattttatt ggattatgcg 300

caaggcgcaa tttggcgttc gcaaggaaaa catcaaaaag ccattacact ttaccgtaat 360

attcttgttc gacatcctaa tcttgttgcc gtccgtctag acttagctgc tatgctttat 420

gaggataagc aaacccgtaa ttcacaatat gaatttgatg ccgccaaaaa gcaaggttta 480

ccagaagatg tccttcctac tattgccctt tatgaaaacg ctatggggca aaataaatgg 540

caattttcag gcagtctgag ttacacccaa gacaacaata tcaacaacgt ttcagctgag 600

cgtgaaattc atcttcctca gtttggtaac ttggcttttg aaaaaaattc tgattatctg 660

ccacaaaaag ggcatggttt tacctacgcc ttatccgttg atcgagatat caatcttaaa 720

aacaaccatt attttgctct ttcaggcgat gtcgatggtg ttagctattg gaataatcat 780

gattatgatg atcaaacagc aaaggtcagt cttggttata aaaataaaag ttttaaaaca 840

gatagttttg ttatgccatt tttagaaaag cgtcgctacg gaaatcatcc ttattacacg 900

cgtacaggtg tagatttagg tgtttcacgt tggataaaac caaatttacg tctatctgcc 960

aacggaacct ttgcacaaaa agattatgca tataccaaac gacaagggaa agattatcag 1020

attggatttg gggcgaccta cctgatgaat gataaaacct atttcttagg aggtttgaat 1080

tatgcgcgtg acaaagttga aaatttcgca ggcagcagct ccaaacggat aggaggttac 1140

ttaggttggg ggcaaatttg gggtgaaaat ttcaatagcc gccttatcat caatcgctac 1200

aatgaacgct ttgatggaaa acattacgtc tttaccgacc gtcatcgtac agataatgca 1260

gtagttacca atttaagcct ctggcacaat aaactgagtt ttctaggaat tacgccgaga 1320

ttaaattggc gatatgcgaa caataacagc aatattaacg aacttcatag ttatactaaa 1380

aatcgtgtat ttatagattt tgagaaaacg ttctga 1416

<210> 454

<211> 471

<212> PRT

<213> Neisseria sp. oral taxon 014 SLAM 1

<400> 454

Met Val Thr Ala Glu Thr Ile Ala Asn Pro Glu Thr Glu Ala Asp Arg

1 5 10 15

Gln Met Glu Arg Ile Gln Glu Met Ala Ile Pro Lys Pro Pro Glu Val

20 25 30

Gly Thr Ser Leu Leu Asn Gly Val Lys Ala Ser Leu Asn Glu His Thr

35 40 45

Gln Thr Leu Thr Leu Asp Asp Leu Ala Lys Gln Pro Glu Leu Ala Glu

50 55 60

Pro Leu Leu Asn Gln Ala Leu Gln Ala Arg Asn Tyr Ile Ala Ala Glu

65 70 75 80

Gln Leu Leu Pro Ile Tyr Arg Lys Trp Asp Gly Tyr Asp Pro Ile Leu

85 90 95

Leu Asp Tyr Ala Gln Gly Ala Ile Trp Arg Ser Gln Gly Lys His Gln
100 105 110
Lys Ala Ile Thr Leu Tyr Arg Asn Ile Leu Val Arg His Pro Asn Leu
115 120 125
Val Ala Val Arg Leu Asp Leu Ala Ala Met Leu Tyr Glu Asp Lys Gln
130 135 140
Thr Arg Asn Ser Gln Tyr Glu Phe Asp Ala Ala Lys Lys Gln Gly Leu

145 150 155 160
Pro Glu Asp Val Leu Pro Thr Ile Ala Leu Tyr Glu Asn Ala Met Gly
165 170 175
Gln Asn Lys Trp Gln Phe Ser Gly Ser Leu Ser Tyr Thr Gln Asp Asn
180 185 190
Asn Ile Asn Asn Val Ser Ala Glu Arg Glu Ile His Leu Pro Gln Phe
195 200 205
Gly Asn Leu Ala Phe Glu Lys Asn Ser Asp Tyr Leu Pro Gln Lys Gly

210 215 220
His Gly Phe Thr Tyr Ala Leu Ser Val Asp Arg Asp Ile Asn Leu Lys
225 230 235 240
Asn Asn His Tyr Phe Ala Leu Ser Gly Asp Val Asp Gly Val Ser Tyr
245 250 255
Trp Asn Asn His Asp Tyr Asp Asp Gln Thr Ala Lys Val Ser Leu Gly
260 265 270
Tyr Lys Asn Lys Ser Phe Lys Thr Asp Ser Phe Val Met Pro Phe Leu

275 280 285
Glu Lys Arg Arg Tyr Gly Asn His Pro Tyr Tyr Thr Arg Thr Gly Val
290 295 300
Asp Leu Gly Val Ser Arg Trp Ile Lys Pro Asn Leu Arg Leu Ser Ala
305 310 315 320
Asn Gly Thr Phe Ala Gln Lys Asp Tyr Ala Tyr Thr Lys Arg Gln Gly
325 330 335
Lys Asp Tyr Gln Ile Gly Phe Gly Ala Thr Tyr Leu Met Asn Asp Lys

340 345 350

Thr Tyr Phe Leu Gly Gly Leu Asn Tyr Ala Arg Asp Lys Val Glu Asn

355 360 365

Phe Ala Gly Ser Ser Ser Lys Arg Ile Gly Gly Tyr Leu Gly Trp Gly

370 375 380

Gln Ile Trp Gly Glu Asn Phe Asn Ser Arg Leu Ile Ile Asn Arg Tyr

385 390 395 400

Asn Glu Arg Phe Asp Gly Lys His Tyr Val Phe Thr Asp Arg His Arg

405 410 415

Thr Asp Asn Ala Val Val Thr Asn Leu Ser Leu Trp His Asn Lys Leu

420 425 430

Ser Phe Leu Gly Ile Thr Pro Arg Leu Asn Trp Arg Tyr Ala Asn Asn

435 440 445

Asn Ser Asn Ile Asn Glu Leu His Ser Tyr Thr Lys Asn Arg Val Phe

450 455 460

Ile Asp Phe Glu Lys Thr Phe

465 470

<210> 455

<211> 1470

<212> DNA

<213> Neisseria sp. oral taxon 014 SLAM 2

<400> 455

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tttctcaccg cccccgtcct tgccgcgcca cgttccgact tttcagacaa ccgtaccgcg 120

caacgcctgt ggcaggatac ccgccaaacc atgcaggaac aggaacaaaa agtgcgcgaa 180

taccgcctcg acattccagc cgaaaacatc gggcagacag ccgaaaccga ccccgaagcc 240

gaccaaggcg aagccctgtt taacgcagtt aaccgcagcg actggcaaac cgtgcgctcc 300

ctgctcgaca gctatacccg acaaaccgaa tacgaccccg acatcgccct ctttgcccgc 360

gcctcgcttg cccgcggcga aggcaggtgg aaagccgcca aacaagacta cgaaaccctg 420

ctgcaacgcc atcccgactt cacgcgcgga cggctcgatt acgcccgcct gctctttgag 480

ggccgtctga accgcgaagc cgccgccgag ttcgcccgcc tccaaaacga agacctgccc 540

gaagccgtca aagaaaacat cgcccatttc caagatgctc tgaaccaacg ccaaagttgg 600

cagggcagcc tttccgtcgg cgccgtccac aacagcaaca tcaacgaagg cagcggcaaa 660

gtttggtgca aaaccgaaat cgccggcgaa tgctgggaag aattttcagg cgacaagccc 720

atttccgcca acggcatcaa atacgaagcc gccgctgtcc gccgctggca gattaaagga 780

catcacggca tcgccgcccg cgcgctcggc tacggccgct tctaccgcga ccatcgggac 840

ttcaacgaac acacgctcaa cctcagcgca ggttaccagt ttgaaaacca ccgccacacc 900

ttcgccctcg ccccgcttgt cgaatggaac ggcagcggcg gcaaaaccct caaccgcgcc 960

tacggcgtac gcagcgaatg gaacctcgac cgtgaaagct ggacatggaa caccgaagcc 1020

gagtggaaac acctctccta ttccgacaaa acccgtctgc tcgacggcag tctcttctcc 1080

gtttacaaca ccctgtccta tttcccgcgt aacgacctca tgctctacgg cggcatagac 1140

tggcagcagc gcaaagccaa agaccatgtg gacagttacc gccaaatctc cgcacggctg 1200

ggtgccgcaa aaatctttga agccggcttc gatgcctcac tctccgccac cttcggcctg 1260

cgcagccacc gtgaagagaa cgccgtactc gaacaacgcc gccgcgacaa agaacagacc 1320

tacttcctca gcataggtgc agaccgctgg aaagccgccg gcctcaaacc cgtcctcagc 1380

tacaaacacc gccgcgtcag cggcaacacc gactggctat acagctacaa gcaaaacgaa 1440

ataggcctgt cgctggtgaa atcgttttaa 1470

<210> 456

<211> 489

<212> PRT

<213> Neisseria sp. oral taxon 014 SLAM 2

<400> 456

Met Lys Pro Ala Asp Arg Lys Ala Asp Thr Met Tyr Lys Pro Ser Ala

1 5 10 15

Cys Leu Ile Leu Phe Leu Thr Ala Pro Val Leu Ala Ala Pro Arg Ser

20 25 30

Asp Phe Ser Asp Asn Arg Thr Ala Gln Arg Leu Trp Gln Asp Thr Arg

35 40 45

Gln Thr Met Gln Glu Gln Glu Gln Lys Val Arg Glu Tyr Arg Leu Asp

50 55 60

Ile Pro Ala Glu Asn Ile Gly Gln Thr Ala Glu Thr Asp Pro Glu Ala

65 70 75 80

Asp Gln Gly Glu Ala Leu Phe Asn Ala Val Asn Arg Ser Asp Trp Gln

85 90 95

Thr Val Arg Ser Leu Leu Asp Ser Tyr Thr Arg Gln Thr Glu Tyr Asp

100 105 110

Pro Asp Ile Ala Leu Phe Ala Arg Ala Ser Leu Ala Arg Gly Glu Gly

115 120 125

Arg Trp Lys Ala Ala Lys Gln Asp Tyr Glu Thr Leu Leu Gln Arg His

130 135 140

Pro Asp Phe Thr Arg Gly Arg Leu Asp Tyr Ala Arg Leu Leu Phe Glu

145 150 155 160

Gly Arg Leu Asn Arg Glu Ala Ala Ala Glu Phe Ala Arg Leu Gln Asn

165 170 175

Glu Asp Leu Pro Glu Ala Val Lys Glu Asn Ile Ala His Phe Gln Asp

180 185 190

Ala Leu Asn Gln Arg Gln Ser Trp Gln Gly Ser Leu Ser Val Gly Ala

195 200 205

Val His Asn Ser Asn Ile Asn Glu Gly Ser Gly Lys Val Trp Cys Lys

210 215 220

Thr Glu Ile Ala Gly Glu Cys Trp Glu Glu Phe Ser Gly Asp Lys Pro

225 230 235 240

Ile Ser Ala Asn Gly Ile Lys Tyr Glu Ala Ala Ala Val Arg Arg Trp

245 250 255

Gln Ile Lys Gly His His Gly Ile Ala Ala Arg Ala Leu Gly Tyr Gly

260 265 270

Arg Phe Tyr Arg Asp His Arg Asp Phe Asn Glu His Thr Leu Asn Leu

275 280 285

Ser Ala Gly Tyr Gln Phe Glu Asn His Arg His Thr Phe Ala Leu Ala

290 295 300

Pro Leu Val Glu Trp Asn Gly Ser Gly Gly Lys Thr Leu Asn Arg Ala

305 310 315 320

Tyr Gly Val Arg Ser Glu Trp Asn Leu Asp Arg Glu Ser Trp Thr Trp

325 330 335

Asn Thr Glu Ala Glu Trp Lys His Leu Ser Tyr Ser Asp Lys Thr Arg
340 345 350
Leu Leu Asp Gly Ser Leu Phe Ser Val Tyr Asn Thr Leu Ser Tyr Phe
355 360 365
Pro Arg Asn Asp Leu Met Leu Tyr Gly Gly Ile Asp Trp Gln Gln Arg
370 375 380
Lys Ala Lys Asp His Val Asp Ser Tyr Arg Gln Ile Ser Ala Arg Leu

385 390 395 400
Gly Ala Ala Lys Ile Phe Glu Ala Gly Phe Asp Ala Ser Leu Ser Ala
405 410 415
Thr Phe Gly Leu Arg Ser His Arg Glu Glu Asn Ala Val Leu Glu Gln
420 425 430
Arg Arg Arg Asp Lys Glu Gln Thr Tyr Phe Leu Ser Ile Gly Ala Asp
435 440 445
Arg Trp Lys Ala Ala Gly Leu Lys Pro Val Leu Ser Tyr Lys His Arg

450 455 460
Arg Val Ser Gly Asn Thr Asp Trp Leu Tyr Ser Tyr Lys Gln Asn Glu
465 470 475 480
Ile Gly Leu Ser Leu Val Lys Ser Phe
485

<210> 457
<211> 1230
<212> DNA
<213> Neisseria sp. oral taxon 014 SLAM 3
<400> 457
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ttggcgcaat accgcacccg tcccgaccgc gaccaaatcc tgtacgatta cgcactgggc 120

gcgctgcgcc gttcgcagtt gcgtcatgac gaagcggtgg cgctctatcg cggcatcgtg 180
ctgcggcagc ccgatttggc gtatccgcgt ttcgatttgg gcgtgatgtt gtttgaaaac 240
aaacaatacc gcgaagcggc ggcggaactg gaacgcgcca agccggattt gcaacccgac 300
atgcaacagc tcgccgacca ttacctgaag gccgtcaaag acgcacaaag ctggcaaccc 360
gaagcctcgc tgcaatatga ggcgacggat aatgtcaaca gtgcttccgc taccgaaatc 420

atcgaatggg gcgggcggca gtggcacaaa accgccgaca gcctgccgca aagcgcgcac 480

ggcttccgct acggcttggg cttgtcgcgc gaaatcaatc tgggcggcca tcatttcgcc 540

tacggcaacc tcagcggcga cggcgtacat tactgggaca atcgggaatt taacgagcaa 600

agcgtcaatc tggcggcggg ctacaaaaac cgctcgataa cgcgctcgtt cggcatcgtg 660

ccgtttgcag aacaaaactg gctcggcggc aaccgctaca accgctcgtt cggtgcccat 720

accgacttct cacgccgtct gaacgcccga tggcgcgtaa tgctgaatgc gggatacgtc 780

cgaaaacact atcaggacca ccgcatggcg gcacgttacg actcaggaat gccgctggcg 840

ggcgccacgc tgttgtatac cgcgccgaaa aactggctgt tttacggcgg tgcggactgg 900

tcgcacgaca tcaccaagga ggcggaacag gcatcggtac gcaaaggcgt ccggctgggt 960

atggtaaagt ttttttcaga cggcctcggc ctgcgcgcaa acctgcgcta cacccgccgc 1020

acattcgacg cacccggaga gctggtttac cgctttatcc gcaaagaccg tgaatatcag 1080

gccaatgcct caatctggca cgacaaaatc gcatggaaag gtttggtacc gcacctgaat 1140

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tggtttgtca gcgtggaaaa gcagttttga 1230

<210> 458

<211> 409

<212> PRT

<213> Neisseria sp. oral taxon 014 SLAM 3

<400> 458

Met Glu Glu Arg Ile Asn Arg Ala Val Ile Arg Gln Asp Trp Asp Ala

1 5 10 15

Leu Thr Asp Leu Leu Ala Gln Tyr Arg Thr Arg Pro Asp Arg Asp Gln

20 25 30

Ile Leu Tyr Asp Tyr Ala Leu Gly Ala Leu Arg Arg Ser Gln Leu Arg

35 40 45

His Asp Glu Ala Val Ala Leu Tyr Arg Gly Ile Val Leu Arg Gln Pro

50 55 60

Asp Leu Ala Tyr Pro Arg Phe Asp Leu Gly Val Met Leu Phe Glu Asn

65 70 75 80

Lys Gln Tyr Arg Glu Ala Ala Ala Glu Leu Glu Arg Ala Lys Pro Asp

85 90 95

Leu Gln Pro Asp Met Gln Gln Leu Ala Asp His Tyr Leu Lys Ala Val
100 105 110
Lys Asp Ala Gln Ser Trp Gln Pro Glu Ala Ser Leu Gln Tyr Glu Ala
115 120 125
Thr Asp Asn Val Asn Ser Ala Ser Ala Thr Glu Ile Ile Glu Trp Gly

130 135 140
Gly Arg Gln Trp His Lys Thr Ala Asp Ser Leu Pro Gln Ser Ala His
145 150 155 160
Gly Phe Arg Tyr Gly Leu Gly Leu Ser Arg Glu Ile Asn Leu Gly Gly
165 170 175
His His Phe Ala Tyr Gly Asn Leu Ser Gly Asp Gly Val His Tyr Trp
180 185 190
Asp Asn Arg Glu Phe Asn Glu Gln Ser Val Asn Leu Ala Ala Gly Tyr

195 200 205
Lys Asn Arg Ser Ile Thr Arg Ser Phe Gly Ile Val Pro Phe Ala Glu
210 215 220
Gln Asn Trp Leu Gly Gly Asn Arg Tyr Asn Arg Ser Phe Gly Ala His
225 230 235 240
Thr Asp Phe Ser Arg Arg Leu Asn Ala Arg Trp Arg Val Met Leu Asn
245 250 255
Ala Gly Tyr Val Arg Lys His Tyr Gln Asp His Arg Met Ala Ala Arg

260 265 270
Tyr Asp Ser Gly Met Pro Leu Ala Gly Ala Thr Leu Leu Tyr Thr Ala
275 280 285
Pro Lys Asn Trp Leu Phe Tyr Gly Gly Ala Asp Trp Ser His Asp Ile
290 295 300
Thr Lys Glu Ala Glu Gln Ala Ser Val Arg Lys Gly Val Arg Leu Gly
305 310 315 320
Met Val Lys Phe Phe Ser Asp Gly Leu Gly Leu Arg Ala Asn Leu Arg

325 330 335
Tyr Thr Arg Arg Thr Phe Asp Ala Pro Gly Glu Leu Val Tyr Arg Phe

340 345 350

Ile Arg Lys Asp Arg Glu Tyr Gln Ala Asn Ala Ser Ile Trp His Asp

355 360 365

Lys Ile Ala Trp Lys Gly Leu Val Pro His Leu Asn Met Arg Tyr Leu

370 375 380

Arg Thr Asp Ser Asn Met Ser Gly Phe Tyr Ser Arg Arg Asn Met Gln

385 390 395 400

Trp Phe Val Ser Val Glu Lys Gln Phe

405

<210> 459

<211> 1467

<212> DNA

<213> Neisseria sp. oral taxon 014 SLAM 4

<400> 459

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gacagggaag accgcttcat gcagctcaaa cagggaacgg aactccgccg cgcacagcag 120

gaaaggaacg aagcggacaa tacggcgatt gagttcggcg cgggagaagt gcaggacggc 180

gaagatttag cgttgtcgct gatgaaggcg gtcaacgcgc aaaacgaaga ggaaacggcg 240

cggctgttgg acatttaccg ccgtcaggat gattacgacc ccgatatagt gctgtttgcc 300

gaggccaatc aggcggtgtt ccgcgacgat ttgaaggccg cgctggcgaa ataccgcgag 360

ctttaccgca aaaatcccga atttctgcgc ggccgcctgg atttggcgcg gctgctgttt 420

atagacaaac aaaacaaaga atcggcggca ttgttcgacg gcatcgatat tcccgaagtg 480

cccgccgtca atgagaaaat caaagtgttt gccgacgctt tgaagaaacg cgatgcgtgg 540

agcggttcgg tttcgttcgg cgcgggttac gacaccaact taaaccagtc gtcgggcgcg 600

acggttgtcc gcaatcagac aagctgcggt ttcgattcga acgggcagcc gattctggac 660

gacgccggaa tgctgtcctg ccgcaacgaa cggcttgacg cctacgcgcc cgatgcgttg 720

aaaaaccgga tgtgggtata tgaagccaac ttaagcagac gcatttcgct caacggccac 780

cacggcctgc aactgggcgg ctacgcatgg ggccggctct atcccggcaa caaggaatac 840

ggcgaacaca atatcaacgt cagccccgct tacagttttc agagcaaaga ccattccttc 900

agtatcggcc cgcaggtgca atacgaatgg tcgggcggca aactgcgcga cagcagcgct 960

ggcatcagca tggcatacag ccgcaccttt tccgaccaag cctcgctggg cgtgcagctc 1020

gaccacaaat acgaccgcta ccgcggcgaa ttaaaacatt tcaacggccc gcagacgctt 1080

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taccagttgg acatcaaatt cgaccgccct ttcctccgcg gcttcgtacc cgtcctcacc 1380
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atgtttaaag tggaatacgg attctga 1467

<210> 460
<211> 488
<212> PRT
<213> Neisseria sp. oral taxon 014 SLAM 4
<400> 460

Met Lys Arg Leu Leu Ile Leu Pro Val Phe Leu Ser Leu Leu Pro His
1 5 10 15
Ala Phe Ala Asp Asp Arg Glu Asp Arg Phe Met Gln Leu Lys Gln Gly
20 25 30
Thr Glu Leu Arg Arg Ala Gln Gln Glu Arg Asn Glu Ala Asp Asn Thr
35 40 45
Ala Ile Glu Phe Gly Ala Gly Glu Val Gln Asp Gly Glu Asp Leu Ala
50 55 60
Leu Ser Leu Met Lys Ala Val Asn Ala Gln Asn Glu Glu Glu Thr Ala
65 70 75 80
Arg Leu Leu Asp Ile Tyr Arg Arg Gln Asp Asp Tyr Asp Pro Asp Ile
85 90 95
Val Leu Phe Ala Glu Ala Asn Gln Ala Val Phe Arg Asp Asp Leu Lys
100 105 110
Ala Ala Leu Ala Lys Tyr Arg Glu Leu Tyr Arg Lys Asn Pro Glu Phe
115 120 125
Leu Arg Gly Arg Leu Asp Leu Ala Arg Leu Leu Phe Ile Asp Lys Gln
130 135 140

Asn Lys Glu Ser Ala Ala Leu Phe Asp Gly Ile Asp Ile Pro Glu Val
145 150 155 160
Pro Ala Val Asn Glu Lys Ile Lys Val Phe Ala Asp Ala Leu Lys Lys
165 170 175
Arg Asp Ala Trp Ser Gly Ser Val Ser Phe Gly Ala Gly Tyr Asp Thr

180 185 190
Asn Leu Asn Gln Ser Ser Gly Ala Thr Val Val Arg Asn Gln Thr Ser
195 200 205
Cys Gly Phe Asp Ser Asn Gly Gln Pro Ile Leu Asp Asp Ala Gly Met
210 215 220
Leu Ser Cys Arg Asn Glu Arg Leu Asp Ala Tyr Ala Pro Asp Ala Leu
225 230 235 240
Lys Asn Arg Met Trp Val Tyr Glu Ala Asn Leu Ser Arg Arg Ile Ser

245 250 255
Leu Asn Gly His His Gly Leu Gln Leu Gly Gly Tyr Ala Trp Gly Arg
260 265 270
Leu Tyr Pro Gly Asn Lys Glu Tyr Gly Glu His Asn Ile Asn Val Ser
275 280 285
Pro Ala Tyr Ser Phe Gln Ser Lys Asp His Ser Phe Ser Ile Gly Pro
290 295 300
Gln Val Gln Tyr Glu Trp Ser Gly Gly Lys Leu Arg Asp Ser Ser Ala

305 310 315 320
Gly Ile Ser Met Ala Tyr Ser Arg Thr Phe Ser Asp Gln Ala Ser Leu
325 330 335
Gly Val Gln Leu Asp His Lys Tyr Asp Arg Tyr Arg Gly Glu Leu Lys
340 345 350
His Phe Asn Gly Pro Gln Thr Leu Leu Phe Thr Thr Ala Ile Tyr Ala
355 360 365
Leu Pro Lys Asp Trp Leu Val Phe Gly Gly Tyr Asp Tyr Leu Arg Lys

370 375 380
Asn Ser Arg Glu Lys Val Asp Ser Tyr Arg Arg His Gly Leu Arg Ala

385 390 395 400

Gly Val Asn Lys Arg Phe Glu Ser Gly Ile Asp Ala Thr Phe Gln Ala

405 410 415

Ile Trp Arg Lys Thr Ala Tyr Gln Asp Tyr His Ala Trp Leu Glu Thr

420 425 430

Arg Arg Arg Asp Phe Glu Arg Thr Tyr Gln Leu Asp Ile Lys Phe Asp

435 440 445

Arg Pro Phe Leu Arg Gly Phe Val Pro Val Leu Thr Val Lys His Thr

450 455 460

Asp Asn Lys Ser Ser Ser Trp Leu Asn Arg Tyr Lys Arg Asn Glu Tyr

465 470 475 480

Met Phe Lys Val Glu Tyr Gly Phe

485

<210> 461

<211> 1482

<212> DNA

<213> Neisseria sp. oral taxon 014 SLAM 5

<400> 461

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atccccgcct ttgccgacga tgacgacacg cgtatgctgc gcgacggggt tcagcgtcaa 120

atcaggcagt atcaggaagc ggaagcattt tcagacggcc tttcagatga aagccgcatt 180

aacatcggcg gcgagactta tcatgtgccg cacacggaac acgatttggc cttgggcatt 240

tattacgcgg tcaacgacag gcagtggaac aaagtgaggg aatttctgac gcactaccgc 300

acccttccg gccacaaacc gcatctggtg ctgatggccg aggggttgct ggcgcgttcg 360

cagggcgatg tttccggcgc gctggaaaag atgaaagcgg cgcaacaggc tgcgcccgac 420

gatgtccgca tagggttgga actggcacgg ctttacggtg aagacaatca gacccgcgaa 480

gcaaaagccg gtttcgaaaa ggttttgcaa ggcgggatgc cgtctgaaac caaagagacg 540

gtgcaaaact atctcgacat cctcgataaa cgcagccgct ggcacggcga catttccgtc 600

gggcgcggtt acagcgacaa catcaatcaa ggcaacggca aacgcgaatg cgtgggcgaa 660

ttgatgggcg aatgtttcag ctaccgctcc ctgcccaagc ccgtcggctc ggcgttttgg 720

caatacagcg ccgccgcctc gaaatccgtt ccgctcaagg gccatcacaa cctcatcctg 780

cgcccgattg cctacggcag ccgatttgac cgcgccgaca cccaaagcga accgattgaa 840

aaatacagtg aaaacaccgc cctgctgtcc gccggctacc aatacgccga tgccgacgat 900

gacctgacgc tgaccccgta tttcgaacat tactttcgcg gcggccgcag ccgttaccgc 960
gcatggggcg cggatatgaa ctgggaacgg aatctggggc gaaaatggtc ggtcaacgcc 1020
cgactggaag gcaaacgggt caaatatctg gaaagcgagc gcggatatta cagcgactac 1080
agcctttata cttccggcgc aggattgggc tacacgtttt cagacggcct cggcctgttc 1140
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accgcccgca tcggcggcta taaaattttc ggcaacggta tctatctcaa cgccgccgcc 1260
cttcaccgcc tcagccgcta cgacgaaggc agctaccaca ccgacggcaa acgccgccgc 1320

gacaggcaga ccatttttac caccgctttg ggcgcatcga aatggcagtt taaatacatc 1380
tctcccgaat taagattcaa gcggacggtc agccgcagca attcggattt ttatgtttac 1440
cgacagaatg aaatcgcact gaatttgaga taccgttttt aa 1482

<210> 462
<211> 493
<212> PRT
<213> Neisseria sp. oral taxon 014 SLAM 5
<400> 462

Met Trp Lys Pro Glu Met Lys Asn Arg Ala Cys Leu Phe Ala Leu Leu
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Leu Pro Leu Ser Ile Pro Ala Phe Ala Asp Asp Asp Asp Thr Arg Met

20 25 30
Leu Arg Asp Gly Val Gln Arg Gln Ile Arg Gln Tyr Gln Glu Ala Glu
35 40 45
Ala Phe Ser Asp Gly Leu Ser Asp Glu Ser Arg Ile Asn Ile Gly Gly
50 55 60
Glu Thr Tyr His Val Pro His Thr Glu His Asp Leu Ala Leu Gly Ile
65 70 75 80
Tyr Tyr Ala Val Asn Asp Arg Gln Trp Asn Lys Val Arg Glu Phe Leu

85 90 95
Thr His Tyr Arg Thr Leu Ser Gly His Lys Pro His Leu Val Leu Met
100 105 110
Ala Glu Gly Leu Leu Ala Arg Ser Gln Gly Asp Val Ser Gly Ala Leu

115 120 125

Glu Lys Met Lys Ala Ala Gln Gln Ala Ala Pro Asp Asp Val Arg Ile

130 135 140

Gly Leu Glu Leu Ala Arg Leu Tyr Gly Glu Asp Asn Gln Thr Arg Glu

145 150 155 160

Ala Lys Ala Gly Phe Glu Lys Val Leu Gln Gly Gly Met Pro Ser Glu

165 170 175

Thr Lys Glu Thr Val Gln Asn Tyr Leu Asp Ile Leu Asp Lys Arg Ser

180 185 190

Arg Trp His Gly Asp Ile Ser Val Gly Arg Gly Tyr Ser Asp Asn Ile

195 200 205

Asn Gln Gly Asn Gly Lys Arg Glu Cys Val Gly Glu Leu Met Gly Glu

210 215 220

Cys Phe Ser Tyr Arg Ser Leu Pro Lys Pro Val Gly Ser Ala Phe Trp

225 230 235 240

Gln Tyr Ser Ala Ala Ala Ser Lys Ser Val Pro Leu Lys Gly His His

245 250 255

Asn Leu Ile Leu Arg Pro Ile Ala Tyr Gly Ser Arg Phe Asp Arg Ala

260 265 270

Asp Thr Gln Ser Glu Pro Ile Glu Lys Tyr Ser Glu Asn Thr Ala Leu

275 280 285

Leu Ser Ala Gly Tyr Gln Tyr Ala Asp Ala Asp Asp Asp Leu Thr Leu

290 295 300

Thr Pro Tyr Phe Glu His Tyr Phe Arg Gly Gly Arg Ser Arg Tyr Arg

305 310 315 320

Ala Trp Gly Ala Asp Met Asn Trp Glu Arg Asn Leu Gly Arg Lys Trp

325 330 335

Ser Val Asn Ala Arg Leu Glu Gly Lys Arg Val Lys Tyr Leu Glu Ser

340 345 350

Glu Arg Gly Tyr Tyr Ser Asp Tyr Ser Leu Tyr Thr Ser Gly Ala Gly

355 360 365

Leu Gly Tyr Thr Phe Ser Asp Gly Leu Gly Leu Phe Gly Gly Ile Asp

370 375 380

Leu Thr Arg Arg Lys Tyr Pro Asp Ala Phe Ala Arg Ser Arg Glu Tyr

385 390 395 400

Thr Ala Arg Ile Gly Gly Tyr Lys Ile Phe Gly Asn Gly Ile Tyr Leu

405 410 415

Asn Ala Ala Ala Leu His Arg Leu Ser Arg Tyr Asp Glu Gly Ser Tyr

420 425 430

His Thr Asp Gly Lys Arg Arg Arg Asp Arg Gln Thr Ile Phe Thr Thr

435 440 445

Ala Leu Gly Ala Ser Lys Trp Gln Phe Lys Tyr Ile Ser Pro Glu Leu

450 455 460

Arg Phe Lys Arg Thr Val Ser Arg Ser Asn Ser Asp Phe Tyr Val Tyr

465 470 475 480

Arg Gln Asn Glu Ile Ala Leu Asn Leu Arg Tyr Arg Phe

485 490

<210> 463

<211> 1440

<212> DNA

<213> Neisseria sp. oral taxon 020 SLAM 1

<400> 463

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gcgcttgtgc cagagggaga gggaggcgga gtattctttg tcgtcgcggc ggatggcgag 180

gaagtcggcg gcgtcgtagc ggcggccgta gccggcggag agggcggtgc cgagtccttt 240

tccccagacg cgcacggcgg acgcgcggat gccgcgcctg tggtaggcgt cgtcggtgcg 300

ggcgcgtttg cgggagaagt tggcgccgag ggtaaagtat tggcgcgggc tgtgttggaa 360

tatccaggtg gcggacaggc tgctgttgcg gccttcgagg aatttgcgcg tgtcgtagtg 420

ctggtagtcc gattcggcgg cggcagcgag gcggtggcgc gggctgaggc tgcgctgcca 480

ttcggcgcgc aggccggttt cgcgggagta gggttcggta ccgtaccaac ggcgctcgta 540

ataggggagc agggcggctt cgctgcggcc gctttggtag gcggcgccca gggcggtgcg 600

gacggtgaga tcgttgtagc ggtggttgtc ccaataaaat ttgccgtaga ggtcggtttc 660

gctgcgcagg agcagattgt cggcgaggtt gaagtcgcgg gcgaggccgg cggagtagga 720

gaggccgcgg gctttttcgg gggcgggcag cgtccattcg ccgttgccgt agcgcagggt 780

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gcggtcgtct ttcagtgcct gcgccagacg gaggcggacg aggaaggcgt cgggcatttg 1020

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gaggtcgaag cgggtgtcgg gttggctgag ggcggagcgt gcggcggggt tcggcaactc 1380

gtcggcacgc gctgcggaca gggtggcaag caggagcagg aagggtaggc gtttgggcat 1440

<210> 464

<211> 479

<212> PRT

<213> Neisseria sp. oral taxon 020 SLAM 1

<400> 464

Met Pro Lys Arg Leu Pro Phe Leu Leu Leu Leu Ala Thr Leu Ser Ala
1 5 10 15

Ala Arg Ala Asp Glu Leu Pro Asn Pro Ala Ala Arg Ser Ala Leu Ser
20 25 30

Gln Pro Asp Thr Arg Phe Asp Leu Thr Gly Ser Asp Glu Leu Pro Ala
35 40 45

Pro Ala Ser Ala Pro Glu Ser Ser Val Ser Gln Asn Gly Gly Thr Leu
50 55 60

Thr Cys Ser Asn Pro Glu Glu Leu Leu Gln His Pro Gly Leu Leu His
65 70 75 80

Arg Ala Leu Ser Ser Ser Val Ile Ala Ala Asn Thr Ala Ala Ile Lys
85 90 95

Leu Leu Leu Pro Val Tyr Arg Arg Leu Pro Glu Gly Gln Asp Pro Val
100 105 110
Leu Leu Glu Thr Ala Glu Gly Met Ala Ala Gln Ser Asp Gly Arg Tyr
115 120 125

Arg Glu Ala Val Arg Arg Leu Gln Asn Ala Arg Arg Gln Met Pro Asp
130 135 140
Ala Phe Leu Val Arg Leu Arg Leu Ala Gln Ala Leu Lys Asp Asp Arg
145 150 155 160
Arg Asn Val Ser Ala Gln Ala His Tyr Thr Asn Leu Leu Ala Pro Pro
165 170 175
Asp Leu Asp Pro Gln Thr Arg Ala Ala Leu Gln Ser Gln Leu Asp Glu
180 185 190

Ile Arg Ser Arg Ser Arg Trp Thr Pro Arg Leu Ser Ala Asn Tyr Thr
195 200 205
Arg Asp Asn Asn Val Asn Asn Ala Ala Lys Glu His Thr Leu Arg Tyr
210 215 220
Gly Asn Gly Glu Trp Thr Leu Pro Ala Pro Glu Lys Ala Arg Gly Leu
225 230 235 240
Ser Tyr Ser Ala Gly Leu Ala Arg Asp Phe Asn Leu Ala Asp Asn Leu
245 250 255

Leu Leu Arg Ser Glu Thr Asp Leu Tyr Gly Lys Phe Tyr Trp Asp Asn
260 265 270
His Arg Tyr Asn Asp Leu Thr Val Arg Thr Ala Leu Gly Ala Ala Tyr
275 280 285
Gln Ser Gly Arg Ser Glu Ala Ala Leu Leu Pro Tyr Tyr Glu Arg Arg
290 295 300
Trp Tyr Gly Thr Glu Pro Tyr Ser Arg Glu Thr Gly Leu Arg Ala Glu
305 310 315 320

Trp Gln Arg Ser Leu Ser Pro Arg His Arg Leu Ala Ala Ala Ala Glu
325 330 335
Ser Asp Tyr Gln His Tyr Asp Thr Arg Lys Phe Leu Glu Gly Arg Asn

340 345 350

Ser Ser Leu Ser Ala Thr Trp Ile Phe Gln His Ser Pro Arg Gln Tyr

355 360 365

Phe Thr Leu Gly Ala Asn Phe Ser Arg Lys Arg Ala Arg Thr Asp Asp

370 375 380

Ala Tyr His Arg Arg Gly Ile Arg Ala Ser Ala Val Arg Val Trp Gly

385 390 395 400

Lys Gly Leu Gly Thr Ala Leu Ser Ala Gly Tyr Gly Arg Arg Tyr Asp

405 410 415

Ala Ala Asp Phe Leu Ala Ile Arg Arg Asp Asp Lys Glu Tyr Ser Ala

420 425 430

Ser Leu Ser Leu Trp His Lys Arg Leu Ser Leu Trp Gly Val Thr Pro

435 440 445

Arg Leu Val Thr Val Trp Gln Lys Thr Thr Ser Asn His Pro Leu Tyr

450 455 460

Gly Tyr Arg Lys Ala Asn Ala Tyr Leu Gln Ile Ser Lys Ser Phe

465 470 475

<210> 465

<211> 1515

<212> DNA

<213> Neisseria sp. oral taxon 020 SLAM 2

<400> 465

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cgcgacgtgg gcggcgatat cggctatcgg cagcagcaga tcgagcgcaa cgacagcctg 180

cgcagaaaaa ataccgacgg cgcacaggaa gacgacacgc ctgatttaag cgacgaagat 240

ttgaaaaaaa atcccgaaat cgccaaccac atcctgaaca ccgccatgct gcgcgaagac 300

tgggatacgc tggaacacat catgggtttc taccgcgaca ttcccggcca cgatcccgtt 360

atgtacgatt ttgttcaagg cgcgctttgg cgcgctcagg gcaagcacgg caaagccatc 420

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gcaggcatgc tgtttgaaaa ccgcgcctat cgggatgcgg caaaagaatt cgggcaggta 540

aaaaaggaag acatcgaacc ggaagccgcc gcacaagccg acgcctattt gcaggccgtg 600

aaacaggcca atccgtggca gttcaagctg cgcggcggcc tgcaatacag cagcaacacc 660
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aaagtcaaaa gcaatatcta cgccttcccc cgcaacaaaa aacaggtatt gctgactctg 1500
gaaaaagaat tctga 1515
<210> 466
<211> 504
<212> PRT
<213> Neisseria sp. oral taxon 020 SLAM 2
<400> 466
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1 5 10 15
Leu Thr Gln Gln Thr Ala Leu Ala Asp Asp Pro Ser Ala Lys Thr Ser
20 25 30

Ile Arg Asp Asp Phe Gly Ile Phe Arg Asp Val Gly Gly Asp Ile Gly
35 40 45
Tyr Arg Gln Gln Gln Ile Glu Arg Asn Asp Ser Leu Arg Arg Lys Asn
50 55 60
Thr Asp Gly Ala Gln Glu Asp Asp Thr Pro Asp Leu Ser Asp Glu Asp

65 70 75 80

Leu Lys Lys Asn Pro Glu Ile Ala Asn His Ile Leu Asn Thr Ala Met
85 90 95

Leu Arg Glu Asp Trp Asp Thr Leu Glu His Ile Met Gly Phe Tyr Arg
100 105 110

Asp Ile Pro Gly His Asp Pro Val Met Tyr Asp Phe Val Gln Gly Ala
115 120 125

Leu Trp Arg Ala Gln Gly Lys His Gly Lys Ala Ile Lys Thr Tyr Arg
130 135 140

Lys Ile Leu Asp Lys Gln Pro Asp Leu Ser Tyr Val Arg Leu Asp Leu
145 150 155 160

Ala Gly Met Leu Phe Glu Asn Arg Ala Tyr Arg Asp Ala Ala Lys Glu
165 170 175

Phe Gly Gln Val Lys Lys Glu Asp Ile Glu Pro Glu Ala Ala Ala Gln
180 185 190

Ala Asp Ala Tyr Leu Gln Ala Val Lys Gln Ala Asn Pro Trp Gln Phe
195 200 205

Lys Leu Arg Gly Gly Leu Gln Tyr Ser Ser Asn Thr Asn Asn Ala Thr
210 215 220

Ser Asn Asp Tyr Phe Leu Trp Pro Phe Ala Val Ile Asp Gly Val Thr
225 230 235 240

Tyr Tyr Tyr Lys Leu Pro Arg Asp Pro Glu Ser Leu Pro Arg Ser Gly
245 250 255

His Gly Tyr Ser Tyr Gly Ala Gln Leu Gln Lys Asp Phe Asn Leu Ser
260 265 270

Gly Asn His Asn Ile Gly Phe Asn Ile Glu Ala Asp Gly Val His Tyr
275 280 285

Pro Gly Arg His Glu Asp Asn Glu Phe Ser Leu Ser Ala Asp Ala Gly
290 295 300

Tyr Lys Tyr Gln Asn Leu Asn Asn Thr Phe Thr Leu Thr Pro Leu Val
305 310 315 320

Ser Ala Ser Trp Leu Gly Gly Arg Pro Tyr Ser Arg Ser Ile Gly Ala
325 330 335
Ala Ala Ser Ala Ser Arg Trp Val Thr Pro Arg Leu Gln Leu Ser Gly
340 345 350

Ser Tyr Ser Ala Leu Arg Arg Lys Tyr Arg Asp Glu Arg Tyr Glu Gly
355 360 365
Tyr Asp Ser Thr Ala Asn Ser Leu Ser Leu Ser Ser Val Tyr Ala Leu
370 375 380
Thr Gly Asn Trp Phe Val Phe Gly Gly Ala Ala Val Gln Arg Glu Asn
385 390 395 400
Thr Arg Asp Lys Glu Glu Thr Ser Thr Arg Arg Ser Leu Ser Leu Gly
405 410 415

Thr Leu Tyr Arg Phe Asp Asn Gly Ile Asn Phe Arg Ile Gly Gly Arg
420 425 430
His Val Ser Arg Arg Phe Ala Asn Pro Ala Thr Leu Tyr Gly Gly Asp
435 440 445
Ile Arg Arg Asp Lys Glu Ile Tyr Ala Asp Ala Ser Val Trp Lys Glu
450 455 460
Lys Trp Leu Pro Gly Gly Ile Thr Pro Lys Leu Glu Phe Ser Tyr Leu
465 470 475 480

Lys Val Lys Ser Asn Ile Tyr Ala Phe Pro Arg Asn Lys Lys Gln Val
485 490 495
Leu Leu Thr Leu Glu Lys Glu Phe
500

<210> 467
<211> 1458
<212> DNA
<213> Neisseria sp. oral taxon 020 SLAM 3
<400> 467
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aacgaagaca cccgcctgca actgagatac ggcatagaag agcggcagca gcggcaggaa 120

ggggaaacgg tgggcgattt gtctttcggc gcagccgcgc cgcaggaaga cgacaatctg 180

ccgaccgcgc tgatgaaggc ggtgaacgcg caaaacgaag gcgaaacgct gcgcctgctc 240
gaaatctaca aggcgcagcc cgatgccgat cccgatatgg tgctgtttgc cgaagccaat 300
ctggccgtat tccgcgacga tttgccgggc gcgctggcac gctatcggga gctgtatgcg 360
cgcaatccgc agtttgtccg cgccaagctc gatttggcgc gtttgctgtt tgtcgacaag 420
cagaacaggg aatcggcggc gctgttcggc agcatcgata ttcccgaacg ccccgccgtc 480
aacgaaaaaa tcaaaggctt ctccgacgcg ctctccaaac gcgacgcatg gagcggctcg 540
ctctccgtcg gcttgggaca cgacagcaat ctgaaccgct cctccgctgc caccatgctg 600

cgcgaacagc aaagctgcgg cttcgattcc aacggacagc cgattttgga cgccaacggc 660
aatttcacct gccgcagcga atggctgccg atgaaaaccc ccgatgcgct aagcggccgc 720
atgtgggcat acgaagccgc cgtcagtcgc cgcctctcgc tcaaaggcca ccacggcata 780
cagttttccg gctacgcgct gggcaaaatc taccccggaa accgcgacta caccgaacac 840
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ccacaaatcc aatatgattg ggtaggcggc aaaatgcagg acagcaatgc gggcgtcagc 960
gtgtcctaca accgcacttt cgccgacaaa gcctcgctgg gcgtgcagat agagcacaaa 1020

tacgaccgct accgcagcgg ctacgaacat ttcaacggcc cgcaatcgtt gctgtttgcc 1080
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caggacttcc atgcctggct ggacacgcgg cgcaaagaca gcgaacgcac ctaccaactt 1320
gacctcaaac tcaaccgccc cgccctgcgc ggcttcgttc ccatcctcag cctgaagcac 1380
accgacaacc gcagcacctc gtgggtcaac cgctacaaac gcaacgaaat caccttcaag 1440

ctgcaatacg ggttttga 1458

<210> 468

<211> 485

<212> PRT

<213> Neisseria sp. oral taxon 020 SLAM 3

<400> 468

Met Lys Tyr Arg Leu Phe Leu Leu Pro Leu Leu Leu Leu Ser Leu Pro
1 5 10 15
Ala Arg Ala Asp Asn Glu Asp Thr Arg Leu Gln Leu Arg Tyr Gly Ile

20 25 30

Glu Glu Arg Gln Gln Arg Gln Glu Gly Glu Thr Val Gly Asp Leu Ser

35 40 45

Phe Gly Ala Ala Ala Pro Gln Glu Asp Asp Asn Leu Pro Thr Ala Leu

50 55 60

Met Lys Ala Val Asn Ala Gln Asn Glu Gly Glu Thr Leu Arg Leu Leu

65 70 75 80

Glu Ile Tyr Lys Ala Gln Pro Asp Ala Asp Pro Asp Met Val Leu Phe

85 90 95

Ala Glu Ala Asn Leu Ala Val Phe Arg Asp Asp Leu Pro Gly Ala Leu

100 105 110

Ala Arg Tyr Arg Glu Leu Tyr Ala Arg Asn Pro Gln Phe Val Arg Ala

115 120 125

Lys Leu Asp Leu Ala Arg Leu Leu Phe Val Asp Lys Gln Asn Arg Glu

130 135 140

Ser Ala Ala Leu Phe Gly Ser Ile Asp Ile Pro Glu Arg Pro Ala Val

145 150 155 160

Asn Glu Lys Ile Lys Gly Phe Ser Asp Ala Leu Ser Lys Arg Asp Ala

165 170 175

Trp Ser Gly Ser Leu Ser Val Gly Leu Gly His Asp Ser Asn Leu Asn

180 185 190

Arg Ser Ser Ala Ala Thr Met Leu Arg Glu Gln Gln Ser Cys Gly Phe

195 200 205

Asp Ser Asn Gly Gln Pro Ile Leu Asp Ala Asn Gly Asn Phe Thr Cys

210 215 220

Arg Ser Glu Trp Leu Pro Met Lys Thr Pro Asp Ala Leu Ser Gly Arg

225 230 235 240

Met Trp Ala Tyr Glu Ala Ala Val Ser Arg Arg Leu Ser Leu Lys Gly

245 250 255

His His Gly Ile Gln Phe Ser Gly Tyr Ala Leu Gly Lys Ile Tyr Pro

260 265 270

Gly Asn Arg Asp Tyr Thr Glu His Ser Val Ser Leu Ser Pro Ala Tyr
275 280 285
Ser Phe Gln Asn Lys Asp Thr Ser Phe Ser Ile Gly Pro Gln Ile Gln
290 295 300

Tyr Asp Trp Val Gly Gly Lys Met Gln Asp Ser Asn Ala Gly Val Ser
305 310 315 320
Val Ser Tyr Asn Arg Thr Phe Ala Asp Lys Ala Ser Leu Gly Val Gln
325 330 335
Ile Glu His Lys Tyr Asp Arg Tyr Arg Ser Gly Tyr Glu His Phe Asn
340 345 350
Gly Pro Gln Ser Leu Leu Phe Ala Thr Gly Val Tyr Val Leu Pro Lys
355 360 365

Asn Trp Val Leu Phe Gly Gly Tyr Asp Phe Leu Arg Lys Asn Ser Arg
370 375 380
Glu Lys Val Asp Ser Tyr Arg Arg His Gly Leu Arg Gly Gly Ile Ser
385 390 395 400
Lys Arg Phe Asp Ser Gly Ile Glu Ala Thr Phe Gln Thr Ile Trp Arg
405 410 415
Lys Thr Ala Tyr Gln Asp Phe His Ala Trp Leu Asp Thr Arg Arg Lys
420 425 430

Asp Ser Glu Arg Thr Tyr Gln Leu Asp Leu Lys Leu Asn Arg Pro Ala
435 440 445
Leu Arg Gly Phe Val Pro Ile Leu Ser Leu Lys His Thr Asp Asn Arg
450 455 460
Ser Thr Ser Trp Val Asn Arg Tyr Lys Arg Asn Glu Ile Thr Phe Lys
465 470 475 480
Leu Gln Tyr Gly Phe
485

<210> 469
<211> 1464
<212> DNA

<213> Neisseria sp. oral taxon 020 SLAM 4

<400> 469

atgaaaaaac accttctgcc gcttatcctg cttgtcctgc ccgccgccgc gctggccgac 60

gaagacgaca cccgtatgct gctcgacggc gcgcaaaagg aaatgcgccg ccaacaggac 120

gcggcggcgt tttcagacgg cctctccgac agcggcagta tcgaaatcga cggtgaaacc 180

tatatcgtgc cgcacaccgc ccacgatttg gaattgggca tttattacgc gatagacggg 240

cggcaatggg gcaaggtgcg cgagtttgcc gccgcctacc gccgcctgcc cgaacacaaa 300

acccatctgg cgctgatggc cgaaggcttg gccgaacgcg ccgagggcaa agtcggcgcc 360

gctttgaaaa aaatgaaagc cgcacacgca gccgcgccgg atgatgtgcg cgtcggtttg 420

gagctggcgc ggctctacgg cgaagacaac caaaaccgcg aatcgcaggc gcagttcaaa 480

gaagtattga aaggagagat gccgtctgaa acccgcgcag ccgtgcaaag ctatctcgac 540

atcctcgaca aacgccgccg ctggcacggc agcatcagca taggcggcgg ctataacgac 600

aacatcaatc agggcaacgg caagcgcgaa tgtgtcggct cgtttatggg gcagtgtttc 660

agctaccgcc ccctgccctc gcccgtcggt tcgccgtttt ggcaatacag cgccgttgcc 720

gcgaaaaaaa tcccgctgcg cggccaccac aacctgctgc tgcgcccgct ctcctacggt 780

acgaaatacc gccgcgacga cagtcagtcg gagccgcccg aaccgtacag cgaaaacacc 840

gccgccctct acgcgggcta cgaacacaac accgccgaca gcgatttcac gtttaccccc 900

tatttcgaac actactaccg cggcagccgc agccgctacc gcgcatgggg cgcggaagcc 960

gcgtgggaaa aaaacctcac ggccaaatgg tcgctcaacg tccgcgccga agccaagcgg 1020

gtgaaatacc tcgaacagga gcggcagtat tacagcgact acaccctcta caccggcggc 1080

gcagggctgg gctacacctt ttcagacggc ctcggcctct acggcggcat cgacctcgcc 1140

cgccgcaaat acccctacgc cgcctcgcgc agcaaggaat acaccgcccg catcggcggc 1200

tacaaaatgt ttaaaaacgg catttatttc aacgccgccg ccctctaccg tctcagccac 1260

tacgacgccg gcagctacct caccgccggc gaaccgcgcc gcgaccgcca aaccatcctc 1320

accgccgccc tcggcgcatc caaactttcc tttaaaagca tctaccccga attgcgcgtc 1380

aaacgcaccg tcggccgcag caatgccgat ctctttgcct acaagcaaaa cgaaatcgcc 1440

ctggctttga aataccggtt ttaa 1464

<210> 470

<211> 487

<212> PRT

<213> Neisseria sp. oral taxon 020 SLAM 4

<400> 470

Met Lys Lys His Leu Leu Pro Leu Ile Leu Leu Val Leu Pro Ala Ala
1 5 10 15

Ala Leu Ala Asp Glu Asp Asp Thr Arg Met Leu Leu Asp Gly Ala Gln
20 25 30

Lys Glu Met Arg Arg Gln Gln Asp Ala Ala Ala Phe Ser Asp Gly Leu
35 40 45

Ser Asp Ser Gly Ser Ile Glu Ile Asp Gly Glu Thr Tyr Ile Val Pro
50 55 60

His Thr Ala His Asp Leu Glu Leu Gly Ile Tyr Tyr Ala Ile Asp Gly
65 70 75 80

Arg Gln Trp Gly Lys Val Arg Glu Phe Ala Ala Ala Tyr Arg Arg Leu
85 90 95

Pro Glu His Lys Thr His Leu Ala Leu Met Ala Glu Gly Leu Ala Glu
100 105 110

Arg Ala Glu Gly Lys Val Gly Ala Ala Leu Lys Lys Met Lys Ala Ala
115 120 125

His Ala Ala Ala Pro Asp Asp Val Arg Val Gly Leu Glu Leu Ala Arg
130 135 140

Leu Tyr Gly Glu Asp Asn Gln Asn Arg Glu Ser Gln Ala Gln Phe Lys
145 150 155 160

Glu Val Leu Lys Gly Glu Met Pro Ser Glu Thr Arg Ala Ala Val Gln
165 170 175

Ser Tyr Leu Asp Ile Leu Asp Lys Arg Arg Arg Trp His Gly Ser Ile
180 185 190

Ser Ile Gly Gly Gly Tyr Asn Asp Asn Ile Asn Gln Gly Asn Gly Lys
195 200 205

Arg Glu Cys Val Gly Ser Phe Met Gly Gln Cys Phe Ser Tyr Arg Pro
210 215 220

Leu Pro Ser Pro Val Gly Ser Pro Phe Trp Gln Tyr Ser Ala Val Ala
225 230 235 240

Ala Lys Lys Ile Pro Leu Arg Gly His His Asn Leu Leu Leu Arg Pro
245 250 255
Leu Ser Tyr Gly Thr Lys Tyr Arg Arg Asp Asp Ser Gln Ser Glu Pro
260 265 270

Pro Glu Pro Tyr Ser Glu Asn Thr Ala Ala Leu Tyr Ala Gly Tyr Glu
275 280 285
His Asn Thr Ala Asp Ser Asp Phe Thr Phe Thr Pro Tyr Phe Glu His
290 295 300
Tyr Tyr Arg Gly Ser Arg Ser Arg Tyr Arg Ala Trp Gly Ala Glu Ala
305 310 315 320
Ala Trp Glu Lys Asn Leu Thr Ala Lys Trp Ser Leu Asn Val Arg Ala
325 330 335

Glu Ala Lys Arg Val Lys Tyr Leu Glu Gln Glu Arg Gln Tyr Tyr Ser
340 345 350
Asp Tyr Thr Leu Tyr Thr Gly Gly Ala Gly Leu Gly Tyr Thr Phe Ser
355 360 365
Asp Gly Leu Gly Leu Tyr Gly Gly Ile Asp Leu Ala Arg Arg Lys Tyr
370 375 380
Pro Tyr Ala Ala Ser Arg Ser Lys Glu Tyr Thr Ala Arg Ile Gly Gly
385 390 395 400

Tyr Lys Met Phe Lys Asn Gly Ile Tyr Phe Asn Ala Ala Ala Leu Tyr
405 410 415
Arg Leu Ser His Tyr Asp Ala Gly Ser Tyr Leu Thr Ala Gly Glu Pro
420 425 430
Arg Arg Asp Arg Gln Thr Ile Leu Thr Ala Ala Leu Gly Ala Ser Lys
435 440 445
Leu Ser Phe Lys Ser Ile Tyr Pro Glu Leu Arg Val Lys Arg Thr Val
450 455 460

Gly Arg Ser Asn Ala Asp Leu Phe Ala Tyr Lys Gln Asn Glu Ile Ala
465 470 475 480
Leu Ala Leu Lys Tyr Arg Phe

485

<210> 471

<211> 1311

<212> DNA

<213> Novosphingobium sp. AP12 SLAM 1

<400> 471

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gttcccgcgc aaattaaact ctcggccgcg cagatctttg cgttggccga gcaagcgggt 120

cgggcaggcg atttcgccac cgccgagacc gcctatcggg ccctcacacg ggacgccgac 180

ctcgaggttc gcaccgaggc ccggttccgt ctcggcctga tgctggccga cgatctcaag 240

cgctacagcg atgccgcgct cgagtttcgc cgtatcctcg acgacaagcc cggcgccgcg 300

cgggtgcgct tggaactagc gcgcatgcaa gcaatgctcg gcaacatggc cggcgcccgc 360

aaggaactac gcgcggcgca ggccgcgggg cttccttcgt ctgtggaaca gctggtgcgc 420

ttctattcgc gctcgctcaa tgcccgcaag ccgctgggcg gctcgatcga agtggcgctt 480

gcgccggaca gcaacatcaa tcgcgccacc cgttcggata cgctgggcac ggtgatcggc 540

gacttctcgc tcgacgacga tgcccgcgcc aaatcgggtg taggcctcga cctgcaggga 600

cagggctatt ttcgccttgg catcgagccg gggaccgacc tcctggtgcg tgcctcgacc 660

gacgcgacgc tctaccgcga gaaggatttc agcgacatca gcttggcgct ccaggccggg 720

ccgcaataca cttggggcgg caaccagctg accttctcgg caggcccggc gcgtcgctgg 780

tacggcggcc gactgttcag caccaccatg gggggcgggg tgagttggca gcgaccggtg 840

ggcaagcggg ggcaggtgcg cctcgacggc aacatcgccc atgtgaccaa ccggcgcaat 900

gcgctgcaga cggcggatga cttcacgctc tccgccagct tcgatcgggc tttcagcgcg 960

cgtttcggcg gcggcgtgca ggctttcggt ttccgcgaag cagcacgcga cccgggttac 1020

tcgctggcga tgggcggaac gtccgcctac cttttcctcg aactgggtcg caccacgctg 1080

gtgggtactg tcggttacag ccacctcgaa gcggatgccc gcctgttcct ctacccgaac 1140

cgccgcatcg aagaccgcta cagtgccagc atggcagcga ctttgcgcgc gttgcacctg 1200

ggcagcttcg cgccgctggt gcgcctcaag tgggagcgta accgttcctc aatcgagatt 1260

tacgactacc gccgcgtcgt cgccgagttc ggcgtcacgt cggcattctg a 1311

<210> 472

<211> 436

<212> PRT

<213> Novosphingobium sp. AP12 SLAM 1

<400> 472

Met Leu Ala Gly Ile Ala Ala Gly Ala Gly Ala Gln Asp Gln Gly Val

1 5 10 15

Pro Pro Ala Pro Val Pro Ala Gln Ile Lys Leu Ser Ala Ala Gln Ile

20 25 30

Phe Ala Leu Ala Glu Gln Ala Gly Arg Ala Gly Asp Phe Ala Thr Ala

35 40 45

Glu Thr Ala Tyr Arg Ala Leu Thr Arg Asp Ala Asp Leu Glu Val Arg

50 55 60

Thr Glu Ala Arg Phe Arg Leu Gly Leu Met Leu Ala Asp Asp Leu Lys

65 70 75 80

Arg Tyr Ser Asp Ala Ala Leu Glu Phe Arg Arg Ile Leu Asp Asp Lys

85 90 95

Pro Gly Ala Ala Arg Val Arg Leu Glu Leu Ala Arg Met Gln Ala Met

100 105 110

Leu Gly Asn Met Ala Gly Ala Arg Lys Glu Leu Arg Ala Ala Gln Ala

115 120 125

Ala Gly Leu Pro Ser Ser Val Glu Gln Leu Val Arg Phe Tyr Ser Arg

130 135 140

Ser Leu Asn Ala Arg Lys Pro Leu Gly Gly Ser Ile Glu Val Ala Leu

145 150 155 160

Ala Pro Asp Ser Asn Ile Asn Arg Ala Thr Arg Ser Asp Thr Leu Gly

165 170 175

Thr Val Ile Gly Asp Phe Ser Leu Asp Asp Asp Ala Arg Ala Lys Ser

180 185 190

Gly Val Gly Leu Asp Leu Gln Gly Gln Gly Tyr Phe Arg Leu Gly Ile

195 200 205

Glu Pro Gly Thr Asp Leu Leu Val Arg Ala Ser Thr Asp Ala Thr Leu

210 215 220

Tyr Arg Glu Lys Asp Phe Ser Asp Ile Ser Leu Ala Leu Gln Ala Gly

225 230 235 240

Pro Gln Tyr Thr Trp Gly Gly Asn Gln Leu Thr Phe Ser Ala Gly Pro
245 250 255
Ala Arg Arg Trp Tyr Gly Gly Arg Leu Phe Ser Thr Thr Met Gly Gly

260 265 270
Gly Val Ser Trp Gln Arg Pro Val Gly Lys Arg Gly Gln Val Arg Leu
275 280 285
Asp Gly Asn Ile Ala His Val Thr Asn Arg Arg Asn Ala Leu Gln Thr
290 295 300
Ala Asp Asp Phe Thr Leu Ser Ala Ser Phe Asp Arg Ala Phe Ser Ala
305 310 315 320
Arg Phe Gly Gly Gly Val Gln Ala Phe Gly Phe Arg Glu Ala Ala Arg

325 330 335
Asp Pro Gly Tyr Ser Leu Ala Met Gly Gly Thr Ser Ala Tyr Leu Phe
340 345 350
Leu Glu Leu Gly Arg Thr Thr Leu Val Gly Thr Val Gly Tyr Ser His
355 360 365
Leu Glu Ala Asp Ala Arg Leu Phe Leu Tyr Pro Asn Arg Arg Ile Glu
370 375 380
Asp Arg Tyr Ser Ala Ser Met Ala Ala Thr Leu Arg Ala Leu His Leu

385 390 395 400
Gly Ser Phe Ala Pro Leu Val Arg Leu Lys Trp Glu Arg Asn Arg Ser
405 410 415
Ser Ile Glu Ile Tyr Asp Tyr Arg Arg Val Val Ala Glu Phe Gly Val
420 425 430
Thr Ser Ala Phe
435

<210> 473
<211> 1356
<212> DNA
<213> Novosphingobium sp. PP1Y SLAM 1
<400> 473

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gcgggctttt cgccaactgt taaggcacag accgccgagg cgcagggagc ggcacagacg 120

gcccggcttt ccggcaccca attgcttgcc ttcgccaatc gcgctcgcga tgaggggcgc 180

ttcgagattg ccgaagcggc ctatcgcgcg ctgtttgcag atccttcggt acaagtccgc 240

agtgaggcac gattccggtt ggcgatgctt tatgtaggca cgcgtcggct gtcgcaggct 300

gcagtgctgt ttcgcgaaat cctcgacgaa cagcccgacg cgcagcgggt ccgcctcgaa 360

ctggcgcatg ttctggatct catgggcgat gaggtgggcg cacggcgtgc ccttcgcgaa 420

gcacaggcgg gcaagcttcc cccggaagtg gcacgcttcg tcgatcgcta ttccgccgcg 480

ctcagggcgc aaaagcccct tggtgccagc ttcgaccttg ccctggcacc ggacagcaac 540

atcaaccgtg ccacccggtc ctcgacgctc ggaaccgtgt tcggcgattt cgtcctcgac 600

gacgaagcgc gccagcgctc gggtatcggg cttgccctgc gcgggcaggc ctatgcgcgt 660

ctgccaatcg gcgccagcgt aaacttgctc gcaaaactgt ccggttccgc ggacctctat 720

cgcgcccacg acttcaatga cattgccgtt gcagcaacgg tcggtcccga attgcggctg 780

ggtgccgatc gcctttccct ggatggcgga gcgctctggc gctactttgg cggccgaccc 840

tattcacgcg cggtcacggc agaggcgacg tacctgcatc ccctgggccg caaggcccag 900

ctgcgcgccg tggccaacgc ggcccttatc gacaatcgcc gcaattcctt gctcgatggc 960

cacagctttt cggcaacgct cggctatgag cgggcgattt caggccggtc cggcgcgggg 1020

ctgaccgtca gcatcgaccg gcaggcgacg cgcgatcccg gatatgccac ctggggctgg 1080

caaacatcgg ccttcgccta tcgcgacctg ggcgcgctca ccctcgtcgg gacgctggga 1140

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aattaccgtg ccagcctggg agcgaccttt cgagcctttc gaattgcaag cttcgcgcct 1260

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ttgcgaatgg agttcggctt tacgcggtcc ttctag 1356

<210> 474

<211> 451

<212> PRT

<213> Novosphingobium sp. PP1Y SLAM 1

<400> 474

Met Ala Gly Ser Gly Cys Ser Pro Ala Ala Cys Ala Gly Ala Val Leu

1 5 10 15

Ala Leu Ala Ile Ala Gly Phe Ser Pro Thr Val Lys Ala Gln Thr Ala

20 25 30

Glu Ala Gln Gly Ala Ala Gln Thr Ala Arg Leu Ser Gly Thr Gln Leu

35 40 45

Leu Ala Phe Ala Asn Arg Ala Arg Asp Glu Gly Arg Phe Glu Ile Ala

50 55 60

Glu Ala Ala Tyr Arg Ala Leu Phe Ala Asp Pro Ser Val Gln Val Arg

65 70 75 80

Ser Glu Ala Arg Phe Arg Leu Ala Met Leu Tyr Val Gly Thr Arg Arg

85 90 95

Leu Ser Gln Ala Ala Val Leu Phe Arg Glu Ile Leu Asp Glu Gln Pro

100 105 110

Asp Ala Gln Arg Val Arg Leu Glu Leu Ala His Val Leu Asp Leu Met

115 120 125

Gly Asp Glu Val Gly Ala Arg Arg Ala Leu Arg Glu Ala Gln Ala Gly

130 135 140

Lys Leu Pro Pro Glu Val Ala Arg Phe Val Asp Arg Tyr Ser Ala Ala

145 150 155 160

Leu Arg Ala Gln Lys Pro Leu Gly Ala Ser Phe Asp Leu Ala Leu Ala

165 170 175

Pro Asp Ser Asn Ile Asn Arg Ala Thr Arg Ser Ser Thr Leu Gly Thr

180 185 190

Val Phe Gly Asp Phe Val Leu Asp Asp Glu Ala Arg Gln Arg Ser Gly

195 200 205

Ile Gly Leu Ala Leu Arg Gly Gln Ala Tyr Ala Arg Leu Pro Ile Gly

210 215 220

Ala Ser Val Asn Leu Leu Ala Lys Leu Ser Gly Ser Ala Asp Leu Tyr

225 230 235 240

Arg Ala His Asp Phe Asn Asp Ile Ala Val Ala Ala Thr Val Gly Pro

245 250 255

Glu Leu Arg Leu Gly Ala Asp Arg Leu Ser Leu Asp Gly Gly Ala Leu

260 265 270

Trp Arg Tyr Phe Gly Gly Arg Pro Tyr Ser Arg Ala Val Thr Ala Glu
275 280 285

Ala Thr Tyr Leu His Pro Leu Gly Arg Lys Ala Gln Leu Arg Ala Val
290 295 300

Ala Asn Ala Ala Leu Ile Asp Asn Arg Arg Asn Ser Leu Leu Asp Gly
305 310 315 320

His Ser Phe Ser Ala Thr Leu Gly Tyr Glu Arg Ala Ile Ser Gly Arg
325 330 335

Ser Gly Ala Gly Leu Thr Val Ser Ile Asp Arg Gln Ala Thr Arg Asp
340 345 350

Pro Gly Tyr Ala Thr Trp Gly Trp Gln Thr Ser Ala Phe Ala Tyr Arg
355 360 365

Asp Leu Gly Ala Leu Thr Leu Val Gly Thr Leu Gly Met Gly Arg Leu
370 375 380

Lys Ala Asp Arg Arg Ile Leu Leu Tyr Pro Asp Arg Arg Ser Asp Arg
385 390 395 400

Asn Tyr Arg Ala Ser Leu Gly Ala Thr Phe Arg Ala Phe Arg Ile Ala
405 410 415

Ser Phe Ala Pro Phe Ile Arg Ala Thr Phe Glu Arg Asn Arg Ser Ser
420 425 430

Leu Glu Ile His Asp Tyr Arg Arg Leu Arg Met Glu Phe Gly Phe Thr
435 440 445

Arg Ser Phe
450

<210> 475

<211> 1326

<212> DNA

<213> Novosphingobium sp. Rr 2-17 SLAM 1

<400> 475

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gcgacgcccg ccaccgcccc caaacgctca catgaactct cggcaatcga ggtgttcacc 120

gttgctgagc gtgcgcagag tgcaggacac tatgaggaag cgatccgtct ctatgacgcc 180

ctgacgcagg accgcaatgc cgacgtgcgg gcagaggccc gcttccgcaa gggcatgctg 240

ttggccagcc tgaagcgcta tcgcaaggcc gcgacggcct ttcgcgagct gctcgatgag 300
acacccgatg ccgcccccgt gcggctggaa ctggcccagg tcctggcact gatgggtgac 360
gagggcggcg cccggcgcga gttacgccaa gtgcaggcaa ccggactgcc ggaacaagtg 420
gcgcgtgcgg tcggccagtt cgacacggcg ctgcgttcgc ataagcgcgc gggactaagg 480
ctagagttcg cactcgcacc cgataccaac atcaatcggg cgaccgaagt tcgcacgctg 540
gataccgtca tcgcaccttt gacgctatcc cgcgatgccc gggcccagtc agggctaggc 600
gtccatctgt cggccgacgg atacctgaag gtccccatcg gtgcagggat cagcgtggtg 660

ccccggatca acagccttgc cacgctttat ggcaagagcg aattcgacga tataacagtc 720
acggccttgg tcgggctgga agtgcagcgt cagcatgacc ggttcagccc ctcgattgga 780
cacggctggc gctggtacgg caagcgttcc tacatgcaca ccgatgtcgc cacgctggac 840
tggatccatg tgctgggtca aacagcgcag ttgagcggtt cggtaagtgc ggccactacc 900
gactatcagc tcaataacct acaggacggt gcgctctatt ccgtgagtgt tggtgtcgag 960
cgggcactgt cggcgcgcag cggtgttagc gtcgcgctta atgccgtgcg ccagaccgca 1020
cgcgatcccg gttatgcgac agcatcggga ggcgtgcgtc tgctcggctg gcgggaggcg 1080

ggtcgaacca cactgttcgc ctcagcgacg ctccagcgta ccgaaggtga cgccgccctt 1140
gcgctgttcg gcaagcgtcg tcgtgagtgg ttcgccagcg tacgcgcagg ggccaccttg 1200
cgggctctga ctgtgcacgg tttcgccccc tacgtgcggg tcggctatga gcgcaatgca 1260
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ttctag 1326

<210> 476
<211> 441
<212> PRT
<213> Novosphingobium sp. Rr 2-17 SLAM 1
<400> 476

Met Ile Val Cys Phe Ala Ala Ala Ala Ala Pro Phe Val Leu Ala Ser

1 5 10 15

Ala Ala Ser Pro Ala Thr Pro Ala Thr Ala Pro Lys Arg Ser His Glu
20 25 30

Leu Ser Ala Ile Glu Val Phe Thr Val Ala Glu Arg Ala Gln Ser Ala
35 40 45

Gly His Tyr Glu Glu Ala Ile Arg Leu Tyr Asp Ala Leu Thr Gln Asp

50 55 60

Arg Asn Ala Asp Val Arg Ala Glu Ala Arg Phe Arg Lys Gly Met Leu

65 70 75 80

Leu Ala Ser Leu Lys Arg Tyr Arg Lys Ala Ala Thr Ala Phe Arg Glu

85 90 95

Leu Leu Asp Glu Thr Pro Asp Ala Ala Pro Val Arg Leu Glu Leu Ala

100 105 110

Gln Val Leu Ala Leu Met Gly Asp Glu Gly Gly Ala Arg Arg Glu Leu

115 120 125

Arg Gln Val Gln Ala Thr Gly Leu Pro Glu Gln Val Ala Arg Ala Val

130 135 140

Gly Gln Phe Asp Thr Ala Leu Arg Ser His Lys Arg Ala Gly Leu Arg

145 150 155 160

Leu Glu Phe Ala Leu Ala Pro Asp Thr Asn Ile Asn Arg Ala Thr Glu

165 170 175

Val Arg Thr Leu Asp Thr Val Ile Ala Pro Leu Thr Leu Ser Arg Asp

180 185 190

Ala Arg Ala Gln Ser Gly Leu Gly Val His Leu Ser Ala Asp Gly Tyr

195 200 205

Leu Lys Val Pro Ile Gly Ala Gly Ile Ser Val Val Pro Arg Ile Asn

210 215 220

Ser Leu Ala Thr Leu Tyr Gly Lys Ser Glu Phe Asp Asp Ile Thr Val

225 230 235 240

Thr Ala Leu Val Gly Leu Glu Val Gln Arg Gln His Asp Arg Phe Ser

245 250 255

Pro Ser Ile Gly His Gly Trp Arg Trp Tyr Gly Lys Arg Ser Tyr Met

260 265 270

His Thr Asp Val Ala Thr Leu Asp Trp Ile His Val Leu Gly Gln Thr

275 280 285

Ala Gln Leu Ser Gly Ser Val Ser Ala Ala Thr Thr Asp Tyr Gln Leu

290 295 300

Asn Asn Leu Gln Asp Gly Ala Leu Tyr Ser Val Ser Val Gly Val Glu

305 310 315 320

Arg Ala Leu Ser Ala Arg Ser Gly Val Ser Val Ala Leu Asn Ala Val

325 330 335

Arg Gln Thr Ala Arg Asp Pro Gly Tyr Ala Thr Ala Ser Gly Gly Val

340 345 350

Arg Leu Leu Gly Trp Arg Glu Ala Gly Arg Thr Thr Leu Phe Ala Ser

355 360 365

Ala Thr Leu Gln Arg Thr Glu Gly Asp Ala Ala Leu Ala Leu Phe Gly

370 375 380

Lys Arg Arg Arg Glu Trp Phe Ala Ser Val Arg Ala Gly Ala Thr Leu

385 390 395 400

Arg Ala Leu Thr Val His Gly Phe Ala Pro Tyr Val Arg Val Gly Tyr

405 410 415

Glu Arg Asn Ala Ser Ser Val Asp Leu Tyr Asp Tyr Arg Arg Phe Thr

420 425 430

Ser Glu Phe Gly Ile Thr Ser Ala Phe

435 440

<210> 477

<211> 1113

<212> DNA

<213> O. batsensis SLAM 1

<400> 477

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ctggaacggc tggtcgcgcg ccggccggac gtcgcgcggt tccggatcgc tcttgccgaa 120

gttctggtgg acgccgggca gaccgagcgg gcgcgcctgc atctggacga atcccttggc 180

ggcatcgcct cggacgtgga tcagagccgt gcccggaaac tgctgacggc gctggacacg 240

aaaaagacct tcagtggcca tttcaacctg tccttcgtgc cttcgaccaa cgccgcccag 300

cagacgaact cccgtaccgt caccatcggc ggccgcgatt tcgtgattgc cgacagcgcg 360

cgcaagtcac cggcgatagg gctggccctc gacctcggag tgcaggcggt gccgcagatc 420

ggtccccgca cgcgtctgcg ctttggcctg tccgccgatg cgcgtgtctt cgacgaccgc 480

gcgcgggacg atctgacgct gagagccgag gtcgcgctgc gctatgaacc cacaccatcg 540

ctcgcgctgg aggtcggcac gacctacacg cgccgctggc ttgacgggac gggctattcc 600

cgcgcgccgg gtctcttttt cggggtctcc gcctatcccg atgcacaaag ccggttgcag 660

gtggtggcga gcctcgacga gcttcgacac gagaccgcga cggggctcga cggacagcgc 720

tggcttgccg ccgtctccta tacccgggcg gtcacgccgc aattgcagct gcgggccagt 780

ctcggtgccg aacacatggg agcggcggcc ccgagttctg cctatcgtgc gttttggtcg 840

gggatcggca tgagctatta ctttcggggc gggttgcggc tgggcgccga tgcgtcgctg 900

cgccgtgcca gctacaacgg cgtctcgccg ctgttcggca agcagcgccg cgacacgcag 960

ttccgggcct cgatcgaagc ctcgcacagc cgtttcaacc tgtccggatt tgcgccggtc 1020

atgggggtgg actacacccg tcgcgcggcg aacatcaccg tctactccta tgacgagttc 1080

agtgcgaggg tcggcttgac gaaacggttc tga 1113

<210> 478

<211> 370

<212> PRT

<213> O. batsensis SLAM 1

<400> 478

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1 5 10 15

Ala Leu Pro Leu Leu Glu Arg Leu Val Ala Arg Arg Pro Asp Val Ala
20 25 30

Arg Phe Arg Ile Ala Leu Ala Glu Val Leu Val Asp Ala Gly Gln Thr
35 40 45

Glu Arg Ala Arg Leu His Leu Asp Glu Ser Leu Gly Gly Ile Ala Ser
50 55 60

Asp Val Asp Gln Ser Arg Ala Arg Lys Leu Leu Thr Ala Leu Asp Thr
65 70 75 80

Lys Lys Thr Phe Ser Gly His Phe Asn Leu Ser Phe Val Pro Ser Thr
85 90 95

Asn Ala Ala Gln Gln Thr Asn Ser Arg Thr Val Thr Ile Gly Gly Arg
100 105 110

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Asp Phe Val Ile Ala Asp Ser Ala Arg Lys Ser Pro Ala Ile Gly Leu
        115                 120                 125
Ala Leu Asp Leu Gly Val Gln Ala Val Pro Gln Ile Gly Pro Arg Thr
    130                 135                 140

Arg Leu Arg Phe Gly Leu Ser Ala Asp Ala Arg Val Phe Asp Asp Arg
145                 150                 155                 160
Ala Arg Asp Asp Leu Thr Leu Arg Ala Glu Val Ala Leu Arg Tyr Glu
                165                 170                 175
Pro Thr Pro Ser Leu Ala Leu Glu Val Gly Thr Thr Tyr Thr Arg Arg
            180                 185                 190
Trp Leu Asp Gly Thr Gly Tyr Ser Arg Ala Pro Gly Leu Phe Phe Gly
        195                 200                 205

Val Ser Ala Tyr Pro Asp Ala Gln Ser Arg Leu Gln Val Val Ala Ser
    210                 215                 220
Leu Asp Glu Leu Arg His Glu Thr Ala Thr Gly Leu Asp Gly Gln Arg
225                 230                 235                 240
Trp Leu Ala Ala Val Ser Tyr Thr Arg Ala Val Thr Pro Gln Leu Gln
                245                 250                 255
Leu Arg Ala Ser Leu Gly Ala Glu His Met Gly Ala Ala Ala Pro Ser
            260                 265                 270

Ser Ala Tyr Arg Ala Phe Trp Ser Gly Ile Gly Met Ser Tyr Tyr Phe
        275                 280                 285
Arg Gly Gly Leu Arg Leu Gly Ala Asp Ala Ser Leu Arg Arg Ala Ser
    290                 295                 300
Tyr Asn Gly Val Ser Pro Leu Phe Gly Lys Gln Arg Arg Asp Thr Gln
305                 310                 315                 320
Phe Arg Ala Ser Ile Glu Ala Ser His Ser Arg Phe Asn Leu Ser Gly
                325                 330                 335

Phe Ala Pro Val Met Gly Val Asp Tyr Thr Arg Arg Ala Ala Asn Ile
            340                 345                 350
Thr Val Tyr Ser Tyr Asp Glu Phe Ser Ala Arg Val Gly Leu Thr Lys
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355 360 365

Arg Phe

370

<210> 479

<211> 1020

<212> DNA

<213> O. symbiont SLAM Rs1

<400> 479

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aacgttgctg ctgacgtccg tatgtttaag ggttaaatgg ggtttgaaac cgaacagtga 120

ccaacgtgaa ctctttagac ttagggtcag atttttctct ctgtctttgc gtcgctcgcc 180

caagatgtta ctgaatttat ggtaggtctg ttggcgtact gagctagata aggtcgcgct 240

aacggtattg ttgaaggttt tcgatacccc caatctaatc cctatttgac gataggcgta 300

aggtcgatct tgcgctagcc ggttcagcca atccgcaccg gcaaatacca cccagttatt 360

attcagccct tgccaagcgg tgatgttggt cgaataagag gggccgtcgt aacgttgaaa 420

atggctcttt ttgtagcgta attctttgta gtccgcactc actttaaaca tgcgctgatt 480

agatatttta tgcgtccaat cgccgtggag tccccaggcg ctaaacagag atttgtcggc 540

gtaggttgaa tattcaaatg agggggccaa ccgtagctga tcagtgaaat tttgaaagcg 600

ataacctagt tgggtgttga atgtgctctg gtcgtaaccc ggatgatcat cgtacttttt 660

accgtataac attgattggc tatacagggc atgatgtcta gcaataggta gcgctttgct 720

agcggtgaat tcgtaatcta agccacgggt ggagatagcc ttgggaatgc tgcgctggta 780

aacgcactgt ccccgatagg ttaatagaca agattgattt tctgaggatt ggttgaggtt 840

gtctttccag acactgccaa tcgcaaaaaa tagcgaccag tcactgcgtt gctccaatgc 900

tttgctaaaa ctttgcacac tgcggtttac ccccgcgtgt tgcgtgtcat cagtgtctaa 960

atattcggca atttcagtaa aaataccccct cgcctcttta tcttgatgat cttcaaacaa 1020

<210> 480

<211> 339

<212> PRT

<213> O. symbiont SLAM Rs1

<400> 480

Met Phe Glu Asp His Gln Asp Lys Glu Ala Arg Gly Ile Phe Thr Glu

1 5 10 15

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Ile Ala Glu Tyr Leu Asp Thr Asp Asp Thr Gln His Ala Gly Val Asn
            20                  25                  30
Arg Ser Val Gln Ser Phe Ser Lys Ala Leu Glu Gln Arg Ser Asp Trp
        35                  40                  45

Ser Leu Phe Phe Ala Ile Gly Ser Val Trp Lys Asp Asn Leu Asn Gln
    50                  55                  60
Ser Ser Glu Asn Gln Ser Cys Leu Leu Thr Tyr Arg Gly Gln Cys Val
65                  70                  75                  80
Tyr Gln Arg Ser Ile Pro Lys Ala Ile Ser Thr Arg Gly Leu Asp Tyr
                85                  90                  95
Glu Phe Thr Ala Ser Lys Ala Leu Pro Ile Ala Arg His His Ala Leu
            100                 105                 110

Tyr Ser Gln Ser Met Leu Tyr Gly Lys Lys Tyr Asp Asp His Pro Gly
        115                 120                 125
Tyr Asp Gln Ser Thr Phe Asn Thr Gln Leu Gly Tyr Arg Phe Gln Asn
    130                 135                 140
Phe Thr Asp Gln Leu Arg Leu Ala Pro Ser Phe Glu Tyr Ser Thr Tyr
145                 150                 155                 160
Ala Asp Lys Ser Leu Phe Ser Ala Trp Gly Leu His Gly Asp Trp Thr
                165                 170                 175

His Lys Ile Ser Asn Gln Arg Met Phe Lys Val Ser Ala Asp Tyr Lys
            180                 185                 190
Glu Leu Arg Tyr Lys Lys Ser His Phe Gln Arg Tyr Asp Gly Pro Ser
        195                 200                 205
Tyr Ser Thr Asn Ile Thr Ala Trp Gln Gly Leu Asn Asn Asn Trp Val
    210                 215                 220
Val Phe Ala Gly Ala Asp Trp Leu Asn Arg Leu Ala Gln Asp Arg Pro
225                 230                 235                 240

Tyr Ala Tyr Arg Gln Ile Gly Ile Arg Leu Gly Val Ser Lys Thr Phe
                245                 250                 255
Asn Asn Thr Val Ser Ala Thr Leu Ser Ser Ser Val Arg Gln Gln Thr
```

260 265 270

Tyr His Lys Phe Ser Asn Ile Leu Gly Glu Arg Arg Lys Asp Arg Glu

275 280 285

Lys Asn Leu Thr Leu Ser Leu Lys Ser Ser Arg Trp Ser Leu Phe Gly

290 295 300

Phe Lys Pro His Leu Thr Leu Lys His Thr Asp Val Ser Ser Asn Val

305 310 315 320

Asp Trp Leu Tyr Ser Arg Arg Ser Asn Glu Ile Ser Leu Lys Leu Glu

325 330 335

Arg Ser Phe

<210> 481

<211> 1284

<212> DNA

<213> Oceanicola sp. S124 SLAM 1

<400> 481

atggcgatgg tggtgttgtt cgggctctct gtcctggcgg cgcccccggc ccgcgcctcg 60

ggatcgcccg tcgaggcggt acaggggctg gtccaggccg gagagctgga gctggcccgt 120

gatcagctgc tggcctggca gccgcagtcc gccgccgagg ccgaacgtcg cctctggctt 180

ctggccgtgg tctatcgcga aggcgggcgc cccgacctgg cgttgatcgt gctggaagac 240

ctggtggccc ggcgccccga cgtcgcccgc ttccggctgg agctggccga caccctggcc 300

cgcctgggcc agcaggatcg cgcagcctat cactatgacc tcgcccgtgg aggagagctc 360

agcgacgctc agcgggccca tgcggccagc aatgccaccc ggatggagac ccccagcccc 420

tggacgggca acttcgggat cgcgctggtg ccttccagca accccggccg caagacccag 480

gaagagacgc tggatctcgg cttcggcacc gctgtcctca gccaggaatc gcgggcccag 540

ccggcgaccg ggctcgaggt cggcgcacgg ctggcctatg cgcaccggat ctcgcagcgg 600

cttcagggac aggtggcagt gaacctgaac gggcggctgt tcgcggatcg cgacgacaac 660

gatgtgaccg gcagcatcga ggcggggctg gtgcatcgcc tgggcccgga tgcgctgttg 720

cgtacgacgc tcagttacca gcgccgcgat ctcggcggcg atctctattc gcgcgggccg 780

ggtttcgggg tgaacctgat gctgcgcagc ggagcgcggg ggcgtatcgg gctggggctg 840

accctgagcg acctgaccta tcccggtgcc ccgggggcgg acgggctgcg cagcgtcgcc 900

atgctcagct acgatcacgc cctttcgccg accttcggcc tgcgcaccct gctgcgctac 960

gagcgcgtcg acgcggtcaa cgccgatgtc gccgccacca gctgggaggc ggggctgggc 1020

gccagccagg tcttccgggg cgggctgatc ctggacgccg acctgcggct gcgccggtcc 1080

gggcgtgacg gcccgcatgg gctgtttggc gtggtgcagc aggaccgtcg ccagaccctc 1140

tcgctgcggt tgcgccacag cgaggtctcc tggcgcggct tcgcccccta tgtcgagctg 1200

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ctgggtctga cgcgccggtt ctga 1284

<210> 482

<211> 427

<212> PRT

<213> Oceanicola sp. S124 SLAM 1

<400> 482

Met Ala Met Val Val Leu Phe Gly Leu Ser Val Leu Ala Ala Pro Pro
1 5 10 15

Ala Arg Ala Ser Gly Ser Pro Val Glu Ala Val Gln Gly Leu Val Gln
20 25 30

Ala Gly Glu Leu Glu Leu Ala Arg Asp Gln Leu Leu Ala Trp Gln Pro
35 40 45

Gln Ser Ala Ala Glu Ala Glu Arg Arg Leu Trp Leu Leu Ala Val Val
50 55 60

Tyr Arg Glu Gly Gly Arg Pro Asp Leu Ala Leu Ile Val Leu Glu Asp
65 70 75 80

Leu Val Ala Arg Arg Pro Asp Val Ala Arg Phe Arg Leu Glu Leu Ala
85 90 95

Asp Thr Leu Ala Arg Leu Gly Gln Gln Asp Arg Ala Ala Tyr His Tyr
100 105 110

Asp Leu Ala Arg Gly Gly Glu Leu Ser Asp Ala Gln Arg Ala His Ala
115 120 125

Ala Ser Asn Ala Thr Arg Met Glu Thr Pro Ser Pro Trp Thr Gly Asn
130 135 140

Phe Gly Ile Ala Leu Val Pro Ser Ser Asn Pro Gly Arg Lys Thr Gln

145 150 155 160

Glu Glu Thr Leu Asp Leu Gly Phe Gly Thr Ala Val Leu Ser Gln Glu

165 170 175

Ser Arg Ala Gln Pro Ala Thr Gly Leu Glu Val Gly Ala Arg Leu Ala

180 185 190

Tyr Ala His Arg Ile Ser Gln Arg Leu Gln Gly Gln Val Ala Val Asn

195 200 205

Leu Asn Gly Arg Leu Phe Ala Asp Arg Asp Asp Asn Asp Val Thr Gly

210 215 220

Ser Ile Glu Ala Gly Leu Val His Arg Leu Gly Pro Asp Ala Leu Leu

225 230 235 240

Arg Thr Thr Leu Ser Tyr Gln Arg Arg Asp Leu Gly Gly Asp Leu Tyr

245 250 255

Ser Arg Gly Pro Gly Phe Gly Val Asn Leu Met Leu Arg Ser Gly Ala

260 265 270

Arg Gly Arg Ile Gly Leu Gly Leu Thr Leu Ser Asp Leu Thr Tyr Pro

275 280 285

Gly Ala Pro Gly Ala Asp Gly Leu Arg Ser Val Ala Met Leu Ser Tyr

290 295 300

Asp His Ala Leu Ser Pro Thr Phe Gly Leu Arg Thr Leu Leu Arg Tyr

305 310 315 320

Glu Arg Val Asp Ala Val Asn Ala Asp Val Ala Ala Thr Ser Trp Glu

325 330 335

Ala Gly Leu Gly Ala Ser Gln Val Phe Arg Gly Gly Leu Ile Leu Asp

340 345 350

Ala Asp Leu Arg Leu Arg Arg Ser Gly Arg Asp Gly Pro His Gly Leu

355 360 365

Phe Gly Val Val Gln Gln Asp Arg Arg Gln Thr Leu Ser Leu Arg Leu

370 375 380

Arg His Ser Glu Val Ser Trp Arg Gly Phe Ala Pro Tyr Val Glu Leu

385 390 395 400

Thr Ala Glu Arg Gln Arg Ser Ser Ile Pro Tyr Tyr Ser Tyr Asp Ala
405 410 415

Gln Asp Leu Thr Leu Gly Leu Thr Arg Arg Phe
420 425

<210> 483

<211> 1371

<212> DNA

<213> P. aeruginosa SLAM 1

<400> 483

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gaagggcaga cctaccaggt gcccgacctg ctggaggcgc tggaaccggc gatctacatc 120

gtcatcaaca gcaaccagtg ggtccagctg ccggacttca tcgcgcgcta tcgtcagttg 180

cccggccacc ggccggccct ggcggcaatg gccgagagcc tgatggcgcg caaccgcggc 240

gactacccga cagccttgcg gcgcatgctg gaggcccgcg aggaagaacc gcaagacgcg 300

cggatacgcc tcgaatccgc tcgcctgctg ttcgaggaca accaggacac gcaggccgga 360

gaggcgtttt cccggttgca gggcacagga ctgccgccct atgcggaaat actggtgcaa 420

cagtaccggc aagccctgga cattcgctcc gattggcatg gcaccgccgc gctgggctgg 480

ggctacaacg acaacatcaa ccaggccaac ggctatcgcc gctgcgagtg gtacgtaccg 540

gtagccgacc tgtgtgcctt cgaacgggta atgccggagg ccatcggctc ggaactgctc 600

aactatgaag cctccctgca gcgtcgcatc aacctggccg gcaatcacaa cctgcaggtg 660

cgcccggtca gctacggcaa ctattactca tccaccgaca cgtcctcggc ctcccgcctc 720

cacgactaca gcaacagcct gtccgtcctg caggtcggct accagtacct ggacgcccgc 780

gacagcctgt cactgacgcc ctacttcgag tactactacc gcaatcgcca tggagactat 840

ctcgcccacg gcctgcaatt ggagtggcgg cgctcgttga accagcggtg gcagttgggc 900

agcagcctgg acgccaagcg ctacgaatac agttcccgcg ggcaactgac aggcgccgac 960

tacaaccagt accagtggga cctgttcgcg tccttcatgc cgcaacccac caccaacctg 1020

tacgcggggg tgaatctcgg tcgccggcgc tatgcgctag accaggccag cagcagggac 1080

tgggcgatcc gcggcggact ctaccatgcg ttcgccggcg aacccggcct gtacgtgaac 1140

gcgctgggta tctaccgaaa cacccgcaac gaggcgttcg atgccttcct gggcgcgcgc 1200

cggcatgacc agcagcaggt gtacatcctc ggggtcggcg ccaacggctg gaaattcgcc 1260

ggcctcgtcc cggaactacg ggttcgccac agcatcaacc gcagcaatct ggactgggcg 1320

ttcggctaca ggcagaccga gctcagcctg atgttgcgca aggacttctg a 1371

<210> 484

<211> 456

<212> PRT

<213> P. aeruginosa SLAM 1

<400> 484

Met Asn Gln Lys Ser Gln Ala Glu Gln Ser Leu Ala Ala Pro Pro Gly
1 5 10 15

Thr Leu Leu Tyr Glu Gly Gln Thr Tyr Gln Val Pro Asp Leu Leu Glu
20 25 30

Ala Leu Glu Pro Ala Ile Tyr Ile Val Ile Asn Ser Asn Gln Trp Val
35 40 45

Gln Leu Pro Asp Phe Ile Ala Arg Tyr Arg Gln Leu Pro Gly His Arg
50 55 60

Pro Ala Leu Ala Ala Met Ala Glu Ser Leu Met Ala Arg Asn Arg Gly
65 70 75 80

Asp Tyr Pro Thr Ala Leu Arg Arg Met Leu Glu Ala Arg Glu Glu Glu
85 90 95

Pro Gln Asp Ala Arg Ile Arg Leu Glu Ser Ala Arg Leu Leu Phe Glu
100 105 110

Asp Asn Gln Asp Thr Gln Ala Gly Glu Ala Phe Ser Arg Leu Gln Gly
115 120 125

Thr Gly Leu Pro Pro Tyr Ala Glu Ile Leu Val Gln Gln Tyr Arg Gln
130 135 140

Ala Leu Asp Ile Arg Ser Asp Trp His Gly Thr Ala Ala Leu Gly Trp
145 150 155 160

Gly Tyr Asn Asp Asn Ile Asn Gln Ala Asn Gly Tyr Arg Arg Cys Glu
165 170 175

Trp Tyr Val Pro Val Ala Asp Leu Cys Ala Phe Glu Arg Val Met Pro
180 185 190

Glu Ala Ile Gly Ser Glu Leu Leu Asn Tyr Glu Ala Ser Leu Gln Arg
195 200 205

Arg Ile Asn Leu Ala Gly Asn His Asn Leu Gln Val Arg Pro Val Ser
210 215 220
Tyr Gly Asn Tyr Tyr Ser Ser Thr Asp Thr Ser Ser Ala Ser Arg Leu
225 230 235 240

His Asp Tyr Ser Asn Ser Leu Ser Val Leu Gln Val Gly Tyr Gln Tyr
245 250 255
Leu Asp Ala Arg Asp Ser Leu Ser Leu Thr Pro Tyr Phe Glu Tyr Tyr
260 265 270
Tyr Arg Asn Arg His Gly Asp Tyr Leu Ala His Gly Leu Gln Leu Glu
275 280 285
Trp Arg Arg Ser Leu Asn Gln Arg Trp Gln Leu Gly Ser Ser Leu Asp
290 295 300

Ala Lys Arg Tyr Glu Tyr Ser Ser Arg Gly Gln Leu Thr Gly Ala Asp
305 310 315 320
Tyr Asn Gln Tyr Gln Trp Asp Leu Phe Ala Ser Phe Met Pro Gln Pro
325 330 335
Thr Thr Asn Leu Tyr Ala Gly Val Asn Leu Gly Arg Arg Arg Tyr Ala
340 345 350
Leu Asp Gln Ala Ser Ser Arg Asp Trp Ala Ile Arg Gly Gly Leu Tyr
355 360 365

His Ala Phe Ala Gly Glu Pro Gly Leu Tyr Val Asn Ala Leu Gly Ile
370 375 380
Tyr Arg Asn Thr Arg Asn Glu Ala Phe Asp Ala Phe Leu Gly Ala Arg
385 390 395 400
Arg His Asp Gln Gln Gln Val Tyr Ile Leu Gly Val Gly Ala Asn Gly
405 410 415
Trp Lys Phe Ala Gly Leu Val Pro Glu Leu Arg Val Arg His Ser Ile
420 425 430

Asn Arg Ser Asn Leu Asp Trp Ala Phe Gly Tyr Arg Gln Thr Glu Leu
435 440 445
Ser Leu Met Leu Arg Lys Asp Phe

450 455

<210> 485

<211> 1458

<212> DNA

<213> P. alcalifaciens SLAM 1

<400> 485

gtgattttgc ctacctgtat ttttatggaa aaagaacagg aaagagagat gaaaaaaata 60

ataaacaata ttgaggtatt aattctatta ttgttttctg caaattcatt ttctgaaaaa 120

aattatgggt atcaacaata tgaacagata attgaagttt taacggaaat aaataacaca 180

aggaataaat cacccattat aatcccactt aaaattaata aaactgtcga cgaccttggt 240

tttattcttt atgatttaac caatcggcag cagtttcaaa aaatcgatga actattacct 300

gattatctaa atgataaaaa tcacgataaa ggtatggtgg attatatttc agcagaaagg 360

gcttatttta atggtgatta cccattgtca cttaagtttt atttaaaaat agttaatgaa 420

aaccctaact cagtgttttc tgaaatgaaa ctggctcatg tctatataaa aaatagctat 480

caccgtgaag cattaagttt atataaaaag ataaaagata aatatcgagt aaatctatct 540

gaagagagaa taaaacagat agataatgaa attacagcat tagaaaatcg cactcattgg 600

cagggaaatt tcaatgctga tttaaaatat gatacgaact ataccgaggc tcatggtaat 660

ggtgagcagc aatgtagtgc aatgtggtgt atgcaaggta gcgaaattaa atctggtttg 720

gtgtatggct tttcaggaaa tgccaataaa gtcctttggc agaatcgagg acattcactg 780

ttggccagcc ttggtggaca tgtatgggaa ttccctcatc gctcagtaaa aaggcgcttt 840

tcaagttatt catcagtaag ctatcagtat ctttatggta ataaaaaggt cgcttttttca 900

ccgattgtag atattaattg gcgagggcat ctgtttgacc attacagtgt tggtgcgcgc 960

attactgggg aatattctcc cagcagtaaa ctttatttac tgtctaacat aacgtataaa 1020

aatcaaactt tcttcggaaa gcgagcatcg cgttcaggtt acgatattaa ttacagtatg 1080

acagcaattt atttagttaa tccacaatgg agcttattct caaatttata tggtggcaaa 1140

aatattgaaa aatataaaag tgatagctat caattgtcag ggttaaccgt ggactcaatc 1200

aatgtatttg gctcgaataa gttagtcaat aaattaacaa gtagcaatca taagtttttt 1260

gattttgaca gtgcacttaa tacaaagcga cacgatgagt catgggcgtt aaatagccaa 1320

ataactctat tgggacacaa atttttatca ttaacaccaa cactctatgt taattacaaa 1380

ttcaatgata gcagtgcaag aataagctat tcctataata aaagcgaagt gggtttaaat 1440

ttaagtaaaa cgttttag 1458

<210> 486

<211> 485

<212> PRT

<213> P. alcalifaciens SLAM 1

<400> 486

Met Ile Leu Pro Thr Cys Ile Phe Met Glu Lys Glu Gln Glu Arg Glu
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Met Lys Lys Ile Ile Asn Asn Ile Glu Val Leu Ile Leu Leu Leu Phe
20 25 30

Ser Ala Asn Ser Phe Ser Glu Lys Asn Tyr Gly Tyr Gln Gln Tyr Glu
35 40 45

Gln Ile Ile Glu Val Leu Thr Glu Ile Asn Asn Thr Arg Asn Lys Ser
50 55 60

Pro Ile Ile Ile Pro Leu Lys Ile Asn Lys Thr Val Asp Asp Leu Gly
65 70 75 80

Phe Ile Leu Tyr Asp Leu Thr Asn Arg Gln Gln Phe Gln Lys Ile Asp
85 90 95

Glu Leu Leu Pro Asp Tyr Leu Asn Asp Lys Asn His Asp Lys Gly Met
100 105 110

Val Asp Tyr Ile Ser Ala Glu Arg Ala Tyr Phe Asn Gly Asp Tyr Pro
115 120 125

Leu Ser Leu Lys Phe Tyr Leu Lys Ile Val Asn Glu Asn Pro Asn Ser
130 135 140

Val Phe Ser Glu Met Lys Leu Ala His Val Tyr Ile Lys Asn Ser Tyr
145 150 155 160

His Arg Glu Ala Leu Ser Leu Tyr Lys Lys Ile Lys Asp Lys Tyr Arg
165 170 175

Val Asn Leu Ser Glu Glu Arg Ile Lys Gln Ile Asp Asn Glu Ile Thr
180 185 190

Ala Leu Glu Asn Arg Thr His Trp Gln Gly Asn Phe Asn Ala Asp Leu
195 200 205

Lys Tyr Asp Thr Asn Tyr Thr Glu Ala His Gly Asn Gly Glu Gln Gln

210 215 220

Cys Ser Ala Met Trp Cys Met Gln Gly Ser Glu Ile Lys Ser Gly Leu
225 230 235 240

Val Tyr Gly Phe Ser Gly Asn Ala Asn Lys Val Leu Trp Gln Asn Arg
245 250 255

Gly His Ser Leu Leu Ala Ser Leu Gly Gly His Val Trp Glu Phe Pro
260 265 270

His Arg Ser Val Lys Arg Arg Phe Ser Ser Tyr Ser Ser Val Ser Tyr
275 280 285

Gln Tyr Leu Tyr Gly Asn Lys Lys Val Ala Phe Ser Pro Ile Val Asp
290 295 300

Ile Asn Trp Arg Gly His Leu Phe Asp His Tyr Ser Val Gly Ala Arg
305 310 315 320

Ile Thr Gly Glu Tyr Ser Pro Ser Ser Lys Leu Tyr Leu Leu Ser Asn
325 330 335

Ile Thr Tyr Lys Asn Gln Thr Phe Phe Gly Lys Arg Ala Ser Arg Ser
340 345 350

Gly Tyr Asp Ile Asn Tyr Ser Met Thr Ala Ile Tyr Leu Val Asn Pro
355 360 365

Gln Trp Ser Leu Phe Ser Asn Leu Tyr Gly Gly Lys Asn Ile Glu Lys
370 375 380

Tyr Lys Ser Asp Ser Tyr Gln Leu Ser Gly Leu Thr Val Asp Ser Ile
385 390 395 400

Asn Val Phe Gly Ser Asn Lys Leu Val Asn Lys Leu Thr Ser Ser Asn
405 410 415

His Lys Phe Phe Asp Phe Asp Ser Ala Leu Asn Thr Lys Arg His Asp
420 425 430

Glu Ser Trp Ala Leu Asn Ser Gln Ile Thr Leu Leu Gly His Lys Phe
435 440 445

Leu Ser Leu Thr Pro Thr Leu Tyr Val Asn Tyr Lys Phe Asn Asp Ser
450 455 460

Ser Ala Arg Ile Ser Tyr Ser Tyr Asn Lys Ser Glu Val Gly Leu Asn
465 470 475 480

Leu Ser Lys Thr Phe
485

<210> 487

<211> 1488

<212> DNA

<213> P. asymbiotica SLAM 1

<400> 487

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ttgcaggatc aagaaaaagc actcgtcact gatgaaatag tcaatcagaa tagtgataat 180

ttatcgatag tacttaatgg tttgactttt agcgtcgaaa ataatgtcaa tgatattggt 240

caggcattgt atttggccat taatcatcaa caagttaagg atgttgagcg ctttttagcg 300

atgtatcaga agttacctag gcatgatacc caattggtcc attttgctca ggcaaatctt 360

gcacgttcac agggtgattt agtgacggca gaacagcatt atcaagctat cttgcaccag 420

caacctgatt ttacccgcgc taaattagag ttagccaggg tctattatga aaatcaaaaa 480

aataaagagg ccagcttact gtttaatgaa attgctgcgg ctaatcacaa taacgaaaat 540

aaattaccac cggcagtcat taagaatata accagttatc aggatgccat tagtttgcgt 600

aattcatggc gtggatcttt ttctgtaggc tatattttta acgataacac taatatgtct 660

ccgaatcagc ctcctgtttg cacccagtat tatgaaaatg gtagttgcag gacagaacgt 720

aaattgcctt tggcgaagaa ggcgagtgga atgagttatg atgccacgtt gcgtaaggta 780

tattcgttaa gtggtcatca tggtatattt ctgcgttcga tgacttatgg cgaaagttac 840

catcatcata gtgatgagaa tgaaaatacc acttctgctt atttgggtta taactataaa 900

gcgctaaaga atgatttcct gctggggcca attcttgagt ttaatcatgt tggcaatcgt 960

ttccgctatc gtactactgg aacgaaagcg gaatggatga atattttatc tcaaaatttg 1020

gcattaaatt tagaaggaga atataagcag tttcgttatc ataaacttta taatcataat 1080

gacggtaata tgacttctgt ttatgctacg ttatcttatt atttaacgga tcaaacaatt 1140

acctttgcgg gtgtcgattg ggttaataaa accagtgttg aaaaagcgga tgattatcag 1200

cagaaagggg taagagcagg tatttctacc caattatatc cgggaattaa tgcggtggta 1260

tttactgctt tacgtcagcg gcaatttggt gattacagtg tgccactaaa tgcacatcgt 1320

aaagataatg aacaattcta ttcggcaatt gtcagtatgc ctaaatttga agtgtttggt 1380

ttaaccccag tgatcactta tcgatacaga aaaaataata gcaatgtcga ttggttatat 1440

tcatatagta agaatgaggt tttagttaag ttcgaaaaat atttttga 1488

<210> 488

<211> 495

<212> PRT

<213> P. asymbiotica SLAM 1

<400> 488

Met Leu Asn Ala Pro Ile Ser Arg Phe Ile Leu Leu Met Ser Cys Leu
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Phe Ile Gln Ser Ser Leu Val Leu Ala Asp Glu Asp Thr Gly Arg Arg
20 25 30

Leu Trp His Asn Val Gln Arg Asn Leu Gln Asp Gln Glu Lys Ala Leu
35 40 45

Val Thr Asp Glu Ile Val Asn Gln Asn Ser Asp Asn Leu Ser Ile Val
50 55 60

Leu Asn Gly Leu Thr Phe Ser Val Glu Asn Asn Val Asn Asp Ile Gly
65 70 75 80

Gln Ala Leu Tyr Leu Ala Ile Asn His Gln Gln Val Lys Asp Val Glu
85 90 95

Arg Phe Leu Ala Met Tyr Gln Lys Leu Pro Arg His Asp Thr Gln Leu
100 105 110

Val His Phe Ala Gln Ala Asn Leu Ala Arg Ser Gln Gly Asp Leu Val
115 120 125

Thr Ala Glu Gln His Tyr Gln Ala Ile Leu His Gln Gln Pro Asp Phe
130 135 140

Thr Arg Ala Lys Leu Glu Leu Ala Arg Val Tyr Tyr Glu Asn Gln Lys
145 150 155 160

Asn Lys Glu Ala Ser Leu Leu Phe Asn Glu Ile Ala Ala Ala Asn His
165 170 175

Asn Asn Glu Asn Lys Leu Pro Pro Ala Val Ile Lys Asn Ile Thr Ser
180 185 190

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Tyr Gln Asp Ala Ile Ser Leu Arg Asn Ser Trp Arg Gly Ser Phe Ser
        195                 200                 205

Val Gly Tyr Ile Phe Asn Asp Asn Thr Asn Met Ser Pro Asn Gln Pro
    210                 215                 220
Pro Val Cys Thr Gln Tyr Tyr Glu Asn Gly Ser Cys Arg Thr Glu Arg
225                 230                 235                 240
Lys Leu Pro Leu Ala Lys Lys Ala Ser Gly Met Ser Tyr Asp Ala Thr
                245                 250                 255
Leu Arg Lys Val Tyr Ser Leu Ser Gly His His Gly Ile Phe Leu Arg
            260                 265                 270

Ser Met Thr Tyr Gly Glu Ser Tyr His His His Ser Asp Glu Asn Glu
        275                 280                 285
Asn Thr Thr Ser Ala Tyr Leu Gly Tyr Asn Tyr Lys Ala Leu Lys Asn
    290                 295                 300
Asp Phe Leu Leu Gly Pro Ile Leu Glu Phe Asn His Val Gly Asn Arg
305                 310                 315                 320
Phe Arg Tyr Arg Thr Thr Gly Thr Lys Ala Glu Trp Met Asn Ile Leu
                325                 330                 335

Ser Gln Asn Leu Ala Leu Asn Leu Glu Gly Glu Tyr Lys Gln Phe Arg
            340                 345                 350
Tyr His Lys Leu Tyr Asn His Asn Asp Gly Asn Met Thr Ser Val Tyr
        355                 360                 365
Ala Thr Leu Ser Tyr Tyr Leu Thr Asp Gln Thr Ile Thr Phe Ala Gly
    370                 375                 380
Val Asp Trp Val Asn Lys Thr Ser Val Glu Lys Ala Asp Asp Tyr Gln
385                 390                 395                 400

Gln Lys Gly Val Arg Ala Gly Ile Ser Thr Gln Leu Tyr Pro Gly Ile
                405                 410                 415
Asn Ala Val Val Phe Thr Ala Leu Arg Gln Arg Gln Phe Gly Asp Tyr
            420                 425                 430
Ser Val Pro Leu Asn Ala His Arg Lys Asp Asn Glu Gln Phe Tyr Ser
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435 440 445

Ala Ile Val Ser Met Pro Lys Phe Glu Val Phe Gly Leu Thr Pro Val

450 455 460

Ile Thr Tyr Arg Tyr Arg Lys Asn Asn Ser Asn Val Asp Trp Leu Tyr

465 470 475 480

Ser Tyr Ser Lys Asn Glu Val Leu Val Lys Phe Glu Lys Tyr Phe

485 490 495

<210> 489

<211> 1440

<212> DNA

<213> P. bettyae SLAM 1

<400> 489

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cttattgaaa aagatcagtt tttaacgaca atgatgatta atcatcaaga aattgggatt 180

ggcaataata ttgaagaagt cctcaccgca ctttttttag ctattaatca taaacaaaca 240

gatgatattg agcgtttatt agctatttat caaaccatgc ctgaggcaga agaaggaatg 300

attactttca gtttagctaa tattgctttt aatcgtggag atactaaaaa agcgattcag 360

ctttatgaaa aactggtaaa aacagataat gatttttttac gtgggaaact tgatcttgcc 420

cgtttatatt tttttgatta tcaaaataaa gaatcccacc aattattttc tgaaattaat 480

ttatctgagt ccccaagtct tatggaaaaa gttaatgaat ttcagttatc tcttgataac 540

cgagaagatt ggcatggaag tttttcccta ggagctattt atcactctaa tttgaatcag 600

tctgcgaata agacaactga atgggttgtg aatacgccat tttggggaga aataacgact 660

atcagacatt cacctcaagt aatcaaatct catggtttag gttttgaagg tgcattgaat 720

aaatatacgg ctataaaaaa tcatcatggc ataatgttta aaggctctgc aaatggagag 780

ttttttcaaa atcatagttt ttataatgaa cattatttct cactaggctt aggttatcgc 840

tataaaaatc aacgtcatca agttgatatt tatccttttat cagaagctag ttatactaat 900

aatcaatggt attctactcg ccaagggatt caagcagaat attcacaaga tattggagat 960

gatgcctatt tttcttttac tttatcttat aaaaatgaac gttatcgaga acataattta 1020

aaaatatata atggtaatat tgcttctgtt tttttattta gtgcttatgc attgcctcat 1080

gattgggtta tctttggtgg gctagattat ttacaaaaaa atgggacgga agataaatct 1140

gatcaatatg aacgtaaagg attacggtta gggattaata aagcttttga tatcggattg 1200

gatctaactt taagtgtaaa ttatcgaaaa actgattatc gtcagtatag tgaattatta 1260

tcagaaaaac gtcatgataa agaatatctt tattctgcaa atttaaaatt ccctaaattg 1320

agtttttatg gtattactcc tcagcttagt ctaagtcgaa ctcaagtaaa atctaatgta 1380

gattggttgt ataattacaa taatcatgaa attgggttat ggtttgaaaa acgtttttaa 1440

<210> 490

<211> 479

<212> PRT

<213> P. bettyae SLAM 1

<400> 490

Met Asp Tyr Arg Phe Leu Phe Leu Leu Phe Phe Cys Ser Gly Ala Leu

1 5 10 15

Ala Asp Asn Gln Asp Thr Glu Phe Arg Leu Gln Gln Glu Val Glu Gln

20 25 30

Gln Gln Lys Ala Gln Glu Glu Gln Leu Ile Glu Lys Asp Gln Phe Leu

35 40 45

Thr Thr Met Met Ile Asn His Gln Glu Ile Gly Ile Gly Asn Asn Ile

50 55 60

Glu Glu Val Leu Thr Ala Leu Phe Leu Ala Ile Asn His Lys Gln Thr

65 70 75 80

Asp Asp Ile Glu Arg Leu Leu Ala Ile Tyr Gln Thr Met Pro Glu Ala

85 90 95

Glu Glu Gly Met Ile Thr Phe Ser Leu Ala Asn Ile Ala Phe Asn Arg

100 105 110

Gly Asp Thr Lys Lys Ala Ile Gln Leu Tyr Glu Lys Leu Val Lys Thr

115 120 125

Asp Asn Asp Phe Leu Arg Gly Lys Leu Asp Leu Ala Arg Leu Tyr Phe

130 135 140

Phe Asp Tyr Gln Asn Lys Glu Ser His Gln Leu Phe Ser Glu Ile Asn

145 150 155 160

Leu Ser Glu Ser Pro Ser Leu Met Glu Lys Val Asn Glu Phe Gln Leu

165 170 175

Ser Leu Asp Asn Arg Glu Asp Trp His Gly Ser Phe Ser Leu Gly Ala

180 185 190

Ile Tyr His Ser Asn Leu Asn Gln Ser Ala Asn Lys Thr Thr Glu Trp

195 200 205

Val Val Asn Thr Pro Phe Trp Gly Glu Ile Thr Thr Ile Arg His Ser

210 215 220

Pro Gln Val Ile Lys Ser His Gly Leu Gly Phe Glu Gly Ala Leu Asn

225 230 235 240

Lys Tyr Thr Ala Ile Lys Asn His His Gly Ile Met Phe Lys Gly Ser

245 250 255

Ala Asn Gly Glu Phe Phe Gln Asn His Ser Phe Tyr Asn Glu His Tyr

260 265 270

Phe Ser Leu Gly Leu Gly Tyr Arg Tyr Lys Asn Gln Arg His Gln Val

275 280 285

Asp Ile Tyr Pro Leu Ser Glu Ala Ser Tyr Thr Asn Asn Gln Trp Tyr

290 295 300

Ser Thr Arg Gln Gly Ile Gln Ala Glu Tyr Ser Gln Asp Ile Gly Asp

305 310 315 320

Asp Ala Tyr Phe Ser Phe Thr Leu Ser Tyr Lys Asn Glu Arg Tyr Arg

325 330 335

Glu His Asn Leu Lys Ile Tyr Asn Gly Asn Ile Ala Ser Val Phe Leu

340 345 350

Phe Ser Ala Tyr Ala Leu Pro His Asp Trp Val Ile Phe Gly Gly Leu

355 360 365

Asp Tyr Leu Gln Lys Asn Gly Thr Glu Asp Lys Ser Asp Gln Tyr Glu

370 375 380

Arg Lys Gly Leu Arg Leu Gly Ile Asn Lys Ala Phe Asp Ile Gly Leu

385 390 395 400

Asp Leu Thr Leu Ser Val Asn Tyr Arg Lys Thr Asp Tyr Arg Gln Tyr

405 410 415

Ser Glu Leu Leu Ser Glu Lys Arg His Asp Lys Glu Tyr Leu Tyr Ser

420 425 430

Ala Asn Leu Lys Phe Pro Lys Leu Ser Phe Tyr Gly Ile Thr Pro Gln

435 440 445

Leu Ser Leu Ser Arg Thr Gln Val Lys Ser Asn Val Asp Trp Leu Tyr

450 455 460

Asn Tyr Asn Asn His Glu Ile Gly Leu Trp Phe Glu Lys Arg Phe

465 470 475

<210> 491

<211> 1299

<212> DNA

<213> P. bettyae SLAM 2

<400> 491

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tctttttag aagaacaact taaacaagct atttatcatc aacaacttga taatattcag 120

attttactca agaactatca acaggaagta gactcagatt tgattcttat tgcttatgct 180

caagcaaaag tagcctatct tctgcaagat tatgcaaaag cgatttctat ttatcggcaa 240

ataattagcc aaaaacctca attaatttca atgcgaatgg aactagccgt tgctttattt 300

gtagatcacc aagataatgc agctaaactt caatttgaga gagttaaatc agctctagag 360

ttacctaata gtgcttatca gaaagttgaa agctacttgg cagcaattaa tcggcgtaat 420

gaatggcaag ctaactttac gttatcttat ttaagaacag acaatgtaga aaatgtatct 480

aacgatttaa acattgaaaa tacaggtttt attaaaagta aaaaaatgtt gccacaaaaa 540

gctcatggtt ttgcttatag tatagatttt ggaaaagatt ttaatttaat aaattcccat 600

tatattagta ttcaaaacga aacttatggt aagaattact gggataatca caactttgat 660

gacctttcaa ctcgaatatt attcggttat gcgtataaaa aaatggataa tacttttcgt 720

attcagcctt tttatgataa gcgttggtat ggaaatcatt cttttcattg gtctaatggt 780

attcaattca cttatgattt ttatttttct aaacaatgga aaaatcagac aataatgtct 840

ttcgaaaatc gatcgttttt taatgaagat ttgcaatcag gttatattaa aacattgtct 900

gatactataa tttggtatac caatcctcaa cagctttttt atttaggtgg tgctatttca 960

caggaaaaaa caaacgatag acagtatggc tcaacgagta aaaatattcg tttgggatgg 1020

cttcaagaat atcaatgggg tatttctagc cagctcagtt tttcatttac ttatcgaaaa 1080

tttcacgatg aagctatatt agcggggatt ttacctctta ataaaactag acgagacttt 1140

atttatattc tgaatactaa aatttggaaa agagattggt atttttgggg cgttacccca 1200

aaactgaatt tggtttggaa gaaacagaaa agtaatttag acattttata ttcttataaa 1260

gataagcaaa taacaattct gtttgaaaaa acctttttag 1299

<210> 492

<211> 432

<212> PRT

<213> P. bettyae SLAM 2

<400> 492

Met Arg Phe Phe Leu Leu Gly Leu Ile Phe Cys Ile Ser Gln Ile Ala
1 5 10 15

Ser Ala Ser Asn Ser Phe Leu Glu Glu Gln Leu Lys Gln Ala Ile Tyr
20 25 30

His Gln Gln Leu Asp Asn Ile Gln Ile Leu Leu Lys Asn Tyr Gln Gln
35 40 45

Glu Val Asp Ser Asp Leu Ile Leu Ile Ala Tyr Ala Gln Ala Lys Val
50 55 60

Ala Tyr Leu Leu Gln Asp Tyr Ala Lys Ala Ile Ser Ile Tyr Arg Gln
65 70 75 80

Ile Ile Ser Gln Lys Pro Gln Leu Ile Ser Met Arg Met Glu Leu Ala
85 90 95

Val Ala Leu Phe Val Asp His Gln Asp Asn Ala Ala Lys Leu Gln Phe
100 105 110

Glu Arg Val Lys Ser Ala Leu Glu Leu Pro Asn Ser Ala Tyr Gln Lys
115 120 125

Val Glu Ser Tyr Leu Ala Ala Ile Asn Arg Arg Asn Glu Trp Gln Ala
130 135 140

Asn Phe Thr Leu Ser Tyr Leu Arg Thr Asp Asn Val Glu Asn Val Ser
145 150 155 160

Asn Asp Leu Asn Ile Glu Asn Thr Gly Phe Ile Lys Ser Lys Lys Met
165 170 175

Leu Pro Gln Lys Ala His Gly Phe Ala Tyr Ser Ile Asp Phe Gly Lys

180 185 190

Asp Phe Asn Leu Ile Asn Ser His Tyr Ile Ser Ile Gln Asn Glu Thr
195 200 205
Tyr Gly Lys Asn Tyr Trp Asp Asn His Asn Phe Asp Asp Leu Ser Thr
210 215 220
Arg Ile Leu Phe Gly Tyr Ala Tyr Lys Lys Met Asp Asn Thr Phe Arg
225 230 235 240
Ile Gln Pro Phe Tyr Asp Lys Arg Trp Tyr Gly Asn His Ser Phe His
245 250 255

Trp Ser Asn Gly Ile Gln Phe Thr Tyr Asp Phe Tyr Phe Ser Lys Gln
260 265 270
Trp Lys Asn Gln Thr Ile Met Ser Phe Glu Asn Arg Ser Phe Phe Asn
275 280 285
Glu Asp Leu Gln Ser Gly Tyr Ile Lys Thr Leu Ser Asp Thr Ile Ile
290 295 300
Trp Tyr Thr Asn Pro Gln Gln Leu Phe Tyr Leu Gly Gly Ala Ile Ser
305 310 315 320

Gln Glu Lys Thr Asn Asp Arg Gln Tyr Gly Ser Thr Ser Lys Asn Ile
325 330 335
Arg Leu Gly Trp Leu Gln Glu Tyr Gln Trp Gly Ile Ser Ser Gln Leu
340 345 350
Ser Phe Ser Phe Thr Tyr Arg Lys Phe His Asp Glu Ala Ile Leu Ala
355 360 365
Gly Ile Leu Pro Leu Asn Lys Thr Arg Arg Asp Phe Ile Tyr Ile Leu
370 375 380

Asn Thr Lys Ile Trp Lys Arg Asp Trp Tyr Phe Trp Gly Val Thr Pro
385 390 395 400
Lys Leu Asn Leu Val Trp Lys Lys Gln Lys Ser Asn Leu Asp Ile Leu
405 410 415
Tyr Ser Tyr Lys Asp Lys Gln Ile Thr Ile Leu Phe Glu Lys Thr Phe
420 425 430

<210> 493

<211> 1464

<212> DNA

<213> P. bettyae SLAM 3

<400> 493

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tcggcagtac ccggttcaga acccgttccc gaaatacaag gtgcggaagc ttataaagca 120

gtagatgaca atgccgattt ggaattcatc cgcaaacagc aaaaacgccc acaaagacaa 180

attactgtgg atgtaccaca ggaacatcaa ggcatacaaa ttactgaggc agatttatta 240

atgcagcccc agttattaca tcaattaatg atggcgttag ttcagcggca aaatgttacc 300

gctttgcgtt tgttactgcc tatttataaa aaatcagcaa attatgatca cgaacttgcc 360

gaatatgtcg aagcgcgtat tgctcaagat gacggcaaca tgaaattcgc tataaaaact 420

taccgcactt tattgactcg tgatcccagc ctgtttttag tgcgctttaa tttagcgtct 480

gcgctttatc tggataaaca atatgcacaa gtgcggtccg aattagccga aattcgtaaa 540

gaacaacaat taccacagga ttttcttgct tttgctcatg agttggagtt agccactgaa 600

cagcaaaata cttggtcatg ggattttaat ttggggtatg tgcaggataa aaatgtcaat 660

aatgcacctg atcagcagga aataaaaacg acaaatggca cttggacatt acctaaaccc 720

gaatctgcac acggtataag ttattttgct acggtaaata aagattggtt tttgctgaat 780

aattggggct ggcgagcgca aggttatggg tttggtaaat attattggga caataaaaaa 840

tacaatgaca tgcaataccg ctttagtact ggtcctgtat ggcagtccgt ggatactgaa 900

ctgaccttca tgccgtttta cggtatgcgt tattatggtg aacgtgctta tgcggaaacc 960

atcggattac gttccgtact gaattatcac gttaatggaa aatggcgaat ttctaccgca 1020

cttgaaggtg gtaaacgtac tcaccccaaa cgagaatatc taaatgggcg ttatgcactt 1080

gggagctttt cactgggtta tgctatttca cctcaccaat atcttcattt aagtgtggat 1140

actgggtatc gtggtgctca agatcctagc gatgcttatc atcatcgtgg cgtacgtatg 1200

ggatatacct tgttattacc aaagaatatc gtggttaaaa cagatgttag ctatagtttg 1260

cgtcaatatc tgggccacaa tctatttaat gtggtgcagc ggaataaagt ttttggtgca 1320

tcgtttagtt tatggaagac cgattggcaa tggaaaggat ttatgccgaa atttaatatt 1380

gattatgagc gtacgtgcag taattatgtt atagcaacct accataaaac caatatttac 1440

cttgatattt ctaaatcatt ttag 1464

<210> 494

<211> 487

<212> PRT

<213> P. bettyae SLAM 4

<400> 494

Met Lys Lys Ala Ile Phe Cys Leu Leu Ile Val Phe Thr Gly Ser Tyr
1 5 10 15

Ser Ala Phe Thr Ser Ala Val Pro Gly Ser Glu Pro Val Pro Glu Ile
20 25 30

Gln Gly Ala Glu Ala Tyr Lys Ala Val Asp Asp Asn Ala Asp Leu Glu
35 40 45

Phe Ile Arg Lys Gln Gln Lys Arg Pro Gln Arg Gln Ile Thr Val Asp
50 55 60

Val Pro Gln Glu His Gln Gly Ile Gln Ile Thr Glu Ala Asp Leu Leu
65 70 75 80

Met Gln Pro Gln Leu Leu His Gln Leu Met Met Ala Leu Val Gln Arg
85 90 95

Gln Asn Val Thr Ala Leu Arg Leu Leu Leu Pro Ile Tyr Lys Lys Ser
100 105 110

Ala Asn Tyr Asp His Glu Leu Ala Glu Tyr Val Glu Ala Arg Ile Ala
115 120 125

Gln Asp Asp Gly Asn Met Lys Phe Ala Ile Lys Thr Tyr Arg Thr Leu
130 135 140

Leu Thr Arg Asp Pro Ser Leu Phe Leu Val Arg Phe Asn Leu Ala Ser
145 150 155 160

Ala Leu Tyr Leu Asp Lys Gln Tyr Ala Gln Val Arg Ser Glu Leu Ala
165 170 175

Glu Ile Arg Lys Glu Gln Gln Leu Pro Gln Asp Phe Leu Ala Phe Ala
180 185 190

His Glu Leu Glu Leu Ala Thr Glu Gln Gln Asn Thr Trp Ser Trp Asp
195 200 205

Phe Asn Leu Gly Tyr Val Gln Asp Lys Asn Val Asn Asn Ala Pro Asp

210 215 220

Gln Gln Glu Ile Lys Thr Thr Asn Gly Thr Trp Thr Leu Pro Lys Pro
225 230 235 240
Glu Ser Ala His Gly Ile Ser Tyr Phe Ala Thr Val Asn Lys Asp Trp
245 250 255
Phe Leu Leu Asn Asn Trp Gly Trp Arg Ala Gln Gly Tyr Gly Phe Gly
260 265 270
Lys Tyr Tyr Trp Asp Asn Lys Lys Tyr Asn Asp Met Gln Tyr Arg Phe
275 280 285

Ser Thr Gly Pro Val Trp Gln Ser Val Asp Thr Glu Leu Thr Phe Met
290 295 300
Pro Phe Tyr Gly Met Arg Tyr Tyr Gly Glu Arg Ala Tyr Ala Glu Thr
305 310 315 320
Ile Gly Leu Arg Ser Val Leu Asn Tyr His Val Asn Gly Lys Trp Arg
325 330 335
Ile Ser Thr Ala Leu Glu Gly Gly Lys Arg Thr His Pro Lys Arg Glu
340 345 350

Tyr Leu Asn Gly Arg Tyr Ala Leu Gly Ser Phe Ser Leu Gly Tyr Ala
355 360 365
Ile Ser Pro His Gln Tyr Leu His Leu Ser Val Asp Thr Gly Tyr Arg
370 375 380
Gly Ala Gln Asp Pro Ser Asp Ala Tyr His His Arg Gly Val Arg Met
385 390 395 400
Gly Tyr Thr Leu Leu Leu Pro Lys Asn Ile Val Val Lys Thr Asp Val
405 410 415

Ser Tyr Ser Leu Arg Gln Tyr Leu Gly His Asn Leu Phe Asn Val Val
420 425 430
Gln Arg Asn Lys Val Phe Gly Ala Ser Phe Ser Leu Trp Lys Thr Asp
435 440 445
Trp Gln Trp Lys Gly Phe Met Pro Lys Phe Asn Ile Asp Tyr Glu Arg
450 455 460

Thr Cys Ser Asn Tyr Val Ile Ala Thr Tyr His Lys Thr Asn Ile Tyr
465 470 475 480

Leu Asp Ile Ser Lys Ser Phe
485

<210> 495

<211> 1446

<212> DNA

<213> P. bettyae SLAM 4

<400> 495

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caacgtgaaa gtcatacctt aaatgtctct cagcctataa atgaaatcat tattgaggga 180

caatcttttg aagtagcacc aaatgccttg tcagtgggac aagccctata tattgcgtta 240

aatcaacagc tatggcagta cgtagagaag cttttagagc aatataaaac atttgatgag 300

cataaacctg aattaatttg gtttgccgaa ggtgcactag ctcgtgaacg tggtgatttt 360

gctttagctg cacaacgcta tcatcaattg ctgcaagtgc aacctgattt tctgagagga 420

caattagatt tagcgagaat tttatttgaa gataaaaaaa atgcagaatc taccgcactt 480

ttccgtaaaa tagctgaaca accgcttcct agcagtgtac ttggtaacat acaggattat 540

cagttggcat tgaaacaacg tgaaagttgg tctagttctc tgacatttgg ttatttgtat 600

aataaaaatt taaatcagtc accacagaaa gaacaatgtt tattagaaaa taaaggtcag 660

tgtctaatta atcgacattc gccaaaagct attaatgctc atggttggcg ttatgatttt 720

aacacccaac gtcgaatttc attgcgtggc catcatggtt tagcatttta tttcaatagc 780

tatggtcaat tttatccgca tgaacatgac tataatgaaa acacactaaa aacctatggg 840

ggttacagct tccagagtgc aaacacagaa atcaccgttg cacctttct ggaacataat 900

acttttggca atcaccgtaa ttatcacagt tggggagggc actttgaatg gacgcaaaat 960

ctttcacccc gtcatttatg gaatatgcaa tttgagcaga aaagattgcg atatagtgag 1020

cattatagca gtttctctaa ggcgaattta agttcattgt tcagtacttg gtattatttg 1080

tattcaccaa aaacaacgtt attcggtggg gtggattggc aatatcgtta cactcctgat 1140

caggcacaag cttatcattt agtaggtaca cgcttaggtc ttaatcatca attcgatttt 1200

ggattaaatg cgactgtgat gacattgtta cgtcgctata attatcaagg gtatcatgca 1260

gcattagagg tgacaaggaa ggactaccaa cagatctata tagcactctt taaaatgcct 1320

caatggagct taaaaggatt tacgcctaat ttgttattta aacatactcg taatcgcagc 1380

aatgctgatt atgtttattc ctacaaacaa agcgaggtac aactgaattt tgaatttcaa 1440

ttttaa 1446

<210> 496

<211> 481

<212> PRT

<213> P. bettyae SLAM 4

<400> 496

Met Lys Lys Tyr Tyr Leu Ile Cys Leu Leu Ser Cys Tyr Cys Thr Thr
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Thr Phe Ala Asp Ile Gln Glu Gln Asp Ala Leu Arg Leu Trp Lys Gln
20 25 30

His Ile Gln Gln Leu Thr Gln Gln Gln Arg Glu Ser His Thr Leu Asn
35 40 45

Val Ser Gln Pro Ile Asn Glu Ile Ile Ile Glu Gly Gln Ser Phe Glu
50 55 60

Val Ala Pro Asn Ala Leu Ser Val Gly Gln Ala Leu Tyr Ile Ala Leu
65 70 75 80

Asn Gln Gln Leu Trp Gln Tyr Val Glu Lys Leu Leu Glu Gln Tyr Lys
85 90 95

Thr Phe Asp Glu His Lys Pro Glu Leu Ile Trp Phe Ala Glu Gly Ala
100 105 110

Leu Ala Arg Glu Arg Gly Asp Phe Ala Leu Ala Ala Gln Arg Tyr His
115 120 125

Gln Leu Leu Gln Val Gln Pro Asp Phe Leu Arg Gly Gln Leu Asp Leu
130 135 140

Ala Arg Ile Leu Phe Glu Asp Lys Lys Asn Ala Glu Ser Thr Ala Leu
145 150 155 160

Phe Arg Lys Ile Ala Glu Gln Pro Leu Pro Ser Ser Val Leu Gly Asn
165 170 175

Ile Gln Asp Tyr Gln Leu Ala Leu Lys Gln Arg Glu Ser Trp Ser Ser

180 185 190

Ser Leu Thr Phe Gly Tyr Leu Tyr Asn Lys Asn Leu Asn Gln Ser Pro
195 200 205

Gln Lys Glu Gln Cys Leu Leu Glu Asn Lys Gly Gln Cys Leu Ile Asn
210 215 220

Arg His Ser Pro Lys Ala Ile Asn Ala His Gly Trp Arg Tyr Asp Phe
225 230 235 240

Asn Thr Gln Arg Arg Ile Ser Leu Arg Gly His His Gly Leu Ala Phe
245 250 255

Tyr Phe Asn Ser Tyr Gly Gln Phe Tyr Pro His Glu His Asp Tyr Asn
260 265 270

Glu Asn Thr Leu Lys Thr Tyr Gly Gly Tyr Ser Phe Gln Ser Ala Asn
275 280 285

Thr Glu Ile Thr Val Ala Pro Phe Leu Glu His Asn Thr Phe Gly Asn
290 295 300

His Arg Asn Tyr His Ser Trp Gly Gly His Phe Glu Trp Thr Gln Asn
305 310 315 320

Leu Ser Pro Arg His Leu Trp Asn Met Gln Phe Glu Gln Lys Arg Leu
325 330 335

Arg Tyr Ser Glu His Tyr Ser Ser Phe Ser Lys Ala Asn Leu Ser Ser
340 345 350

Leu Phe Ser Thr Trp Tyr Tyr Leu Tyr Ser Pro Lys Thr Thr Leu Phe
355 360 365

Gly Gly Val Asp Trp Gln Tyr Arg Tyr Thr Pro Asp Gln Ala Gln Ala
370 375 380

Tyr His Leu Val Gly Thr Arg Leu Gly Leu Asn His Gln Phe Asp Phe
385 390 395 400

Gly Leu Asn Ala Thr Val Met Thr Leu Leu Arg Arg Tyr Asn Tyr Gln
405 410 415

Gly Tyr His Ala Ala Leu Glu Val Thr Arg Lys Asp Tyr Gln Gln Ile
420 425 430

Tyr Ile Ala Leu Phe Lys Met Pro Gln Trp Ser Leu Lys Gly Phe Thr
435 440 445

Pro Asn Leu Leu Phe Lys His Thr Arg Asn Arg Ser Asn Ala Asp Tyr
450 455 460

Val Tyr Ser Tyr Lys Gln Ser Glu Val Gln Leu Asn Phe Glu Phe Gln
465 470 475 480

Phe

<210> 497

<211> 1464

<212> DNA

<213> P. burhodogranariea SLAM 1

<400> 497

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aatcaaccgt tgatattaaa aagcactgaa ccctttatta aaaatgaaat aattattaac 180

tttgataata aaaactataa aataaataat aatgttaatg aaatgggaat ggcgatttat 240

atcgcattaa atcgtgggca atatcaggat gttcacagat tattacctta ttatcaaaaa 300

ttgcctgaat atgattattt attagttaaa tttgctgaag cacaatttgc aagaatagat 360

aaaaattaca ttaaagctat ctctgattat caacagatct taacattaaa gcctgatttt 420

ttacgtgtag aactcgaact tgcacgaacc tattatgaag ataagcaaaa caaagaagca 480

ttattactat ttaaaataat attggataaa tatgctcagc agcttccagc taatgtatca 540

attgtaattg gtcaatttac aactgaactg aataaaaaaa accgttggtc aggaagtttt 600

tctacaggct atggttataa ttcgaatatt aaccaagtgc ccaataatga tagaaaaacc 660

tgttaccaga atttacaaca gcatctttgc tatggcggta gtcaagcaga taaaggcagt 720

aagtttattt atgatggaga tattaatcgg tcatttgcgt tttatcagca ccaaagtgtt 780

cagtttaaag cttactcctt tggcagccac tatgagagaa atgctgatta taatgaaaat 840

accaccaata taagactgta ctatcaatat catgatgcca acaaatcgtt atcaataggg 900

ccaataaccg aattgaaatt tgtgggaggc aaacggcgct attatggtgt gggaacgggg 960

attgacgcag agtatcgttt ttcaccccaa ttttcgttaa ctgcgatgat agattctaaa 1020

aaaatgattt atcgtactcc ttaccaaagt aatgatggaa ataaaagtaa tctctactta 1080

acgggaattt atgcgttaac ccctgaggct gttctctttg gtggaattga tagttcactt 1140

gttaataaaa aatatgaaag tgatagctat cggcaatacg gtgctagagt tggtgtcttt 1200

aaaaaattta atcaagacgt aaattttctt gggctaatat cttataaaaa tacgcgattt 1260

aatgatgctc aatatgaatt taatcataaa gtcagaaatg atgatgaaca gctctattta 1320

acgaagctca gcattccaaa atacagtttt atgacattga ttccctctat ctcttataag 1380

tacagaatta ataatagcag tattgatacg ttgtactctt ataaacaaag tgaagttgaa 1440

tttaaattgg aaaaacgttt ttaa 1464

<210> 498

<211> 487

<212> PRT

<213> P. burhodogranariea SLAM 1

<400> 498

Met Leu Lys Arg Gln Phe Ser Ile Leu Leu Phe Phe Phe Phe Tyr Ser
1 5 10 15

Tyr Pro Val Ser Gly Val Ser Asp Gly Leu Glu Asn Tyr Arg Phe Leu
20 25 30

Leu Lys Gly Lys Thr Gly Leu Asn Asn Gln Pro Leu Ile Leu Lys Ser
35 40 45

Thr Glu Pro Phe Ile Lys Asn Glu Ile Ile Ile Asn Phe Asp Asn Lys
50 55 60

Asn Tyr Lys Ile Asn Asn Asn Val Asn Glu Met Gly Met Ala Ile Tyr
65 70 75 80

Ile Ala Leu Asn Arg Gly Gln Tyr Gln Asp Val His Arg Leu Leu Pro
85 90 95

Tyr Tyr Gln Lys Leu Pro Glu Tyr Asp Tyr Leu Leu Val Lys Phe Ala
100 105 110

Glu Ala Gln Phe Ala Arg Ile Asp Lys Asn Tyr Ile Lys Ala Ile Ser
115 120 125

Asp Tyr Gln Gln Ile Leu Thr Leu Lys Pro Asp Phe Leu Arg Val Glu
130 135 140

Leu Glu Leu Ala Arg Thr Tyr Tyr Glu Asp Lys Gln Asn Lys Glu Ala
145 150 155 160

Leu Leu Leu Phe Lys Ile Ile Leu Asp Lys Tyr Ala Gln Gln Leu Pro

165 170 175

Ala Asn Val Ser Ile Val Ile Gly Gln Phe Thr Thr Glu Leu Asn Lys

180 185 190

Lys Asn Arg Trp Ser Gly Ser Phe Ser Thr Gly Tyr Gly Tyr Asn Ser

195 200 205

Asn Ile Asn Gln Val Pro Asn Asn Asp Arg Lys Thr Cys Tyr Gln Asn

210 215 220

Leu Gln Gln His Leu Cys Tyr Gly Gly Ser Gln Ala Asp Lys Gly Ser

225 230 235 240

Lys Phe Ile Tyr Asp Gly Asp Ile Asn Arg Ser Phe Ala Phe Tyr Gln

245 250 255

His Gln Ser Val Gln Phe Lys Ala Tyr Ser Phe Gly Ser His Tyr Glu

260 265 270

Arg Asn Ala Asp Tyr Asn Glu Asn Thr Thr Asn Ile Arg Leu Tyr Tyr

275 280 285

Gln Tyr His Asp Ala Asn Lys Ser Leu Ser Ile Gly Pro Ile Thr Glu

290 295 300

Leu Lys Phe Val Gly Gly Lys Arg Arg Tyr Tyr Gly Val Gly Thr Gly

305 310 315 320

Ile Asp Ala Glu Tyr Arg Phe Ser Pro Gln Phe Ser Leu Thr Ala Met

325 330 335

Ile Asp Ser Lys Lys Met Ile Tyr Arg Thr Pro Tyr Gln Ser Asn Asp

340 345 350

Gly Asn Lys Ser Asn Leu Tyr Leu Thr Gly Ile Tyr Ala Leu Thr Pro

355 360 365

Glu Ala Val Leu Phe Gly Gly Ile Asp Ser Ser Leu Val Asn Lys Lys

370 375 380

Tyr Glu Ser Asp Ser Tyr Arg Gln Tyr Gly Ala Arg Val Gly Val Phe

385 390 395 400

Lys Lys Phe Asn Gln Asp Val Asn Phe Leu Gly Leu Ile Ser Tyr Lys

405 410 415

Asn Thr Arg Phe Asn Asp Ala Gln Tyr Glu Phe Asn His Lys Val Arg

420 425 430

Asn Asp Asp Glu Gln Leu Tyr Leu Thr Lys Leu Ser Ile Pro Lys Tyr

435 440 445

Ser Phe Met Thr Leu Ile Pro Ser Ile Ser Tyr Lys Tyr Arg Ile Asn

450 455 460

Asn Ser Ser Ile Asp Thr Leu Tyr Ser Tyr Lys Gln Ser Glu Val Glu

465 470 475 480

Phe Lys Leu Glu Lys Arg Phe

485

<210> 499

<211> 1473

<212> DNA

<213> P. cremoricolorata SLAM 1

<400> 499

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gacgacaccc gcctgctgct gaacaagatc gaacaacgcg gcgaagcccg tgagcgggcc 120

aaccgcggcg cgcccgatcc ggcacagcac aatgcttcgc tgatcaccat cgagggccag 180

acctacaacg tgcagaacac cctgcaggat cttgcgccgg ccatttacgt gtcgatcaac 240

ctgcgccagt ggggcaaggt ccgtcagttc gtcgagcgct accggcagtt gcccggtcat 300

gagccagcgc tggtggaaat ggccgagggc ctgttggccc gccagcagcg ccagcacaag 360

cgggccatcg atcacctgcg ccgcgccatc gagctgaacc cgcgcttcgt gcgtgcgcaa 420

ctggaattgg cccgcaccct gttcgaagac aaccagaccc ttgaggccga acgcctgttc 480

cgccaggtcg ccaacgaaac cgtgcccgag tcgctgcatg gcgtgctcgg tgagtaccag 540

caggccatcg acctgcgccg gcaatggcac ggatccgcct cgctcgggct gggctacaac 600

agcaacatca accagggcaa tggcatggtt acccaccgcc tggtctgtac gatcttcgat 660

gaatgtttcg actatgcccg gcaaatgccc aagcccaagg gttctgcaag tctggtctat 720

gacgtcaccg ccgagcggcg ctttcagctg accggcaatc accacctgct gctgcgcggc 780

ctgagctacg gcaaccagtt cgacaagcat ggcgaggacg acccacaaat ctggtacgac 840

gacaacacca cggtgctcta cgccggctac aacttccaga gcgtgctcaa cgacgtgtcg 900

ttgatgccgc tgttcgagaa ctactacaac gaccaccaca ccaagtacca ggccaccggt 960

gtgcgcggtg agtggaagca caacctcagc gagcgcctgc aactgggcgg ccaggcgcag 1020

ttcaagcatt accgtttcca gggtgagcag cgcgagtact tcgatgacta cgatgagcgc 1080

cagctggggg catcgctgtc gtacctgctc gatgcgcaga ccttgctgtt cggtggactg 1140

acctacaccc ggcgtgaaca aaaagccgcg gcgtcgagca accgcgaggc gatggtcagc 1200

ctgggcgcct tccacagctt cgacgccggg ctgaccctga gcgccgtggg cctgtaccgg 1260

caaacccgct atgacgcggc agatcttttc ctcggtggcc ggcgcgagga tcgccagcag 1320

gtctatatcg ccaacctggg catgccgcgc ctggccttcg ccggcgtggt gccgaacctc 1380

tacgtcaagc gcacggtgac cgccagcagc atcgattggg cctatgccta ccggcagacc 1440

gagctggcgc tgaaattcga gaagaccttc tga 1473

<210> 500

<211> 490

<212> PRT

<213> P. cremoricolorata SLAM 1

<400> 500

Met Gly Arg Ile Leu Leu Gly Leu Ser Leu Leu Tyr Thr Ala Val Val

1 5 10 15

Gln Ala Asp Asp Asp Asp Thr Arg Leu Leu Leu Asn Lys Ile Glu Gln

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Arg Gly Glu Ala Arg Glu Arg Ala Asn Arg Gly Ala Pro Asp Pro Ala

35 40 45

Gln His Asn Ala Ser Leu Ile Thr Ile Glu Gly Gln Thr Tyr Asn Val

50 55 60

Gln Asn Thr Leu Gln Asp Leu Ala Pro Ala Ile Tyr Val Ser Ile Asn

65 70 75 80

Leu Arg Gln Trp Gly Lys Val Arg Gln Phe Val Glu Arg Tyr Arg Gln

85 90 95

Leu Pro Gly His Glu Pro Ala Leu Val Glu Met Ala Glu Gly Leu Leu

100 105 110

Ala Arg Gln Gln Arg Gln His Lys Arg Ala Ile Asp His Leu Arg Arg

115 120 125

Ala Ile Glu Leu Asn Pro Arg Phe Val Arg Ala Gln Leu Glu Leu Ala

130 135 140

Arg Thr Leu Phe Glu Asp Asn Gln Thr Leu Glu Ala Glu Arg Leu Phe
145 150 155 160
Arg Gln Val Ala Asn Glu Thr Val Pro Glu Ser Leu His Gly Val Leu
165 170 175
Gly Glu Tyr Gln Gln Ala Ile Asp Leu Arg Arg Gln Trp His Gly Ser
180 185 190
Ala Ser Leu Gly Leu Gly Tyr Asn Ser Asn Ile Asn Gln Gly Asn Gly

195 200 205

Met Val Thr His Arg Leu Val Cys Thr Ile Phe Asp Glu Cys Phe Asp
210 215 220
Tyr Ala Arg Gln Met Pro Lys Pro Lys Gly Ser Ala Ser Leu Val Tyr
225 230 235 240
Asp Val Thr Ala Glu Arg Arg Phe Gln Leu Thr Gly Asn His His Leu
245 250 255
Leu Leu Arg Gly Leu Ser Tyr Gly Asn Gln Phe Asp Lys His Gly Glu

260 265 270

Asp Asp Pro Gln Ile Trp Tyr Asp Asp Asn Thr Thr Val Leu Tyr Ala
275 280 285
Gly Tyr Asn Phe Gln Ser Val Leu Asn Asp Val Ser Leu Met Pro Leu
290 295 300
Phe Glu Asn Tyr Tyr Asn Asp His His Thr Lys Tyr Gln Ala Thr Gly
305 310 315 320
Val Arg Gly Glu Trp Lys His Asn Leu Ser Glu Arg Leu Gln Leu Gly

325 330 335

Gly Gln Ala Gln Phe Lys His Tyr Arg Phe Gln Gly Glu Gln Arg Glu
340 345 350
Tyr Phe Asp Asp Tyr Asp Glu Arg Gln Leu Gly Ala Ser Leu Ser Tyr
355 360 365
Leu Leu Asp Ala Gln Thr Leu Leu Phe Gly Gly Leu Thr Tyr Thr Arg

370 375 380

Arg Glu Gln Lys Ala Ala Ala Ser Ser Asn Arg Glu Ala Met Val Ser

385 390 395 400

Leu Gly Ala Phe His Ser Phe Asp Ala Gly Leu Thr Leu Ser Ala Val

405 410 415

Gly Leu Tyr Arg Gln Thr Arg Tyr Asp Ala Ala Asp Leu Phe Leu Gly

420 425 430

Gly Arg Arg Glu Asp Arg Gln Gln Val Tyr Ile Ala Asn Leu Gly Met

435 440 445

Pro Arg Leu Ala Phe Ala Gly Val Val Pro Asn Leu Tyr Val Lys Arg

450 455 460

Thr Val Thr Ala Ser Ser Ile Asp Trp Ala Tyr Ala Tyr Arg Gln Thr

465 470 475 480

Glu Leu Ala Leu Lys Phe Glu Lys Thr Phe

485 490

<210> 501

<211> 1524

<212> DNA

<213> P. dagmatis SLAM 1

<400> 501

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ttaatcagcc aaacatcttc cgcaaatgat actgttgttc aagttgacaa ctctcgacca 120

gaagaatctt tccgccaacc aacagcaatc aaacaagaac aaatgccttc tcgagcaagt 180

tctccggcaa taactacgcc tcaaaaacag caattatcta tcaccccaga acaattatta 240

cagcgccctg atttattaat ccgagcatta attcctgcat taagaaataa tgatatgcgg 300

gtcacagagt tattattgcc aatttatgaa aaattacctg aacaagaccc tattctattg 360

aattgggctc gcgcaatggt ggcgaaaaaa caaggtagat taaatgattc catccgttta 420

tatcgtgagg tgattgcaga acagcccaaa atacagcctg cacgcttaca attagcaatt 480

gtattaatgc aaaaccgtga atacgatgcc gcaaaagatc aattccaaca attacgtgca 540

gaaaatttac ccccacaatt aatacaaatt attgataact acgttaaggc tatcaacgag 600

caagacagct ggagcttcta cagtggaggc aattatttga acgagaaaaa cgtgaataat 660

gctcccaaaa aagggactaa agctggcaac ttcacaccat caagtgaacc tgaaagtgca 720

gaaggaatca gctactattt cgggataaat aaaacttggt caattaaaca tggttttttc 780

actgaatttg atgccgatct aaatggtaaa tattattgga ataaccgtaa atatgatgaa 840

gtatcattgc gtggcggtct tggtgttggt tatcgtaatg ctaaaacaga agtaaaattc 900

atcccttatt tagagcaatt ttggtatgct ggtggtgaaa atgccaaaaa agatgcccgt 960

acgttacacc gatactcaaa aaccagtggc gtagctttcg atattagcta ttggttaaac 1020

ccacattgga aaatctctac cgcacttgaa tacggtgaac agcgttatct cgatccgaga 1080

cgtagaaaat ccaacggcaa tttctattca gcaacaaata cattgatata tttcccaaat 1140

agccaacaat attggtttgc gggcttagat ttttatcgaa aaaacgccca ttggaaggca 1200

aatgcctttg atcgccctgc tgcacgttta ggctggggac aagagtggcc aaaagggatt 1260

tcaacccgtt tacagatcag ctatgcaaaa cgatcttacc gtatgccatc agcacctcaa 1320

aatgcaattt ttgcaccaat tttctttaaa tttgcgcaga aaaatcaaga atatggtgtg 1380

aacctaacta tatggcatcg tagtattcac tggctaggca ttactcctaa aatcacttgg 1440

tcataccaaa aaaccgatag taacaaccca tttgcacgtt atgaccgcaa ccgtgtttat 1500

ctaagtgtaa gtaaaaattt ttaa 1524

<210> 502

<211> 507

<212> PRT

<213> P. dagmatis SLAM 1

<400> 502

Met Lys Gln Lys Ser Leu Ser Leu Phe Thr Tyr Phe Ala Ala Leu Phe
1 5 10 15

Ala Val Ser Ser Leu Ile Ser Gln Thr Ser Ser Ala Asn Asp Thr Val
20 25 30

Val Gln Val Asp Asn Ser Arg Pro Glu Glu Ser Phe Arg Gln Pro Thr
35 40 45

Ala Ile Lys Gln Glu Gln Met Pro Ser Arg Ala Ser Ser Pro Ala Ile
50 55 60

Thr Thr Pro Gln Lys Gln Gln Leu Ser Ile Thr Pro Glu Gln Leu Leu
65 70 75 80

Gln Arg Pro Asp Leu Leu Ile Arg Ala Leu Ile Pro Ala Leu Arg Asn

85 90 95

Asn Asp Met Arg Val Thr Glu Leu Leu Leu Pro Ile Tyr Glu Lys Leu
100 105 110
Pro Glu Gln Asp Pro Ile Leu Leu Asn Trp Ala Arg Ala Met Val Ala
115 120 125
Lys Lys Gln Gly Arg Leu Asn Asp Ser Ile Arg Leu Tyr Arg Glu Val
130 135 140
Ile Ala Glu Gln Pro Lys Ile Gln Pro Ala Arg Leu Gln Leu Ala Ile
145 150 155 160

Val Leu Met Gln Asn Arg Glu Tyr Asp Ala Ala Lys Asp Gln Phe Gln
165 170 175
Gln Leu Arg Ala Glu Asn Leu Pro Pro Gln Leu Ile Gln Ile Ile Asp
180 185 190
Asn Tyr Val Lys Ala Ile Asn Glu Gln Asp Ser Trp Ser Phe Tyr Ser
195 200 205
Gly Gly Asn Tyr Leu Asn Glu Lys Asn Val Asn Asn Ala Pro Lys Lys
210 215 220

Gly Thr Lys Ala Gly Asn Phe Thr Pro Ser Ser Glu Pro Glu Ser Ala
225 230 235 240
Glu Gly Ile Ser Tyr Tyr Phe Gly Ile Asn Lys Thr Trp Ser Ile Lys
245 250 255
His Gly Phe Phe Thr Glu Phe Asp Ala Asp Leu Asn Gly Lys Tyr Tyr
260 265 270
Trp Asn Asn Arg Lys Tyr Asp Glu Val Ser Leu Arg Gly Gly Leu Gly
275 280 285

Val Gly Tyr Arg Asn Ala Lys Thr Glu Val Lys Phe Ile Pro Tyr Leu
290 295 300
Glu Gln Phe Trp Tyr Ala Gly Gly Glu Asn Ala Lys Lys Asp Ala Arg
305 310 315 320
Thr Leu His Arg Tyr Ser Lys Thr Ser Gly Val Ala Phe Asp Ile Ser
325 330 335

Tyr Trp Leu Asn Pro His Trp Lys Ile Ser Thr Ala Leu Glu Tyr Gly
340 345 350

Glu Gln Arg Tyr Leu Asp Pro Arg Arg Arg Lys Ser Asn Gly Asn Phe
355 360 365
Tyr Ser Ala Thr Asn Thr Leu Ile Tyr Phe Pro Asn Ser Gln Gln Tyr
370 375 380
Trp Phe Ala Gly Leu Asp Phe Tyr Arg Lys Asn Ala His Trp Lys Ala
385 390 395 400
Asn Ala Phe Asp Arg Pro Ala Ala Arg Leu Gly Trp Gly Gln Glu Trp
405 410 415

Pro Lys Gly Ile Ser Thr Arg Leu Gln Ile Ser Tyr Ala Lys Arg Ser
420 425 430
Tyr Arg Met Pro Ser Ala Pro Gln Asn Ala Ile Phe Ala Pro Ile Phe
435 440 445
Phe Lys Phe Ala Gln Lys Asn Gln Glu Tyr Gly Val Asn Leu Thr Ile
450 455 460
Trp His Arg Ser Ile His Trp Leu Gly Ile Thr Pro Lys Ile Thr Trp
465 470 475 480

Ser Tyr Gln Lys Thr Asp Ser Asn Asn Pro Phe Ala Arg Tyr Asp Arg
485 490 495
Asn Arg Val Tyr Leu Ser Val Ser Lys Asn Phe
500 505

<210> 503
<211> 1500
<212> DNA
<213> P. fluorescens SLAM 1
<400> 503
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ctgttcatgg cccctgcgct atttgctgcc gaccaggaca ccagcttgcg cctgaaccag 120
accatcgagt accgcgccaa tcagcaagag cgcgagttgc tcaaggatga attgcccagc 180

gacggcgccg cgccactctt gaacatcgac ggccaggact acaccgtcgg caacaacctg 240

gatgaattgg gccgcgcggt gtacgtgtcc ctctcacgcc agaactggcc acaggccagg 300

gactatctca aacgctacac cgccctgccc ggccatgatc cgatgctcac cgcctatgcc 360

aaaggtggcc tggcccgcgc cgaaggcgac ctggagcaag ccgaagatta ttaccgccaa 420

ttgctggcga tacagtccga cttcctgccg ggccgcctgg agctggcgcg ggtgctgttc 480

gagaaccgca aggatggcga gtccaacgcc gtattccaac agatcagcag tggcctcagc 540

ccctccgacg cgcaggccat gggcctgggc aagaccgtcg acagtttcaa gcaggccctg 600

gatcaccgcg aagactggca aggctccttc gccattggcc cgacctgggg caaaaacctc 660

aatcagtccc ccgaaagcac agtgacgtat cgctacgtca ctgccgaaga aaccattctg 720

gtccaacgct cgctgcccaa ggctgtgtct gcccacggcg cggattacga ggccacgctc 780

aacaaacgca tcgccctcag cggtcatcac ggggtgttca tgcgctcgct gttgtacggc 840

caggcgtatg aaaaggagag caagtacaac gaaagcaccc ttatcaacaa cgccggctac 900

agctatcacg atgcgaaaaa ccagtactcc ctcgggccat cgtatgagtt caacaccatc 960

gccgacaacg ccatgtacag cgcctggggg ttgcggggcg aatggattca cacgttatcg 1020

gctacgcgca tgttcaagct ggaaggcgaa tacaaggaca tggcctacaa gcacgacctc 1080

aacagcaacc tcgacggcgg cattagctcg gtctacgcca ctctgtggca ggccctgccc 1140

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gatgaccgac gcagcgacga tgaacagggc tacaccttta tcctgcgcgc cccacgcctg 1380

gcggtgatgg aagtggtgcc cagtctgacg gtcaaataca acaaggtcgt aagcaatgtc 1440

gactggcttt attcctacga caaaaacagc atcagcctaa agctggaaaa gcagttttaa 1500

<210> 504

<211> 477

<212> PRT

<213> P. fluorescens SLAM 1

<400> 504

Met Ala Pro Ala Leu Phe Ala Ala Asp Gln Asp Thr Ser Leu Arg Leu

1 5 10 15

Asn Gln Thr Ile Glu Tyr Arg Ala Asn Gln Gln Glu Arg Glu Leu Leu

20 25 30

Lys Asp Glu Leu Pro Ser Asp Gly Ala Ala Pro Leu Leu Asn Ile Asp

35 40 45

Gly Gln Asp Tyr Thr Val Gly Asn Asn Leu Asp Glu Leu Gly Arg Ala
50 55 60
Val Tyr Val Ser Leu Ser Arg Gln Asn Trp Pro Gln Ala Arg Asp Tyr
65 70 75 80
Leu Lys Arg Tyr Thr Ala Leu Pro Gly His Asp Pro Met Leu Thr Ala
85 90 95
Tyr Ala Lys Gly Gly Leu Ala Arg Ala Glu Gly Asp Leu Glu Gln Ala
100 105 110

Glu Asp Tyr Tyr Arg Gln Leu Leu Ala Ile Gln Ser Asp Phe Leu Pro
115 120 125
Gly Arg Leu Glu Leu Ala Arg Val Leu Phe Glu Asn Arg Lys Asp Gly
130 135 140
Glu Ser Asn Ala Val Phe Gln Gln Ile Ser Ser Gly Leu Ser Pro Ser
145 150 155 160
Asp Ala Gln Ala Met Gly Leu Gly Lys Thr Val Asp Ser Phe Lys Gln
165 170 175

Ala Leu Asp His Arg Glu Asp Trp Gln Gly Ser Phe Ala Ile Gly Pro
180 185 190
Thr Trp Gly Lys Asn Leu Asn Gln Ser Pro Glu Ser Thr Val Thr Tyr
195 200 205
Arg Tyr Val Thr Ala Glu Glu Thr Ile Leu Val Gln Arg Ser Leu Pro
210 215 220
Lys Ala Val Ser Ala His Gly Ala Asp Tyr Glu Ala Thr Leu Asn Lys
225 230 235 240

Arg Ile Ala Leu Ser Gly His His Gly Val Phe Met Arg Ser Leu Leu
245 250 255
Tyr Gly Gln Ala Tyr Glu Lys Glu Ser Lys Tyr Asn Glu Ser Thr Leu
260 265 270
Ile Asn Asn Ala Gly Tyr Ser Tyr His Asp Ala Lys Asn Gln Tyr Ser
275 280 285

Leu Gly Pro Ser Tyr Glu Phe Asn Thr Ile Ala Asp Asn Ala Met Tyr
290 295 300

Ser Ala Trp Gly Leu Arg Gly Glu Trp Ile His Thr Leu Ser Ala Thr
305 310 315 320
Arg Met Phe Lys Leu Glu Gly Glu Tyr Lys Asp Met Ala Tyr Lys His
325 330 335
Asp Leu Asn Ser Asn Leu Asp Gly Gly Ile Ser Ser Val Tyr Ala Thr
340 345 350
Leu Trp Gln Ala Leu Pro Gln Arg Trp Thr Leu Phe Gly Gly Val Asp
355 360 365

Leu Ser Gln Arg Asn Ala Arg Asp Arg Thr Gln Ala Tyr Leu Gln Lys
370 375 380
Gly Val Arg Leu Gly Val Ala Lys Asp Phe Glu Val Gly Val Ser Ala
385 390 395 400
Val Leu Phe Ala Ser Tyr Arg Lys Arg Gln Tyr Asp Ala Tyr Ser Ala
405 410 415
Leu Val Asp Asp Arg Arg Ser Asp Asp Glu Gln Gly Tyr Thr Phe Ile
420 425 430

Leu Arg Ala Pro Arg Leu Ala Val Met Glu Val Val Pro Ser Leu Thr
435 440 445
Val Lys Tyr Asn Lys Val Val Ser Asn Val Asp Trp Leu Tyr Ser Tyr
450 455 460
Asp Lys Asn Ser Ile Ser Leu Lys Leu Glu Lys Gln Phe
465 470 475

<210> 505
<211> 1455
<212> DNA
<213> P. geniculata SLAM 1
<400> 505

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caggacgatc ttcgtcgtgt gcttgaacag ggcaccgaac tgcgccacca gcagcaggac 120

cagcagcgcc tgcagcaggc cgagtcggag cggccgacca tcaccatcga cggccagacg 180

ctgcgcgtgg agcgcaccgt cgatgatctt ggccaggccc tttacctctc tctgcagcat 240

cagcaatggc aggccgccgc tgcgttcctc gatgagtaca tcgaactgcc ggggcatgac 300

cccctgctgc gccactatgc gcaggggcgc ctggcgcggg tggcgggcga ccatcgtcgc 360

gcggcgatgg agtacgaagc gctgctggcg gcgcagccgg atttcctgcc ggcccgcctc 420

gagctggcac gtgtctatgc ggaagaccag cgcgatcgcg atgcggccgc gctgttcacc 480

gccatcgctg caggcatcaa tgccgatgat ccggccacgg ccggcgtccg cgcgcgcgtg 540

gacggttacc tgggtgccct gcaggcgcgc cagcgctgga aaggcgcgct gtccgccggc 600

ccggcatgga gtgacaacat caaccgcagt tcggccagtc gcacctgcct gttcggcgtg 660

ggcgacgcct gcatcatcga acggaaactg ccggacgccc agcgcgcggc gggcctcgac 720

tacgacgcca gcctggaacg gcgctgggtg ctcggcgggc atcatgggct gtacgtgcgc 780

ggtctcgcct tcggccaggc atggcgcggg cacagtgcgt acaacgagct caatgccaac 840

gtgcaggcgg gttacagctg gcgtagtgca cggcagaccg tgatgctcgc ccccagctat 900

gactatcagg ccctgggcaa ccatgcgctg cagggcggca gtggcgtgca cgcggaatgg 960

cagtacgccc tggatgcacg cagcctgctc aagctggagg ctgactggaa gcgccagcgc 1020

tatcgccagc agggccttgc cagcaactac gacggcgagc tggcatcgct gtacgccacc 1080

tggttccgcg cgctcaatcc acgctggacg gtcttcgccg ggctggatgt caccgacagc 1140

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cagtggagtg gcaccacggc caccgtattc gtgtcgctgc gccagcgcga ctacgacacc 1260

tggagtccgt tgctggaggc gcgcaggcag gacgacgaac agaacctgat cgccatcgtg 1320

cgcagcgagc gcttggccgt ggccgggctg gtacccagcc tgagcctgcg ctacgcgcgc 1380

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gaacgggcct tctga 1455

<210> 506

<211> 484

<212> PRT

<213> P. geniculata SLAM 1

<400> 506

Met Arg His Ser Ile Phe Leu Val Val Leu Leu Leu Ala Ala Thr Glu

1 5 10 15

Val Arg Ala Gln Gln Asp Asp Leu Arg Arg Val Leu Glu Gln Gly Thr

20 25 30

Glu Leu Arg His Gln Gln Gln Asp Gln Gln Arg Leu Gln Gln Ala Glu
35 40 45
Ser Glu Arg Pro Thr Ile Thr Ile Asp Gly Gln Thr Leu Arg Val Glu
50 55 60
Arg Thr Val Asp Asp Leu Gly Gln Ala Leu Tyr Leu Ser Leu Gln His
65 70 75 80
Gln Gln Trp Gln Ala Ala Ala Ala Phe Leu Asp Glu Tyr Ile Glu Leu
85 90 95

Pro Gly His Asp Pro Leu Leu Arg His Tyr Ala Gln Gly Ala Leu Ala
100 105 110
Arg Val Ala Gly Asp His Arg Arg Ala Ala Met Glu Tyr Glu Ala Leu
115 120 125
Leu Ala Ala Gln Pro Asp Phe Leu Pro Ala Arg Leu Glu Leu Ala Arg
130 135 140
Val Tyr Ala Glu Asp Gln Arg Asp Arg Asp Ala Ala Ala Leu Phe Thr
145 150 155 160

Ala Ile Ala Ala Gly Ile Asn Ala Asp Asp Pro Ala Thr Ala Gly Val
165 170 175
Arg Ala Arg Val Asp Gly Tyr Leu Gly Ala Leu Gln Ala Arg Gln Arg
180 185 190
Trp Lys Gly Ala Leu Ser Ala Gly Pro Ala Trp Ser Asp Asn Ile Asn
195 200 205
Arg Ser Ser Ala Ser Arg Thr Cys Leu Phe Gly Val Gly Asp Ala Cys
210 215 220

Ile Ile Glu Arg Lys Leu Pro Asp Ala Gln Arg Ala Ala Gly Leu Asp
225 230 235 240
Tyr Asp Ala Ser Leu Glu Arg Arg Trp Val Leu Gly Gly His His Gly
245 250 255
Leu Tyr Val Arg Gly Leu Ala Phe Gly Gln Ala Trp Arg Gly His Ser
260 265 270

Ala Tyr Asn Glu Leu Asn Ala Asn Val Gln Ala Gly Tyr Ser Trp Arg
275 280 285

Ser Ala Arg Gln Thr Val Met Leu Ala Pro Ser Tyr Asp Tyr Gln Ala
290 295 300
Leu Gly Asn His Ala Leu Gln Gly Gly Ser Gly Val His Ala Glu Trp
305 310 315 320
Gln Tyr Ala Leu Asp Ala Arg Ser Leu Leu Lys Leu Glu Ala Asp Trp
325 330 335
Lys Arg Gln Arg Tyr Arg Gln Gln Gly Leu Ala Ser Asn Tyr Asp Gly
340 345 350

Glu Leu Ala Ser Leu Tyr Ala Thr Trp Phe Arg Ala Leu Asn Pro Arg
355 360 365
Trp Thr Val Phe Ala Gly Leu Asp Val Thr Asp Ser Ser Ala Ala Asp
370 375 380
Ala Ala Asn Gly Phe Arg Gln Arg Gly Leu Arg Leu Gly Ala Ala Arg
385 390 395 400
Gln Trp Ser Gly Thr Thr Ala Thr Val Phe Val Ser Leu Arg Gln Arg
405 410 415

Asp Tyr Asp Thr Trp Ser Pro Leu Leu Glu Ala Arg Arg Gln Asp Asp
420 425 430
Glu Gln Asn Leu Ile Ala Ile Val Arg Ser Glu Arg Leu Ala Val Ala
435 440 445
Gly Leu Val Pro Ser Leu Ser Leu Arg Tyr Ala Arg Ile Asp Ser Asn
450 455 460
Val Gly Trp Leu Tyr Ser His Asp Arg Ser Leu Leu Ser Leu Lys Trp
465 470 475 480

Glu Arg Ala Phe

<210> 507
<211> 1485
<212> DNA

<213> P. halotolerans SLAM 1

<400> 507

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gtggcgcaga tggcccacgc cgatccggat accaatctcc gtctggaaca gaacaccagc 120

ctgcaagccc gggagaaaga acaaagcctg ctggaagaag aacaggcccg tgaacaggcc 180

gaagcactgg tcattgacgg ccagatatat caggttgagg acaacctgaa cgcactggga 240

caggcgattt atctgtcggt caaatcccgg cgttgggtgg cggttcgcgg ctttctgacc 300

cgctatctgg cactgcccgg ccatgacatg atgctggtgc actatgcaca gggggcgtta 360

gcccgctcag acggtgaatt cgcacaggca gaacagtcat accgggcgct gttgcagtta 420

cagccggatt ttctgccggg tcagcttgaa ctggcgcgtg tgttgttcga aaaccagaaa 480

aaccgcgatg ccctgaggct gtttgaagac attcgcgtcg ctctgcccat tcatgacccc 540

aaagcgcagg gagtcatgaa aacggtcgat gctttttctc aggcgctggc ataccgggat 600

agctggcagg gcgcgctttc tttcgggccc ggcttcaaca ataatctgaa tctctcttca 660

gaaagttata cctgcttact cctgatgccg aatggcgagt gcctggtgga gcggaaaaca 720

ccgacagccg aatcggcata cggcacgacc tttgaagcca gtctgaataa acgcatttcc 780

ctgagcggcc atcatggcat cagctttctt ggtctggctt atggcgagaa ctatattcac 840

cacagtccgt acaatgaaca taccctgttg agctatctgg gttacagcta tcacaccgcc 900

aactatcagt tgttcgcagc acctttgttt gaataccgca cgcaaggaaa cgatgcgctc 960

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aagctggaag ctgaggcgaa agatctgcaa tttctgcctg acgggctgga tgttcaatcc 1080

ggctggcaat acgccgggta tgccacgctc tggcaccagt tgccgggaca gtggctgctg 1140

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aaaggcgtcc ggcttggtgt tcagcgttct tgggaggtgg ggattgaaac ctcactcttc 1260

acgtcgttcc ggcagcggga atatcaggcc tacagtcctt tgctggaagc gacccgaaaa 1320

gacgatgagc aaagctacac gctggaaacc cgtttcaccg gattacgttt ttgggatctg 1380

acaccagtgc tgacgctagc gcacaaccgg gtcagcagta atgtggactg gctgtacagc 1440

catgaccaaa gcgaggtgag tctgaaaatc gaaaagcgtt tctga 1485

<210> 508

<211> 1284

<212> DNA

<213> P. halotolerans SLAM 1

<400> 508

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cgcggaccgg acggcgcgct gctggcgcgg cttatggcct taggggacca tgacggcgcg 120

cgagcccatc ttgccgccgc cgtctccgaa ccggcgctgc atgcccttta tcgcacccat 180

ctcgaaggat tgatcgcccg gcagcagggc aggtcggccg atgccgttgc gctttttcgc 240

gccgttctgg ccatcgaccc cggtttcgtt gcggcgcgtg tcgaactggc aaaaagtctg 300

ctcgccacgc gcaatttcga aggcgcgcag caccatctcg atagtctcgc gctcaacgcc 360

gacgacgcaa ttcgcacgat tgcgcaggcg ggcctcgacc atatccgggc caatcgcggt 420

tatggcgcgc agatgcattt ttccatcgcg ccatcgagca atctcaaccg gggcagcgcg 480

caccggattt ttgccgcagg cgggatggat tttgcgatcg accccgattc gcgccggacc 540

gcggggacgg gcatcaccat cgggggcagc gcctatcaca gcttttccct tggcaacggg 600

caggccgtca ttgcaaatgc ggcggtcgat ctgaccaccg atatcgaggg cacacgggcc 660

gaacagcttt cgctgagcgc ggggctgaac tggcaggggc gtttgggcaa ttcccggttt 720

ggcctcggcc cgattgccga tgtgagctat tcagggttcg atccgcatct ggtgcgctat 780

ggcttgagcg ggacgctcaa tgttccggtt ggcgggcaaa atctcgtggg gctgagcttt 840

acggtgctgg ggcaggacta tgcctcgcag gcctatcgca acgggtttcg ggtgctggcg 900

ggggcgcaag tgacccatgc cttcaccccg gccgtgcggg cgagcctgca actgggcgcg 960

gatatcgagc gtacgcaagc cgctcatctc gaccgggatg gggtgtttgg agacgtacgg 1020

gtggtgagcg attggcgggg cggattttcg acggcgctgt ttgtgcgcta cgctcgcgac 1080

cagtatctgg gcaattaccc cggcaccggc acgccgcgcc tcgatgagcg gttgagcgcc 1140

gggatcacgg tttccaacag ccagatcgat ctgggcggtt ttacgccggc gctgagctac 1200

agctatacgc ggcaattttc caatgtgagc tttttcgacc atgacagcca cgatgtcagc 1260

ctggggttga ccaaggcgtt ctag 1284

<210> 509

<211> 494

<212> PRT

<213> P. halotolerans SLAM 1

<400> 509

Met Pro Tyr Leu Ser Arg Leu Ser Ser Val Val Gly Leu Ala Leu Leu

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Ser Phe Leu Phe Val Ala Gln Met Ala His Ala Asp Pro Asp Thr Asn

20 25 30

Leu Arg Leu Glu Gln Asn Thr Ser Leu Gln Ala Arg Glu Lys Glu Gln

35 40 45

Ser Leu Leu Glu Glu Glu Gln Ala Arg Glu Gln Ala Glu Ala Leu Val

50 55 60

Ile Asp Gly Gln Ile Tyr Gln Val Glu Asp Asn Leu Asn Ala Leu Gly

65 70 75 80

Gln Ala Ile Tyr Leu Ser Val Lys Ser Arg Arg Trp Val Ala Val Arg

85 90 95

Gly Phe Leu Thr Arg Tyr Leu Ala Leu Pro Gly His Asp Met Met Leu

100 105 110

Val His Tyr Ala Gln Gly Ala Leu Ala Arg Ser Asp Gly Glu Phe Ala

115 120 125

Gln Ala Glu Gln Ser Tyr Arg Ala Leu Leu Gln Leu Gln Pro Asp Phe

130 135 140

Leu Pro Gly Gln Leu Glu Leu Ala Arg Val Leu Phe Glu Asn Gln Lys

145 150 155 160

Asn Arg Asp Ala Leu Arg Leu Phe Glu Asp Ile Arg Val Ala Leu Pro

165 170 175

Ile His Asp Pro Lys Ala Gln Gly Val Met Lys Thr Val Asp Ala Phe

180 185 190

Ser Gln Ala Leu Ala Tyr Arg Asp Ser Trp Gln Gly Ala Leu Ser Phe

195 200 205

Gly Pro Gly Phe Asn Asn Asn Leu Asn Leu Ser Ser Glu Ser Tyr Thr

210 215 220

Cys Leu Leu Leu Met Pro Asn Gly Glu Cys Leu Val Glu Arg Lys Thr

225 230 235 240

Pro Thr Ala Glu Ser Ala Tyr Gly Thr Thr Phe Glu Ala Ser Leu Asn

245 250 255

Lys Arg Ile Ser Leu Ser Gly His His Gly Ile Ser Phe Leu Gly Leu

260 265 270

Ala Tyr Gly Glu Asn Tyr Ile His His Ser Pro Tyr Asn Glu His Thr

275 280 285

Leu Leu Ser Tyr Leu Gly Tyr Ser Tyr His Thr Ala Asn Tyr Gln Leu

290 295 300

Phe Ala Ala Pro Leu Phe Glu Tyr Arg Thr Gln Gly Asn Asp Ala Leu

305 310 315 320

Tyr Gln Ala Trp Gly Gly Lys Leu Ser Gly Leu Tyr Leu Phe Ser Ala

325 330 335

Ala Thr Ala Phe Lys Leu Glu Ala Glu Ala Lys Asp Leu Gln Phe Leu

340 345 350

Pro Asp Gly Leu Asp Val Gln Ser Gly Trp Gln Tyr Ala Gly Tyr Ala

355 360 365

Thr Leu Trp His Gln Leu Pro Gly Gln Trp Leu Leu Phe Gly Gly Leu

370 375 380

Asp Trp Thr Asp Lys His Ala Gln Gln Ala Val His Ala Tyr Gln Met

385 390 395 400

Lys Gly Val Arg Leu Gly Val Gln Arg Ser Trp Glu Val Gly Ile Glu

405 410 415

Thr Ser Leu Phe Thr Ser Phe Arg Gln Arg Glu Tyr Gln Ala Tyr Ser

420 425 430

Pro Leu Leu Glu Ala Thr Arg Lys Asp Asp Glu Gln Ser Tyr Thr Leu

435 440 445

Glu Thr Arg Phe Thr Gly Leu Arg Phe Trp Asp Leu Thr Pro Val Leu

450 455 460

Thr Leu Ala His Asn Arg Val Ser Ser Asn Val Asp Trp Leu Tyr Ser

465 470 475 480

His Asp Gln Ser Glu Val Ser Leu Lys Ile Glu Lys Arg Phe

485 490

<210> 510

<211> 427

<212> PRT

<213> P. halotolerans SLAM 1

<400> 510

Met Arg Ile Leu Ile Leu Ala Leu Ala Leu Gly Leu Thr Leu Thr Gly
1 5 10 15
Ala Val Ala Ala Arg Gly Pro Asp Gly Ala Leu Leu Ala Arg Leu Met
20 25 30
Ala Leu Gly Asp His Asp Gly Ala Arg Ala His Leu Ala Ala Ala Val
35 40 45
Ser Glu Pro Ala Leu His Ala Leu Tyr Arg Thr His Leu Glu Gly Leu
50 55 60

Ile Ala Arg Gln Gln Gly Arg Ser Ala Asp Ala Val Ala Leu Phe Arg
65 70 75 80
Ala Val Leu Ala Ile Asp Pro Gly Phe Val Ala Ala Arg Val Glu Leu
85 90 95
Ala Lys Ser Leu Leu Ala Thr Arg Asn Phe Glu Gly Ala Gln His His
100 105 110
Leu Asp Ser Leu Ala Leu Asn Ala Asp Asp Ala Ile Arg Thr Ile Ala
115 120 125

Gln Ala Gly Leu Asp His Ile Arg Ala Asn Arg Gly Tyr Gly Ala Gln
130 135 140
Met His Phe Ser Ile Ala Pro Ser Ser Asn Leu Asn Arg Gly Ser Ala
145 150 155 160
His Arg Ile Phe Ala Ala Gly Gly Met Asp Phe Ala Ile Asp Pro Asp
165 170 175
Ser Arg Arg Thr Ala Gly Thr Gly Ile Thr Ile Gly Gly Ser Ala Tyr
180 185 190

His Ser Phe Ser Leu Gly Asn Gly Gln Ala Val Ile Ala Asn Ala Ala
195 200 205
Val Asp Leu Thr Thr Asp Ile Glu Gly Thr Arg Ala Glu Gln Leu Ser
210 215 220
Leu Ser Ala Gly Leu Asn Trp Gln Gly Arg Leu Gly Asn Ser Arg Phe
225 230 235 240
Gly Leu Gly Pro Ile Ala Asp Val Ser Tyr Ser Gly Phe Asp Pro His

245 250 255

Leu Val Arg Tyr Gly Leu Ser Gly Thr Leu Asn Val Pro Val Gly Gly
260 265 270
Gln Asn Leu Val Gly Leu Ser Phe Thr Val Leu Gly Gln Asp Tyr Ala
275 280 285
Ser Gln Ala Tyr Arg Asn Gly Phe Arg Val Leu Ala Gly Ala Gln Val
290 295 300
Thr His Ala Phe Thr Pro Ala Val Arg Ala Ser Leu Gln Leu Gly Ala
305 310 315 320

Asp Ile Glu Arg Thr Gln Ala Ala His Leu Asp Arg Asp Gly Val Phe
325 330 335
Gly Asp Val Arg Val Val Ser Asp Trp Arg Gly Gly Phe Ser Thr Ala
340 345 350
Leu Phe Val Arg Tyr Ala Arg Asp Gln Tyr Leu Gly Asn Tyr Pro Gly
355 360 365
Thr Gly Thr Pro Arg Leu Asp Glu Arg Leu Ser Ala Gly Ile Thr Val
370 375 380

Ser Asn Ser Gln Ile Asp Leu Gly Gly Phe Thr Pro Ala Leu Ser Tyr
385 390 395 400
Ser Tyr Thr Arg Gln Phe Ser Asn Val Ser Phe Phe Asp His Asp Ser
405 410 415
His Asp Val Ser Leu Gly Leu Thr Lys Ala Phe
420 425

<210> 511
<211> 1365
<212> DNA
<213> P. hauseri SLAM 1
<400> 511
atgcgttatt atcaaaaacg aatgaaatta tttattatca ttagtgtgtt acttattcca 60

ttaaaaataa acgccaacga aaataatgcg attttattct cctattcttc acctcaacac 120
caagttgcac aaatagggca acaactttat cgcgctttac agcaacagca gtggaaaaag 180

gctgaagaac tattactgga ctatcaacaa ttacctttac atgaaacact attaattaat 240

tacgctaaag cgcttttagc tcaaataaaa ggtgattttt taaacgccga attttattat 300

cagcagcaac ttaaacaaaa agtcgatttt atcccagcgc aaacagggtt aattcagctt 360

tattttcatt tacgagaata taaaaaagca caacgacaac ttaatcaatt gagcaatatg 420

attgatttac ctaaagatat tatccaatct attgcgtttt atagagctaa attagcctct 480

tattttcaag gccaacgttt ctatcaactt agtttctttt atgatgataa tattaatcat 540

gcacctgatt tagctgaaaa aattgtctct caatctactc aaagaaaaat gacgctaaga 600

ggtgctaaac ccattgtatc aacaggactt gctcattatt tttcttttta tcagcctttt 660

attctttatt ctcaccatac tttttcttct tatacttatg cacgatatat cgattatcac 720

tcttaccgta gtgctaattt tcttgcgtta tatacccaac tgggctatcg ctaccaaaaa 780

cctcaatatc aatggtcaat cacaccttat tacgaaataa aaaaaacacc aactcaatat 840

gaatatcaag cctggggaag tgaaacacaa ttttcttatt tgattaataa aaagcaaact 900

attaatttaa gtttggatta taaaataaag aaatatcaag aaacgttaaa gaatttaaat 960

actcagcgac tgagttatag cactaatcat aactattatt taaataatag agtgaattta 1020

cttaatcaat taaattatca attaggtcgt aaaaaaaaca ctttattaaa ttatcagctg 1080

tatggtataa aaactggcgt ttattatcca ttgtcagtaa attggcatat gtctcttttt 1140

ttacagtatc aatttaaaca atttaataac tataatcctt tattaaaaaa gagaagaaaa 1200

gacaatagct ttatttttac aaccaatatt aaaaataaat cacccttat tttagggttt 1260

tatcccgcaa tagagttacg ttatacccga agattaagca atgtggattg gttatatcaa 1320

tatcagcaac atgaagtatt atttaaatta gaaaaacaat tttaa 1365

<210> 512

<211> 454

<212> PRT

<213> P. hauseri SLAM 1

<400> 512

Met Arg Tyr Tyr Gln Lys Arg Met Lys Leu Phe Ile Ile Ile Ser Val
1 5 10 15

Leu Leu Ile Pro Leu Lys Ile Asn Ala Asn Glu Asn Asn Ala Ile Leu
20 25 30

Phe Ser Tyr Ser Ser Pro Gln His Gln Val Ala Gln Ile Gly Gln Gln
35 40 45

Leu Tyr Arg Ala Leu Gln Gln Gln Gln Trp Lys Lys Ala Glu Glu Leu
50 55 60
Leu Leu Asp Tyr Gln Gln Leu Pro Leu His Glu Thr Leu Leu Ile Asn
65 70 75 80
Tyr Ala Lys Ala Leu Leu Ala Gln Ile Lys Gly Asp Phe Leu Asn Ala
85 90 95
Glu Phe Tyr Tyr Gln Gln Gln Leu Lys Gln Lys Val Asp Phe Ile Pro
100 105 110

Ala Gln Thr Gly Leu Ile Gln Leu Tyr Phe His Leu Arg Glu Tyr Lys
115 120 125
Lys Ala Gln Arg Gln Leu Asn Gln Leu Ser Asn Met Ile Asp Leu Pro
130 135 140
Lys Asp Ile Ile Gln Ser Ile Ala Phe Tyr Arg Ala Lys Leu Ala Ser
145 150 155 160
Tyr Phe Gln Gly Gln Arg Phe Tyr Gln Leu Ser Phe Phe Tyr Asp Asp
165 170 175

Asn Ile Asn His Ala Pro Asp Leu Ala Glu Lys Ile Val Ser Gln Ser
180 185 190
Thr Gln Arg Lys Met Thr Leu Arg Gly Ala Lys Pro Ile Val Ser Thr
195 200 205
Gly Leu Ala His Tyr Phe Ser Phe Tyr Gln Pro Phe Ile Leu Tyr Ser
210 215 220
His His Thr Phe Ser Ser Tyr Thr Tyr Ala Arg Tyr Ile Asp Tyr His
225 230 235 240

Ser Tyr Arg Ser Ala Asn Phe Leu Ala Leu Tyr Thr Gln Leu Gly Tyr
245 250 255
Arg Tyr Gln Lys Pro Gln Tyr Gln Trp Ser Ile Thr Pro Tyr Tyr Glu
260 265 270
Ile Lys Lys Thr Pro Thr Gln Tyr Glu Tyr Gln Ala Trp Gly Ser Glu
275 280 285
Thr Gln Phe Ser Tyr Leu Ile Asn Lys Lys Gln Thr Ile Asn Leu Ser

290 295 300

Leu Asp Tyr Lys Ile Lys Lys Tyr Gln Glu Thr Leu Lys Asn Leu Asn
305 310 315 320
Thr Gln Arg Leu Ser Tyr Ser Thr Asn His Asn Tyr Tyr Leu Asn Asn
325 330 335
Arg Val Asn Leu Leu Asn Gln Leu Asn Tyr Gln Leu Gly Arg Lys Lys
340 345 350
Asn Thr Leu Leu Asn Tyr Gln Leu Tyr Gly Ile Lys Thr Gly Val Tyr
355 360 365

Tyr Pro Leu Ser Val Asn Trp His Met Ser Leu Phe Leu Gln Tyr Gln
370 375 380
Phe Lys Gln Phe Asn Asn Tyr Asn Pro Leu Leu Lys Lys Arg Arg Lys
385 390 395 400
Asp Asn Ser Phe Ile Phe Thr Thr Asn Ile Lys Asn Lys Ser Pro Phe
405 410 415
Ile Leu Gly Phe Tyr Pro Ala Ile Glu Leu Arg Tyr Thr Arg Arg Leu
420 425 430

Ser Asn Val Asp Trp Leu Tyr Gln Tyr Gln Gln His Glu Val Leu Phe
435 440 445
Lys Leu Glu Lys Gln Phe
450

<210> 513
<211> 1500
<212> DNA
<213> P. luminescens
<400> 513
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tttatagagc catctctagt gttggcagat gaagataccg gtagaagatt gtggtataac 120
gtacagcgaa atttgcagga tcaagaaaaa gcgttggtca cagatgaaac cgtggataaa 180
aaaacggatc atttattgat agtccttaat ggtcaaacgt ttagtgttga aaacaatgtg 240

aatgatattg gtcaggcgct ttatttagcc attaatcatc aacaagtgca ggatgttgag 300

cgttttttat cgatgtacca gaaattacct ggacatgata cccaattggt ccattttgct 360

caggcaaatc tggcgcgttt acaaggtgac ttagtagcag cagaacagca ttatcaggcc 420

atcttgcagc aacaacctga ttttacccgg gctaaattag agttagccag agtctattat 480

gagaatcaaa agaatagaga agccagctta ctatttaatg agatttcagc agttagtcgc 540

gataatgaaa ataaattacc accagcagtc attaagaata taactaatta tcaggaggcg 600

attaatttgc gtaattcctg gcgtggatct ttctccgtag gatatatctt taacgataac 660

acgaatatgt cgtcagataa gcctcctgtt tgcactctct atcgtgaaaa tggtgagtgt 720

gcggttgaac gtaagctgcc tatggcaaag aaagcgaatg gtattagtta tgatgctacg 780

ttacgtaaga tatatccgct aagtggtcac cacggtgtct ttttacgttc gatgacttat 840

ggggaaagtt atcgtcatca tagtgaggag aatgaaaata cgacttctgc ttattttggt 900

tatagttata aagcgcaaaa aaatgatttc ctaatggggc cagttgttga gtttaattct 960

gttggtaacc attcccgtta tcgtactacg ggaataaaat ctgaatggat gaatatttta 1020

tctgaaaatt tggtattgaa tttggaaggt gaatataagc agtttcgtta tcataaactt 1080

tataatcata atgacggtaa tatggcctct gtttatgcca ccttatctta ttatttaact 1140

gatcagacaa ttacctttgc gggtggtgat tgggttaata aaactagtgt tgagaaagct 1200

gacgattatc aacaaaaagg tgtgagagca ggcatttcaa ctcaattgta tccgggaatt 1260

aatgcagtgg tatttactgt attacgccag cggcaatttg gtgattacag tgtgcctcta 1320

aatgcacgtc gtaaagataa tgaacaattc tatgcggcaa ttgtgagtat gcctaaattt 1380

gaagttttcg gtttaacccc agtaattact tatcggttta gaaaaaataa tagtaatgtt 1440

gattggctct attcctataa taagaatgaa gtgttagtca agtttgaaaa gtatttttga 1500

<210> 514

<211> 499

<212> PRT

<213> P. luminescens SLAM 1

<400> 514

Met Ile Leu Pro Met Leu Asn Thr Ser Ile Val Arg Phe Thr Leu Leu

1 5 10 15

Ile Ser Cys Leu Phe Ile Glu Pro Ser Leu Val Leu Ala Asp Glu Asp

20 25 30

Thr Gly Arg Arg Leu Trp Tyr Asn Val Gln Arg Asn Leu Gln Asp Gln

35 40 45

Glu Lys Ala Leu Val Thr Asp Glu Thr Val Asp Lys Lys Thr Asp His

50 55 60

Leu Leu Ile Val Leu Asn Gly Gln Thr Phe Ser Val Glu Asn Asn Val

65 70 75 80

Asn Asp Ile Gly Gln Ala Leu Tyr Leu Ala Ile Asn His Gln Gln Val

85 90 95

Gln Asp Val Glu Arg Phe Leu Ser Met Tyr Gln Lys Leu Pro Gly His

100 105 110

Asp Thr Gln Leu Val His Phe Ala Gln Ala Asn Leu Ala Arg Leu Gln

115 120 125

Gly Asp Leu Val Ala Ala Glu Gln His Tyr Gln Ala Ile Leu Gln Gln

130 135 140

Gln Pro Asp Phe Thr Arg Ala Lys Leu Glu Leu Ala Arg Val Tyr Tyr

145 150 155 160

Glu Asn Gln Lys Asn Arg Glu Ala Ser Leu Leu Phe Asn Glu Ile Ser

165 170 175

Ala Val Ser Arg Asp Asn Glu Asn Lys Leu Pro Pro Ala Val Ile Lys

180 185 190

Asn Ile Thr Asn Tyr Gln Glu Ala Ile Asn Leu Arg Asn Ser Trp Arg

195 200 205

Gly Ser Phe Ser Val Gly Tyr Ile Phe Asn Asp Asn Thr Asn Met Ser

210 215 220

Ser Asp Lys Pro Pro Val Cys Thr Leu Tyr Arg Glu Asn Gly Glu Cys

225 230 235 240

Ala Val Glu Arg Lys Leu Pro Met Ala Lys Lys Ala Asn Gly Ile Ser

245 250 255

Tyr Asp Ala Thr Leu Arg Lys Ile Tyr Pro Leu Ser Gly His His Gly

260 265 270

Val Phe Leu Arg Ser Met Thr Tyr Gly Glu Ser Tyr Arg His His Ser

275 280 285

Glu Glu Asn Glu Asn Thr Thr Ser Ala Tyr Phe Gly Tyr Ser Tyr Lys

290 295 300

Ala Gln Lys Asn Asp Phe Leu Met Gly Pro Val Val Glu Phe Asn Ser

305 310 315 320

Val Gly Asn His Ser Arg Tyr Arg Thr Thr Gly Ile Lys Ser Glu Trp

325 330 335

Met Asn Ile Leu Ser Glu Asn Leu Val Leu Asn Leu Glu Gly Glu Tyr

340 345 350

Lys Gln Phe Arg Tyr His Lys Leu Tyr Asn His Asn Asp Gly Asn Met

355 360 365

Ala Ser Val Tyr Ala Thr Leu Ser Tyr Tyr Leu Thr Asp Gln Thr Ile

370 375 380

Thr Phe Ala Gly Gly Asp Trp Val Asn Lys Thr Ser Val Glu Lys Ala

385 390 395 400

Asp Asp Tyr Gln Gln Lys Gly Val Arg Ala Gly Ile Ser Thr Gln Leu

405 410 415

Tyr Pro Gly Ile Asn Ala Val Val Phe Thr Val Leu Arg Gln Arg Gln

420 425 430

Phe Gly Asp Tyr Ser Val Pro Leu Asn Ala Arg Arg Lys Asp Asn Glu

435 440 445

Gln Phe Tyr Ala Ala Ile Val Ser Met Pro Lys Phe Glu Val Phe Gly

450 455 460

Leu Thr Pro Val Ile Thr Tyr Arg Phe Arg Lys Asn Asn Ser Asn Val

465 470 475 480

Asp Trp Leu Tyr Ser Tyr Asn Lys Asn Glu Val Leu Val Lys Phe Glu

485 490 495

Lys Tyr Phe

<210> 515

<211> 1353

<212> DNA

<213> P. mirabilis SLAM 1

<400> 515

atgcgttatt atcaaaggct aataaagtca ttatttatta ttaatatctt atttcattcg 60

tcacaggggg cggcaacaca acctaatcaa gagcagctta ataaagagaa ggtcgctcaa 120

ttaggtcaac aactgtatca ccatttacag caacagcagt ggtatcaagc ggaaaaacta 180

ttagttaatt atcagcaatt accattacac gaaactttat tagtctatta tgctcaagca 240

ctattagcac agaagaatgg taatttctta caagctgaat tttattatca gcagcaactt 300

aagcagcaag cagattttat tccggcacaa acaggtctaa ttcagctcta cttttctcaa 360

ggagaatata aaaaagcaca ataccagcta aatcaattaa gtcgtttatc gggattatca 420

cctgccatta atcaagcaat tatctattat cagaaacagc ttaacgatta ttttaaagct 480

aggcgttttt atcaaatcag tttttttttat gatgataata ttaatcatgc accttatctt 540

gatgagcaaa ttgtttcgca atcaacgcaa gtcatcatga ccagaaaagg cgctcaacct 600

atagcatcga tgggggttag tcatcttttt tctttctatc agcccacttt tatttacgct 660

aataataccc tatcaggcta tttttcagca cgctaccgtg attattttgc atataaacaa 720

gctaatttta cacatttata tactcaatta agttatcagt accaaaaaaa ggattatcgg 780

tggaccttat ctccttatta tgaaataaaa tcacctaaaa aggcgtttga gtatcaatct 840

attggggtat ataccgggct atttttctct attaataaat atcattctat taatttatct 900

ataaattatt atataaagaa atataataaa gaattaataa acttaaataa tcataagcag 960

ctatatgcta ttagctatta ctatacatta gcagagaatg ttcaattagt taatcaatta 1020

aactattata gtagtcgtaa aaaaaatact ttattaaatt atcagcaata tgatataaaa 1080

acgggtgttt attacttatt accaaaaaat tggcaagttt ctctttcttt acaatatcaa 1140

tttaaaagtt ttaataatta taatccatta ttaaataaga aaagagaaga taatggcttt 1200

gtttttacaa caactattaa aaataaagca cctattatct ggggttttta tccagcaata 1260

gaattaagtt atacccgtag attaagcaat gtggattggt tatatcaata tcagcagcat 1320

gaagtcttat ttaaattaga aaaacaattt taa 1353

<210> 516

<400> 516

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<210> 517

<211> 1524

<212> DNA

<213> P. multocida SLAM 1

<400> 517

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agccgaccag atgaaacatt ttcccagacg tcacctaaac agcatctctt ttctcagaaa 180

ccgactgaac ccacatcaag tgcgagcagt cagcaaattt cgttgaccat tgaacaactt 240

gctagcagac ctgatttggt gcttcgcgcc ttaatcccag cattaaaaaa taatgatatg 300

cgcggtgttg aaatcctcct acctatttat gctaaacaat cacccgatcc ctttttatta 360

aaatgggcac aggcaatggt tgctcgtaaa caaggcaaat taaatgaatc cgtgcgttta 420

tatcgccaaa ttattgcaga aaagcccaat ttacaacctg cacgcttaca actcgctatc 480

gccttaacgc aaaaccgtga aaatgaagct gcgaaagcac aatttaacca actgcgttca 540

gaaaacttac ccgcgccttt actgaccctc attgatagct atattgatgc gattaaccaa 600

cgcgatagct ggaatgtgta tggcggagta aattatttgc atgagaacaa tgtcaataat 660

gcaccgccta aaggtaccaa agcggaaggc ttcaccccgt caagtcaacc agaaaaagca 720

catggtttaa gttattttat taatttaagt aaaaattggt cattagccca cggctttttc 780

acagaattta gtgccgatat caatggaaaa tattattggg ataatcataa gtatgatgag 840

ttttcgactc gcctcaatct aggtggtggt taccgtaatg ccaaaacaga agtgaaactt 900

ataccttttcg tggaacaatt ttggtatgtg ggcggtgaaa atgcaaaaaa ggatgcacgt 960

acattacacc gttattctaa aagctcaggt atcaaccttg acgtggacta ttggttgaca 1020

cccaattgga aaatctccac ggttctggaa tataccgaac aacgttatat ccagcctcaa 1080

cggcaaaact caaatggaaa tagctattcc attagcaata ctctgatata tatgccaaat 1140

agccaacaat tttggtttgt tggactcgat tattatcaaa aaaatacccg gctaaaagcc 1200

tatgcttttg aacgtcaagg aatacgtcta ggttgggggc aagaatggcc gaaaggcatt 1260

tcaacgcgtt tacaaacaag ctatgccacg cgtacttatc gagcaccttc agcagaaaag 1320

aatatgattt tcgcgccgag ttttttttaaa gttgtgcaaa aaaatcacga atacggtgtc 1380

aattttacga tttggcatcg tagtcttcac tggttgggga tcacgcctaa aatcacttgg 1440

gcatatcaaa aaaccaccag taacaatcct ttttccgaat atgaccggaa tcggatttat 1500

ttaaccttca gtaaaacatt ttaa 1524

<210> 518

<211> 507

<212> PRT

<213> P. multocida SLAM 1

<400> 518

Met Asn Leu Met Ile Asn Leu Lys Pro Leu Thr Phe Leu Pro Phe Phe
1 5 10 15
Gly Arg Leu Val Phe Leu Ser Gly Val Ile Tyr Asn Thr Ala Trp Ala
20 25 30
Asn Thr Val Ile Pro Val Asp Asn Ser Arg Pro Asp Glu Thr Phe Ser

35 40 45
Gln Thr Ser Pro Lys Gln His Leu Phe Ser Gln Lys Pro Thr Glu Pro
50 55 60
Thr Ser Ser Ala Ser Ser Gln Gln Ile Ser Leu Thr Ile Glu Gln Leu
65 70 75 80
Ala Ser Arg Pro Asp Leu Val Leu Arg Ala Leu Ile Pro Ala Leu Lys
85 90 95
Asn Asn Asp Met Arg Gly Val Glu Ile Leu Leu Pro Ile Tyr Ala Lys

100 105 110
Gln Ser Pro Asp Pro Phe Leu Leu Lys Trp Ala Gln Ala Met Val Ala
115 120 125
Arg Lys Gln Gly Lys Leu Asn Glu Ser Val Arg Leu Tyr Arg Gln Ile
130 135 140
Ile Ala Glu Lys Pro Asn Leu Gln Pro Ala Arg Leu Gln Leu Ala Ile
145 150 155 160
Ala Leu Thr Gln Asn Arg Glu Asn Glu Ala Ala Lys Ala Gln Phe Asn

165 170 175
Gln Leu Arg Ser Glu Asn Leu Pro Ala Pro Leu Leu Thr Leu Ile Asp
180 185 190
Ser Tyr Ile Asp Ala Ile Asn Gln Arg Asp Ser Trp Asn Val Tyr Gly
195 200 205
Gly Val Asn Tyr Leu His Glu Asn Asn Val Asn Asn Ala Pro Pro Lys
210 215 220
Gly Thr Lys Ala Glu Gly Phe Thr Pro Ser Ser Gln Pro Glu Lys Ala

225 230 235 240
His Gly Leu Ser Tyr Phe Ile Asn Leu Ser Lys Asn Trp Ser Leu Ala

245 250 255

His Gly Phe Phe Thr Glu Phe Ser Ala Asp Ile Asn Gly Lys Tyr Tyr

260 265 270

Trp Asp Asn His Lys Tyr Asp Glu Phe Ser Thr Arg Leu Asn Leu Gly

275 280 285

Gly Gly Tyr Arg Asn Ala Lys Thr Glu Val Lys Leu Ile Pro Phe Val

290 295 300

Glu Gln Phe Trp Tyr Val Gly Gly Glu Asn Ala Lys Lys Asp Ala Arg

305 310 315 320

Thr Leu His Arg Tyr Ser Lys Ser Ser Gly Ile Asn Leu Asp Val Asp

325 330 335

Tyr Trp Leu Thr Pro Asn Trp Lys Ile Ser Thr Val Leu Glu Tyr Thr

340 345 350

Glu Gln Arg Tyr Ile Gln Pro Gln Arg Gln Asn Ser Asn Gly Asn Ser

355 360 365

Tyr Ser Ile Ser Asn Thr Leu Ile Tyr Met Pro Asn Ser Gln Gln Phe

370 375 380

Trp Phe Val Gly Leu Asp Tyr Tyr Gln Lys Asn Thr Arg Leu Lys Ala

385 390 395 400

Tyr Ala Phe Glu Arg Gln Gly Ile Arg Leu Gly Trp Gly Gln Glu Trp

405 410 415

Pro Lys Gly Ile Ser Thr Arg Leu Gln Thr Ser Tyr Ala Thr Arg Thr

420 425 430

Tyr Arg Ala Pro Ser Ala Glu Lys Asn Met Ile Phe Ala Pro Ser Phe

435 440 445

Phe Lys Val Val Gln Lys Asn His Glu Tyr Gly Val Asn Phe Thr Ile

450 455 460

Trp His Arg Ser Leu His Trp Leu Gly Ile Thr Pro Lys Ile Thr Trp

465 470 475 480

Ala Tyr Gln Lys Thr Thr Ser Asn Asn Pro Phe Ser Glu Tyr Asp Arg

485 490 495

Asn Arg Ile Tyr Leu Thr Phe Ser Lys Thr Phe

500 505

<210> 519

<211> 1467

<212> DNA

<213> P. parafulva SLAM 1

<400> 519

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gctcaatccg atcaggatac agacctgcgg ctcaatcaga caattgacta ccgtgccaca 120

gtggaagacc ggggtttcca gcaggcgcct ggcaccctgt ctctcctgtc cgtggatggc 180

catacctatc aagttggcaa taacctggat gatctggggc gggcgctgta tctctcggta 240

cagcggcagc agtgggcgga tgtgatcttt tttcgagcac gctacgcggc acttccagat 300

catgacccca tgcttctggc ctatgccgat ggtgcacgcg cacgcgccga tgggcaattg 360

agtcaagccg aagttgatta tcggcactta ctggccctgc agccagactt cttgccaggc 420

caactcgaac tggcgagggt gctatttgaa aatcgtaaag atcgggagtc ggcggacgct 480

ttcagccgta tccgctcgtc ccttgaccct gcagacacgc aaaatcgagg gttgctccag 540

agcatcagta gtttcaccca ggcactcgat cggcgaggtc aatggcaagg ctcgttggcc 600

gtagggccca cgtggagtaa taacctcaac cggtcctcgg agagccgaac cacctaccgc 660

cttgcatcca gcgagggtgt atacgtgata gaaagaagga tgcccaaggc cgtttctgga 720

gacggcatag attacgaggc gaccctgaat aaacgcgcag ccctttctgg gcatcacggc 780

gcctacatcc gagcgcttgc gtatggccaa gcctataagg ggcaaggcaa atataacgag 840

gatacattga ctgctcatgc aggctacagc taccaaaatg cacgcaatca atacagccta 900

ggaccacttt tcgagttcaa ccgcatgggc agtgatccga tgtcaactgc ctggggcctg 960

cgcggtgaat ggatgcacaa cctgagtgcc acacgtttgc tcaaactgga ggttgaatac 1020

aaagacctcg cctaccgagg gctgtatgca agcgcttaca atggtagcgt cacctcgacg 1080

tacgcgacac tttggcaagc aatgccccaa caatggttgc tgttcggagg cttcgatttc 1140

acggaccggc gcgcgaaaaa tgacgttgaa acttatttcc aaaaggggct gcgtgcgggg 1200

gtagccaagg aatttggttc aggcttgagt acagtactgt tcgcctcttg gcggacccgg 1260

caatatgccg gtttcagcgc gccccttaat gcgcgccgac acgaagagga gagtggctat 1320

accttcatcg ctcgagcgcc gcggttggct gttagcgggc tagtacccag cctcgtcgtc 1380

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agcgtcaagt tggaaaaagt gttctag 1467

<210> 520

<211> 488

<212> PRT

<213> P. parafulva SLAM 1

<400> 520

Met Pro His Cys Tyr Arg Ser Phe Val Gly Ile Phe Phe Ala Val Phe
1 5 10 15

Phe Pro Ser His Ala Gln Ser Asp Gln Asp Thr Asp Leu Arg Leu Asn
20 25 30

Gln Thr Ile Asp Tyr Arg Ala Thr Val Glu Asp Arg Gly Phe Gln Gln
35 40 45

Ala Pro Gly Thr Leu Ser Leu Leu Ser Val Asp Gly His Thr Tyr Gln
50 55 60

Val Gly Asn Asn Leu Asp Asp Leu Gly Arg Ala Leu Tyr Leu Ser Val
65 70 75 80

Gln Arg Gln Gln Trp Ala Asp Val Ile Phe Phe Arg Ala Arg Tyr Ala
85 90 95

Ala Leu Pro Asp His Asp Pro Met Leu Leu Ala Tyr Ala Asp Gly Ala
100 105 110

Arg Ala Arg Ala Asp Gly Gln Leu Ser Gln Ala Glu Val Asp Tyr Arg
115 120 125

His Leu Leu Ala Leu Gln Pro Asp Phe Leu Pro Gly Gln Leu Glu Leu
130 135 140

Ala Arg Val Leu Phe Glu Asn Arg Lys Asp Arg Glu Ser Ala Asp Ala
145 150 155 160

Phe Ser Arg Ile Arg Ser Ser Leu Asp Pro Ala Asp Thr Gln Asn Arg
165 170 175

Gly Leu Leu Gln Ser Ile Ser Ser Phe Thr Gln Ala Leu Asp Arg Arg
180 185 190

Gly Gln Trp Gln Gly Ser Leu Ala Val Gly Pro Thr Trp Ser Asn Asn

195 200 205

Leu Asn Arg Ser Ser Glu Ser Arg Thr Thr Tyr Arg Leu Ala Ser Ser

210 215 220

Glu Gly Val Tyr Val Ile Glu Arg Arg Met Pro Lys Ala Val Ser Gly

225 230 235 240

Asp Gly Ile Asp Tyr Glu Ala Thr Leu Asn Lys Arg Ala Ala Leu Ser

245 250 255

Gly His His Gly Ala Tyr Ile Arg Ala Leu Ala Tyr Gly Gln Ala Tyr

260 265 270

Lys Gly Gln Gly Lys Tyr Asn Glu Asp Thr Leu Thr Ala His Ala Gly

275 280 285

Tyr Ser Tyr Gln Asn Ala Arg Asn Gln Tyr Ser Leu Gly Pro Leu Phe

290 295 300

Glu Phe Asn Arg Met Gly Ser Asp Pro Met Ser Thr Ala Trp Gly Leu

305 310 315 320

Arg Gly Glu Trp Met His Asn Leu Ser Ala Thr Arg Leu Leu Lys Leu

325 330 335

Glu Val Glu Tyr Lys Asp Leu Ala Tyr Arg Gly Leu Tyr Ala Ser Ala

340 345 350

Tyr Asn Gly Ser Val Thr Ser Thr Tyr Ala Thr Leu Trp Gln Ala Met

355 360 365

Pro Gln Gln Trp Leu Leu Phe Gly Gly Phe Asp Phe Thr Asp Arg Arg

370 375 380

Ala Lys Asn Asp Val Glu Thr Tyr Phe Gln Lys Gly Leu Arg Ala Gly

385 390 395 400

Val Ala Lys Glu Phe Gly Ser Gly Leu Ser Thr Val Leu Phe Ala Ser

405 410 415

Trp Arg Thr Arg Gln Tyr Ala Gly Phe Ser Ala Pro Leu Asn Ala Arg

420 425 430

Arg His Glu Glu Glu Ser Gly Tyr Thr Phe Ile Ala Arg Ala Pro Arg

435 440 445

Leu Ala Val Ser Gly Leu Val Pro Ser Leu Val Val Lys Tyr Asn Asp
450 455 460

Val Arg Ser Asn Ile Ala Trp Leu Tyr Ser His Glu Arg Ser Ser Val
465 470 475 480

Ser Val Lys Leu Glu Lys Val Phe
485

<210> 521

<211> 1470

<212> DNA

<213> P. pelagia SLAM 1

<400> 521

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atacacgccg ctgaccaaga caccaccctg cgtctcaatc agcacattga aggcaacgct 120

aacgcacagg agcaggagtt gctacaaggc gaactggatg accaaccgac cattaccctc 180

aatggcgaaa ccctcgccat cggcaacaat gccaatgatc tgggccgggc gctctatctt 240

tcgctcagcc atcagcaatg gcaggccgcc agcgccttcc tgctacgcta ccgcggcctg 300

cccaacgccg accccatgtt gctgcactac gccgacggcg tgctgcagcg cgttcgcggc 360

caactaggca atgccgagac acagttccgc gcactgctgc agcgccagcc cgactttctg 420

cccgggaaac tggagctggc ccgcgtgctg tttgaaaacc agcaggacca ggcagccgaa 480

accctgtttc ggcagatccg cgccggcctg cccgcggacg acgcccacac tctgggcgta 540

cgcaccagcg tcgagcgctt tctcgcagca ctggatcagc gtcaggactg gcaaggttca 600

atcaacctgg gcccgacctg ggtcgacaat ctgaaccaga gttcggaaag caatacttgc 660

ctgctggcca ccaacggcgg cacctgtatt gtgcgccgca ccctgcccga ggcgatcagc 720

gccacaggcc tcgattacga ggccaccctc aaccgtcgtg ttgcgctctc gggccatcac 780

gggctatacg cccgcgccct gctgtatggc tacagctacc gcaactacag cgagtacaac 840

gaaagcaccc tgatcgccaa tcttggctac agctaccgca gcgcgcgcaa tcagtattcg 900

ctggctccct ccttcgaaac caatcgcatc ggcaacgatg gcatgtattc cgcctggggc 960

gcccgcgccg aatggctgca tcagctcagc cgccgcagcg cggtaaagct ggaagcgacc 1020

taccgcgaca tgcgctatca ggacccgctg taccgctaca acaacggcgg caacagcgca 1080

ctctatgcca ctggctggca tgtgctttcg ccgcgctgga cgctgttcgg cggcctcgat 1140

ctgagcgaaa ggcgcaccga ggagccggtc tacggttatc agcagggcgg cgcgagattg 1200

ggtgccgcgc tgaccctgca aagcgggatt cgcgccagcc tgttcagctc gttccgacac 1260

cgcgaatacg ccgagtacag cccactgctc ggcgcccgtc gccgtgatgg cgagactaat 1320

cacacgctga tcgtcagctt gccgggacta gcttggcagg gtattacccc tagcctcagt 1380

ctcaagcaca ccgaagtgcg cagtagcgtc gactggcttt actcctacca gcgcacccag 1440

accagtttcc gtctggaaaa actgttttga 1470

<210> 522

<211> 489

<212> PRT

<213> P. pelagia SLAM 1

<400> 522

Met Thr Arg His Pro Leu His Leu Ile Leu Ile Met Leu Leu Leu Leu
1 5 10 15

Gly Ser Ala Ala Ile His Ala Ala Asp Gln Asp Thr Thr Leu Arg Leu
20 25 30

Asn Gln His Ile Glu Gly Asn Ala Asn Ala Gln Glu Gln Glu Leu Leu
35 40 45

Gln Gly Glu Leu Asp Asp Gln Pro Thr Ile Thr Leu Asn Gly Glu Thr
50 55 60

Leu Ala Ile Gly Asn Asn Ala Asn Asp Leu Gly Arg Ala Leu Tyr Leu
65 70 75 80

Ser Leu Ser His Gln Gln Trp Gln Ala Ala Ser Ala Phe Leu Leu Arg
85 90 95

Tyr Arg Gly Leu Pro Asn Ala Asp Pro Met Leu Leu His Tyr Ala Asp
100 105 110

Gly Val Leu Gln Arg Val Arg Gly Gln Leu Gly Asn Ala Glu Thr Gln
115 120 125

Phe Arg Ala Leu Leu Gln Arg Gln Pro Asp Phe Leu Pro Gly Lys Leu
130 135 140

Glu Leu Ala Arg Val Leu Phe Glu Asn Gln Gln Asp Gln Ala Ala Glu
145 150 155 160

Thr Leu Phe Arg Gln Ile Arg Ala Gly Leu Pro Ala Asp Asp Ala His
165 170 175

Thr Leu Gly Val Arg Thr Ser Val Glu Arg Phe Leu Ala Ala Leu Asp
180 185 190
Gln Arg Gln Asp Trp Gln Gly Ser Ile Asn Leu Gly Pro Thr Trp Val
195 200 205
Asp Asn Leu Asn Gln Ser Ser Glu Ser Asn Thr Cys Leu Leu Ala Thr
210 215 220

Asn Gly Gly Thr Cys Ile Val Arg Arg Thr Leu Pro Glu Ala Ile Ser
225 230 235 240
Ala Thr Gly Leu Asp Tyr Glu Ala Thr Leu Asn Arg Arg Val Ala Leu
245 250 255
Ser Gly His His Gly Leu Tyr Ala Arg Ala Leu Leu Tyr Gly Tyr Ser
260 265 270
Tyr Arg Asn Tyr Ser Glu Tyr Asn Glu Ser Thr Leu Ile Ala Asn Leu
275 280 285

Gly Tyr Ser Tyr Arg Ser Ala Arg Asn Gln Tyr Ser Leu Ala Pro Ser
290 295 300
Phe Glu Thr Asn Arg Ile Gly Asn Asp Gly Met Tyr Ser Ala Trp Gly
305 310 315 320
Ala Arg Ala Glu Trp Leu His Gln Leu Ser Arg Arg Ser Ala Val Lys
325 330 335
Leu Glu Ala Thr Tyr Arg Asp Met Arg Tyr Gln Asp Pro Leu Tyr Arg
340 345 350

Tyr Asn Asn Gly Gly Asn Ser Ala Leu Tyr Ala Thr Gly Trp His Val
355 360 365
Leu Ser Pro Arg Trp Thr Leu Phe Gly Gly Leu Asp Leu Ser Glu Arg
370 375 380
Arg Thr Glu Glu Pro Val Tyr Gly Tyr Gln Gln Gly Gly Ala Arg Leu
385 390 395 400
Gly Ala Ala Leu Thr Leu Gln Ser Gly Ile Arg Ala Ser Leu Phe Ser
405 410 415

Ser Phe Arg His Arg Glu Tyr Ala Glu Tyr Ser Pro Leu Leu Gly Ala

420 425 430

Arg Arg Arg Asp Gly Glu Thr Asn His Thr Leu Ile Val Ser Leu Pro

435 440 445

Gly Leu Ala Trp Gln Gly Ile Thr Pro Ser Leu Ser Leu Lys His Thr

450 455 460

Glu Val Arg Ser Ser Val Asp Trp Leu Tyr Ser Tyr Gln Arg Thr Gln

465 470 475 480

Thr Ser Phe Arg Leu Glu Lys Leu Phe

485

<210> 523

<211> 1482

<212> DNA

<213> P. pelagia SLAM 2

<400> 523

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gtctgggccg atgacgacga tacgcgcttt ctgcaggatc agacccgccg cagtatcgag 120

cagaaggccc aggccgagga ggcgctggca gcgccgcccg gtacgctgat gtatgaaggc 180

cagcgctacc aggtgacgag cacgctggag gcgctgacgc cagccatcta tgtggccatc 240

aataccaacc agtggacgca gttgccggac tttgtcgccc gttaccgtga gctgccgggg 300

caccggccag cgctggcgaa tatggcggaa agcctgctgg cgcgcttcga tgggaattat 360

ccgctggcgt tgcagcgcat ggagcaggcc agcggacagg agccggaaga tgcccgtatc 420

cagctggagc tggcgcgcct gtggtttgag gatcatcagg aaaagcgcgc agaggagggc 480

tttgccaggg tgctcaatat gggcttgccc gagcaggcgc agatgctggt gcagcagtac 540

cggcaggcaa tggatattcg cgcgagctgg catggcagcg cggcggtggg ggtcggctat 600

aacgataata tcaatcaggc caacggctat tacagttgcc tgagttcttt tttcggtatt 660

tgctttttcg agcggaaaat gccggatccg gttgagtccg ggctggcgag ctatgagttg 720

tcattgcagc gccgatataa cctggcgggt aatcacaacc tgcaactgcg gcccatgagt 780

tatggcacct attattccaa aaccaatccg tctgatacgg caaccatgca ggattacagc 840

accaacctgg cacaactgca gatgggttat cagtacctga atgcgcggaa cagtatcagc 900

gttatgccct atgcggagca ttactaccgc aaccgtgcca gcgaatatct ggcgcagggc 960

ctgcaactgg aatggcagca cacgttaagc cgcaaatggc aactgagcac cagcctggat 1020

accaagcgtt acgaatacac cagcaagggg cagcgcctgg gggcggatta tgaaatgcac 1080

cagtggggcg ttacggctgc ctatatgcct ggcgtcaata ccagcctgta cggcggtgtg 1140

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ggcggcgttt accacgcctt tgccggtcgg gctggctttt ttgtcaatgg catgggcatc 1260

taccgggaaa cccgcaacga cgcctacgac ttcttccttg gtgaacggcg ctacgacaag 1320

cagcaggtgt atatcctcag cgccggggcg aacggctgga agatcgctgg cctgaccccg 1380

gagctgcgcg tgcgccatag catcaaccac agcagcaatc tggattgggc gttcggcttc 1440

aagcagacgg agctaagctt gatgttgcgc aggaatttct ga 1482

<210> 524

<211> 493

<212> PRT

<213> P. pelagia SLAM 2

<400> 524

Met Pro Cys Arg Phe Arg Ala Val Trp Leu Leu Ser Leu Ala Cys Leu
1 5 10 15

Val Ala Pro Gly Val Trp Ala Asp Asp Asp Asp Thr Arg Phe Leu Gln
20 25 30

Asp Gln Thr Arg Arg Ser Ile Glu Gln Lys Ala Gln Ala Glu Glu Ala
35 40 45

Leu Ala Ala Pro Pro Gly Thr Leu Met Tyr Glu Gly Gln Arg Tyr Gln
50 55 60

Val Thr Ser Thr Leu Glu Ala Leu Thr Pro Ala Ile Tyr Val Ala Ile
65 70 75 80

Asn Thr Asn Gln Trp Thr Gln Leu Pro Asp Phe Val Ala Arg Tyr Arg
85 90 95

Glu Leu Pro Gly His Arg Pro Ala Leu Ala Asn Met Ala Glu Ser Leu
100 105 110

Leu Ala Arg Phe Asp Gly Asn Tyr Pro Leu Ala Leu Gln Arg Met Glu
115 120 125

Gln Ala Ser Gly Gln Glu Pro Glu Asp Ala Arg Ile Gln Leu Glu Leu
130 135 140

Ala Arg Leu Trp Phe Glu Asp His Gln Glu Lys Arg Ala Glu Glu Gly

145 150 155 160

Phe Ala Arg Val Leu Asn Met Gly Leu Pro Glu Gln Ala Gln Met Leu

165 170 175

Val Gln Gln Tyr Arg Gln Ala Met Asp Ile Arg Ala Ser Trp His Gly

180 185 190

Ser Ala Ala Val Gly Val Gly Tyr Asn Asp Asn Ile Asn Gln Ala Asn

195 200 205

Gly Tyr Tyr Ser Cys Leu Ser Ser Phe Phe Gly Ile Cys Phe Phe Glu

210 215 220

Arg Lys Met Pro Asp Pro Val Glu Ser Gly Leu Ala Ser Tyr Glu Leu

225 230 235 240

Ser Leu Gln Arg Arg Tyr Asn Leu Ala Gly Asn His Asn Leu Gln Leu

245 250 255

Arg Pro Met Ser Tyr Gly Thr Tyr Tyr Ser Lys Thr Asn Pro Ser Asp

260 265 270

Thr Ala Thr Met Gln Asp Tyr Ser Thr Asn Leu Ala Gln Leu Gln Met

275 280 285

Gly Tyr Gln Tyr Leu Asn Ala Arg Asn Ser Ile Ser Val Met Pro Tyr

290 295 300

Ala Glu His Tyr Tyr Arg Asn Arg Ala Ser Glu Tyr Leu Ala Gln Gly

305 310 315 320

Leu Gln Leu Glu Trp Gln His Thr Leu Ser Arg Lys Trp Gln Leu Ser

325 330 335

Thr Ser Leu Asp Thr Lys Arg Tyr Glu Tyr Thr Ser Lys Gly Gln Arg

340 345 350

Leu Gly Ala Asp Tyr Glu Met His Gln Trp Gly Val Thr Ala Ala Tyr

355 360 365

Met Pro Gly Val Asn Thr Ser Leu Tyr Gly Gly Val Thr Leu Thr Arg

370 375 380

Arg Lys Tyr Glu Val Asp Gln Ala Ser Ser Lys Glu Trp Gly Met Arg

385 390 395 400

Gly Gly Val Tyr His Ala Phe Ala Gly Arg Ala Gly Phe Phe Val Asn
405 410 415
Gly Met Gly Ile Tyr Arg Glu Thr Arg Asn Asp Ala Tyr Asp Phe Phe
420 425 430
Leu Gly Glu Arg Arg Tyr Asp Lys Gln Gln Val Tyr Ile Leu Ser Ala
435 440 445

Gly Ala Asn Gly Trp Lys Ile Ala Gly Leu Thr Pro Glu Leu Arg Val
450 455 460
Arg His Ser Ile Asn His Ser Ser Asn Leu Asp Trp Ala Phe Gly Phe
465 470 475 480
Lys Gln Thr Glu Leu Ser Leu Met Leu Arg Arg Asn Phe
485 490

<210> 525
<211> 1554
<212> DNA
<213> P. phenylpyruvicus SLAM 1
<400> 525
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gcagcagaaa aagagaccgc tgataagctt ctagaacttc aacgagaaga tataaatgtg 180
agtaaagctg caccaactgc taatttatct acgtctgaaa cacaaaatgc actaaacgaa 240
agagggcaga gatcaaaatc tcagcgctat aaccttgaag cacttaaagc cgatccaata 300
gcttttacta agttcttgaa tgctgctttg gctgctcaag atatggtcac agtcaaagaa 360
ctgttacctc attacaaagc actcaatgta aatgatccgc tgttgattaa gttcgctgat 420
gctctagtgt atcgaagtga agggcagcat aagaaagcca ttgctatcta caaagatatg 480

ttggcagaca acccagactt ccaccctgtg cgccttaatc tggctcaagc tttatatgca 540
gacaaacaat acagtgtggc tcatgaccag ctgcaaaagc tacgtggtgc cgatattcca 600
gagccagtta tggtcaatgt cgagcgttta attcagcgta ttgatgagca ggaacagtgg 660
cgatttaatg catcagtacg atatgtatat gatgataatt taaatgatgt tcctgatgtt 720
atgcctaatg gttacagggc tcctaaagag gagggtaaag ggattcaagt atcaggcagt 780
gccaataaac gttttaattt agataaaaac ttttatgccg aagtaggggg caacgcaacc 840

ctaaaaggct actgggataa tagtgaatac aatgactacc tgcttacagc ttcagcaggt 900

gtgggttatg atgatgccaa aaatgacgtt tcaatcagcc cttttgtaac caagcgtttt 960

tatagtgagg atccttatag cttgcgtaaa ggtgttaata tcagtggctc tcgctgggta 1020

aaacccaagc tcaaattgac tgctagtagc atgtattcaa acgaaacgtt cgatgatgaa 1080

agaaataaag caagagagac agatgcacta tttctaggat tgaatgcttt atatattaaa 1140

gatgccaaag aatactttta cggcggtata ggtaggtata ataatgacgt accagaacga 1200

agcttcttaa cctatgatag aaactcagtt aacgtaggtt ggggacgaga atggacccaa 1260

ggaatatcga ccatagcctc attgaactat ggggttaaaa aatatgataa tcctgcaggg 1320

gacttttatg gtgagggttt aaatttcttt tataatactt acggcggtga gcctggttca 1380

agccgtgaag ataagacaac ttcgttgggc ttacaagtat ggaagcgtga tttaacggta 1440

ttgggtctaa cccctcgtct agtatttgat tacgagaaga cttcaagtaa cttcaaatat 1500

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<210> 526

<211> 517

<212> PRT

<213> P. plecoglossicida SLAM 1

<400> 526

Met Ile Tyr Pro His Leu Leu Lys Thr Leu Thr Thr Ser Ala Val Leu
1 5 10 15

Phe Thr Ala Ala Tyr Ala Pro Leu Ile Tyr Ala Ala Asp Asp Pro Gln
20 25 30

Pro Leu Asp Asp Asn Asp Arg Tyr Ala Ala Glu Lys Glu Thr Ala Asp
35 40 45

Lys Leu Leu Glu Leu Gln Arg Glu Asp Ile Asn Val Ser Lys Ala Ala
50 55 60

Pro Thr Ala Asn Leu Ser Thr Ser Glu Thr Gln Asn Ala Leu Asn Glu
65 70 75 80

Arg Gly Gln Arg Ser Lys Ser Gln Arg Tyr Asn Leu Glu Ala Leu Lys
85 90 95

Ala Asp Pro Ile Ala Phe Thr Lys Phe Leu Asn Ala Ala Leu Ala Ala
100 105 110

Gln Asp Met Val Thr Val Lys Glu Leu Leu Pro His Tyr Lys Ala Leu
115 120 125
Asn Val Asn Asp Pro Leu Leu Ile Lys Phe Ala Asp Ala Leu Val Tyr
130 135 140

Arg Ser Glu Gly Gln His Lys Lys Ala Ile Ala Ile Tyr Lys Asp Met
145 150 155 160
Leu Ala Asp Asn Pro Asp Phe His Pro Val Arg Leu Asn Leu Ala Gln
165 170 175
Ala Leu Tyr Ala Asp Lys Gln Tyr Ser Val Ala His Asp Gln Leu Gln
180 185 190
Lys Leu Arg Gly Ala Asp Ile Pro Glu Pro Val Met Val Asn Val Glu
195 200 205

Arg Leu Ile Gln Arg Ile Asp Glu Gln Glu Gln Trp Arg Phe Asn Ala
210 215 220
Ser Val Arg Tyr Val Tyr Asp Asp Asn Leu Asn Asp Val Pro Asp Val
225 230 235 240
Met Pro Asn Gly Tyr Arg Ala Pro Lys Glu Glu Gly Lys Gly Ile Gln
245 250 255
Val Ser Gly Ser Ala Asn Lys Arg Phe Asn Leu Asp Lys Asn Phe Tyr
260 265 270

Ala Glu Val Gly Gly Asn Ala Thr Leu Lys Gly Tyr Trp Asp Asn Ser
275 280 285
Glu Tyr Asn Asp Tyr Leu Leu Thr Ala Ser Ala Gly Val Gly Tyr Asp
290 295 300
Asp Ala Lys Asn Asp Val Ser Ile Ser Pro Phe Val Thr Lys Arg Phe
305 310 315 320
Tyr Ser Glu Asp Pro Tyr Ser Leu Arg Lys Gly Val Asn Ile Ser Gly
325 330 335

Ser Arg Trp Val Lys Pro Lys Leu Lys Leu Thr Ala Ser Ser Met Tyr
340 345 350
Ser Asn Glu Thr Phe Asp Asp Glu Arg Asn Lys Ala Arg Glu Thr Asp

355 360 365

Ala Leu Phe Leu Gly Leu Asn Ala Leu Tyr Ile Lys Asp Ala Lys Glu

370 375 380

Tyr Phe Tyr Gly Gly Ile Gly Arg Tyr Asn Asn Asp Val Pro Glu Arg

385 390 395 400

Ser Phe Leu Thr Tyr Asp Arg Asn Ser Val Asn Val Gly Trp Gly Arg

405 410 415

Glu Trp Thr Gln Gly Ile Ser Thr Ile Ala Ser Leu Asn Tyr Gly Val

420 425 430

Lys Lys Tyr Asp Asn Pro Ala Gly Asp Phe Tyr Gly Glu Gly Leu Asn

435 440 445

Phe Phe Tyr Asn Thr Tyr Gly Gly Glu Pro Gly Ser Ser Arg Glu Asp

450 455 460

Lys Thr Thr Ser Leu Gly Leu Gln Val Trp Lys Arg Asp Leu Thr Val

465 470 475 480

Leu Gly Leu Thr Pro Arg Leu Val Phe Asp Tyr Glu Lys Thr Ser Ser

485 490 495

Asn Phe Lys Tyr Tyr Asp Asp Arg Asp Asp Lys Thr Ala Thr Ile Leu

500 505 510

Leu Thr Lys Ser Phe

515

<210> 527

<211> 1491

<212> DNA

<213> P. plecoglossicida SLAM 1

<400> 527

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caggccatcg aacagcgtgc agtctcacaa gagcgtgcac tgctggaaag cagcgtgcca 180

accggcccgg atgcgccgct attggagtta gatggccaat actatggcat cggcaatacc 240

gtagatgaac tcggcgcagc ggtttacctg tccatcgagc gcaaacaatg gcctgctgct 300

agcgactatc tggcccgtta caccgctcta cctgaacatg accctatgct cattgcctat 360

gcgcatgggg cgctggcccg cacaaaaggc aacctcgaac tggcagagtc ttactaccgc 420

gaactgttga caatgcagtc tgactttcta ccgggccaac ttgaattagc ccgtgtgctg 480
tttgagagcc gcaaggatcg cgagtccact tcagccttcc aacagattcg agcagagctc 540
gatgcttcgg atgcccgggc aatgggcctc ggcagatccg tcgacagctt cctcgaagtg 600
ctggatgagc gcgaacggtg gcatggctcg ctcgcggtgg gcccgatatg ggccagtaat 660
ctgaaccagt cttcagaagg cgtccatacg ctgtactcat ttttcggccc cttgacttac 720
aagcagccca aagccgtatc tgcacagggc attgactatg aagccacgtt gagcaagcgt 780
ctgcccgtca gcaaccacca tggcatttat cttcgctcgc tgctgtacgg ccagcactac 840

aaaaacacaa gcctgtataa cgtgagcacg ctgaccaaca acatcggcta cagctaccac 900
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accttgtaca aggcctgggg gctccacggc gaatggcagc gcgtactgtc gagcacgcgc 1020
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ctgaacggta atatgagcac actcttcgcc acactttggc aagcgctacc ttaccagtgg 1140
atgctgttcg gaggcgggga tcttgctgtc cgcaataccc agtatcgaac caacgattac 1200
ttccagaagg ggctgcgcct cggcgtcgcc aaagaattcg acatgggcgt cagcgcggtg 1260

ttgttcacgt cctaccggca gcgccagtat gacggctaca acgcttggtt gggggaccgg 1320
cgcaatgaag atgagcaaag ctatacgctc tcggtgcgcg caccccgctt agcaatatac 1380
ggtgcggtgc ccagccttac cgcgaaatat taccaaaaca aaagcaatat cgactgggcc 1440
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<210> 528
<211> 496
<212> PRT
<213> P. plecoglossicida SLAM 1
<400> 528

Met Pro Arg Arg Asn Ser Thr His Leu Phe His Leu Leu Phe Thr Phe
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Pro Leu Leu Val Gly Ile Asn Thr Leu Pro Leu Ala Lys Ala Ala Asn
20 25 30

Gln Asp Thr Glu Leu Arg Leu Asn Gln Ala Ile Glu Gln Arg Ala Val
35 40 45

Ser Gln Glu Arg Ala Leu Leu Glu Ser Ser Val Pro Thr Gly Pro Asp

50 55 60

Ala Pro Leu Leu Glu Leu Asp Gly Gln Tyr Tyr Gly Ile Gly Asn Thr
65 70 75 80

Val Asp Glu Leu Gly Ala Ala Val Tyr Leu Ser Ile Glu Arg Lys Gln
85 90 95

Trp Pro Ala Ala Ser Asp Tyr Leu Ala Arg Tyr Thr Ala Leu Pro Glu
100 105 110

His Asp Pro Met Leu Ile Ala Tyr Ala His Gly Ala Leu Ala Arg Thr
115 120 125

Lys Gly Asn Leu Glu Leu Ala Glu Ser Tyr Tyr Arg Glu Leu Leu Thr
130 135 140

Met Gln Ser Asp Phe Leu Pro Gly Gln Leu Glu Leu Ala Arg Val Leu
145 150 155 160

Phe Glu Ser Arg Lys Asp Arg Glu Ser Thr Ser Ala Phe Gln Gln Ile
165 170 175

Arg Ala Glu Leu Asp Ala Ser Asp Ala Arg Ala Met Gly Leu Gly Arg
180 185 190

Ser Val Asp Ser Phe Leu Glu Val Leu Asp Glu Arg Glu Arg Trp His
195 200 205

Gly Ser Leu Ala Val Gly Pro Ile Trp Ala Ser Asn Leu Asn Gln Ser
210 215 220

Ser Glu Gly Val His Thr Leu Tyr Ser Phe Phe Gly Pro Leu Thr Tyr
225 230 235 240

Lys Gln Pro Lys Ala Val Ser Ala Gln Gly Ile Asp Tyr Glu Ala Thr
245 250 255

Leu Ser Lys Arg Leu Pro Val Ser Asn His His Gly Ile Tyr Leu Arg
260 265 270

Ser Leu Leu Tyr Gly Gln His Tyr Lys Asn Thr Ser Leu Tyr Asn Val
275 280 285

Ser Thr Leu Thr Asn Asn Ile Gly Tyr Ser Tyr His Gly Pro Arg Asp
290 295 300

Gln Tyr Ala Phe Gly Pro Thr Phe Glu Leu Asn Thr His Gly Asp Glu
305 310 315 320
Thr Leu Tyr Lys Ala Trp Gly Leu His Gly Glu Trp Gln Arg Val Leu
325 330 335

Ser Ser Thr Arg Met Phe Lys Leu Glu Gly Asp Tyr Lys Lys Ile Ala
340 345 350
Phe Gln Gln Thr Val His Asp Tyr Leu Asn Gly Asn Met Ser Thr Leu
355 360 365
Phe Ala Thr Leu Trp Gln Ala Leu Pro Tyr Gln Trp Met Leu Phe Gly
370 375 380
Gly Gly Asp Leu Ala Val Arg Asn Thr Gln Tyr Arg Thr Asn Asp Tyr
385 390 395 400

Phe Gln Lys Gly Leu Arg Leu Gly Val Ala Lys Glu Phe Asp Met Gly
405 410 415
Val Ser Ala Val Leu Phe Thr Ser Tyr Arg Gln Arg Gln Tyr Asp Gly
420 425 430
Tyr Asn Ala Trp Leu Gly Asp Arg Arg Asn Glu Asp Glu Gln Ser Tyr
435 440 445
Thr Leu Ser Val Arg Ala Pro Arg Leu Ala Ile Tyr Gly Ala Val Pro
450 455 460

Ser Leu Thr Ala Lys Tyr Tyr Gln Asn Lys Ser Asn Ile Asp Trp Ala
465 470 475 480
Tyr Ser Tyr Asp Asn Asn Ser Val Ser Leu Lys Leu Glu Lys Gln Phe
485 490 495

<210> 529
<211> 1431
<212> DNA
<213> P. pneumotropica SLAM 1
<400> 529

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gcagaagtgg ctcaatctaa aagtgatggg ctggacgatc gcattaatat ggcaaaacca 120

aaacttccac aaacagaggc acaaatttct acaccaaaga gagaaaatat ttcaatgagc 180

agtgccgaac tacagcagca tcccaattta atcattcgtg gattagttcc agccgtctta 240

caaaataatg cgaaagccgt agaaatttta ctcccgtttt ataaaaactt acctaatcag 300

gatcccactt tattagcttg gtctgaatca attctagcac gtcatcaagg aaatttttct 360

ctggcagccg agcgttatcg aactttattt agtcagcatt cgcatatcat cgccttacgt 420

tatcagttag cacaagcctt atttttaaac aatgataatg aagcagcaaa agatcaattt 480

caaaaattac gtgcggaaga tatctctccg gaaagcattc aaattattga tcaatattta 540

tctgccttaa acaaacgtaa tcaatggaaa gtaaatggcg ggatcagtta tttaaatgaa 600

tcaaacatca ataacgcccc taaatccggc acaaaaattg gtaattggaa cgcttgggaa 660

aaagaaagtg cacaaggttt ttcctactat ttgaatggag agaaaaaatg gtcttgggcg 720

aataatgtat tcacaaaatt gcaacttgaa gggcaaggtc gatatttttg gaataacaga 780

aaatacaatg agttaaatct tcgcgtagga gcaggtttag gttatcaaac tgcacgtttt 840

gaaaacttac tcacccccct tacagaaaaa cgttggtatg gcggtggctc atcgggtggt 900

gatgcattaa aacaatatgc taaaaattcc ggtatacgat tagaaacaaa ctattggtta 960

aatgaaaaat ggcaaatttc gaccgcactt gagtatggtg aacaacgtta taactggcga 1020

aaacatttaa atggcaataa ttacctttgg tcaaacacct tactttatac tccacaaagc 1080

gggcaatact ggcttatagg catagattat aaccgtgaaa atacacgaga ccatgataac 1140

gcttatcaac gcaaaaatat tcgtctcgct tggggacaag aatggtcatt aggtatttcc 1200

tcccgtttaa atcttgctta tgcaaggcga acatataagg atattgattt ctttcagatt 1260

cgtcagaaaa ataatgagta ttttactgca ttgaccttat ggcatcgcga tttctatttt 1320

ttggggatta ctccaaaact gacgtggact tatcaaaaaa taaaaagcaa tcatcctttt 1380

tatcgttatg ataaaaaccg catttattta gaaatgagca aaatatttta a 1431

<210> 530

<211> 464

<212> PRT

<213> P. pneumotropica SLAM 1

<400> 530

Met Leu Phe Ala Ile Asn Ala Ser Ala Glu Val Ala Gln Ser Lys Ser

1 5 10 15

Asp Gly Leu Asp Asp Arg Ile Asn Met Ala Lys Pro Lys Leu Pro Gln

20 25 30

Thr Glu Ala Gln Ile Ser Thr Pro Lys Arg Glu Asn Ile Ser Met Ser

35 40 45

Ser Ala Glu Leu Gln Gln His Pro Asn Leu Ile Ile Arg Gly Leu Val

50 55 60

Pro Ala Val Leu Gln Asn Asn Ala Lys Ala Val Glu Ile Leu Leu Pro

65 70 75 80

Phe Tyr Lys Asn Leu Pro Asn Gln Asp Pro Thr Leu Leu Ala Trp Ser

85 90 95

Glu Ser Ile Leu Ala Arg His Gln Gly Asn Phe Ser Leu Ala Ala Glu

100 105 110

Arg Tyr Arg Thr Leu Phe Ser Gln His Ser His Ile Ile Ala Leu Arg

115 120 125

Tyr Gln Leu Ala Gln Ala Leu Phe Leu Asn Asn Asp Asn Glu Ala Ala

130 135 140

Lys Asp Gln Phe Gln Lys Leu Arg Ala Glu Asp Ile Ser Pro Glu Ser

145 150 155 160

Ile Gln Ile Ile Asp Gln Tyr Leu Ser Ala Leu Asn Lys Arg Asn Gln

165 170 175

Trp Lys Val Asn Gly Gly Ile Ser Tyr Leu Asn Glu Ser Asn Ile Asn

180 185 190

Asn Ala Pro Lys Ser Gly Thr Lys Ile Gly Asn Trp Asn Ala Trp Glu

195 200 205

Lys Glu Ser Ala Gln Gly Phe Ser Tyr Tyr Leu Asn Gly Glu Lys Lys

210 215 220

Trp Ser Trp Ala Asn Asn Val Phe Thr Lys Leu Gln Leu Glu Gly Gln

225 230 235 240

Gly Arg Tyr Phe Trp Asn Asn Arg Lys Tyr Asn Glu Leu Asn Leu Arg

245 250 255

Val Gly Ala Gly Leu Gly Tyr Gln Thr Ala Arg Phe Glu Asn Leu Leu

260 265 270

Thr Pro Phe Thr Glu Lys Arg Trp Tyr Gly Gly Gly Ser Ser Gly Gly

275 280 285

Asp Ala Leu Lys Gln Tyr Ala Lys Asn Ser Gly Ile Arg Leu Glu Thr

290 295 300

Asn Tyr Trp Leu Asn Glu Lys Trp Gln Ile Ser Thr Ala Leu Glu Tyr

305 310 315 320

Gly Glu Gln Arg Tyr Asn Trp Arg Lys His Leu Asn Gly Asn Asn Tyr

325 330 335

Leu Trp Ser Asn Thr Leu Leu Tyr Thr Pro Gln Ser Gly Gln Tyr Trp

340 345 350

Leu Ile Gly Ile Asp Tyr Asn Arg Glu Asn Thr Arg Asp His Asp Asn

355 360 365

Ala Tyr Gln Arg Lys Asn Ile Arg Leu Ala Trp Gly Gln Glu Trp Ser

370 375 380

Leu Gly Ile Ser Ser Arg Leu Asn Leu Ala Tyr Ala Arg Arg Thr Tyr

385 390 395 400

Lys Asp Ile Asp Phe Phe Gln Ile Arg Gln Lys Asn Asn Glu Tyr Phe

405 410 415

Thr Ala Leu Thr Leu Trp His Arg Asp Phe Tyr Phe Leu Gly Ile Thr

420 425 430

Pro Lys Leu Thr Trp Thr Tyr Gln Lys Ile Lys Ser Asn His Pro Phe

435 440 445

Tyr Arg Tyr Asp Lys Asn Arg Ile Tyr Leu Glu Met Ser Lys Ile Phe

450 455 460

<210> 531

<211> 1458

<212> DNA

<213> P. pneumotropica SLAM 2

<400> 531

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tcggcaagtg ccaatatgca agagcaggac gcactcagat tgtggcgact gtatagtcag 120

caatccgccc aacaacggca ggaacaaaat attgatagtg aacaaccgac taacgaaatc 180

accctagagg gcgaatcttt tcaggttgaa aacaacgtgg aatctgtggg gcaagcgctc 240

tacatcgcat taaatcgcca actatggcga tatgccaagc aatttttggc tcaatatgaa 300

aaatttcccg atcacaaagt ccaattagct tggtttgcca aaggggcatt agccagagaa 360

caaggcgatt tacccgaagc ggaacgttat taccgcaaat tattacaaag cgaaccggat 420

ttcttgcgtg gtcaattgga tttagcccga attttgtttg aagacaaaaa aaacacagaa 480

tcgaccgcac tttttcgcca actttcacac cacccttac cggatggcgt attattaacc 540

attcaggatt accaacaagc gctcaaagaa cgggaaaatt ggaatagctc gctcacttta 600

ggttatttgt atcataaaaa tttgaaccaa tcttcgcaac gccagctatg cctattggaa 660

aaagaggggc aatgttttat taaccgccgt tcgcctgatg ccataaatac ttatggttgg 720

cgttatgatt tcactgctca acgacgtatt tctttacaga atcatcatgg tttggaattt 780

tattttaacg gctacggaca attttatccc cgtcatcacg actatgatga gaataccgtt 840

aaactttatg gtggatacag ctttcgcaat gctaaaacag agatcactgc tgcaccgata 900

ctggaatata gcacctttgg tgatcatcgt tattatcacg gttggggaac tcatcttgag 960

tggacgcaaa acatttcacc acgccacagt tggaataccc aatttgaata taaaaaactg 1020

cgttacagca agcattacag tgcatttgat aaaactgatg tcagtacatt attcggtact 1080

tggtattatc tacttactcc gcaaacaacc ttatttgccg gcgcagattt gtcatatcga 1140

catacaccgg atgatacgca atcctaccgt atgttaggtg cccgtttggg attaaattat 1200

cagtttgatt ttggtttaaa tgcaacggtt ctcgcattat ggcgaaatta taattaccaa 1260

gtctatcacg cggctcttga gctgaaacgt aaagatagac aacaaattta tttagccata 1320

ttaaaaatac caagctggaa ttttaaagac atcacgcctt atctactgct gaaacacacc 1380

cgtaataaga gtaatgcaga ttatgtttat agttataaac aaagtgaaat acagctgaat 1440

tttgagtgga gattttaa 1458

<210> 532

<211> 485

<212> PRT

<213> P. pneumotropica SLAM 2

<400> 532

Met Lys Lys Tyr Tyr Ser Ile Leu Val Gly Ile Leu Phe Cys Val Gly

1 5 10 15

Gly Ser Ser Val Ser Ala Ser Ala Asn Met Gln Glu Gln Asp Ala Leu

20 25 30

Arg Leu Trp Arg Leu Tyr Ser Gln Gln Ser Ala Gln Gln Arg Gln Glu

35 40 45

Gln Asn Ile Asp Ser Glu Gln Pro Thr Asn Glu Ile Thr Leu Glu Gly
50 55 60
Glu Ser Phe Gln Val Glu Asn Asn Val Glu Ser Val Gly Gln Ala Leu
65 70 75 80
Tyr Ile Ala Leu Asn Arg Gln Leu Trp Arg Tyr Ala Lys Gln Phe Leu
85 90 95
Ala Gln Tyr Glu Lys Phe Pro Asp His Lys Val Gln Leu Ala Trp Phe
100 105 110

Ala Lys Gly Ala Leu Ala Arg Glu Gln Gly Asp Leu Pro Glu Ala Glu
115 120 125
Arg Tyr Tyr Arg Lys Leu Leu Gln Ser Glu Pro Asp Phe Leu Arg Gly
130 135 140
Gln Leu Asp Leu Ala Arg Ile Leu Phe Glu Asp Lys Lys Asn Thr Glu
145 150 155 160
Ser Thr Ala Leu Phe Arg Gln Leu Ser His His Pro Leu Pro Asp Gly
165 170 175

Val Leu Leu Thr Ile Gln Asp Tyr Gln Gln Ala Leu Lys Glu Arg Glu
180 185 190
Asn Trp Asn Ser Ser Leu Thr Leu Gly Tyr Leu Tyr His Lys Asn Leu
195 200 205
Asn Gln Ser Ser Gln Arg Gln Leu Cys Leu Leu Glu Lys Glu Gly Gln
210 215 220
Cys Phe Ile Asn Arg Arg Ser Pro Asp Ala Ile Asn Thr Tyr Gly Trp
225 230 235 240

Arg Tyr Asp Phe Thr Ala Gln Arg Arg Ile Ser Leu Gln Asn His His
245 250 255
Gly Leu Glu Phe Tyr Phe Asn Gly Tyr Gly Gln Phe Tyr Pro Arg His
260 265 270
His Asp Tyr Asp Glu Asn Thr Val Lys Leu Tyr Gly Gly Tyr Ser Phe
275 280 285

Arg Asn Ala Lys Thr Glu Ile Thr Ala Ala Pro Ile Leu Glu Tyr Ser
290 295 300

Thr Phe Gly Asp His Arg Tyr Tyr His Gly Trp Gly Thr His Leu Glu
305 310 315 320
Trp Thr Gln Asn Ile Ser Pro Arg His Ser Trp Asn Thr Gln Phe Glu
325 330 335
Tyr Lys Lys Leu Arg Tyr Ser Lys His Tyr Ser Ala Phe Asp Lys Thr
340 345 350
Asp Val Ser Thr Leu Phe Gly Thr Trp Tyr Tyr Leu Leu Thr Pro Gln
355 360 365

Thr Thr Leu Phe Ala Gly Ala Asp Leu Ser Tyr Arg His Thr Pro Asp
370 375 380
Asp Thr Gln Ser Tyr Arg Met Leu Gly Ala Arg Leu Gly Leu Asn Tyr
385 390 395 400
Gln Phe Asp Phe Gly Leu Asn Ala Thr Val Leu Ala Leu Trp Arg Asn
405 410 415
Tyr Asn Tyr Gln Val Tyr His Ala Ala Leu Glu Leu Lys Arg Lys Asp
420 425 430

Arg Gln Gln Ile Tyr Leu Ala Ile Leu Lys Ile Pro Ser Trp Asn Phe
435 440 445
Lys Asp Ile Thr Pro Tyr Leu Leu Leu Lys His Thr Arg Asn Lys Ser
450 455 460
Asn Ala Asp Tyr Val Tyr Ser Tyr Lys Gln Ser Glu Ile Gln Leu Asn
465 470 475 480
Phe Glu Trp Arg Phe
485

<210> 533
<211> 1365
<212> DNA
<213> P. pnomenusa SLAM 1
<400
> 533

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actgccgctg tcggcgggcc gcctgcctcg ccgtccgacg cgggaaacgc cgcgatctcc 120

gaggctcgcg cgctgatgcg cgccaaatcg cccgcacggg cctacgcgtt gctggcgccg 180

ctggagagcc gtctggcggg cgacggcgaa tatgactacc tgctgggtat cgctgccgcg 240

gacagtcatc acctcgaggt tgccgagcgc gcactcaaac gcagcgtggc ggcccgtcct 300

ggcgatggtc cggctcacct cgaactggcg cgcacctatt ttctgctcgg gcagcgcgat 360

aacgcgagac gcgagttcga gggggtggcc gcgggcgagg tccccgaggg tgtgcgtccg 420

gtcatcgagg cctacctgaa cgcgatcaat gcgcctgcgg gcgcgcgtac gtcctggacc 480

ggctacgtgc agggcaacgt cgggcacgat accaatgcca acaacgcgac gacgaattcc 540

gcgatcgcga ttccggcact gggcggcttg atgttcgtcc tcgacggcgc ctcgcgcgga 600

acgccggcga acttcggcga catcagtggc gggctaggcg tgcgacatgc cgtgacggac 660

aacctggtgg tgtcggcatc gggagaggtc gatgtgcgca cctacgccga taaggcgcgc 720

gccttcgatc agggcagcta tttgcttcaa ctgggcgcga actggttgtc cgggccgaac 780

aatttcggac ttcagtacgc caaccagcac atgtgggtcg attcggagag ctaccgcaat 840

ctcaacggct tcaccgcgca gtggacgcgc gatcttggca gcgaccttca ggtggcgacg 900

ttcgcgcagt acacgccgat tcgctacatg ggcacgaatg cgcgcgacgt gaatcgcgcc 960

atcgttggcg cgtcgatcgt caagggattc tcgtcggtct atggcgcgcc ggtcgcttat 1020

gcctcgctgt acgcggggcg agaaaagccc aaggacgact tgtccgccgc gttcggcaat 1080

cggctgtggg gcgcgcgact cggtggcgaa tggcacgtga tgccggatca actgctgttc 1140

gccagcgcta gcatcgagcg acgcaactac gacacgctcg acagtttgtt tctcgtggag 1200

cgcagcgacc gtcagcttga tgtgagggct ggctattcgt acttcgtgac gaaggcgttt 1260

tcgatcacgc cgcaattcag cttcactcgg aatggctcca gccagccgct gtaccagtac 1320

caccgaagtg tctacgaggt cgtggctcgc tatgacttcc gctga 1365

<210> 534

<211> 453

<212> PRT

<213> P. pnomenusa SLAM 1

<400> 534

Met Leu Gly Ala Val Leu Thr His Gly Ala Tyr Ala Ala Gly Thr Leu

1 5 10 15

Val Ala Asp Gly Thr Ala Ala Val Gly Gly Pro Pro Ala Ser Pro Ser

20 25 30

Asp Ala Gly Asn Ala Ala Ile Ser Glu Ala Arg Ala Leu Met Arg Ala

35 40 45

Lys Ser Pro Ala Arg Ala Tyr Ala Leu Leu Ala Pro Leu Glu Ser Arg

50 55 60

Leu Ala Gly Asp Gly Glu Tyr Asp Tyr Leu Leu Gly Ile Ala Ala Ala

65 70 75 80

Asp Ser His His Leu Glu Val Ala Glu Arg Ala Leu Lys Arg Ser Val

85 90 95

Ala Ala Arg Pro Gly Asp Gly Pro Ala His Leu Glu Leu Ala Arg Thr

100 105 110

Tyr Phe Leu Leu Gly Gln Arg Asp Asn Ala Arg Arg Glu Phe Glu Gly

115 120 125

Val Ala Ala Gly Glu Val Pro Glu Gly Val Arg Pro Val Ile Glu Ala

130 135 140

Tyr Leu Asn Ala Ile Asn Ala Pro Ala Gly Ala Arg Thr Ser Trp Thr

145 150 155 160

Gly Tyr Val Gln Gly Asn Val Gly His Asp Thr Asn Ala Asn Asn Ala

165 170 175

Thr Thr Asn Ser Ala Ile Ala Ile Pro Ala Leu Gly Gly Leu Met Phe

180 185 190

Val Leu Asp Gly Ala Ser Arg Gly Thr Pro Ala Asn Phe Gly Asp Ile

195 200 205

Ser Gly Gly Leu Gly Val Arg His Ala Val Thr Asp Asn Leu Val Val

210 215 220

Ser Ala Ser Gly Glu Val Asp Val Arg Thr Tyr Ala Asp Lys Ala Arg

225 230 235 240

Ala Phe Asp Gln Gly Ser Tyr Leu Leu Gln Leu Gly Ala Asn Trp Leu

245 250 255

Ser Gly Pro Asn Asn Phe Gly Leu Gln Tyr Ala Asn Gln His Met Trp

260 265 270

Val Asp Ser Glu Ser Tyr Arg Asn Leu Asn Gly Phe Thr Ala Gln Trp

275 280 285

Thr Arg Asp Leu Gly Ser Asp Leu Gln Val Ala Thr Phe Ala Gln Tyr

290 295 300

Thr Pro Ile Arg Tyr Met Gly Thr Asn Ala Arg Asp Val Asn Arg Ala

305 310 315 320

Ile Val Gly Ala Ser Ile Val Lys Gly Phe Ser Ser Val Tyr Gly Ala

325 330 335

Pro Val Ala Tyr Ala Ser Leu Tyr Ala Gly Arg Glu Lys Pro Lys Asp

340 345 350

Asp Leu Ser Ala Ala Phe Gly Asn Arg Leu Trp Gly Ala Arg Leu Gly

355 360 365

Gly Glu Trp His Val Met Pro Asp Gln Leu Leu Phe Ala Ser Ala Ser

370 375 380

Ile Glu Arg Arg Asn Tyr Asp Thr Leu Asp Ser Leu Phe Leu Val Glu

385 390 395 400

Arg Ser Asp Arg Gln Leu Asp Val Arg Ala Gly Tyr Ser Tyr Phe Val

405 410 415

Thr Lys Ala Phe Ser Ile Thr Pro Gln Phe Ser Phe Thr Arg Asn Gly

420 425 430

Ser Ser Gln Pro Leu Tyr Gln Tyr His Arg Ser Val Tyr Glu Val Val

435 440 445

Ala Arg Tyr Asp Phe

450

<210> 535

<211> 1473

<212> DNA

<213> P. putida SLAM 1

<400> 535

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ctcactgctt tggccgacca ggacaccaac ctgcgcctga accagagcat tgaataccgc 120

gccaaccgtc aggagcgaga gctgctcaag gacgaaatcg ctggcacgac gctggtcatc 180

gatggccaga cgtaccgggt agagaacaac cttgatgacc tgggccgtgc cctttatgtt 240

tcggtgcagc gccagcaatg ggcggctgtg actgcattcc gcgcccgcta cgtcgcgctg 300

ccaggccacg accggatgct gctggcctac gccgatggcg cattggctcg ctcgcgtggc 360

gacttggagc aagccgaggc gcactaccgc cagttgttga cgttgcaggg cgactttctc 420

cccggccagc tcgaactggc ccgggtgctg ttcgaaaacc gcaaggaccg cgagtcggct 480

gaggctttcc gtcagatcag ccaaagcctg ggcccagccg atgcgcgcaa ccagggcctg 540

ggcaataccg tcgacagttt catcgaggcg ctggaccacc gcgaaagctg gcaaggctcg 600

cttgccatcg gcccgacctg gaacgacaac ctcaaccagt cctcggagag caccacccac 660

taccgcctgg aaaccagtga cggggtgtac ctggtcgagc gcaagatgcc caaggcagtg 720

tcggcacaag gcatcgacta cgaagccaca ctgaacaagc gcgtagcgct gtccggccac 780

catggcgtat tcggccgggc gctcgcctac gggcaggctt acgacaaaga gagcaagtac 840

aacgaagaca ccttcatcgg taacaccggc tacagctatc aggacgggcg caaccagtac 900

agcctgggcc cacagttcga atacaaccgc attggcagtg acccgatgta ctcagcctgg 960

ggcctgcgcg gtgaatggat gcacaacctt tcggccacgc gcatgctcaa gctggaaggc 1020

gaatacaagg acatggccta ccgccgccag gccgcggaca cctatgacgg cagcgcagcc 1080

tccgtgtacg ccactttgtg gcaagccctg ccacagcagt gggtgctgtt cggcggcttc 1140

gacctcaccg accgcaacac ccgcgatgct accgaagcct acttccagag gggcctgcgc 1200

ctgggcgttg ccaaggactt cgacatcggc ctgagcactg tgctgttcgc ctcctggcgc 1260

acccgccagt acgacgccta cagtgccttg ctcgatgacc ggcgtcatga agaggagcag 1320

ggctatacct ttatcgtgcg cgcaccgggc ctggccttcc acgacctggt acccagcctg 1380

accttcaagt acaacaaggt gaacagcaac gtcgactggc tgtacagctg ggagcgcaac 1440

agcgtcagcc tcaagctgga gaagcagttc tga 1473

<210> 536

<211> 490

<212> PRT

<213> P. putida SLAM 1

<400> 536

Met Pro Gln Pro Ser Arg Leu His Tyr Val Leu Leu Ser Leu Pro

1 5 10 15

Leu Ser Phe Pro Leu Thr Ala Leu Ala Asp Gln Asp Thr Asn Leu Arg

20 25 30

Leu Asn Gln Ser Ile Glu Tyr Arg Ala Asn Arg Gln Glu Arg Glu Leu

35 40 45

Leu Lys Asp Glu Ile Ala Gly Thr Thr Leu Val Ile Asp Gly Gln Thr
50 55 60
Tyr Arg Val Glu Asn Asn Leu Asp Asp Leu Gly Arg Ala Leu Tyr Val
65 70 75 80
Ser Val Gln Arg Gln Gln Trp Ala Ala Val Thr Ala Phe Arg Ala Arg
85 90 95
Tyr Val Ala Leu Pro Gly His Asp Arg Met Leu Leu Ala Tyr Ala Asp
100 105 110

Gly Ala Leu Ala Arg Ser Arg Gly Asp Leu Glu Gln Ala Glu Ala His
115 120 125
Tyr Arg Gln Leu Leu Thr Leu Gln Gly Asp Phe Leu Pro Gly Gln Leu
130 135 140
Glu Leu Ala Arg Val Leu Phe Glu Asn Arg Lys Asp Arg Glu Ser Ala
145 150 155 160
Glu Ala Phe Arg Gln Ile Ser Gln Ser Leu Gly Pro Ala Asp Ala Arg
165 170 175

Asn Gln Gly Leu Gly Asn Thr Val Asp Ser Phe Ile Glu Ala Leu Asp
180 185 190
His Arg Glu Ser Trp Gln Gly Ser Leu Ala Ile Gly Pro Thr Trp Asn
195 200 205
Asp Asn Leu Asn Gln Ser Ser Glu Ser Thr Thr His Tyr Arg Leu Glu
210 215 220
Thr Ser Asp Gly Val Tyr Leu Val Glu Arg Lys Met Pro Lys Ala Val
225 230 235 240

Ser Ala Gln Gly Ile Asp Tyr Glu Ala Thr Leu Asn Lys Arg Val Ala
245 250 255
Leu Ser Gly His His Gly Val Phe Gly Arg Ala Leu Ala Tyr Gly Gln
260 265 270
Ala Tyr Asp Lys Glu Ser Lys Tyr Asn Glu Asp Thr Phe Ile Gly Asn
275 280 285

Thr Gly Tyr Ser Tyr Gln Asp Gly Arg Asn Gln Tyr Ser Leu Gly Pro
290 295 300

Gln Phe Glu Tyr Asn Arg Ile Gly Ser Asp Pro Met Tyr Ser Ala Trp
305 310 315 320
Gly Leu Arg Gly Glu Trp Met His Asn Leu Ser Ala Thr Arg Met Leu
325 330 335
Lys Leu Glu Gly Glu Tyr Lys Asp Met Ala Tyr Arg Arg Gln Ala Ala
340 345 350
Asp Thr Tyr Asp Gly Ser Ala Ala Ser Val Tyr Ala Thr Leu Trp Gln
355 360 365

Ala Leu Pro Gln Gln Trp Val Leu Phe Gly Gly Phe Asp Leu Thr Asp
370 375 380
Arg Asn Thr Arg Asp Ala Thr Glu Ala Tyr Phe Gln Arg Gly Leu Arg
385 390 395 400
Leu Gly Val Ala Lys Asp Phe Asp Ile Gly Leu Ser Thr Val Leu Phe
405 410 415
Ala Ser Trp Arg Thr Arg Gln Tyr Asp Ala Tyr Ser Ala Leu Leu Asp
420 425 430

Asp Arg Arg His Glu Glu Glu Gln Gly Tyr Thr Phe Ile Val Arg Ala
435 440 445
Pro Gly Leu Ala Phe His Asp Leu Val Pro Ser Leu Thr Phe Lys Tyr
450 455 460
Asn Lys Val Asn Ser Asn Val Asp Trp Leu Tyr Ser Trp Glu Arg Asn
465 470 475 480
Ser Val Ser Leu Lys Leu Glu Lys Gln Phe
485 490

<210> 537

<211> 1500

<212

> DNA

<213> P. rettgeri SLAM 1

<400> 537

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ttaacccctg ccattatgat gcttatagcc gcattctctg catttccagc aagcttggac 120

actgaccgag aacaattgtt atggcaaaaa gacaaacaaa actatcgtga taaaagtgca 180

gtagtcccca ataaagacca attacttctc ccagatgacc tatcaattaa cttaaatggg 240

gaaaattatg cccttgagaa taatgcccaa gacctcgggc aagccattta tctggcaatt 300

aaccacaggc aatttgaaga cgtacagcgc ttattacccc gctaccaaca actagctgat 360

gcggatccac tactcatttt atttgcaaaa gcagaaattg ctaaatcgca aaatcattac 420

cctgaagcga ttgcccacta ccaacaaata ttggcacggt cgccaaagtt tcttcgcata 480

aaattagaac tggcccgggc ttatttcgaa gataaccaaa ataaagagtc tttggcttta 540

ttccaaaatt taatcaacga tgaaacactc gcattaccta cgaatgtgaa gcaaaccatc 600

caacaattta ttagtgctat cgaaaaccgc acagcttgga ctggaagtct ctcctttggc 660

tataaataca acagtaatat caaccaagtt ccagataaaa ataaagtttg ggaaacgcca 720

gggggaacct ggaaaatggc taaccccaaa tcatcaccgg gactcaccta tgatgcaagt 780

ctgagtaaaa ttattcctat ctcgggcaat cattccctgc aaatcaaggg gacatcttat 840

ggtgaccgct atccgcacta tgctgaattc agtgaaaaca cgtcttcttt agcaacttta 900

tatcgtttta atgatgcgaa caccactgtc gcattcggcc cattagttga gttaaaaacg 960

gtcaatgaaa agcgccgtta tttaggcata gggggaaaaa ttgaagctga ctaccaattt 1020

tcacctcgtg tgctcctaag tacctccgct gactaccaac aacttcatta tcaaaaaccg 1080

tatgacagtg ccaatggtaa tcgaagtagc ctacatctaa ccggtgtcta tggtattacc 1140

ccagatacct ccctcttttt gggggctgat gcgactcgtc tcaccacaga agttcgtagc 1200

gatgattatg accaattggg tatccgaggc ggcttttatc acgtgctaac acccgatatt 1260

catttactgg cacttgcaac ttaccgagaa agccaattca aggccttcaa ccaaatgttg 1320

aatgttaaac gccatgatag agaagcgatg tattttgcgc gtcttagttt tccaaattat 1380

tcattgctca catttacgcc ttataccagt taccgctttc gtgataaccg cagttctgca 1440

gatggaattt actcctacca ccagcacgaa atttctattg gattagaaac ccgtttttaa 1500

<210> 538

<211> 499

<212> PRT

<213> P. rettgeri SLAM 1

<400> 538

Met Thr Gly Ser Trp Pro Leu Pro Ile Ile Thr Glu Ala Asn Pro Met

1 5 10 15

Arg Tyr Leu Leu Leu Thr Pro Ala Ile Met Met Leu Ile Ala Ala Phe
20 25 30
Ser Ala Phe Pro Ala Ser Leu Asp Thr Asp Arg Glu Gln Leu Leu Trp
35 40 45
Gln Lys Asp Lys Gln Asn Tyr Arg Asp Lys Ser Ala Val Val Pro Asn
50 55 60
Lys Asp Gln Leu Leu Leu Pro Asp Asp Leu Ser Ile Asn Leu Asn Gly
65 70 75 80

Glu Asn Tyr Ala Leu Glu Asn Asn Ala Gln Asp Leu Gly Gln Ala Ile
85 90 95
Tyr Leu Ala Ile Asn His Arg Gln Phe Glu Asp Val Gln Arg Leu Leu
100 105 110
Pro Arg Tyr Gln Gln Leu Ala Asp Ala Asp Pro Leu Leu Ile Leu Phe
115 120 125
Ala Lys Ala Glu Ile Ala Lys Ser Gln Asn His Tyr Pro Glu Ala Ile
130 135 140

Ala His Tyr Gln Gln Ile Leu Ala Arg Ser Pro Lys Phe Leu Arg Ile
145 150 155 160
Lys Leu Glu Leu Ala Arg Ala Tyr Phe Glu Asp Asn Gln Asn Lys Glu
165 170 175
Ser Leu Ala Leu Phe Gln Asn Leu Ile Asn Asp Glu Thr Leu Ala Leu
180 185 190
Pro Thr Asn Val Lys Gln Thr Ile Gln Gln Phe Ile Ser Ala Ile Glu
195 200 205

Asn Arg Thr Ala Trp Thr Gly Ser Leu Ser Phe Gly Tyr Lys Tyr Asn
210 215 220
Ser Asn Ile Asn Gln Val Pro Asp Lys Asn Lys Val Trp Glu Thr Pro
225 230 235 240
Gly Gly Thr Trp Lys Met Ala Asn Pro Lys Ser Ser Pro Gly Leu Thr
245 250 255

Tyr Asp Ala Ser Leu Ser Lys Ile Ile Pro Ile Ser Gly Asn His Ser
260 265 270

Leu Gln Ile Lys Gly Thr Ser Tyr Gly Asp Arg Tyr Pro His Tyr Ala
275 280 285

Glu Phe Ser Glu Asn Thr Ser Ser Leu Ala Thr Leu Tyr Arg Phe Asn
290 295 300

Asp Ala Asn Thr Thr Val Ala Phe Gly Pro Leu Val Glu Leu Lys Thr
305 310 315 320

Val Asn Glu Lys Arg Arg Tyr Leu Gly Ile Gly Gly Lys Ile Glu Ala
325 330 335

Asp Tyr Gln Phe Ser Pro Arg Val Leu Leu Ser Thr Ser Ala Asp Tyr
340 345 350

Gln Gln Leu His Tyr Gln Lys Pro Tyr Asp Ser Ala Asn Gly Asn Arg
355 360 365

Ser Ser Leu His Leu Thr Gly Val Tyr Gly Ile Thr Pro Asp Thr Ser
370 375 380

Leu Phe Leu Gly Ala Asp Ala Thr Arg Leu Thr Thr Glu Val Arg Ser
385 390 395 400

Asp Asp Tyr Asp Gln Leu Gly Ile Arg Gly Gly Phe Tyr His Val Leu
405 410 415

Thr Pro Asp Ile His Leu Leu Ala Leu Ala Thr Tyr Arg Glu Ser Gln
420 425 430

Phe Lys Ala Phe Asn Gln Met Leu Asn Val Lys Arg His Asp Arg Glu
435 440 445

Ala Met Tyr Phe Ala Arg Leu Ser Phe Pro Asn Tyr Ser Leu Leu Thr
450 455 460

Phe Thr Pro Tyr Thr Ser Tyr Arg Phe Arg Asp Asn Arg Ser Ser Ala
465 470 475 480

Asp Gly Ile Tyr Ser Tyr His Gln His Glu Ile Ser Ile Gly Leu Glu
485 490 495

Thr Arg Phe

<210> 539

<211> 1371

<212> DNA

<213> P. rettgeri SLAM 2

<400> 539

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actaatgatc taagtggtta tagtaacaaa aaacatcaat cagaaataaa taatgtaaaa 120

tatagtaaaa aaaatatcga cgagcttggc tttattcttt atgatctaat tcagcagagg 180

gattttgatg taataaataa aatcattgat aactatgtta gtcataaaga ccatgataaa 240

gaattggtta aatatattta ctctgaaaag gcgatgttaa ataatgaata taacttggca 300

atcaggttat ataatgaaat tttaattcac aagcctaata tgcttttggt tgagttaaaa 360

cttgctcgag cactaactta tgttaaacat tatgaggcag cattatcgat atatcaaaat 420

ataaaaacaa aatatagcgg gggaatatca agtaagttag ttgaatatat tgaaaataaa 480

ataatatatt tagagaataa aaatcgctgg caaggaatgg ttaagctagg ttcaagttat 540

gattttaatt taaatgaagc atcaaatagc cgtgaaatgt actgttttcg tagtaaatgt 600

atgaatagca gcaatcagtc tattgcaggt ggaaaatggc attattacat taaatcaaca 660

aagcgttttc ctctcgtggg taaccattca gggctattat catttggtgc gtttgggtta 720

gaaccgatga aaacagtcac ggctagaaaa ataaatatat ttattagcgg gggttatcaa 780

tttgagaatg cgaatacaaa aatcggcata ttgcccatat ttgaagccaa atggcatgat 840

aaccaatatt ataatttaag cctaggagga aaaatagcaa cagaatatac gttaaatcat 900

cgagtaacta ttttaggtga ttttgaatat aaaaataaaa cgcatcctca tgagtatagt 960

tttaatgatg gtgataaatg gatctattca ctatttggga cctatttagt tgattctcag 1020

ttagtcgctt ttggaggaat acatggagcc aatcgggaaa aacaacgcaa tagtgatagt 1080

tattcacagt atgggattag agccggtttt ttaaaggtca ccggactgtg tgattttctt 1140

gttgcggtag gttacaaaca aacaaatttc gaacagtttg atgtgtattt aaatgtaaaa 1200

agaaaagatc aaaatagata tttaaatgcc caagtgacat ttgataaaaa taaaatatta 1260

acctttacac cttctattta ttttaatagc caagtgaata aaagcacggc agatattatt 1320

tattctttta agcaaagtga agtcggtgtc aatttcacca agaaatttta a 1371

<210> 540

<211> 456

<212> PRT

<213> P. rettgeri SLAM 2

<400> 540

Met Leu Leu Phe Phe Pro Leu His Ser Ile Gln Ala Val Gln Asp Val
1 5 10 15

Asn Glu Glu Val Thr Asn Asp Leu Ser Gly Tyr Ser Asn Lys Lys His
20 25 30

Gln Ser Glu Ile Asn Asn Val Lys Tyr Ser Lys Lys Asn Ile Asp Glu
35 40 45

Leu Gly Phe Ile Leu Tyr Asp Leu Ile Gln Gln Arg Asp Phe Asp Val
50 55 60

Ile Asn Lys Ile Ile Asp Asn Tyr Val Ser His Lys Asp His Asp Lys
65 70 75 80

Glu Leu Val Lys Tyr Ile Tyr Ser Glu Lys Ala Met Leu Asn Asn Glu
85 90 95

Tyr Asn Leu Ala Ile Arg Leu Tyr Asn Glu Ile Leu Ile His Lys Pro
100 105 110

Asn Met Leu Leu Val Glu Leu Lys Leu Ala Arg Ala Leu Thr Tyr Val
115 120 125

Lys His Tyr Glu Ala Ala Leu Ser Ile Tyr Gln Asn Ile Lys Thr Lys
130 135 140

Tyr Ser Gly Gly Ile Ser Ser Lys Leu Val Glu Tyr Ile Glu Asn Lys
145 150 155 160

Ile Ile Tyr Leu Glu Asn Lys Asn Arg Trp Gln Gly Met Val Lys Leu
165 170 175

Gly Ser Ser Tyr Asp Phe Asn Leu Asn Glu Ala Ser Asn Ser Arg Glu
180 185 190

Met Tyr Cys Phe Arg Ser Lys Cys Met Asn Ser Ser Asn Gln Ser Ile
195 200 205

Ala Gly Gly Lys Trp His Tyr Tyr Ile Lys Ser Thr Lys Arg Phe Pro
210 215 220

Leu Val Gly Asn His Ser Gly Leu Leu Ser Phe Gly Ala Phe Gly Leu

225 230 235 240

Glu Pro Met Lys Thr Val Thr Ala Arg Lys Ile Asn Ile Phe Ile Ser

245 250 255

Gly Gly Tyr Gln Phe Glu Asn Ala Asn Thr Lys Ile Gly Ile Leu Pro

260 265 270

Ile Phe Glu Ala Lys Trp His Asp Asn Gln Tyr Tyr Asn Leu Ser Leu

275 280 285

Gly Gly Lys Ile Ala Thr Glu Tyr Thr Leu Asn His Arg Val Thr Ile

290 295 300

Leu Gly Asp Phe Glu Tyr Lys Asn Lys Thr His Pro His Glu Tyr Ser

305 310 315 320

Phe Asn Asp Gly Asp Lys Trp Ile Tyr Ser Leu Phe Gly Thr Tyr Leu

325 330 335

Val Asp Ser Gln Leu Val Ala Phe Gly Gly Ile His Gly Ala Asn Arg

340 345 350

Glu Lys Gln Arg Asn Ser Asp Ser Tyr Ser Gln Tyr Gly Ile Arg Ala

355 360 365

Gly Phe Leu Lys Val Thr Gly Leu Cys Asp Phe Leu Val Ala Val Gly

370 375 380

Tyr Lys Gln Thr Asn Phe Glu Gln Phe Asp Val Tyr Leu Asn Val Lys

385 390 395 400

Arg Lys Asp Gln Asn Arg Tyr Leu Asn Ala Gln Val Thr Phe Asp Lys

405 410 415

Asn Lys Ile Leu Thr Phe Thr Pro Ser Ile Tyr Phe Asn Ser Gln Val

420 425 430

Asn Lys Ser Thr Ala Asp Ile Ile Tyr Ser Phe Lys Gln Ser Glu Val

435 440 445

Gly Val Asn Phe Thr Lys Lys Phe

450 455

<210> 541

<211> 1464

<212> DNA

<213> P. sneebia SLAM 1

<400> 541

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actctctatt ccgctaatat agatactgac cgagaattat tattatggca aaaagaacaa 120

caaataaatc gagaaaacaa taataatatt cctgataaaa accagtcatt attacccgat 180

gatgccatat taaaattaga tggaaaaacc tattctgtaa aaaagaatat taatgattta 240

ggtaaagcga tttatttatc tattactcaa catcaattcg atgatataca acaattactc 300

aatcattatc aatatttccc tgatcatgac ccattattag ttttatttgc gcatgctgaa 360

attgaaaaat ataataatca ttattctcaa gccataaact attatcgaga gatattagaa 420

ctatcgccaa atttttacg tgtaaaacta gaattagctc gtacttattt tgaagataaa 480

caaaataatg aatcgttaaa gatatttaat aatatcatta atgatactgc acttttatta 540

cctgaaagta ctcgccacat tattcaaaaa tttattatta ctttagaaaa acgcattagc 600

tggtctggta atttctctgt tgcttatacc tataatagta atattaacca aacaccaaag 660

aagaataaga tatgggaaat acccggtgga gtttggcaaa ctgaagcacc tattgcttat 720

ggtggacttt cttatgatgc cagtttagat aaggcgattc ccctctttgg tcatcactcc 780

ttacagatta aagcgtctag ttacggcgac cattacccac actatgcaga attcagtgaa 840

aacacctcaa ctttagcgac cctatatcaa tttaacaatg cggataccac attatcattt 900

ggcccgcaaa ttgagctaaa aacgatagat aatcagcacc ttcatactgg tattggccta 960

cgaatagaga gcgattatca gttctctccc cgttttatgg taagtgcttc tgccaattat 1020

cattggctta attatcaaaa aacttatgcc ggcagcgatg gatctcgcag caacttatta 1080

ctcacgggaa tttatggtct taccacagat acatcacttt ttttaggtac agatgccact 1140

caagttacta cccaaacccg cagtgatgat tacgaccaat taggattaag aagcggtttt 1200

tttagtgtgt tatctcctga tattcatttg ctaacccttg ccacactgcg ctatagccaa 1260

tttcaagctt tcaactcaat gctgaatgta aaacgtgatg atcgcgaagc aatgctattt 1320

acacgtttaa gttttccggg ctattcagtg ctcacattaa caccctacac cagttaccgc 1380

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gccggatttg aaactcgatt ttaa 1464

<210> 542

<211> 487

<212> PRT

<213> P. sneebia SLAM 1

<400> 542

Met Gln Ile Ala Pro Leu Phe Ser Ile Ile Ile Ile Phe Ile Ser Ser
1 5 10 15

Leu Met Pro Leu Thr Leu Tyr Ser Ala Asn Ile Asp Thr Asp Arg Glu
20 25 30

Leu Leu Leu Trp Gln Lys Glu Gln Gln Ile Asn Arg Glu Asn Asn Asn
35 40 45

Asn Ile Pro Asp Lys Asn Gln Ser Leu Leu Pro Asp Asp Ala Ile Leu

50 55 60

Lys Leu Asp Gly Lys Thr Tyr Ser Val Lys Lys Asn Ile Asn Asp Leu
65 70 75 80

Gly Lys Ala Ile Tyr Leu Ser Ile Thr Gln His Gln Phe Asp Asp Ile
85 90 95

Gln Gln Leu Leu Asn His Tyr Gln Tyr Phe Pro Asp His Asp Pro Leu
100 105 110

Leu Val Leu Phe Ala His Ala Glu Ile Glu Lys Tyr Asn Asn His Tyr

115 120 125

Ser Gln Ala Ile Asn Tyr Tyr Arg Glu Ile Leu Glu Leu Ser Pro Asn
130 135 140

Phe Leu Arg Val Lys Leu Glu Leu Ala Arg Thr Tyr Phe Glu Asp Lys
145 150 155 160

Gln Asn Asn Glu Ser Leu Lys Ile Phe Asn Asn Ile Ile Asn Asp Thr
165 170 175

Ala Leu Leu Leu Pro Glu Ser Thr Arg His Ile Ile Gln Lys Phe Ile

180 185 190

Ile Thr Leu Glu Lys Arg Ile Ser Trp Ser Gly Asn Phe Ser Val Ala
195 200 205

Tyr Thr Tyr Asn Ser Asn Ile Asn Gln Thr Pro Lys Lys Asn Lys Ile
210 215 220

Trp Glu Ile Pro Gly Gly Val Trp Gln Thr Glu Ala Pro Ile Ala Tyr
225 230 235 240

Gly Gly Leu Ser Tyr Asp Ala Ser Leu Asp Lys Ala Ile Pro Leu Phe

245 250 255

Gly His His Ser Leu Gln Ile Lys Ala Ser Ser Tyr Gly Asp His Tyr

260 265 270

Pro His Tyr Ala Glu Phe Ser Glu Asn Thr Ser Thr Leu Ala Thr Leu

275 280 285

Tyr Gln Phe Asn Asn Ala Asp Thr Thr Leu Ser Phe Gly Pro Gln Ile

290 295 300

Glu Leu Lys Thr Ile Asp Asn Gln His Leu His Thr Gly Ile Gly Leu

305 310 315 320

Arg Ile Glu Ser Asp Tyr Gln Phe Ser Pro Arg Phe Met Val Ser Ala

325 330 335

Ser Ala Asn Tyr His Trp Leu Asn Tyr Gln Lys Thr Tyr Ala Gly Ser

340 345 350

Asp Gly Ser Arg Ser Asn Leu Leu Leu Thr Gly Ile Tyr Gly Leu Thr

355 360 365

Thr Asp Thr Ser Leu Phe Leu Gly Thr Asp Ala Thr Gln Val Thr Thr

370 375 380

Gln Thr Arg Ser Asp Asp Tyr Asp Gln Leu Gly Leu Arg Ser Gly Phe

385 390 395 400

Phe Ser Val Leu Ser Pro Asp Ile His Leu Leu Thr Leu Ala Thr Leu

405 410 415

Arg Tyr Ser Gln Phe Gln Ala Phe Asn Ser Met Leu Asn Val Lys Arg

420 425 430

Asp Asp Arg Glu Ala Met Leu Phe Thr Arg Leu Ser Phe Pro Gly Tyr

435 440 445

Ser Val Leu Thr Leu Thr Pro Tyr Thr Ser Tyr Arg Phe Arg Asp Asn

450 455 460

Gln Ser Ser Ala Asp Gly Ile Tyr Ser Tyr Arg Gln His Glu Phe Ser

465 470 475 480

Ala Gly Phe Glu Thr Arg Phe

485

<210> 543

<211> 1461

<212> DNA

<213> P. stuartii SLAM 1

<400> 543

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aaatctcccg ttattgaaaa taataaaccg tttattaaag atgacatcaa aattaatttc 180

gatggtaaag aatatcaggt tagtaatacg cttaatgaga tgggaatggc tatttatatt 240

gccttaaatc gtgggcaata cgatgacgta gaacgtctat tatcatatta ccaacaatta 300

agtggatatg acgttttact tgttgagttt gctaaagcac aaatggcacg tgcaaatcat 360

gattatgctc aggctatttt tcactaccaa actattttag cgctaaaacc tgatttttg 420

cgtgtcgagc tggaattagc tcgaacttat tttgaagatc aacaaaataa tgaggcatct 480

tcacagttta aacgggtatt ggaaaagtat cagcagcagt taccacaaag tgtattagct 540

acaatttcac aatttattac ggaattaagt aaacgaaata gttggtcagg aagtttttcg 600

gtaggttacg gttacaactc taatattaat caagtaccgg gggataaaag acagcgttgc 660

tacagaaatg cagtgcagca gttttgttat agtgctggat tggcggataa aggcaccaaa 720

tttatctatg atggtgatat taaacgtacc ttttcacttt accagcatca cagtttactg 780

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agccacatac gggtttatta tcaatatcag gatgcaaaaa aatcattcgc tattggccca 900

attagtgaat ttaaatgggt aggagagcgg cgacactatt atggtgttgg agtgggaatg 960

gaagcggagt atcgtttttt accccagttt tcgctgagta cagtgattga tcaccaaaaa 1020

ataaactatc gttcacctta tcaaagccaa gatggtaata agagtcaggc ttatatcaca 1080

gggatttatg ctcttagctc agatgcagtg atatttggtg gtgtagatag tgggtatgtg 1140

aataaggttt atgatagtga cagttataaa caatatggca taagaggagg aatatttaag 1200

gacgttagtc agtattatca tctattgggg atcgccagtt ataagcaaac tcgatttaat 1260

gctccgcaat atgcgttggg aagtcaaaat cgaatggatg atgaacaact gtatttggct 1320

aagttaagtt tacctaaata cagtattgcc acaatgacac catccatttc ttataggtat 1380

agagtcaata aaagtaatat tgatgcactg tattcatacc aacaaagtga aattgaaatt 1440

agattagaaa aacgctttta a 1461

<210> 544

<211> 486

<212> PRT

<213> P. stuartii SLAM 1

<400> 544

Met Gly Leu Phe Arg Ala Gly Ile Leu Trp Leu Leu Leu Tyr Ser Ser
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Val Ala Ile Gly Glu Ile Ser Asp Ile Asp Asn Tyr Arg Phe Leu Leu
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Lys Asp Lys Ala Glu Phe Ser Arg Lys Ser Pro Val Ile Glu Asn Asn
35 40 45
Lys Pro Phe Ile Lys Asp Asp Ile Lys Ile Asn Phe Asp Gly Lys Glu
50 55 60
Tyr Gln Val Ser Asn Thr Leu Asn Glu Met Gly Met Ala Ile Tyr Ile
65 70 75 80
Ala Leu Asn Arg Gly Gln Tyr Asp Asp Val Glu Arg Leu Leu Ser Tyr
85 90 95

Tyr Gln Gln Leu Ser Gly Tyr Asp Val Leu Leu Val Glu Phe Ala Lys
100 105 110
Ala Gln Met Ala Arg Ala Asn His Asp Tyr Ala Gln Ala Ile Phe His
115 120 125
Tyr Gln Thr Ile Leu Ala Leu Lys Pro Asp Phe Leu Arg Val Glu Leu
130 135 140
Glu Leu Ala Arg Thr Tyr Phe Glu Asp Gln Gln Asn Asn Glu Ala Ser
145 150 155 160

Ser Gln Phe Lys Arg Val Leu Glu Lys Tyr Gln Gln Gln Leu Pro Gln
165 170 175
Ser Val Leu Ala Thr Ile Ser Gln Phe Ile Thr Glu Leu Ser Lys Arg
180 185 190
Asn Ser Trp Ser Gly Ser Phe Ser Val Gly Tyr Gly Tyr Asn Ser Asn
195 200 205
Ile Asn Gln Val Pro Gly Asp Lys Arg Gln Arg Cys Tyr Arg Asn Ala

210 215 220

Val Gln Gln Phe Cys Tyr Ser Ala Gly Leu Ala Asp Lys Gly Thr Lys
225 230 235 240
Phe Ile Tyr Asp Gly Asp Ile Lys Arg Thr Phe Ser Leu Tyr Gln His
245 250 255
His Ser Leu Leu Phe Lys Ala Tyr Thr Tyr Gly Asn Lys Tyr Asp Gly
260 265 270
Ala Ala Glu Tyr Asn Glu Asn Thr Ser His Ile Arg Val Tyr Tyr Gln
275 280 285

Tyr Gln Asp Ala Lys Lys Ser Phe Ala Ile Gly Pro Ile Ser Glu Phe
290 295 300
Lys Trp Val Gly Glu Arg Arg His Tyr Tyr Gly Val Gly Val Gly Met
305 310 315 320
Glu Ala Glu Tyr Arg Phe Leu Pro Gln Phe Ser Leu Ser Thr Val Ile
325 330 335
Asp His Gln Lys Ile Asn Tyr Arg Ser Pro Tyr Gln Ser Gln Asp Gly
340 345 350

Asn Lys Ser Gln Ala Tyr Ile Thr Gly Ile Tyr Ala Leu Ser Ser Asp
355 360 365
Ala Val Ile Phe Gly Gly Val Asp Ser Gly Tyr Val Asn Lys Val Tyr
370 375 380
Asp Ser Asp Ser Tyr Lys Gln Tyr Gly Ile Arg Gly Gly Ile Phe Lys
385 390 395 400
Asp Val Ser Gln Tyr Tyr His Leu Leu Gly Ile Ala Ser Tyr Lys Gln
405 410 415

Thr Arg Phe Asn Ala Pro Gln Tyr Ala Leu Gly Ser Gln Asn Arg Met
420 425 430
Asp Asp Glu Gln Leu Tyr Leu Ala Lys Leu Ser Leu Pro Lys Tyr Ser
435 440 445
Ile Ala Thr Met Thr Pro Ser Ile Ser Tyr Arg Tyr Arg Val Asn Lys
450 455 460

Ser Asn Ile Asp Ala Leu Tyr Ser Tyr Gln Gln Ser Glu Ile Glu Ile
465 470 475 480

Arg Leu Glu Lys Arg Phe
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<210> 545

<211> 1479

<212> DNA

<213> P. stutzeri SLAM 1

<400> 545

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cagaaggccc aggccgagga ggcgctggcg gcgccgcccg gtacgctgat gtacgagggc 180

cggcgctacc aggtgccgag caccctggag gcactgacgc cggccatcta cgtggccatc 240

aataccaacc agtggaccca gttgccggat ttcatcgccc gttaccgtga actgccgggg 300

catcggccgg cgctggcgaa catggcggaa agcctgctgg cgcgcttcga gggggactat 360

ccgctggcgt tgcagcgcat ggagctggcc agtgaacagg agccgcggga tgcacgcatc 420

ctgctggagc tggcgcgcct gtggttcgag ggttaccagg aaaagcgcgc gcgggagggc 480

tttgccaggg cgctggaggc ggggctgccg cccgaggtac agatgctgat ccagcagtat 540

cacctggcga tggaaatccg tgccgactgg catggcagtg cggcgctagg ctggggctac 600

aacgacaata tcaaccaggc taatggccac tacagctgcc tcagcgagtt cgccggcatc 660

tgtttcttcg agcgcaggat gcccgaggcc atcgattccg aaatggtcaa ctacgagctg 720

tcgttgcagc gccgcttcaa cctgtccggt aaccacaacc tgcagctgcg tcccctcagc 780

tacggcaact actattcgac gaccgatccg tccacgactt cccgtatcaa ggactacagc 840

aacaacctgg cgatcctgca ggcgggctac cagtacctgg atgcccgcga caatatctcg 900

ctcgctccct atgtcgagca ctactaccgc aaccgtgcca gcgactacct ggcccatggc 960

ctgcaactgg agtggagcca ctcgctgaac cgccagtggc agctgggcac cagcctggat 1020

gccaagcgct acgagtacag ttccaggggc ctgctgaccg gtgccgacta cgaccagtac 1080

cagtggaacc tgttcgcctc cttctcgccc agcacccgca ccagcctgta cggcggctta 1140

agcctcaccc gcaagaagta cgaggtggat caggccagca gccgcgactg ggccgtgcgc 1200

ggcggggtct atcatctctt tgccggcagc gccgggttgt tcgtcaacgc gctgggcatc 1260

taccgggaaa gccgcaacga tgcctacgat ttcttcctcg gcgaacgccg gtacgacaag 1320

cagcaggtgt atatcctcag cgccggggtg aacgcctggc aggtcgccgg gctggttccg 1380

gagttgcgcg tgcggcacag catcaaccac agcaatctgg attgggcgtt cggcttcgag 1440

cagacggagg tgagcctgat gctgcgcaag agcttctga 1479

<210> 546

<211> 492

<212> PRT

<213> P. stutzeri SLAM 1

<400> 546

Met Ser Cys Arg Phe Arg Ala Val Trp Leu Leu Ser Leu Ala Cys Leu
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Val Ala Pro Ala Val Trp Ala Asp Asp Asp Asp Thr Leu Phe Leu Gln
20 25 30

Asp Gln Thr Arg Arg Thr Ile Glu Gln Lys Ala Gln Ala Glu Glu Ala
35 40 45

Leu Ala Ala Pro Pro Gly Thr Leu Met Tyr Glu Gly Arg Arg Tyr Gln
50 55 60

Val Pro Ser Thr Leu Glu Ala Leu Thr Pro Ala Ile Tyr Val Ala Ile
65 70 75 80

Asn Thr Asn Gln Trp Thr Gln Leu Pro Asp Phe Ile Ala Arg Tyr Arg
85 90 95

Glu Leu Pro Gly His Arg Pro Ala Leu Ala Asn Met Ala Glu Ser Leu
100 105 110

Leu Ala Arg Phe Glu Gly Asp Tyr Pro Leu Ala Leu Gln Arg Met Glu
115 120 125

Leu Ala Ser Glu Gln Glu Pro Arg Asp Ala Arg Ile Leu Leu Glu Leu
130 135 140

Ala Arg Leu Trp Phe Glu Gly Tyr Gln Glu Lys Arg Ala Arg Glu Gly
145 150 155 160

Phe Ala Arg Ala Leu Glu Ala Gly Leu Pro Pro Glu Val Gln Met Leu
165 170 175

Ile Gln Gln Tyr His Leu Ala Met Glu Ile Arg Ala Asp Trp His Gly

180 185 190

Ser Ala Ala Leu Gly Trp Gly Tyr Asn Asp Asn Ile Asn Gln Ala Asn
195 200 205
Gly His Tyr Ser Cys Leu Ser Glu Phe Ala Gly Ile Cys Phe Phe Glu
210 215 220
Arg Arg Met Pro Glu Ala Ile Asp Ser Glu Met Val Asn Tyr Glu Leu
225 230 235 240
Ser Leu Gln Arg Arg Phe Asn Leu Ser Gly Asn His Asn Leu Gln Leu
245 250 255

Arg Pro Leu Ser Tyr Gly Asn Tyr Tyr Ser Thr Thr Asp Pro Ser Thr
260 265 270
Thr Ser Arg Ile Lys Asp Tyr Ser Asn Asn Leu Ala Ile Leu Gln Ala
275 280 285
Gly Tyr Gln Tyr Leu Asp Ala Arg Asp Asn Ile Ser Leu Ala Pro Tyr
290 295 300
Val Glu His Tyr Tyr Arg Asn Arg Ala Ser Asp Tyr Leu Ala His Gly
305 310 315 320

Leu Gln Leu Glu Trp Ser His Ser Leu Asn Arg Gln Trp Gln Leu Gly
325 330 335
Thr Ser Leu Asp Ala Lys Arg Tyr Glu Tyr Ser Ser Arg Gly Leu Leu
340 345 350
Thr Gly Ala Asp Tyr Asp Gln Tyr Gln Trp Asn Leu Phe Ala Ser Phe
355 360 365
Ser Pro Ser Thr Arg Thr Ser Leu Tyr Gly Gly Leu Ser Leu Thr Arg
370 375 380

Lys Lys Tyr Glu Val Asp Gln Ala Ser Ser Arg Asp Trp Ala Val Arg
385 390 395 400
Gly Gly Val Tyr His Leu Phe Ala Gly Ser Ala Gly Leu Phe Val Asn
405 410 415
Ala Leu Gly Ile Tyr Arg Glu Ser Arg Asn Asp Ala Tyr Asp Phe Phe
420 425 430

Leu Gly Glu Arg Arg Tyr Asp Lys Gln Gln Val Tyr Ile Leu Ser Ala
435 440 445

Gly Val Asn Ala Trp Gln Val Ala Gly Leu Val Pro Glu Leu Arg Val
450 455 460
Arg His Ser Ile Asn His Ser Asn Leu Asp Trp Ala Phe Gly Phe Glu
465 470 475 480
Gln Thr Glu Val Ser Leu Met Leu Arg Lys Ser Phe
485 490

<210> 547
<211> 1539
<212> DNA
<213> P. temperata SLAM 1
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caagaaaaag aattcgttac tgatgaaact gtaaatgaga atactgatca tttatcgata 240
gtccttaatg gtcagacttt cagtgttgag aataatgtga atgaggttgg tcaggcgctg 300
tatttagcta ttaatcatca acaagtaaag gatgttgagc gttttttgtc gatgtatcag 360
aagttaccta ggcatgacat gcaattggta cattttgctc aggcgaatct tgcccgttcg 420
cagggtaatt tagtagcggc agaacagcat tatcaggcta ttttgcacca gcaacctgat 480

tttacccgtg ctaaattgga gttagccagg gtctattatg agaaccagaa aaataaagag 540
gcaggtttac tgtttaatga gatttctgcg gcaaatcacg acaacgaaaa taaattacca 600
ccagcagtca ttaagaatat aaccagctat caggatgcga ttgaattgcg taatgcctgg 660
cgtgggtctt ttgccgtagg atatattttt aacgacaata ctaatatgtc accaaataag 720
cctcctgttt gcaaggaata tgctgaaaat ggcagttgta tagttgaacg taagttgcct 780
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aatgattttc tgataggtcc aattattgag tttaatcatg ttggtaatca ttctcgttat 1020
cgcaccacag gaatgaaaac tgaatggatg aatattctat caaaaaatct ggcattgaat 1080

cttgaaggtg aatataaaca gtttcgttat cataaacttt ataatcataa tgacggtaat 1140

atgacttctg tttatgccac cttatcttat tatttaactg atcagacaat tacctttact 1200

ggtggtgatt gggttaataa aaccagtgtt gagaaaacgg atgattatca acagaaaggc 1260

atacgagcgg gtatttctac ccagttgtat ccgggaatta atgcggtggt atttaccgca 1320

ttacgacaga ggcagtttgg agattacagt gtaccattaa gtgcacgccg taaagacaat 1380

gaacaactct attcggccat cctcagtatg cctaaatttg atgtttttgg cttaactccg 1440

gtaatcactt atcggtacag aaaaaacaat agcaatgtcg attggctata ctcatataac 1500

aaaaacgaag tgttaattaa gtttgaaaaa tatttttga 1539

<210> 548

<211> 512

<212> PRT

<213> P. temperata SLAM 1

<400> 548

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Pro Met Leu Asn Ile Pro Ile Ile Arg Phe Thr Ile Leu Ile Ser Cys
20 25 30

Leu Phe Ile Tyr Pro Ser Leu Val Leu Ala Asp Glu Asp Ala Gly Arg
35 40 45

Arg Leu Trp His Asn Val Gln Arg Asn Leu Gln Asp Gln Glu Lys Glu
50 55 60

Phe Val Thr Asp Glu Thr Val Asn Glu Asn Thr Asp His Leu Ser Ile
65 70 75 80

Val Leu Asn Gly Gln Thr Phe Ser Val Glu Asn Asn Val Asn Glu Val
85 90 95

Gly Gln Ala Leu Tyr Leu Ala Ile Asn His Gln Gln Val Lys Asp Val
100 105 110

Glu Arg Phe Leu Ser Met Tyr Gln Lys Leu Pro Arg His Asp Met Gln
115 120 125

Leu Val His Phe Ala Gln Ala Asn Leu Ala Arg Ser Gln Gly Asn Leu
130 135 140

Val Ala Ala Glu Gln His Tyr Gln Ala Ile Leu His Gln Gln Pro Asp
145 150 155 160
Phe Thr Arg Ala Lys Leu Glu Leu Ala Arg Val Tyr Tyr Glu Asn Gln
165 170 175
Lys Asn Lys Glu Ala Gly Leu Leu Phe Asn Glu Ile Ser Ala Ala Asn
180 185 190
His Asp Asn Glu Asn Lys Leu Pro Pro Ala Val Ile Lys Asn Ile Thr
195 200 205

Ser Tyr Gln Asp Ala Ile Glu Leu Arg Asn Ala Trp Arg Gly Ser Phe
210 215 220
Ala Val Gly Tyr Ile Phe Asn Asp Asn Thr Asn Met Ser Pro Asn Lys
225 230 235 240
Pro Pro Val Cys Lys Glu Tyr Ala Glu Asn Gly Ser Cys Ile Val Glu
245 250 255
Arg Lys Leu Pro Leu Ala Lys Lys Ala Asn Gly Ile Ser Tyr Asp Ala
260 265 270

Thr Leu Arg Lys Ile Tyr Gln Leu Ser Gly His His Gly Ile Ser Leu
275 280 285
Arg Ser Met Thr Tyr Gly Glu Ser Tyr Arg His His Ser Asp Glu Asn
290 295 300
Glu Asn Thr Thr Ser Ala Tyr Leu Gly Tyr Asn Tyr Lys Ala Gln Lys
305 310 315 320
Asn Asp Phe Leu Ile Gly Pro Ile Ile Glu Phe Asn His Val Gly Asn
325 330 335

His Ser Arg Tyr Arg Thr Thr Gly Met Lys Thr Glu Trp Met Asn Ile
340 345 350
Leu Ser Lys Asn Leu Ala Leu Asn Leu Glu Gly Glu Tyr Lys Gln Phe
355 360 365
Arg Tyr His Lys Leu Tyr Asn His Asn Asp Gly Asn Met Thr Ser Val
370 375 380
Tyr Ala Thr Leu Ser Tyr Tyr Leu Thr Asp Gln Thr Ile Thr Phe Thr

385 390 395 400

Gly Gly Asp Trp Val Asn Lys Thr Ser Val Glu Lys Thr Asp Asp Tyr
405 410 415
Gln Gln Lys Gly Ile Arg Ala Gly Ile Ser Thr Gln Leu Tyr Pro Gly
420 425 430
Ile Asn Ala Val Val Phe Thr Ala Leu Arg Gln Arg Gln Phe Gly Asp
435 440 445
Tyr Ser Val Pro Leu Ser Ala Arg Arg Lys Asp Asn Glu Gln Leu Tyr
450 455 460

Ser Ala Ile Leu Ser Met Pro Lys Phe Asp Val Phe Gly Leu Thr Pro
465 470 475 480
Val Ile Thr Tyr Arg Tyr Arg Lys Asn Asn Ser Asn Val Asp Trp Leu
485 490 495
Tyr Ser Tyr Asn Lys Asn Glu Val Leu Ile Lys Phe Glu Lys Tyr Phe
500 505 510

<210> 549
<211> 1362
<212> DNA
<213> P. vulgaris SLAM 1
<400> 549

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gaaagattac tgctttatta tcaacaacaa cctcaacatg aagcattact tgttaattac 240
gcaaaggcgt tattggcaca aaacagaggt gatttttaa acgctgaatt ttattatcag 300
caacaactta agcaaaaagc cgattttatc ccagctcaaa ctgggctaat tcaactttac 360
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ccttacttat ctgaaaaaat tgtctctcaa tccactcaag gaaaaacgac gctaagaggt 600
gcaaaaccta ttgcatctac aggaattact cattattttt ctttttatca acctttttatt 660

atttattctt actatacttt ttcttcttat acttatgcta gatatataga ttatcactct 720

catcgtaacg ccaatttttt tgcattatat acacaactgg gttatcgcta tcaaaaacct 780

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tatcaagcat ggggaaatga aacacagctt tcttatttta ttaataaaaa gcaaactatt 900

aatttaagct tggattataa aataaagaaa tatcaaaaaa cgttaaataa tttaaatagt 960

aagcgattta gttatagtgc ttaccataac tattatttta ataataaaat acacttagtt 1020

aatcaattaa attatcagtt agttcgtaaa aaaaacactt tattaaatta tcatctgtat 1080

ggtataaaaa ctggtattta ttatccattg tcagctaatt ggcatatctc tctttttta 1140

cagtatcaat ttaaatattt taataactat aatcctttat taaaaaagag aagaaaagat 1200

aatagtatta tttttacaac caatattaaa agcaaatcac ctttgtttt agggttttat 1260

cccacaattg aattacgtta tacccgaaga ttaagcaatg tggattggtt atatcaatat 1320

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<210> 550

<211> 453

<212> PRT

<213> P. vulgaris SLAM 1

<400> 550

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20 25 30

Leu Tyr Tyr Leu Glu Thr Thr Ser Thr Ala Lys Val Gly Gln Gln Leu
35 40 45

Tyr His Tyr Leu Gln Gln Gln Gln Trp Gln Lys Ala Glu Arg Leu Leu
50 55 60

Leu Tyr Tyr Gln Gln Gln Pro Gln His Glu Ala Leu Leu Val Asn Tyr
65 70 75 80

Ala Lys Ala Leu Leu Ala Gln Asn Arg Gly Asp Phe Leu Asn Ala Glu
85 90 95

Phe Tyr Tyr Gln Gln Gln Leu Lys Gln Lys Ala Asp Phe Ile Pro Ala
100 105 110

Gln Thr Gly Leu Ile Gln Leu Tyr Phe His Leu Arg Glu Tyr Lys Lys
115 120 125
Ala Gln Gln Gln Leu Asn Gln Leu Ser Asn Ile Ile Asp Leu Ser Lys
130 135 140
Asp Ile Ile Gln Ser Ile Glu Phe Tyr Lys Val Lys Leu Ala Ser Tyr
145 150 155 160
Phe Gln Gly Gln Arg Phe Tyr Gln Leu Gly Phe Phe Tyr Asp Asp Asn
165 170 175

Ile Asn His Ala Pro Tyr Leu Ser Glu Lys Ile Val Ser Gln Ser Thr
180 185 190
Gln Gly Lys Thr Thr Leu Arg Gly Ala Lys Pro Ile Ala Ser Thr Gly
195 200 205
Ile Thr His Tyr Phe Ser Phe Tyr Gln Pro Phe Ile Ile Tyr Ser Tyr
210 215 220
Tyr Thr Phe Ser Ser Tyr Thr Tyr Ala Arg Tyr Ile Asp Tyr His Ser
225 230 235 240

His Arg Asn Ala Asn Phe Phe Ala Leu Tyr Thr Gln Leu Gly Tyr Arg
245 250 255
Tyr Gln Lys Pro Gln Tyr Gln Trp Ser Ile Thr Pro Tyr Tyr Glu Ile
260 265 270
Lys Ser Ser Arg Glu Gln Tyr Glu Tyr Gln Ala Trp Gly Asn Glu Thr
275 280 285
Gln Leu Ser Tyr Phe Ile Asn Lys Lys Gln Thr Ile Asn Leu Ser Leu
290 295 300

Asp Tyr Lys Ile Lys Lys Tyr Gln Lys Thr Leu Asn Asn Leu Asn Ser
305 310 315 320
Lys Arg Phe Ser Tyr Ser Ala Tyr His Asn Tyr Tyr Phe Asn Asn Lys
325 330 335
Ile His Leu Val Asn Gln Leu Asn Tyr Gln Leu Val Arg Lys Lys Asn
340 345 350
Thr Leu Leu Asn Tyr His Leu Tyr Gly Ile Lys Thr Gly Ile Tyr Tyr

355 360 365

Pro Leu Ser Ala Asn Trp His Ile Ser Leu Phe Leu Gln Tyr Gln Phe
370 375 380
Lys Tyr Phe Asn Asn Tyr Asn Pro Leu Leu Lys Lys Arg Arg Lys Asp
385 390 395 400
Asn Ser Ile Ile Phe Thr Thr Asn Ile Lys Ser Lys Ser Pro Phe Val
405 410 415
Leu Gly Phe Tyr Pro Thr Ile Glu Leu Arg Tyr Thr Arg Arg Leu Ser
420 425 430

Asn Val Asp Trp Leu Tyr Gln Tyr Gln Gln His Glu Val Leu Phe Lys
435 440 445
Leu Glu Lys Gln Phe
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<210> 551
<211> 1266
<212> DNA
<213> Phyllobacterium sp. YR531 SLAM 1
<400> 551

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gcgacttctg gtgatggtgg gaaagccaat caagttgccc agatatttac tgaagcgctt 180
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ggcgggagct tggacggcgt taaataccgt gatcgggcct ttgacgagct gtcaggacaa 660

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gcgcgaacct cttttgcgtg ggaggggcat aattggggtt atggcgtcca gggatatgtt 780

cagaagcggc taggcaacag cggtgacacc attcggatga cggcccgtat gcgttatctg 840

gattacgatg ttcaggatta ccatgatggt gtggaaacga ccattggcct tcgatatcag 900

cacgtgtttt ctgcttcttt actggccagt gtcggcgcta ccgcgacgcg gatgaatgcc 960

cagaacttta acgcctatac aagcatccgc cccaatttag aagtttactc cgatctacca 1020

ttgggtattc ttggtagtgt tgcggcggga tatgagttcc gaaactttga cggcaaattt 1080

cccatgactg gcaaaggaag ggaggacagg cagttcagcg cgagtgttgg actgacactg 1140

agaaagctga gttataaaaa tattgcgccc cggctggaat atggttatcg catcaatagc 1200

tcgaatgttg atctctacga ttacgattcg cacaattttg gaatttatct gacgaagaag 1260

tactag 1266

<210> 552

<211> 421

<212> PRT

<213> Phyllobacterium sp. YR531 SLAM 1

<400> 552

Met Ser Phe Phe Gly Ala Glu Pro Thr His Ala Ser Val Gln Gln Gly
1 5 10 15

Pro Ser Tyr Ser Phe Ala Gln Val Arg Ala Leu Ile Glu Ala Ser Glu
20 25 30

Tyr Asp Glu Ala Arg Asn Leu Val Ala Thr Ser Gly Asp Gly Gly Lys
35 40 45

Ala Asn Gln Val Ala Gln Ile Phe Thr Glu Ala Leu Ile Leu Lys His
50 55 60

Gln Arg Gln Phe Gln Ala Ser Ala Glu Lys Met Gln Gln Ile Ile Ile
65 70 75 80

Ala Tyr Pro Gln Tyr Asp Arg Val Arg Gln Glu Leu Ala His Thr Tyr
85 90 95

Phe Leu Leu Gly Asp Gly Glu His Ala Lys Tyr Gln Phe Glu Leu Leu
100 105 110

Ala Ala Ser Ser Gln Ser Pro Asp Phe Arg Ser Leu Tyr Asn Asn Tyr
115 120 125

Ile Asp Ala Ile Asp Ala Lys Arg Pro Trp Thr Leu Asp Gly Tyr Ile

130 135 140

Ala Leu Ala Pro Ser Thr Asn Ile Thr Arg Gly Ala Ser Glu Asp Thr
145 150 155 160
Ile Phe Ile Ala Gly Ile Pro Phe Thr Pro Lys Asn Gln Lys Gln Ser
165 170 175
Gly Val Gly Leu Asn Tyr Gly Val Ser Gly Thr Tyr Gln Phe Lys Leu
180 185 190
Asp Glu Arg Phe Ala Leu Ala Phe Gly Gly Ser Leu Asp Gly Val Lys
195 200 205

Tyr Arg Asp Arg Ala Phe Asp Glu Leu Ser Gly Gln Val Phe Ser Glu
210 215 220
Leu Ser Tyr Arg Thr His Asp Trp Arg Phe Gly Ile Gly Pro Thr Leu
225 230 235 240
Ala Arg Thr Ser Phe Ala Trp Glu Gly His Asn Trp Gly Tyr Gly Val
245 250 255
Gln Gly Tyr Val Gln Lys Arg Leu Gly Asn Ser Gly Asp Thr Ile Arg
260 265 270

Met Thr Ala Arg Met Arg Tyr Leu Asp Tyr Asp Val Gln Asp Tyr His
275 280 285
Asp Gly Val Glu Thr Thr Ile Gly Leu Arg Tyr Gln His Val Phe Ser
290 295 300
Ala Ser Leu Leu Ala Ser Val Gly Ala Thr Ala Thr Arg Met Asn Ala
305 310 315 320
Gln Asn Phe Asn Ala Tyr Thr Ser Ile Arg Pro Asn Leu Glu Val Tyr
325 330 335

Ser Asp Leu Pro Leu Gly Ile Leu Gly Ser Val Ala Ala Gly Tyr Glu
340 345 350
Phe Arg Asn Phe Asp Gly Lys Phe Pro Met Thr Gly Lys Gly Arg Glu
355 360 365
Asp Arg Gln Phe Ser Ala Ser Val Gly Leu Thr Leu Arg Lys Leu Ser
370 375 380

Tyr Lys Asn Ile Ala Pro Arg Leu Glu Tyr Gly Tyr Arg Ile Asn Ser
385 390 395 400

Ser Asn Val Asp Leu Tyr Asp Tyr Asp Ser His Asn Phe Gly Ile Tyr
405 410 415

Leu Thr Lys Lys Tyr
420

<210> 553

<211> 1335

<212> DNA

<213> Polaromonas sp. CF318 SLAM 1

<400> 553

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aacggcctag cgcacgcgga agtcgacgca ctggtcagca acgcccgtag tctgctggac 120

caaagccagg cgcaaaaagc cttcgatctg ctggagccgc aagaggcggc gcgcgcgggc 180

gacccggact tcgacaccgt gctgggcatt gccgcgaacg agaccggcca gtacacccgc 240

gcggtattcg ccctggaacg cgtgctggcc gtgcagccca gcaactcccg ggcacgtgcc 300

gaactcggcc gcgcgctgtt ctccgtcggt gacaccaagg cctcgcggca agtgctgctg 360

gaaaccaagc aggacaacat ccctgccgaa gccgccgcca ccatagacca gttcctgcag 420

gccatagacc gcaccgaaga agccgcccgc tcgtcggtca agcccttcct ggaagccagc 480

ataggttacg acaccaacat caacagcggc cccggcaacc cgaatgtggc cgtgcccgct 540

ttcggcggcc tgatcttcac gctcaatccc gccggcgtcg aaaccaagga cgcgttcatg 600

agcctgggcg gcgggctgtc ggcccgctat gtggtcgacc cgcgctggtc gctgatcggc 660

aacgtctacg gcaacgcgcg cgtcaacagc aaatacaacg acttcaacac cggccaggtc 720

gatgtcaatt tcggcgccag ctaccgctac gacaaacacg agttctcggg cgtcgtgcag 780

gccgggactt acaccgtggc cggctcgcgc gcccgcgacc agcaaggcct ggtcggcgaa 840

tggacctacc gcatcgacgg atttcgccag tggagcacct acatccagtg gggcgacctg 900

agctaccccg gccagtcgct gcgcgacgcg acgcgcacgg tggtcggaac ctcctatgcc 960

cacgccttcc gcgacagcaa catcgtggtc ttcgcgggcg gctacgtcgg aacggaaaag 1020

gagcgcgccg cgggcgttcc gcagctgggc catgaccttg tcggcctgcg caccggcatc 1080

cagaaaacgc tttcggacgc gctggcgctg ttcggcagcc tcgcttacga agaccgcaag 1140

tacggcggcg ccgatccgct cttcctcgtc acccgccatg acaagcagtg gaacctgaac 1200

atgggcctga actgggtgcc cgccaaactg tggcgcgtca cgccccagct ggccctgacc 1260

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cgccgcgact tctga 1335

<210> 554

<211> 444

<212> PRT

<213> Polaromonas sp. CF318 SLAM 1

<400> 554

Met Tyr Ser Lys Asn Lys Leu Phe Ser Gly Gly Val Thr Val Leu Leu

1 5 10 15

Ala Ile Leu Ala Asn Gly Leu Ala His Ala Glu Val Asp Ala Leu Val

20 25 30

Ser Asn Ala Arg Ser Leu Leu Asp Gln Ser Gln Ala Gln Lys Ala Phe

35 40 45

Asp Leu Leu Glu Pro Gln Glu Ala Ala Arg Ala Gly Asp Pro Asp Phe

50 55 60

Asp Thr Val Leu Gly Ile Ala Ala Asn Glu Thr Gly Gln Tyr Thr Arg

65 70 75 80

Ala Val Phe Ala Leu Glu Arg Val Leu Ala Val Gln Pro Ser Asn Ser

85 90 95

Arg Ala Arg Ala Glu Leu Gly Arg Ala Leu Phe Ser Val Gly Asp Thr

100 105 110

Lys Ala Ser Arg Gln Val Leu Leu Glu Thr Lys Gln Asp Asn Ile Pro

115 120 125

Ala Glu Ala Ala Ala Thr Ile Asp Gln Phe Leu Gln Ala Ile Asp Arg

130 135 140

Thr Glu Glu Ala Ala Arg Ser Ser Val Lys Pro Phe Leu Glu Ala Ser

145 150 155 160

Ile Gly Tyr Asp Thr Asn Ile Asn Ser Gly Pro Gly Asn Pro Asn Val

165 170 175

Ala Val Pro Ala Phe Gly Gly Leu Ile Phe Thr Leu Asn Pro Ala Gly

180 185 190

Val Glu Thr Lys Asp Ala Phe Met Ser Leu Gly Gly Gly Leu Ser Ala

195 200 205

Arg Tyr Val Val Asp Pro Arg Trp Ser Leu Ile Gly Asn Val Tyr Gly

210 215 220

Asn Ala Arg Val Asn Ser Lys Tyr Asn Asp Phe Asn Thr Gly Gln Val

225 230 235 240

Asp Val Asn Phe Gly Ala Ser Tyr Arg Tyr Asp Lys His Glu Phe Ser

245 250 255

Gly Val Val Gln Ala Gly Thr Tyr Thr Val Ala Gly Ser Arg Ala Arg

260 265 270

Asp Gln Gln Gly Leu Val Gly Glu Trp Thr Tyr Arg Ile Asp Gly Phe

275 280 285

Arg Gln Trp Ser Thr Tyr Ile Gln Trp Gly Asp Leu Ser Tyr Pro Gly

290 295 300

Gln Ser Leu Arg Asp Ala Thr Arg Thr Val Val Gly Thr Ser Tyr Ala

305 310 315 320

His Ala Phe Arg Asp Ser Asn Ile Val Val Phe Ala Gly Gly Tyr Val

325 330 335

Gly Thr Glu Lys Glu Arg Ala Ala Gly Val Pro Gln Leu Gly His Asp

340 345 350

Leu Val Gly Leu Arg Thr Gly Ile Gln Lys Thr Leu Ser Asp Ala Leu

355 360 365

Ala Leu Phe Gly Ser Leu Ala Tyr Glu Asp Arg Lys Tyr Gly Gly Ala

370 375 380

Asp Pro Leu Phe Leu Val Thr Arg His Asp Lys Gln Trp Asn Leu Asn

385 390 395 400

Met Gly Leu Asn Trp Val Pro Ala Lys Leu Trp Arg Val Thr Pro Gln

405 410 415

Leu Ala Leu Thr Ser Val Lys Ser Asn Val Ala Ile Ser Asp Tyr Lys

420 425 430

Arg Ser Leu Phe Ser Val Thr Val Arg Arg Asp Phe

435 440

<210> 555

<211> 1434

<212> DNA

<213> Providencia rustigianii DSM 4541 SLAM 1

<400> 555

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ctattattgt tttctgcaaa ttcattttct gaacaaaatt atgggcatca acaatatgaa 120

cagataattg aagttttaaa tgaaataaat aacacaagaa ataaatcacc aattataatc 180

cctcttaaaa ttaataaaac tgtcgacgac cttggtttta ttctttatga tttagtcaat 240

cggcagcaat tccaaaaaat tgatgaatta ttacctgtct atctgaatga taaaaatcac 300

gataaaggta tggtggatta tatttcagca gaaagagctt attttaatgg tgattaccca 360

ttgtcactga agttttattt aaaaatagtc actgaaaacc cgagttcagt gttctctgaa 420

atgaagctag ctcatatcta tataaaaaat agctatcatc gtgaagcatt aggtttatat 480

aaaaagataa aaaataaata tcgagtaaat ttacctgaag accgaataaa acagatagat 540

aatgaaatta cagcattaga aaatcgcgct cattggcaag ggaatttcaa tactgactta 600

aagtatgaca ctaactatac ggaggctcac ggtaatgatg aacagcaatg tggtgctatc 660

tggtgcatgc aaggtagtaa aatcaaatcc ggtttggtgt atggcttctc tggaaatgcc 720

aataaaatcc tttggcagaa tcgagggcat tcactgttag ccagtgtcgg tggaaatgta 780

tgggaatatc ctcatcgctc agtaaaacgg cgtttttcaa gttattcatc agtaagctat 840

cagtatcttt acgggaataa aaagatcacg ttttcaccta ttgtagatat taattggcga 900

gggcatttat ttgaccatta cagtgtaggt gcgagcatta ctagcgcata ttctcccagc 960

agtaaacttt atttactgtc taacataatg tataaaaacc aatttttttt cggaaaacga 1020

gaatcgcgtt caggttatga tattaattac agtataacgg caatttattc ggttaatccg 1080

caatggagtt tattctcaaa tttatatggt ggtaaaaata ttgagcaata taaaagtgac 1140

agctatcaag tatcagggtt aaccgtgggg tcaattaatg tatttggcac gaacaagtta 1200

gtcaataaat taataagcag caatcataat tttttcgatt tcgacagttc acttaataca 1260

aagcgacacg atgagtcatg ggctttaaat agccaaataa cgctattagg tcacacattt 1320

ttatcattaa caccaacgct atatattaat tataaattca acgatagtag tgcaaaaata 1380

agctattcct ataataaaag cgaagtgggc attaatttta gtaaaacgtt ttaa 1434

<210> 556

<211> 477

<212> PRT

<213> Providencia rustigianii DSM 4541 SLAM 1

<400> 556

Met Lys Lys Glu Lys Arg Ser Glu Met Lys Lys Ile Ile Asn Lys Ile
1 5 10 15

Glu Val Leu Ile Leu Leu Leu Phe Ser Ala Asn Ser Phe Ser Glu Gln

20 25 30

Asn Tyr Gly His Gln Gln Tyr Glu Gln Ile Ile Glu Val Leu Asn Glu
35 40 45

Ile Asn Asn Thr Arg Asn Lys Ser Pro Ile Ile Ile Pro Leu Lys Ile
50 55 60

Asn Lys Thr Val Asp Asp Leu Gly Phe Ile Leu Tyr Asp Leu Val Asn
65 70 75 80

Arg Gln Gln Phe Gln Lys Ile Asp Glu Leu Leu Pro Val Tyr Leu Asn

85 90 95

Asp Lys Asn His Asp Lys Gly Met Val Asp Tyr Ile Ser Ala Glu Arg
100 105 110

Ala Tyr Phe Asn Gly Asp Tyr Pro Leu Ser Leu Lys Phe Tyr Leu Lys
115 120 125

Ile Val Thr Glu Asn Pro Ser Ser Val Phe Ser Glu Met Lys Leu Ala
130 135 140

His Ile Tyr Ile Lys Asn Ser Tyr His Arg Glu Ala Leu Gly Leu Tyr

145 150 155 160

Lys Lys Ile Lys Asn Lys Tyr Arg Val Asn Leu Pro Glu Asp Arg Ile
165 170 175

Lys Gln Ile Asp Asn Glu Ile Thr Ala Leu Glu Asn Arg Ala His Trp
180 185 190

Gln Gly Asn Phe Asn Thr Asp Leu Lys Tyr Asp Thr Asn Tyr Thr Glu
195 200 205

Ala His Gly Asn Asp Glu Gln Gln Cys Gly Ala Ile Trp Cys Met Gln

210 215 220

Gly Ser Lys Ile Lys Ser Gly Leu Val Tyr Gly Phe Ser Gly Asn Ala

225 230 235 240

Asn Lys Ile Leu Trp Gln Asn Arg Gly His Ser Leu Leu Ala Ser Val

245 250 255

Gly Gly Asn Val Trp Glu Tyr Pro His Arg Ser Val Lys Arg Arg Phe

260 265 270

Ser Ser Tyr Ser Ser Val Ser Tyr Gln Tyr Leu Tyr Gly Asn Lys Lys

275 280 285

Ile Thr Phe Ser Pro Ile Val Asp Ile Asn Trp Arg Gly His Leu Phe

290 295 300

Asp His Tyr Ser Val Gly Ala Ser Ile Thr Ser Ala Tyr Ser Pro Ser

305 310 315 320

Ser Lys Leu Tyr Leu Leu Ser Asn Ile Met Tyr Lys Asn Gln Phe Phe

325 330 335

Phe Gly Lys Arg Glu Ser Arg Ser Gly Tyr Asp Ile Asn Tyr Ser Ile

340 345 350

Thr Ala Ile Tyr Ser Val Asn Pro Gln Trp Ser Leu Phe Ser Asn Leu

355 360 365

Tyr Gly Gly Lys Asn Ile Glu Gln Tyr Lys Ser Asp Ser Tyr Gln Val

370 375 380

Ser Gly Leu Thr Val Gly Ser Ile Asn Val Phe Gly Thr Asn Lys Leu

385 390 395 400

Val Asn Lys Leu Ile Ser Ser Asn His Asn Phe Phe Asp Phe Asp Ser

405 410 415

Ser Leu Asn Thr Lys Arg His Asp Glu Ser Trp Ala Leu Asn Ser Gln

420 425 430

Ile Thr Leu Leu Gly His Thr Phe Leu Ser Leu Thr Pro Thr Leu Tyr

435 440 445

Ile Asn Tyr Lys Phe Asn Asp Ser Ser Ala Lys Ile Ser Tyr Ser Tyr

450 455 460

Asn Lys Ser Glu Val Gly Ile Asn Phe Ser Lys Thr Phe

465 470 475

<210> 557

<211> 1500

<212> DNA

<213> Pseudomonas sp. CBZ-4 SLAM 1

<400> 557

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ctgttcatgg ccccgacggt gttcgccgcc gaccaggaca ccagcctgcg cctcaaccag 120

agcatcgagt accgcgccaa caagcaagag cgcgaattgc tcaaggacga attgcccagt 180

gacggcgccg cgccggcgct gaccatcgac ggccagacct acagcgtcgg caacaacctc 240

gacgagctgg gccgcgcggt gtacctgagt gtccagcgcc agcaatggcc gaacgcccgc 300

gactacctca agcgctacac cgccctgccc ggccacgacc cgatgctcac cgcctacgcc 360

aacggcggcc tggcccgtgc cgatggcgat ctggacagcg ccgaacggta ttaccaggac 420

ctgctggcga tccagcccga cttcctgccc gggcgcctgg aactggcgcg ggtgcagttc 480

gagaaccgca aagaccgcga ttcgaaacac gtcttcgcac agatcagcag cagcctcagc 540

ccgtcggacg cccaggccat gggcctgggc aagaccgtcg acagctttat ccaggccctc 600

gaccaccgcg aagactggca aggctcgttc gccatcggcc cgacctggag cgacaacctc 660

aaccagtcat ccgaaggcag cgtgacttat cgctaccaga ccgctgaaga aacctacgtg 720

gtcaagcaat ccctgcccaa ggccgtgtcg gcccacggcc aggattacga ggccacgctc 780

aacaaacgca tcgccatcag cggccatcac gggctgttcg tgcgctcgct tttgtacggc 840

caagcgtacg aaaaagagag caagtacaac gaagccaccg tgatcaacaa cgccggctac 900

agctaccacg atgcgcgcaa ccagtacgcc ttcgggccgt cgtacgagtt caacaccatt 960

ggcgacaacg ccatgtacag cgcctggggc ctgcgcggtg agtggattca cacgctgtcg 1020

gccacgcgca tgttcaagct cgaaggcgag tacaaggaca tgacgtacaa acaccagatc 1080

aacagcaacc tcgacggcgg tatcagctcg gtctacgcca ccctgtggca ggcattgccc 1140

cggcagtgga cgctgttcgg cggcgtcgac atcaccgaac gcaacgcccg cgaccgcgtc 1200

gcggcgtacc tgcaaaaagg ggtgcgcctg ggcgtcgcca aggatttcga catcggcgtg 1260

agcgccgtgc tgttcgcctc gtaccgcaag cgtcaatacg atgcctacag cgcaatcgtc 1320

gatggccgac gcaatgaaga tgagcaaggc tacaccttca tcctgcgtgc cccacggctg 1380

gcggtgtacg acgtggtgcc cagtcttacg gtcaaataca acaaggtgca gagcaacatc 1440

gactggattt attcctacga caaaaacagc atcagcctaa aactggagaa acagttctag 1500

<210> 558

<211> 477

<212> PRT

<213> Pseudomonas sp. CBZ-4 SLAM 1

<400> 558

Met Ala Pro Thr Val Phe Ala Ala Asp Gln Asp Thr Ser Leu Arg Leu
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Asn Gln Ser Ile Glu Tyr Arg Ala Asn Lys Gln Glu Arg Glu Leu Leu
20 25 30

Lys Asp Glu Leu Pro Ser Asp Gly Ala Ala Pro Ala Leu Thr Ile Asp
35 40 45

Gly Gln Thr Tyr Ser Val Gly Asn Asn Leu Asp Glu Leu Gly Arg Ala
50 55 60

Val Tyr Leu Ser Val Gln Arg Gln Gln Trp Pro Asn Ala Arg Asp Tyr
65 70 75 80

Leu Lys Arg Tyr Thr Ala Leu Pro Gly His Asp Pro Met Leu Thr Ala
85 90 95

Tyr Ala Asn Gly Gly Leu Ala Arg Ala Asp Gly Asp Leu Asp Ser Ala
100 105 110

Glu Arg Tyr Tyr Gln Asp Leu Leu Ala Ile Gln Pro Asp Phe Leu Pro
115 120 125

Gly Arg Leu Glu Leu Ala Arg Val Gln Phe Glu Asn Arg Lys Asp Arg
130 135 140

Asp Ser Lys His Val Phe Ala Gln Ile Ser Ser Ser Leu Ser Pro Ser
145 150 155 160

Asp Ala Gln Ala Met Gly Leu Gly Lys Thr Val Asp Ser Phe Ile Gln
165 170 175

Ala Leu Asp His Arg Glu Asp Trp Gln Gly Ser Phe Ala Ile Gly Pro
180 185 190

Thr Trp Ser Asp Asn Leu Asn Gln Ser Ser Glu Gly Ser Val Thr Tyr

195 200 205

Arg Tyr Gln Thr Ala Glu Glu Thr Tyr Val Val Lys Gln Ser Leu Pro

210 215 220

Lys Ala Val Ser Ala His Gly Gln Asp Tyr Glu Ala Thr Leu Asn Lys

225 230 235 240

Arg Ile Ala Ile Ser Gly His His Gly Leu Phe Val Arg Ser Leu Leu

245 250 255

Tyr Gly Gln Ala Tyr Glu Lys Glu Ser Lys Tyr Asn Glu Ala Thr Val

260 265 270

Ile Asn Asn Ala Gly Tyr Ser Tyr His Asp Ala Arg Asn Gln Tyr Ala

275 280 285

Phe Gly Pro Ser Tyr Glu Phe Asn Thr Ile Gly Asp Asn Ala Met Tyr

290 295 300

Ser Ala Trp Gly Leu Arg Gly Glu Trp Ile His Thr Leu Ser Ala Thr

305 310 315 320

Arg Met Phe Lys Leu Glu Gly Glu Tyr Lys Asp Met Thr Tyr Lys His

325 330 335

Gln Ile Asn Ser Asn Leu Asp Gly Gly Ile Ser Ser Val Tyr Ala Thr

340 345 350

Leu Trp Gln Ala Leu Pro Arg Gln Trp Thr Leu Phe Gly Gly Val Asp

355 360 365

Ile Thr Glu Arg Asn Ala Arg Asp Arg Val Ala Ala Tyr Leu Gln Lys

370 375 380

Gly Val Arg Leu Gly Val Ala Lys Asp Phe Asp Ile Gly Val Ser Ala

385 390 395 400

Val Leu Phe Ala Ser Tyr Arg Lys Arg Gln Tyr Asp Ala Tyr Ser Ala

405 410 415

Ile Val Asp Gly Arg Arg Asn Glu Asp Glu Gln Gly Tyr Thr Phe Ile

420 425 430

Leu Arg Ala Pro Arg Leu Ala Val Tyr Asp Val Val Pro Ser Leu Thr

435 440 445

Val Lys Tyr Asn Lys Val Gln Ser Asn Ile Asp Trp Ile Tyr Ser Tyr

450 455 460

Asp Lys Asn Ser Ile Ser Leu Lys Leu Glu Lys Gln Phe

465 470 475

<210> 559

<211> 1488

<212> DNA

<213> Pseudomonas sp. CBZ-4 SLAM 2

<400> 559

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accgcctggg ccgatgaaga cgacacccgg caactgctga acaagatcga ccgcaccatg 120

gccgagcgcg agcgcgccca tctggtggat accgacccgg ccaaggacaa cgcctcgctg 180

atcaccattg agggccgtac ctacaacgta cagaacaccc tggaagacct cggccctgcg 240

atctacgtca cgctgaattt gcagcagtgg tccaaggtgc gccagttcgt cgagcgctac 300

cgccagttgc ccggccatga gccggcgttg gtgtcgatgg ctgagggcat gctggcccgt 360

caggacaagc actaccgcga agcgattgcc agcctgcgca gggcggtggc gcaaaatcct 420

tcattcgtcc gggcgaagct ggagctggcg cgagcgctgt tcgaagacaa tcaatcccgc 480

gaagccaagg cgttgtttga agaagtggcg caaagcacgg tgcccgagca ggtggtgccg 540

gtgctggagg ggtatcaagg cgcattgcgc gagcgcgaca gttggcatgg ttcggtgtcg 600

atgggcactg gctacaacag caatatcaac caggccaacg gcatgaccac gcgtactcag 660

gtgtgcagtt tttttgagtg cgtcgagacc aaccgcaaga tgcccgtgcc aatcaaatcc 720

tccagcctgg tgtatgacgc ggtggccgag cggcgttttc agatcgaggg caaccaccac 780

ctgctggtgc gcgggttgag ttacggcaat tactaccatc ggcacaagga agacgagccg 840

cagacctatt acgacgacaa caccagtgtg atctacgttg gctacaacta cttgagtgcg 900

ctggatgatg tgtcggtctc accgctgttc gagagttact ggggtgatcg acataacaag 960

tatcaggcga cggggctgcg taccgagtgg aaacacacac tgaccgagcg cttgcaactt 1020

accgcccagg cgcaacagaa gcattttcgc ttccagggtg aagagcgcga ttacttcgag 1080

aattacgacg agcgcatggt gggcggttct gcttcctacc tgctgggtag ccagaccctg 1140

gtgtacggcg gcctgaccta cacgcgccgc acccagccgc aggaatcggc ccgcaacaag 1200

gagtacatgg ccagcctggg tctgtatcgg atgtttgatg tggggatcaa tctgaatgcc 1260

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gaagatcgcc agcagatcta tatcgccaac ctggccgtac cgcgattcaa gttcgccggc 1380

ctggtgccca gcctttacgt gaagcgtacg gtcaacgcga gcagcatcga ctgggcatac 1440

acctaccgcc agaccgaagt ggcactcaaa gtcgaaaaga gcttttag 1488

<210> 560

<211> 495

<212> PRT

<213> Pseudomonas sp. CBZ-4 SLAM 2

<400> 560

Met Pro Leu Cys Leu Pro Leu Arg Leu Ala Leu Thr Leu Phe Leu Ser
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Ser Leu Ala Cys Thr Ala Trp Ala Asp Glu Asp Asp Thr Arg Gln Leu
20 25 30

Leu Asn Lys Ile Asp Arg Thr Met Ala Glu Arg Glu Arg Ala His Leu
35 40 45

Val Asp Thr Asp Pro Ala Lys Asp Asn Ala Ser Leu Ile Thr Ile Glu
50 55 60

Gly Arg Thr Tyr Asn Val Gln Asn Thr Leu Glu Asp Leu Gly Pro Ala
65 70 75 80

Ile Tyr Val Thr Leu Asn Leu Gln Gln Trp Ser Lys Val Arg Gln Phe
85 90 95

Val Glu Arg Tyr Arg Gln Leu Pro Gly His Glu Pro Ala Leu Val Ser
100 105 110

Met Ala Glu Gly Met Leu Ala Arg Gln Asp Lys His Tyr Arg Glu Ala
115 120 125

Ile Ala Ser Leu Arg Arg Ala Val Ala Gln Asn Pro Ser Phe Val Arg
130 135 140

Ala Lys Leu Glu Leu Ala Arg Ala Leu Phe Glu Asp Asn Gln Ser Arg
145 150 155 160

Glu Ala Lys Ala Leu Phe Glu Glu Val Ala Gln Ser Thr Val Pro Glu
165 170 175

Gln Val Val Pro Val Leu Glu Gly Tyr Gln Gly Ala Leu Arg Glu Arg
180 185 190

Asp Ser Trp His Gly Ser Val Ser Met Gly Thr Gly Tyr Asn Ser Asn
195 200 205
Ile Asn Gln Ala Asn Gly Met Thr Thr Arg Thr Gln Val Cys Ser Phe
210 215 220
Phe Glu Cys Val Glu Thr Asn Arg Lys Met Pro Val Pro Ile Lys Ser
225 230 235 240

Ser Ser Leu Val Tyr Asp Ala Val Ala Glu Arg Arg Phe Gln Ile Glu
245 250 255
Gly Asn His His Leu Leu Val Arg Gly Leu Ser Tyr Gly Asn Tyr Tyr
260 265 270
His Arg His Lys Glu Asp Glu Pro Gln Thr Tyr Tyr Asp Asp Asn Thr
275 280 285
Ser Val Ile Tyr Val Gly Tyr Asn Tyr Leu Ser Ala Leu Asp Asp Val
290 295 300

Ser Val Ser Pro Leu Phe Glu Ser Tyr Trp Gly Asp Arg His Asn Lys
305 310 315 320
Tyr Gln Ala Thr Gly Leu Arg Thr Glu Trp Lys His Thr Leu Thr Glu
325 330 335
Arg Leu Gln Leu Thr Ala Gln Ala Gln Gln Lys His Phe Arg Phe Gln
340 345 350
Gly Glu Glu Arg Asp Tyr Phe Glu Asn Tyr Asp Glu Arg Met Val Gly
355 360 365

Gly Ser Ala Ser Tyr Leu Leu Gly Ser Gln Thr Leu Val Tyr Gly Gly
370 375 380
Leu Thr Tyr Thr Arg Arg Thr Gln Pro Gln Glu Ser Ala Arg Asn Lys
385 390 395 400
Glu Tyr Met Ala Ser Leu Gly Leu Tyr Arg Met Phe Asp Val Gly Ile
405 410 415
Asn Leu Asn Ala Thr Ala Leu Tyr Arg Arg Thr Cys Tyr Asp Glu Ala
420 425 430

Asp Ala Phe Leu Gly Gly Leu Arg Glu Asp Arg Gln Gln Ile Tyr Ile

435 440 445

Ala Asn Leu Ala Val Pro Arg Phe Lys Phe Ala Gly Leu Val Pro Ser

450 455 460

Leu Tyr Val Lys Arg Thr Val Asn Ala Ser Ser Ile Asp Trp Ala Tyr

465 470 475 480

Thr Tyr Arg Gln Thr Glu Val Ala Leu Lys Val Glu Lys Ser Phe

485 490 495

<210> 561

<211> 1434

<212> DNA

<213> Pseudomonas sp. FH4 SLAM 1

<400> 561

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gagtaccgcg ccaaccagca agagcgcgag ttgctcaagg atgaactgcc cagcgacggc 120

gccgcgccac tgttgaacat cgatggccag gactacaccg tcggcaacaa cctggatgag 180

ttgggccgtg cggtgtacgt gtccctctcg cgccagaact ggccacaggc cagggactat 240

ctcaaacgct acaccgccct gcccggccac gacccgatgc tcaccgccta tgccaagggc 300

ggcctggccc gcgccgatgg cgatctggaa caggccgaag attattaccg gcagttgctg 360

gcgatacagt ccgacttcct gccgggccgc ctggagctgg cgcgggtgct gttcgagaac 420

cgcaaggatg gcgagtccaa cgccgtattc cagcagatca gcagcggcct cagccccgcc 480

gacgcgcagg ccatgggcct gggcaagacc gtcgacagtt tcaagcaggc cctggatcac 540

cgtgaagact ggcaaggctc cttcgccatc ggcccgacct ggggcaaaaa cctcaatcag 600

tcacccgaaa gcacggtgac gtatcgctac gtcactgccg aagaaaccat tctggtccaa 660

cgctcgctgc ccaaggccgt gtctgcccac ggcgcggatt acgaggccac gctcaacaaa 720

cgcatcgccc tcagcggcca tcacggggta ttcatgcgct cgctgttgta cggccaggcg 780

tatgaaaaag agagcaagta caacgaaggc acagtgatca acaatgccgg ctacagctac 840

cacgatgcca agaaccagta ctccttcggg ccgtcgtatg agttcaacac cattgccgac 900

aacgccatgt acagcgcctg ggggctgcgg ggcgaatgga tccacacgtt atcggccacg 960

cgcatgttca agctcgaagg cgaatacaag gacatggcct acaagcacga cctcaatacc 1020

aacctcgacg gcggcatcag ttcggtctac gccaccctat ggcaggcact gccccagcgc 1080

tggacgctgt tcggcggcgt ggacctgagc cagcgcaacg cccaggaccg tacccaggct 1140

tacctgcaaa aaggtgtgcg gctgggcgtc gccaaggatt tcgaggtggg tgtcagcgcc 1200

gtgctgttcg cgtcataccg caagcgccaa tacgatgcct acagcgcgat tgttgatgac 1260

cgtcgcagcg acgatgaaca aggctacacg tttatcctgc gcgccccacg cctggcggtg 1320

atggatgtgg tgcccagtct gacagtcaag tacaacaagg tcgtaagcaa tgtcgactgg 1380

ctttattcct acgacaaaaa cagcatcagc ctaaagctgg aaaagcagtt ttaa 1434

<210> 562

<211> 477

<212> PRT

<213> Pseudomonas sp. FH4 SLAM 1

<400> 562

Met Ala Pro Ala Val Phe Ala Ala Asp Gln Asp Thr Ser Leu Arg Leu
1 5 10 15

Asn Gln Thr Ile Glu Tyr Arg Ala Asn Gln Gln Glu Arg Glu Leu Leu
20 25 30

Lys Asp Glu Leu Pro Ser Asp Gly Ala Ala Pro Leu Leu Asn Ile Asp
35 40 45

Gly Gln Asp Tyr Thr Val Gly Asn Asn Leu Asp Glu Leu Gly Arg Ala
50 55 60

Val Tyr Val Ser Leu Ser Arg Gln Asn Trp Pro Gln Ala Arg Asp Tyr
65 70 75 80

Leu Lys Arg Tyr Thr Ala Leu Pro Gly His Asp Pro Met Leu Thr Ala
85 90 95

Tyr Ala Lys Gly Gly Leu Ala Arg Ala Asp Gly Asp Leu Glu Gln Ala
100 105 110

Glu Asp Tyr Tyr Arg Gln Leu Leu Ala Ile Gln Ser Asp Phe Leu Pro
115 120 125

Gly Arg Leu Glu Leu Ala Arg Val Leu Phe Glu Asn Arg Lys Asp Gly
130 135 140

Glu Ser Asn Ala Val Phe Gln Gln Ile Ser Ser Gly Leu Ser Pro Ala
145 150 155 160

Asp Ala Gln Ala Met Gly Leu Gly Lys Thr Val Asp Ser Phe Lys Gln

165 170 175

Ala Leu Asp His Arg Glu Asp Trp Gln Gly Ser Phe Ala Ile Gly Pro

180 185 190

Thr Trp Gly Lys Asn Leu Asn Gln Ser Pro Glu Ser Thr Val Thr Tyr

195 200 205

Arg Tyr Val Thr Ala Glu Glu Thr Ile Leu Val Gln Arg Ser Leu Pro

210 215 220

Lys Ala Val Ser Ala His Gly Ala Asp Tyr Glu Ala Thr Leu Asn Lys

225 230 235 240

Arg Ile Ala Leu Ser Gly His His Gly Val Phe Met Arg Ser Leu Leu

245 250 255

Tyr Gly Gln Ala Tyr Glu Lys Glu Ser Lys Tyr Asn Glu Gly Thr Val

260 265 270

Ile Asn Asn Ala Gly Tyr Ser Tyr His Asp Ala Lys Asn Gln Tyr Ser

275 280 285

Phe Gly Pro Ser Tyr Glu Phe Asn Thr Ile Ala Asp Asn Ala Met Tyr

290 295 300

Ser Ala Trp Gly Leu Arg Gly Glu Trp Ile His Thr Leu Ser Ala Thr

305 310 315 320

Arg Met Phe Lys Leu Glu Gly Glu Tyr Lys Asp Met Ala Tyr Lys His

325 330 335

Asp Leu Asn Thr Asn Leu Asp Gly Gly Ile Ser Ser Val Tyr Ala Thr

340 345 350

Leu Trp Gln Ala Leu Pro Gln Arg Trp Thr Leu Phe Gly Gly Val Asp

355 360 365

Leu Ser Gln Arg Asn Ala Gln Asp Arg Thr Gln Ala Tyr Leu Gln Lys

370 375 380

Gly Val Arg Leu Gly Val Ala Lys Asp Phe Glu Val Gly Val Ser Ala

385 390 395 400

Val Leu Phe Ala Ser Tyr Arg Lys Arg Gln Tyr Asp Ala Tyr Ser Ala

405 410 415

Ile Val Asp Asp Arg Arg Ser Asp Asp Glu Gln Gly Tyr Thr Phe Ile
420 425 430

Leu Arg Ala Pro Arg Leu Ala Val Met Asp Val Val Pro Ser Leu Thr
435 440 445

Val Lys Tyr Asn Lys Val Val Ser Asn Val Asp Trp Leu Tyr Ser Tyr
450 455 460

Asp Lys Asn Ser Ile Ser Leu Lys Leu Glu Lys Gln Phe
465 470 475

<210> 563

<211> 1500

<212> DNA

<213> Psychrobacter sp. 1501(2011) SLAM 1

<400> 563

atgattcatt ctcaatataa aaaaatatat ggttttatgc tgctaatatt aagttcaata 60

tcaacagtga gcttcgcaaa tgaagtgcct acggattcta ttgcaccaca agatcattca 120

ctcgaatctt atcaaaatat tgataaagta attgaaccaa tcgaaaatat aaaattagcg 180

actaatctac cttctgaaag taaaagccct aaattgtcta aggaagaaag taaagattat 240

cttaagcaaa accctgaaga gttcgaagaa cttctaagtt tactattggt tcaagggaat 300

gcagaaactc ttaaagaact tttgcctata tatcagcagg tacctaatta cgatccgtct 360

gtaattgact ggggcaacgc tattatagct acccaaaatg gagattttga taaagcagtt 420

gctctatatc gaacccttaa ttctcaactt ccaaatgttg ctatattaag atttcaaatg 480

gcaatggcgc tattttataa ccaacagttt gaagcggcta aattggaatt tgaaaagctg 540

cgtagtggta cagaatctga agaagacata gcggttataa ataaatattt agaagctatt 600

aatgatcagg acagctggga tgtatatgcc tctgtatcct atttagatga ttcaaatata 660

accaattcac ctgaacaagg tactcagctt gataacggca atagtcaagt gacttattcc 720

tccccacgtc aagagggcaa gggactaaac tattatttga gtgctgataa aaaatggaga 780

aaggacaata agcttttcac tgtgcttcat ttaaatagct ttggtaaata ttattgggat 840

aacaaaaatt ttaatgatgt tactgccggt attgggactg gttttggcta tcaaaatgca 900

gcgacagaag ttgaaattgg tccttttac aacaagcgtt ggtatggtca aggcaacaaa 960

ggagatggtg atttacatcc ctatgcagaa actatcggcc tgatgaccca tataaatcaa 1020

tggattaatc ctaagtttcg ataccaaggt gttttaagat atggaaagac cagttatata 1080

gagcaatatg atcataatga tggtaaagat ctatacttat cgaataccgg tatttacttt 1140

ccaaatggtc aacagttttg gatatttggt ttagattatt caaataaaaa ctctgaagac 1200

gattctgcaa cttttgatcg taccggttta aggttaggtt ggggtcaaac atggccaaag 1260

gggtactcta ctaaatttaa tatagggtat gcgcaacgag attataaagc tgaagatttc 1320

ttcggtatta aacgtgaaaa tgaagagtac agtacaggac tatctttttg gaaacgtgat 1380

tttaccgtat tcggtttaac cccccgtctt gagttagatt attacaaagt tgaaagtaac 1440

tctccattcg aagaatacga taaaaccaat gtatcagttg aactcactaa gtctttttga 1500

<210> 564

<211> 499

<212> PRT

<213> Psychrobacter sp. 1501(2011) SLAM 1

<400> 564

Met Ile His Ser Gln Tyr Lys Lys Ile Tyr Gly Phe Met Leu Leu Ile
1 5 10 15

Leu Ser Ser Ile Ser Thr Val Ser Phe Ala Asn Glu Val Pro Thr Asp
20 25 30

Ser Ile Ala Pro Gln Asp His Ser Leu Glu Ser Tyr Gln Asn Ile Asp
35 40 45

Lys Val Ile Glu Pro Ile Glu Asn Ile Lys Leu Ala Thr Asn Leu Pro

50 55 60

Ser Glu Ser Lys Ser Pro Lys Leu Ser Lys Glu Glu Ser Lys Asp Tyr
65 70 75 80

Leu Lys Gln Asn Pro Glu Glu Phe Glu Glu Leu Leu Ser Leu Leu Leu
85 90 95

Val Gln Gly Asn Ala Glu Thr Leu Lys Glu Leu Leu Pro Ile Tyr Gln
100 105 110

Gln Val Pro Asn Tyr Asp Pro Ser Val Ile Asp Trp Gly Asn Ala Ile

115 120 125

Ile Ala Thr Gln Asn Gly Asp Phe Asp Lys Ala Val Ala Leu Tyr Arg
130 135 140

Thr Leu Asn Ser Gln Leu Pro Asn Val Ala Ile Leu Arg Phe Gln Met
145 150 155 160

Ala Met Ala Leu Phe Tyr Asn Gln Gln Phe Glu Ala Ala Lys Leu Glu
165 170 175
Phe Glu Lys Leu Arg Ser Gly Thr Glu Ser Glu Glu Asp Ile Ala Val

180 185 190
Ile Asn Lys Tyr Leu Glu Ala Ile Asn Asp Gln Asp Ser Trp Asp Val
195 200 205
Tyr Ala Ser Val Ser Tyr Leu Asp Asp Ser Asn Ile Thr Asn Ser Pro
210 215 220
Glu Gln Gly Thr Gln Leu Asp Asn Gly Asn Ser Gln Val Thr Tyr Ser
225 230 235 240
Ser Pro Arg Gln Glu Gly Lys Gly Leu Asn Tyr Tyr Leu Ser Ala Asp

245 250 255
Lys Lys Trp Arg Lys Asp Asn Lys Leu Phe Thr Val Leu His Leu Asn
260 265 270
Ser Phe Gly Lys Tyr Tyr Trp Asp Asn Lys Asn Phe Asn Asp Val Thr
275 280 285
Ala Gly Ile Gly Thr Gly Phe Gly Tyr Gln Asn Ala Ala Thr Glu Val
290 295 300
Glu Ile Gly Pro Phe Tyr Asn Lys Arg Trp Tyr Gly Gln Gly Asn Lys

305 310 315 320
Gly Asp Gly Asp Leu His Pro Tyr Ala Glu Thr Ile Gly Leu Met Thr
325 330 335
His Ile Asn Gln Trp Ile Asn Pro Lys Phe Arg Tyr Gln Gly Val Leu
340 345 350
Arg Tyr Gly Lys Thr Ser Tyr Ile Glu Gln Tyr Asp His Asn Asp Gly
355 360 365
Lys Asp Leu Tyr Leu Ser Asn Thr Gly Ile Tyr Phe Pro Asn Gly Gln

370 375 380
Gln Phe Trp Ile Phe Gly Leu Asp Tyr Ser Asn Lys Asn Ser Glu Asp
385 390 395 400
Asp Ser Ala Thr Phe Asp Arg Thr Gly Leu Arg Leu Gly Trp Gly Gln

405 410 415

Thr Trp Pro Lys Gly Tyr Ser Thr Lys Phe Asn Ile Gly Tyr Ala Gln

420 425 430

Arg Asp Tyr Lys Ala Glu Asp Phe Phe Gly Ile Lys Arg Glu Asn Glu

435 440 445

Glu Tyr Ser Thr Gly Leu Ser Phe Trp Lys Arg Asp Phe Thr Val Phe

450 455 460

Gly Leu Thr Pro Arg Leu Glu Leu Asp Tyr Tyr Lys Val Glu Ser Asn

465 470 475 480

Ser Pro Phe Glu Glu Tyr Asp Lys Thr Asn Val Ser Val Glu Leu Thr

485 490 495

Lys Ser Phe

<210> 565

<211> 1475

<212> DNA

<213> Psychrobacter sp. JCM 18903 SLAM 1

<400> 565

atggcagcac cagaattacc agaaataaaa cccgatcttg atcaagctgc ggagttgctt 60

agacgcgaaa atcagacttc tgtgtcagat cctactgcac cctctaccgc tatatcagat 120

tctgaagcac aagatgctat tagaagtcgt cagcaacttg ccaagcaacg gcttataatc 180

tagaagcgct aaaagccaat ccagcagcgt ttagcaagta tttaaatgat gcattgtctg 240

cacaagatat ggtaacggtt aaagagttat tgccgcatta caaagcgtta aaaaccaatg 300

atccaatgct gatcaaattc gctgatgcgc tcatatatcg cagtgaagcc aaaaacaaac 360

aagccattgc catttatcgt gacatgcttg caactgatcc agactttcat ccggtacgtt 420

tgaatatggc cattgccatg caagcagaca agcagtatgt ggcggcaaag gagcagtttc 480

taaaattgca ggcagttgag ttaccagcac ccgtcatggc tagggtgcaa aactcattgg 540

cgcagatcaa tagttcagaa aaatggcaat tcaatgcctc tgccagttat gtaagagaga 600

ataatattaa tgacgcgcca tcgtcatcta ttcaatctga cttagggcgc tcgattgagc 660

aaaaatcagc caatggcctt caggtgtctg ctagcgcgaa taaacgcttt aacttaccga 720

ataatttcta tgctacagtg ggtggtaatg catccctaaa aggatattgg gatgagcctg 780

actataacga ttatctattc actgcctcta cgggagtcgg ctacgatgat gccaaaaacg 840

acgtttcttt gaccccattt atcaccaagc gttattatga tgaagcgccc tatagtttgc 900

gtaaaggcgc aactgtcagc ggctcacgct gggttaagcc caagctaaaa ctgtcagcga 960

ctggtatttt gtccaaagaa acttttgaag atgatagcaa tgcaaatcgc gaaacagatg 1020

gcagattcct tggtttaaat gctttttata ttaaggatgc caaagaatac ttttatgggg 1080

gtgtaggtaa ttatcgaaac gatgtaccca aatcgagtat tattagctat gatcgtaatt 1140

ctgtaaatgc tggttggggt cgtgaatgga ggcgtggact ctccacatta gcaacagtag 1200

gttatggtat caaggactat gacgatcctg cagatgctta tccagcagga agtggagcat 1260

ggaaaggcta ttataatgcg gtaggcggcg tgccgggctc aaccagagaa gacaaatcca 1320

cttcattagg tttgcaagtc tggaaacgtg actttacctt gtatggtttg acaccgcgtt 1380

tggtctttga ttatgaaaca acttcaagta actttgctta ctatgatgat cgggatgaaa 1440

agtctgcaac ggtgttatta acaaagacct tttga 1475

<210> 566

<211> 491

<212> PRT

<213> Psychrobacter sp. JCM 18903 SLAM 1

<400> 566

Met Ala Ala Pro Glu Leu Pro Glu Ile Lys Pro Asp Leu Asp Gln Ala

1 5 10 15

Ala Glu Leu Leu Arg Arg Glu Asn Gln Thr Ser Val Ser Asp Pro Thr

20 25 30

Ala Pro Ser Thr Ala Ile Ser Asp Ser Glu Ala Gln Asp Ala Ile Arg

35 40 45

Ser Arg Gln Gln Leu Ala Lys Gln Arg Leu Tyr Asn Leu Glu Ala Leu

50 55 60

Lys Ala Asn Pro Ala Ala Phe Ser Lys Tyr Leu Asn Asp Ala Leu Ser

65 70 75 80

Ala Gln Asp Met Val Thr Val Lys Glu Leu Leu Pro His Tyr Lys Ala

85 90 95

Leu Lys Thr Asn Asp Pro Met Leu Ile Lys Phe Ala Asp Ala Leu Ile

100 105 110

Tyr Arg Ser Glu Ala Lys Asn Lys Gln Ala Ile Ala Ile Tyr Arg Asp

115 120 125

Met Leu Ala Thr Asp Pro Asp Phe His Pro Val Arg Leu Asn Met Ala

130 135 140

Ile Ala Met Gln Ala Asp Lys Gln Tyr Val Ala Ala Lys Glu Gln Phe

145 150 155 160

Leu Lys Leu Gln Ala Val Glu Leu Pro Ala Pro Val Met Ala Arg Val

165 170 175

Gln Asn Ser Leu Ala Gln Ile Asn Ser Ser Glu Lys Trp Gln Phe Asn

180 185 190

Ala Ser Ala Ser Tyr Val Arg Glu Asn Asn Ile Asn Asp Ala Pro Ser

195 200 205

Ser Ser Ile Gln Ser Asp Leu Gly Arg Ser Ile Glu Gln Lys Ser Ala

210 215 220

Asn Gly Leu Gln Val Ser Ala Ser Ala Asn Lys Arg Phe Asn Leu Pro

225 230 235 240

Asn Asn Phe Tyr Ala Thr Val Gly Gly Asn Ala Ser Leu Lys Gly Tyr

245 250 255

Trp Asp Glu Pro Asp Tyr Asn Asp Tyr Leu Phe Thr Ala Ser Thr Gly

260 265 270

Val Gly Tyr Asp Asp Ala Lys Asn Asp Val Ser Leu Thr Pro Phe Ile

275 280 285

Thr Lys Arg Tyr Tyr Asp Glu Ala Pro Tyr Ser Leu Arg Lys Gly Ala

290 295 300

Thr Val Ser Gly Ser Arg Trp Val Lys Pro Lys Leu Lys Leu Ser Ala

305 310 315 320

Thr Gly Ile Leu Ser Lys Glu Thr Phe Glu Asp Asp Ser Asn Ala Asn

325 330 335

Arg Glu Thr Asp Gly Arg Phe Leu Gly Leu Asn Ala Phe Tyr Ile Lys

340 345 350

Asp Ala Lys Glu Tyr Phe Tyr Gly Gly Val Gly Asn Tyr Arg Asn Asp

355 360 365

Val Pro Lys Ser Ser Ile Ile Ser Tyr Asp Arg Asn Ser Val Asn Ala

370 375 380

Gly Trp Gly Arg Glu Trp Arg Arg Gly Leu Ser Thr Leu Ala Thr Val

385 390 395 400

Gly Tyr Gly Ile Lys Asp Tyr Asp Asp Pro Ala Asp Ala Tyr Pro Ala

405 410 415

Gly Ser Gly Ala Trp Lys Gly Tyr Tyr Asn Ala Val Gly Gly Val Pro

420 425 430

Gly Ser Thr Arg Glu Asp Lys Ser Thr Ser Leu Gly Leu Gln Val Trp

435 440 445

Lys Arg Asp Phe Thr Leu Tyr Gly Leu Thr Pro Arg Leu Val Phe Asp

450 455 460

Tyr Glu Thr Thr Ser Ser Asn Phe Ala Tyr Tyr Asp Asp Arg Asp Glu

465 470 475 480

Lys Ser Ala Thr Val Leu Leu Thr Lys Thr Phe

485 490

<210> 567

<211> 1554

<212> DNA

<213> Psychrobacter sp. PAMC 21119 SLAM 1

<400> 567

atgaacaatc gatatatacg taaaccttta acagcttcaa ttctgctatc tataatggct 60

tttcctctat cggttatggc agcagagccc gtattagaag agatagaacc agagcttgac 120

caagctgccg aactcctcaa gcgtgagaac caaaccgctg tatcagatcc tacagcacct 180

tctaccgttg tctcggatac agaggctcaa cgtgctatca gaagtcgtca gcaacttgct 240

gccgccaccg cttacaattt agaagcctta aaagccaatc cagcagcatt tagcaagtat 300

ttaaacgatg cgttggctgc acaggatatg gtaaccgtca aagaattatt gccgcattat 360

aaagcactag aaaccaatga cccgatgctt attaattttg ctgatgcact cgtatatcgt 420

agtgaagcta aaaacaagca agccatcgcc atctatcgta atatgctagc ggcagaccca 480

gacttccacc cagtacgcct gaatatggca ttggctctgc aagcagacaa acagtatgcc 540

gccgcgaaag accaattctt aaagctacaa tcagtcgact taccggcacc tgttatggct 600

agggttcaag gctcattggc tcagataaac agtctcgaaa actggcgttt tgatgcctct 660

gccagctacg tcaaagatga taacatcaat gatgcgccat caaagactat ccaatctcaa 720

ttaggcaact cagttgagca gaagtcagcc aatggtattc aagtatcagc cagtgcaaac 780

aaacgcttta atttacccga taatttttat gccacggtgg gtggtaatgc ctcactaaaa 840

ggctattggg atgagactga ctataacgac tatttattca cggcttctgc tggtgtcggt 900

tatgatgatg ccaaaaatga tatttccctc acgccatttg tgactaaacg atactatgat 960

gaagagccat atagtctacg taaaggcgtc actgttagtg gttctcgctg ggtaaaacct 1020

aagctgaagc tatcagcgac tggcatttta tctaaagaaa cgtttgaaga tgacgacaat 1080

aaaaatcgcg agactgatgg acagtttttg ggtctaaatg cattctatat taaagatgcc 1140

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atcagctatg accgcaactc tgtaaacgtt ggttggggtc gtgagtggaa gcgaggtatt 1260

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ccagcaggta gtggtgcttt aaatggttac tacaatgctg tcggtggtaa agttggctcg 1380

acaagagaag acaagaccac ctcattaggc ttacaagtct ggaagcgtga cttgactcta 1440

tatggtctga caccgcgact ggtatttgat tatgaccaaa cctcaagtaa ctttgattat 1500

tatgatgatc gcgatgagaa gtcggcaacc atattgttaa ccaagacctt ttaa 1554

<210> 568

<211> 517

<212> PRT

<213> Psychrobacter sp. PAMC 21119 SLAM 1

<400> 568

Met Asn Asn Arg Tyr Ile Arg Lys Pro Leu Thr Ala Ser Ile Leu Leu

1 5 10 15

Ser Ile Met Ala Phe Pro Leu Ser Val Met Ala Ala Glu Pro Val Leu

20 25 30

Glu Glu Ile Glu Pro Glu Leu Asp Gln Ala Ala Glu Leu Leu Lys Arg

35 40 45

Glu Asn Gln Thr Ala Val Ser Asp Pro Thr Ala Pro Ser Thr Val Val

50 55 60

Ser Asp Thr Glu Ala Gln Arg Ala Ile Arg Ser Arg Gln Gln Leu Ala

65 70 75 80

Ala Ala Thr Ala Tyr Asn Leu Glu Ala Leu Lys Ala Asn Pro Ala Ala

85 90 95

Phe Ser Lys Tyr Leu Asn Asp Ala Leu Ala Ala Gln Asp Met Val Thr

100 105 110

Val Lys Glu Leu Leu Pro His Tyr Lys Ala Leu Glu Thr Asn Asp Pro

115 120 125

Met Leu Ile Asn Phe Ala Asp Ala Leu Val Tyr Arg Ser Glu Ala Lys

130 135 140

Asn Lys Gln Ala Ile Ala Ile Tyr Arg Asn Met Leu Ala Ala Asp Pro

145 150 155 160

Asp Phe His Pro Val Arg Leu Asn Met Ala Leu Ala Leu Gln Ala Asp

165 170 175

Lys Gln Tyr Ala Ala Ala Lys Asp Gln Phe Leu Lys Leu Gln Ser Val

180 185 190

Asp Leu Pro Ala Pro Val Met Ala Arg Val Gln Gly Ser Leu Ala Gln

195 200 205

Ile Asn Ser Leu Glu Asn Trp Arg Phe Asp Ala Ser Ala Ser Tyr Val

210 215 220

Lys Asp Asp Asn Ile Asn Asp Ala Pro Ser Lys Thr Ile Gln Ser Gln

225 230 235 240

Leu Gly Asn Ser Val Glu Gln Lys Ser Ala Asn Gly Ile Gln Val Ser

245 250 255

Ala Ser Ala Asn Lys Arg Phe Asn Leu Pro Asp Asn Phe Tyr Ala Thr

260 265 270

Val Gly Gly Asn Ala Ser Leu Lys Gly Tyr Trp Asp Glu Thr Asp Tyr

275 280 285

Asn Asp Tyr Leu Phe Thr Ala Ser Ala Gly Val Gly Tyr Asp Asp Ala

290 295 300

Lys Asn Asp Ile Ser Leu Thr Pro Phe Val Thr Lys Arg Tyr Tyr Asp

305 310 315 320

Glu Glu Pro Tyr Ser Leu Arg Lys Gly Val Thr Val Ser Gly Ser Arg

325 330 335

Trp Val Lys Pro Lys Leu Lys Leu Ser Ala Thr Gly Ile Leu Ser Lys

340 345 350

Glu Thr Phe Glu Asp Asp Asp Asn Lys Asn Arg Glu Thr Asp Gly Gln

355 360 365

Phe Leu Gly Leu Asn Ala Phe Tyr Ile Lys Asp Ala Lys Glu Tyr Phe

370 375 380

Tyr Gly Gly Leu Gly Asn Tyr Gln Asn Asp Val Pro Lys Ser Ser Ile

385 390 395 400

Ile Ser Tyr Asp Arg Asn Ser Val Asn Val Gly Trp Gly Arg Glu Trp

405 410 415

Lys Arg Gly Ile Ser Thr Leu Thr Thr Val Gly Tyr Ala Val Lys Glu

420 425 430

Tyr Asp Asp Pro Ala Asp Ala Tyr Pro Ala Gly Ser Gly Ala Leu Asn

435 440 445

Gly Tyr Tyr Asn Ala Val Gly Gly Lys Val Gly Ser Thr Arg Glu Asp

450 455 460

Lys Thr Thr Ser Leu Gly Leu Gln Val Trp Lys Arg Asp Leu Thr Leu

465 470 475 480

Tyr Gly Leu Thr Pro Arg Leu Val Phe Asp Tyr Asp Gln Thr Ser Ser

485 490 495

Asn Phe Asp Tyr Tyr Asp Asp Arg Asp Glu Lys Ser Ala Thr Ile Leu

500 505 510

Leu Thr Lys Thr Phe

515

<210> 569

<211> 1440

<212> DNA

<213> Psychrobacter sp. PRwf-1 SLAM 1

<400> 569

atgtatttca aacggctttt ttgtcatatc ggtatctcta tgaataaaaa atatcaggct 60

atcgtctatt ttgcagtagc aacggtggcg cacgctcagg aagtgccttt atcacaaacg 120

attttttttg atgaagagcc tcagataaag ccagaattac tgcttgatca ttcaaaaaaa 180

gattcaattc aagttgtttt acctccaaaa aatcaagact tagaatcaca agtgaatttt 240

gcgattatca gcaagaactg ggataagctg acaactttac tagatgaata taaagacaca 300

ccaagtatgg atcctattct atacaattat ggattaggag ctctttacag gcataatggt 360

cgccaagctg aggctattaa gctgtatgaa agcataatac aacaacaacc aaacttgtat 420

tatcctcgtt ttgatctagc aatgatgtta tatgaaaata agcagttcaa tgaggctcaa 480

aatcatttag aggttgttga accccattta tcacctcaga tgcagataat tgtaagtaaa 540

cttttacaag atataaaaaa atcacagcag tggaattacg atgttaactt tagttatgaa 600

aaaacggata acgtcaatca agcctctgat ttaaaggaaa ttgttcttgg tgatgcggtg 660

ttcgttagaa gtgaagactc cctcccacaa gaggcccacg gtattcgcta tggtttaaat 720

agtagtatgg ataaaaatat atttggtaac cattatttag tagctgatgc agaactatca 780

ggtattcatt attgggacaa ttcagattat agtgagatta ctccaaatgc gagcttaggt 840

tatcgcttta aagatattaa acagatgtta ggagttacag cacttgttga taagaacttt 900

ttgggtggag aagattacag tacaaattac ggtggtgtgc tgtcgtataa tcggaagtta 960

tctaatcaac ttcaagtgtc aggaaactat tcacatatcc aaaagaacta tactgaagat 1020

gatttagcta aaaactacga tggacatctc aatgcagctt ctttgcttct cttttaccaa 1080

cccaaattaa aatggctagt ttatgtgggg gcagatgcaa tctatgacag gcttgaggat 1140

aagtctgaat cttcagataa gaaaggtttc agagcaggta ctgtattttc aggagagaaa 1200

tttattgtaa gaacaaacct tcgctactct gaaagggact ttttagataa taactatttg 1260

tataatacga aaagaaagga tgatgagtat caattaagca catcaatagg ccataaagac 1320

ttagtttgga agggattttc tcccaaaatt aattatgaat ttaaaaagat agatagtaac 1380

ttacctcttt atgaaagaaa tgatagtacg gtgttcattg aatttaataa aagcttttaa 1440

<210> 570

<211> 479

<212> PRT

<213> Psychrobacter sp. PRwf-1 SLAM 1

<400> 570

Met Tyr Phe Lys Arg Leu Phe Cys His Ile Gly Ile Ser Met Asn Lys

1 5 10 15

Lys Tyr Gln Ala Ile Val Tyr Phe Ala Val Ala Thr Val Ala His Ala

20 25 30

Gln Glu Val Pro Leu Ser Gln Thr Ile Phe Phe Asp Glu Glu Pro Gln
35 40 45
Ile Lys Pro Glu Leu Leu Leu Asp His Ser Lys Lys Asp Ser Ile Gln
50 55 60
Val Val Leu Pro Pro Lys Asn Gln Asp Leu Glu Ser Gln Val Asn Phe
65 70 75 80
Ala Ile Ile Ser Lys Asn Trp Asp Lys Leu Thr Thr Leu Leu Asp Glu
85 90 95

Tyr Lys Asp Thr Pro Ser Met Asp Pro Ile Leu Tyr Asn Tyr Gly Leu
100 105 110
Gly Ala Leu Tyr Arg His Asn Gly Arg Gln Ala Glu Ala Ile Lys Leu
115 120 125
Tyr Glu Ser Ile Ile Gln Gln Gln Pro Asn Leu Tyr Tyr Pro Arg Phe
130 135 140
Asp Leu Ala Met Met Leu Tyr Glu Asn Lys Gln Phe Asn Glu Ala Gln
145 150 155 160

Asn His Leu Glu Val Val Glu Pro His Leu Ser Pro Gln Met Gln Ile
165 170 175
Ile Val Ser Lys Leu Leu Gln Asp Ile Lys Lys Ser Gln Gln Trp Asn
180 185 190
Tyr Asp Val Asn Phe Ser Tyr Glu Lys Thr Asp Asn Val Asn Gln Ala
195 200 205
Ser Asp Leu Lys Glu Ile Val Leu Gly Asp Ala Val Phe Val Arg Ser
210 215 220

Glu Asp Ser Leu Pro Gln Glu Ala His Gly Ile Arg Tyr Gly Leu Asn
225 230 235 240
Ser Ser Met Asp Lys Asn Ile Phe Gly Asn His Tyr Leu Val Ala Asp
245 250 255
Ala Glu Leu Ser Gly Ile His Tyr Trp Asp Asn Ser Asp Tyr Ser Glu
260 265 270

Ile Thr Pro Asn Ala Ser Leu Gly Tyr Arg Phe Lys Asp Ile Lys Gln
275 280 285

Met Leu Gly Val Thr Ala Leu Val Asp Lys Asn Phe Leu Gly Gly Glu
290 295 300
Asp Tyr Ser Thr Asn Tyr Gly Gly Val Leu Ser Tyr Asn Arg Lys Leu
305 310 315 320
Ser Asn Gln Leu Gln Val Ser Gly Asn Tyr Ser His Ile Gln Lys Asn
325 330 335
Tyr Thr Glu Asp Asp Leu Ala Lys Asn Tyr Asp Gly His Leu Asn Ala
340 345 350

Ala Ser Leu Leu Leu Phe Tyr Gln Pro Lys Leu Lys Trp Leu Val Tyr
355 360 365
Val Gly Ala Asp Ala Ile Tyr Asp Arg Leu Glu Asp Lys Ser Glu Ser
370 375 380
Ser Asp Lys Lys Gly Phe Arg Ala Gly Thr Val Phe Ser Gly Glu Lys
385 390 395 400
Phe Ile Val Arg Thr Asn Leu Arg Tyr Ser Glu Arg Asp Phe Leu Asp
405 410 415

Asn Asn Tyr Leu Tyr Asn Thr Lys Arg Lys Asp Asp Glu Tyr Gln Leu
420 425 430
Ser Thr Ser Ile Gly His Lys Asp Leu Val Trp Lys Gly Phe Ser Pro
435 440 445
Lys Ile Asn Tyr Glu Phe Lys Lys Ile Asp Ser Asn Leu Pro Leu Tyr
450 455 460
Glu Arg Asn Asp Ser Thr Val Phe Ile Glu Phe Asn Lys Ser Phe
465 470 475

<210> 571
<211> 1554
<212> DNA
<213> Psychrobacter sp. PRwf-1 SLAM 2
<400> 571

ctagaaagtc ttagtaaata aaatggtggc tgttttgtca tcacggtcat catagtattt 60

gaagttactt gaggtcttct cataatcaaa taccaagcgt ggggttaagc ctagtaccgt 120

caaatcacgc ttccaaactt gcaaccctaa ggagctggtt ttgtctttgc gatgggtatc 180

attaccctct acgcgataag ttcggtaaaa gaaatctgcg atatcatctg aaggcttatc 240

atagtcttta atagcatagc ttgctgaggc taaagtagag ataccttggt tccattcacg 300

cccccagccc acgtttactg aatttctatc ataacttaag aagctggtct tatcgacatc 360

atttttatag ctacccaaac caccataaaa atactcgttg gcatctttaa tatatagacc 420

attgacccct aaaaacaggc catctgcttc acgcagatct ttgtcatcat catctatggt 480

ttcattagag tacatgcctg ttgccgtcag cttgagcttt ggctgcaccc aacgtgagcc 540

actaagcgtc acccccttc gccagctata cggctcttcc ccataaaagc gcttggtcac 600

aaaaggacta atagacacat cattttggc atcatcataa cccaaggctg tcgaggctgt 660

gaccagataa tcattatact cactattatc ccaatagcct cttagcgagg cattaccacc 720

cacttcagca taaaagtttt tgtctaggtt aatacgttta ctcgcacttc ctgatacctg 780

caaacctttg ccggattcag gcttacttgt ggcacctaat tgagcatcta caatttgcct 840

ttcaggtacc ccatttaagt tcttatcata cacatagctg gcagaagcac taaagcgcca 900

ctgctcctgc tctttgatgc gctcaattaa gcgatcaaca ttggccatta ccggtggtgg 960

aatatccgcg ccacgcagct tctgcaactg gtctgcagca gcggtatact gcttatcagc 1020

atacaacgct tgggccatat taagacgcac tggatgaaag tcagggttgt ctgccaacat 1080

gtctttatat attgcaatag ctttttttgtt ttgtccttca ctacgatata ccaaggcatc 1140

agcgaactta attagcatgg gatcattaac ttctaatgcc ctataatatg ggagcagctc 1200

tttaacagtg gccatatcct gcgctgccaa tgcggcattt aaaaactttg taaaagttac 1260

agggtccgct tttaaagcct ctaaatcata gccttgtata gattgaactt ttttgcgctc 1320

atctagtgct ttttgtgctt cttgcttaga tacggttgct gttggtacgt tcgtgcctaa 1380

ggtaatatct tggcgctcac gtttaattaa ttcatctgcc tggtcattat tatctctagt 1440

ctcctcgata aatccaggag gaatatcgtc agccgcatag accagaggac tataaactgc 1500

gctgagcaat aaggtagaag tggtgagggt tcttaagagg tgcgaatgtg tcat 1554

<210> 572

<211> 517

<212> PRT

<213> Psychrobacter sp. PRwf-1 SLAM 2

<400> 572

Met Thr His Ser His Leu Leu Arg Thr Leu Thr Thr Ser Thr Leu Leu
1 5 10 15
Leu Ser Ala Val Tyr Ser Pro Leu Val Tyr Ala Ala Asp Asp Ile Pro
20 25 30
Pro Gly Phe Ile Glu Glu Thr Arg Asp Asn Asn Asp Gln Ala Asp Glu
35 40 45
Leu Ile Lys Arg Glu Arg Gln Asp Ile Thr Leu Gly Thr Asn Val Pro
50 55 60

Thr Ala Thr Val Ser Lys Gln Glu Ala Gln Lys Ala Leu Asp Glu Arg
65 70 75 80
Lys Lys Val Gln Ser Ile Gln Gly Tyr Asp Leu Glu Ala Leu Lys Ala
85 90 95
Asp Pro Val Thr Phe Thr Lys Phe Leu Asn Ala Ala Leu Ala Ala Gln
100 105 110
Asp Met Ala Thr Val Lys Glu Leu Leu Pro Tyr Tyr Arg Ala Leu Glu
115 120 125

Val Asn Asp Pro Met Leu Ile Lys Phe Ala Asp Ala Leu Val Tyr Arg
130 135 140
Ser Glu Gly Gln Asn Lys Lys Ala Ile Ala Ile Tyr Lys Asp Met Leu
145 150 155 160
Ala Asp Asn Pro Asp Phe His Pro Val Arg Leu Asn Met Ala Gln Ala
165 170 175
Leu Tyr Ala Asp Lys Gln Tyr Thr Ala Ala Ala Asp Gln Leu Gln Lys
180 185 190

Leu Arg Gly Ala Asp Ile Pro Pro Pro Val Met Ala Asn Val Asp Arg
195 200 205
Leu Ile Glu Arg Ile Lys Glu Gln Glu Gln Trp Arg Phe Ser Ala Ser
210 215 220
Ala Ser Tyr Val Tyr Asp Lys Asn Leu Asn Gly Val Pro Glu Arg Gln
225 230 235 240
Ile Val Asp Ala Gln Leu Gly Ala Thr Ser Lys Pro Glu Ser Gly Lys

245 250 255

Gly Leu Gln Val Ser Gly Ser Ala Ser Lys Arg Ile Asn Leu Asp Lys
260 265 270

Asn Phe Tyr Ala Glu Val Gly Gly Asn Ala Ser Leu Arg Gly Tyr Trp
275 280 285

Asp Asn Ser Glu Tyr Asn Asp Tyr Leu Val Thr Ala Ser Thr Ala Leu
290 295 300

Gly Tyr Asp Asp Ala Lys Asn Asp Val Ser Ile Ser Pro Phe Val Thr
305 310 315 320

Lys Arg Phe Tyr Gly Glu Glu Pro Tyr Ser Trp Arg Lys Gly Val Thr
325 330 335

Leu Ser Gly Ser Arg Trp Val Gln Pro Lys Leu Lys Leu Thr Ala Thr
340 345 350

Gly Met Tyr Ser Asn Glu Thr Ile Asp Asp Asp Asp Lys Asp Leu Arg
355 360 365

Glu Ala Asp Gly Leu Phe Leu Gly Val Asn Gly Leu Tyr Ile Lys Asp
370 375 380

Ala Asn Glu Tyr Phe Tyr Gly Gly Leu Gly Ser Tyr Lys Asn Asp Val
385 390 395 400

Asp Lys Thr Ser Phe Leu Ser Tyr Asp Arg Asn Ser Val Asn Val Gly
405 410 415

Trp Gly Arg Glu Trp Asn Gln Gly Ile Ser Thr Leu Ala Ser Ala Ser
420 425 430

Tyr Ala Ile Lys Asp Tyr Asp Lys Pro Ser Asp Asp Ile Ala Asp Phe
435 440 445

Phe Tyr Arg Thr Tyr Arg Val Glu Gly Asn Asp Thr His Arg Lys Asp
450 455 460

Lys Thr Ser Ser Leu Gly Leu Gln Val Trp Lys Arg Asp Leu Thr Val
465 470 475 480

Leu Gly Leu Thr Pro Arg Leu Val Phe Asp Tyr Glu Lys Thr Ser Ser
485 490 495

Asn Phe Lys Tyr Tyr Asp Asp Arg Asp Asp Lys Thr Ala Thr Ile Leu
500 505 510

Phe Thr Lys Thr Phe
515

<210> 573

<211> 1158

<212> DNA

<213> Rhodobacteraceae bacterium PD-2 SLAM 1

<400> 573

atggggaccc aagcggtgcg cgaagccgag ttgcgccgtc tctgggcgct gtccatggcg 60

catgtccggc agggccgtcc ccgcgcagcg cagcccttтc tcgaccggct ggtctctctt 120

gcgcccgatg ccgtcaccta ccgtctggaa cttgccaacg cgctggaggc tgcgggccag 180

cccgagcgcg cgcgttacca ctatgccctc gcgcgcggtg ccgcgctgcc gccgccgctt 240

gccaccgagg tgacgcggcg cattgaccgg attgatcggg cccgggtctg ggaaggcaac 300

ttccgcttcg cgatcgtgcc cgagagcaac ccggcgaaac gaaccgcctc tgacaccatc 360

gtgatcggcg acctgccctt caagctgaag gatagctcac gcgcgcagcc ggcacggggc 420

atcgagcttg gcctcggact tgccgccctg cccaggctgg gaccggatct caggctgcga 480

ctgggggcag ccgtcgatgc gcggctctac gaagaggggg cgcccgacga cgttcaaacg 540

cgggcagagc tggggctgct gcacttcggc gaccgcaacc gcaggctggg cgccgggctt 600

acccttggca agcgctggat cgacggcgag ccctacgcca acacgcgcgg cgtctacctg 660

acctggggcc ggtccatcga cgcccgggcg cgcagcgctc tcaacctgac tctgatccgc 720

gagcgcaccg actatgaagc acccggctcc gagtccgcga cccggtccat tgccgccgca 780

tcgctcagcc atacggtcac gccccggctg caactcagct tcggtttgca actggagcga 840

accgaaagcg cgcttgcaac cgaagcgggg caaggcggag cggtgacgct gggcgcgcgc 900

tacgccttcg aaggagggct gctcgccgag ctgacgctgg cgcttggccg gcatgagcgc 960

gaggggcccg accgcctgct gggcattgtg cgcgaggatc ggcgccagag cctcaccctg 1020

aagctgacgc accgcgactg ggcggtcgca ggctttgcgc cggtgctcga gctgggcgca 1080

gagcggcagg actccaccaa cgacctgtac agctacgaaa accaccgcgc gttgctgggc 1140

atcacccggc ggttctga 1158

<210> 574

<211> 441

<212> PRT

<213> Rhodobacteraceae bacterium PD-2 SLAM 1

<400> 574

Met Thr Arg Leu Ala Ala Gln Gly Ala Arg Arg Leu Leu Ala Gly Leu
1 5 10 15

Phe Leu Ala Leu Ala Leu Val Ser Gln Ala Pro Ala Gln Gln Pro Glu
20 25 30

Glu Ala Leu Ala Arg Ala Glu Ala Gln Val Asn Ala Gly Asp Tyr Asp
35 40 45

Thr Ala Ile Ser Ala Leu Gln Gly Met Gly Thr Gln Ala Val Arg Glu
50 55 60

Ala Glu Leu Arg Arg Leu Trp Ala Leu Ser Met Ala His Val Arg Gln
65 70 75 80

Gly Arg Pro Arg Ala Ala Gln Pro Phe Leu Asp Arg Leu Val Ser Leu
85 90 95

Ala Pro Asp Ala Val Thr Tyr Arg Leu Glu Leu Ala Asn Ala Leu Glu
100 105 110

Ala Ala Gly Gln Pro Glu Arg Ala Arg Tyr His Tyr Ala Leu Ala Arg
115 120 125

Gly Ala Ala Leu Pro Pro Pro Leu Ala Thr Glu Val Thr Arg Arg Ile
130 135 140

Asp Arg Ile Asp Arg Ala Arg Val Trp Glu Gly Asn Phe Arg Phe Ala
145 150 155 160

Ile Val Pro Glu Ser Asn Pro Ala Lys Arg Thr Ala Ser Asp Thr Ile
165 170 175

Val Ile Gly Asp Leu Pro Phe Lys Leu Lys Asp Ser Ser Arg Ala Gln
180 185 190

Pro Ala Arg Gly Ile Glu Leu Gly Leu Gly Leu Ala Ala Leu Pro Arg
195 200 205

Leu Gly Pro Asp Leu Arg Leu Arg Leu Gly Ala Ala Val Asp Ala Arg
210 215 220

Leu Tyr Glu Glu Gly Ala Pro Asp Asp Val Gln Thr Arg Ala Glu Leu

225 230 235 240

Gly Leu Leu His Phe Gly Asp Arg Asn Arg Arg Leu Gly Ala Gly Leu
245 250 255
Thr Leu Gly Lys Arg Trp Ile Asp Gly Glu Pro Tyr Ala Asn Thr Arg
260 265 270
Gly Val Tyr Leu Thr Trp Gly Arg Ser Ile Asp Ala Arg Ala Arg Ser
275 280 285
Ala Leu Asn Leu Thr Leu Ile Arg Glu Arg Thr Asp Tyr Glu Ala Pro
290 295 300

Gly Ser Glu Ser Ala Thr Arg Ser Ile Ala Ala Ala Ser Leu Ser His
305 310 315 320
Thr Val Thr Pro Arg Leu Gln Leu Ser Phe Gly Leu Gln Leu Glu Arg
325 330 335
Thr Glu Ser Ala Leu Ala Thr Glu Ala Gly Gln Gly Gly Ala Val Thr
340 345 350
Leu Gly Ala Arg Tyr Ala Phe Glu Gly Gly Leu Leu Ala Glu Leu Thr
355 360 365

Leu Ala Leu Gly Arg His Glu Arg Glu Gly Pro Asp Arg Leu Leu Gly
370 375 380
Ile Val Arg Glu Asp Arg Arg Gln Ser Leu Thr Leu Lys Leu Thr His
385 390 395 400
Arg Asp Trp Ala Val Ala Gly Phe Ala Pro Val Leu Glu Leu Gly Ala
405 410 415
Glu Arg Gln Asp Ser Thr Asn Asp Leu Tyr Ser Tyr Glu Asn His Arg
420 425 430

Ala Leu Leu Gly Ile Thr Arg Arg Phe
435 440

<210> 575

<211> 1293

<212> DNA

<213> S. bongori SLAM 1

<400> 575

atggcaacac ttttatttgc gatttttct gctccggttt tctcgggaca aaaaggacaa 60

ccggaatata tagctcgcaa gttcattggc tatttaataa ataacaacgc cgagggcgtt 120

aaaaacacgc tgcaacaatg caacaagtgc cttcagaata ttgatccact ttttcttgac 180

tgggctaatg ctattcttga atatcagaag aaaaattatg ctgggtcaat acgatattac 240

agaaagataa tctcatccag acctgactgg tacagtgcga ggttacaact ggccacagca 300

ttatacctaa ataaagatat tcgttcagca gaggaacaac tgaggaaatt gcgtagtgaa 360

aacctgtcag aagaggtggc tagcctcatt gacggattta ttgcccgagt acaaaaagca 420

gatcattggt cattccgtgg tggtctcacg tatctgaacg aaaagaatat taataatgcg 480

ccacccgcca accgcactat cggaggatgg cgatccgaaa aaccgcaatc gggtaaaggc 540

atgatgtact ggggggaggc ggaaaaaaga ttttctcttc cagataattt ttttgttatc 600

acacaactgg cggtagcagg aaaaatatac tggaataatc attcttatga tgagctggat 660

ggcagtattg gtacaggcat gggttaccgg aacgtgaaca ctatggccca gctaatccca 720

ttttacgaaa aaagttatta tggcggagga cggacgtcaa atggtggtct gcagccttac 780

tcaaatactg ttggtattaa aatggaaaca gaattccagc tctcaccacg ctggcgttta 840

tactcggatc taaagctggg taaaaataaa tataaagaaa agaattatct tgatgggcat 900

cgttactctt tgaatgagac cctgatttat tttcccagtc cacgacagta tatttctgcg 960

ggtctgggat acagtatgct cagaacgaaa caaaaagaca gttctttcga taagaccgcc 1020

ttccagaccg gatggatgta tgaatggaat gggggggatat caacgttcct ccaggccgct 1080

tatggctata gaacctacct ggccggggac ttctggggaa taaagcaaac caactatgaa 1140

tacagtactt ctgtcacgat atggcaccgc gatatctatt tttggggaat aacaccaaaa 1200

gtaacatgga gttatcaacg aattgacagt aatcatcctt tctatgatac agaaaggaat 1260

cgtctttttc tgagtttcag taaatatttc tga 1293

<210> 576

<211> 430

<212> PRT

<213> S. bongori SLAM 1

<400> 576

Met Ala Thr Leu Leu Phe Ala Ile Phe Ser Ala Pro Val Phe Ser Gly

1 5 10 15

Gln Lys Gly Gln Pro Glu Tyr Ile Ala Arg Lys Phe Ile Gly Tyr Leu

20 25 30

Ile Asn Asn Asn Ala Glu Gly Val Lys Asn Thr Leu Gln Gln Cys Asn
35 40 45
Lys Cys Leu Gln Asn Ile Asp Pro Leu Phe Leu Asp Trp Ala Asn Ala
50 55 60
Ile Leu Glu Tyr Gln Lys Lys Asn Tyr Ala Gly Ser Ile Arg Tyr Tyr
65 70 75 80
Arg Lys Ile Ile Ser Ser Arg Pro Asp Trp Tyr Ser Ala Arg Leu Gln
85 90 95

Leu Ala Thr Ala Leu Tyr Leu Asn Lys Asp Ile Arg Ser Ala Glu Glu
100 105 110
Gln Leu Arg Lys Leu Arg Ser Glu Asn Leu Ser Glu Glu Val Ala Ser
115 120 125
Leu Ile Asp Gly Phe Ile Ala Arg Val Gln Lys Ala Asp His Trp Ser
130 135 140
Phe Arg Gly Gly Leu Thr Tyr Leu Asn Glu Lys Asn Ile Asn Asn Ala
145 150 155 160

Pro Pro Ala Asn Arg Thr Ile Gly Gly Trp Arg Ser Glu Lys Pro Gln
165 170 175
Ser Gly Lys Gly Met Met Tyr Trp Gly Glu Ala Glu Lys Arg Phe Ser
180 185 190
Leu Pro Asp Asn Phe Phe Val Ile Thr Gln Leu Ala Val Ala Gly Lys
195 200 205
Ile Tyr Trp Asn Asn His Ser Tyr Asp Glu Leu Asp Gly Ser Ile Gly
210 215 220

Thr Gly Met Gly Tyr Arg Asn Val Asn Thr Met Ala Gln Leu Ile Pro
225 230 235 240
Phe Tyr Glu Lys Ser Tyr Tyr Gly Gly Gly Arg Thr Ser Asn Gly Gly
245 250 255
Leu Gln Pro Tyr Ser Asn Thr Val Gly Ile Lys Met Glu Thr Glu Phe
260 265 270

Gln Leu Ser Pro Arg Trp Arg Leu Tyr Ser Asp Leu Lys Leu Gly Lys
275 280 285

Asn Lys Tyr Lys Glu Lys Asn Tyr Leu Asp Gly His Arg Tyr Ser Leu
290 295 300
Asn Glu Thr Leu Ile Tyr Phe Pro Ser Pro Arg Gln Tyr Ile Ser Ala
305 310 315 320
Gly Leu Gly Tyr Ser Met Leu Arg Thr Lys Gln Lys Asp Ser Ser Phe
325 330 335
Asp Lys Thr Ala Phe Gln Thr Gly Trp Met Tyr Glu Trp Asn Gly Gly
340 345 350

Ile Ser Thr Phe Leu Gln Ala Ala Tyr Gly Tyr Arg Thr Tyr Leu Ala
355 360 365
Gly Asp Phe Trp Gly Ile Lys Gln Thr Asn Tyr Glu Tyr Ser Thr Ser
370 375 380
Val Thr Ile Trp His Arg Asp Ile Tyr Phe Trp Gly Ile Thr Pro Lys
385 390 395 400
Val Thr Trp Ser Tyr Gln Arg Ile Asp Ser Asn His Pro Phe Tyr Asp
405 410 415

Thr Glu Arg Asn Arg Leu Phe Leu Ser Phe Ser Lys Tyr Phe
420 425 430

<210> 577
<211> 1509
<212> DNA
<213> S. chinhatense SLAM 1
<400> 577

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gccagcttgt gggcgaccgt tgccaacacg cagacgacaa gcgggcagga cacgcgcctg 120
cggcttgacc agcaggtcga tcgccagcgc gtgaaccagg aatcccgcgc gatcgaggac 180
gctgaagcgc tcgacggtga tacatcttcg ctgaccgtag acggtcagac ttacgcggtt 240
ggcaacactg tcgatgacat cggacaagct ctctatatct cagtgacgcg caaacagtgg 300

cccgacgttc gccgtttcct cgccgcctat cagaagctgg atgggcatga tcccatgctg 360

gtcgaatatg ctcttggtgc gctcgcgcgc gagaaaggcg acctagctac cgcggaacgg 420

cattatcggg cgctgttggc gataaaggcg gattttgtcc ccggtaggct ggaactcgca 480

cgcgtccttt tcgacaatca caaggatcgt gaagctgaca gcgccttccg ggcagcgcgc 540

gatatgctgg ccgatgatgg gtcacaggcg cagggtgtga tcggcacggt cgatgcctat 600

ctgggggcgc tcaagcgccg caggagctgg cagggaagcc ttgctgtcgg gcccggatac 660

agcagcaatc tcaatcagtc gtcggcgagc tacacctgcc tgctggcgac cgacgacggc 720

acctgccttg tcgaccgaca ggttccgccc gcgatcgcgg ccgctggcgt caacttcgaa 780

gccacgctcg cgaaagatgt tccgttgagc ggacatggcg gcctccgggc gcgggcgatc 840

ctgttcggcg atgtctatcc ggaacatcat gcctattccc aggcgacggc gatcatgcgt 900

ctaggctatc aatatcaggc cgcccgcaac gccgtctccc tctcgccctc attcgagatc 960

ggttcgctcg gatcgtcgga gctctacagt gcgccaggtc tgaacgcgga atggacgcac 1020

acggtctcgc cgcggtcgct cttcaaggtt gagggaaatt accgggattt ccgttaccgc 1080

gatgcggctt ttgctccgca aaatgggccg ctcacggatg ttgctatcac aggatggtat 1140

tcgctgacgc cgactttgac cgtgttcggt ggacccgatg tcattgtgaa ggacacgcca 1200

agccttgtcg aagcctatcg ccaatggggt ggtcggctag ggatcaacaa ggctttcggc 1260

aatgtcgcga gcctcttcct catgggatca tatcgctacc gccgccaccg cgcttacagc 1320

gaattgttcg aggcgcagcg caaggatcgc caattcaacg ttatcgggat cgcccgtcta 1380

cccatcctga aagtcgggcc gctcgttccc gaaatcgttg tccagcacac ccgcgtcgag 1440

agcaacatcg actggcttta ttcctacaag cgcacgaccg cgagcgtgag gctcagctat 1500

gccttctga 1509

<210> 578

<211> 502

<212> PRT

<213> S. chinhatense SLAM 1

<400> 578

Met Asp Ile Ser Ala Phe Arg Ile Leu Ile Ser Tyr Glu Pro Leu Leu

1 5 10 15

Leu Ala Leu Ala Ala Ser Leu Trp Ala Thr Val Ala Asn Thr Gln Thr

20 25 30

Thr Ser Gly Gln Asp Thr Arg Leu Arg Leu Asp Gln Gln Val Asp Arg

35 40 45

Gln Arg Val Asn Gln Glu Ser Arg Ala Ile Glu Asp Ala Glu Ala Leu

50 55 60

Asp Gly Asp Thr Ser Ser Leu Thr Val Asp Gly Gln Thr Tyr Ala Val
65 70 75 80

Gly Asn Thr Val Asp Asp Ile Gly Gln Ala Leu Tyr Ile Ser Val Thr
85 90 95

Arg Lys Gln Trp Pro Asp Val Arg Arg Phe Leu Ala Ala Tyr Gln Lys
100 105 110

Leu Asp Gly His Asp Pro Met Leu Val Glu Tyr Ala Leu Gly Ala Leu

115 120 125

Ala Arg Glu Lys Gly Asp Leu Ala Thr Ala Glu Arg His Tyr Arg Ala
130 135 140

Leu Leu Ala Ile Lys Ala Asp Phe Val Pro Gly Arg Leu Glu Leu Ala
145 150 155 160

Arg Val Leu Phe Asp Asn His Lys Asp Arg Glu Ala Asp Ser Ala Phe
165 170 175

Arg Ala Ala Arg Asp Met Leu Ala Asp Asp Gly Ser Gln Ala Gln Gly

180 185 190

Val Ile Gly Thr Val Asp Ala Tyr Leu Gly Ala Leu Lys Arg Arg Arg

195 200 205

Ser Trp Gln Gly Ser Leu Ala Val Gly Pro Gly Tyr Ser Ser Asn Leu
210 215 220

Asn Gln Ser Ser Ala Ser Tyr Thr Cys Leu Leu Ala Thr Asp Asp Gly
225 230 235 240

Thr Cys Leu Val Asp Arg Gln Val Pro Pro Ala Ile Ala Ala Ala Gly

245 250 255

Val Asn Phe Glu Ala Thr Leu Ala Lys Asp Val Pro Leu Ser Gly His

260 265 270

Gly Gly Leu Arg Ala Arg Ala Ile Leu Phe Gly Asp Val Tyr Pro Glu

275 280 285

His His Ala Tyr Ser Gln Ala Thr Ala Ile Met Arg Leu Gly Tyr Gln

290 295 300

Tyr Gln Ala Ala Arg Asn Ala Val Ser Leu Ser Pro Ser Phe Glu Ile

305 310 315 320

Gly Ser Leu Gly Ser Ser Glu Leu Tyr Ser Ala Pro Gly Leu Asn Ala

325 330 335

Glu Trp Thr His Thr Val Ser Pro Arg Ser Leu Phe Lys Val Glu Gly

340 345 350

Asn Tyr Arg Asp Phe Arg Tyr Arg Asp Ala Ala Phe Ala Pro Gln Asn

355 360 365

Gly Pro Leu Thr Asp Val Ala Ile Thr Gly Trp Tyr Ser Leu Thr Pro

370 375 380

Thr Leu Thr Val Phe Gly Gly Pro Asp Val Ile Val Lys Asp Thr Pro

385 390 395 400

Ser Leu Val Glu Ala Tyr Arg Gln Trp Gly Gly Arg Leu Gly Ile Asn

405 410 415

Lys Ala Phe Gly Asn Val Ala Ser Leu Phe Leu Met Gly Ser Tyr Arg

420 425 430

Tyr Arg Arg His Arg Ala Tyr Ser Glu Leu Phe Glu Ala Gln Arg Lys

435 440 445

Asp Arg Gln Phe Asn Val Ile Gly Ile Ala Arg Leu Pro Ile Leu Lys

450 455 460

Val Gly Pro Leu Val Pro Glu Ile Val Val Gln His Thr Arg Val Glu

465 470 475 480

Ser Asn Ile Asp Trp Leu Tyr Ser Tyr Lys Arg Thr Thr Ala Ser Val

485 490 495

Arg Leu Ser Tyr Ala Phe

500

<210> 579

<211> 1317

<212> DNA

<213> S. echinoides SLAM 1

<400> 579

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gcgccgccca cgacccattt gcaggactta tccgcgatcg acgtcttcgg cctcgccgac 120

cgcgcgcgcg cagccggccg gatcgacgat gccaccggct tctatgacgc gctggcgcat 180

gatcccaacg ccgatgtccg cgcggaagca cggtttcgca aagggatgat gcttgccgat 240

cttcggcgct accgcgaggc ggcgcttgcc ttccgtgccg tgcttgacga acaacccaaa 300

gccgcgcgtg cgcggctcga gctggcgcgc atgctggccg cgcttggtga cgaacgcgct 360

gcccgccgcg aactccgcca ggcgcaagcc acgggcctgc cgggctcagt tgccgcagcg 420

gtaggacagt tcgatcaaat cctgcgctcc cacaagcgct tcggcgggtc gttcgaactg 480

gcgctggcac ccgactccaa cgtcaatcgt gcaacgcagg tgcggacgct cgataccatc 540

atcgcgccgc tgacgctctc gaacgacgcc cgcgcgcaat ctggcgtcgg gctacgcctg 600

gctggacaag ggtatgcccg cctcggttta gcggatggcc tcgcactggt tccacgcctc 660

tccacgctgg caaatctata ccgcgcatcc cagtttaacg acatttccgg aactgcgttg 720

atcggcttcg aatggcagcg tcagaaagac cggttcagcc cgtccattgg ccgaacatgg 780

cgctggtatg gcggcgcgct ctacgcgcac acagatgcgg tatcgctcga ctggctgcac 840

atcctcggtc gccgtgcgca attggtcgtc agcgggagcg caagcaaggc gacgtaccgg 900

cgcaatgatc tgcaagacgg cgcgatcggc gatcttaacg tgtcgattga acgcgctttg 960

tcagccaaag ctggcgcaag catcggcgtt tcgatcacac ggcaaaccgc ccgtgatccg 1020

ggatacgcca cgaaagcggc aggcgtttca gcgctcggct ggcgcgaact cggccagacg 1080

accgtgttcg tttcgggagg attgcggcga accgagggcg atgccgccct cttcctgttc 1140

ggcgaccggc gccgcgaatg gttgatgaca gcacgcgcag gggcaacctt ccggcaactt 1200

aaaatcggtg ctttctcccc ttatattcgg gtcagctatg agcggaatgc ctccagcttg 1260

cagctttacc aatacgcacg caccgccagc gaagtcggca tcactcgcgc gttctga 1317

<210> 580

<211> 438

<212> PRT

<213> S. echinoides SLAM 1

<400> 580

Met Ala Gly Leu Thr Leu Ala Leu Ala Ala Pro Ala Ala Val Ala Val

1 5 10 15

Ala Gly Gln Thr Ala Pro Pro Thr Thr His Leu Gln Asp Leu Ser Ala

20 25 30

Ile Asp Val Phe Gly Leu Ala Asp Arg Ala Arg Ala Ala Gly Arg Ile

35 40 45

Asp Asp Ala Thr Gly Phe Tyr Asp Ala Leu Ala His Asp Pro Asn Ala

50 55 60

Asp Val Arg Ala Glu Ala Arg Phe Arg Lys Gly Met Met Leu Ala Asp

65 70 75 80

Leu Arg Arg Tyr Arg Glu Ala Ala Leu Ala Phe Arg Ala Val Leu Asp

85 90 95

Glu Gln Pro Lys Ala Ala Arg Ala Arg Leu Glu Leu Ala Arg Met Leu

100 105 110

Ala Ala Leu Gly Asp Glu Arg Ala Ala Arg Arg Glu Leu Arg Gln Ala

115 120 125

Gln Ala Thr Gly Leu Pro Gly Ser Val Ala Ala Ala Val Gly Gln Phe

130 135 140

Asp Gln Ile Leu Arg Ser His Lys Arg Phe Gly Gly Ser Phe Glu Leu

145 150 155 160

Ala Leu Ala Pro Asp Ser Asn Val Asn Arg Ala Thr Gln Val Arg Thr

165 170 175

Leu Asp Thr Ile Ile Ala Pro Leu Thr Leu Ser Asn Asp Ala Arg Ala

180 185 190

Gln Ser Gly Val Gly Leu Arg Leu Ala Gly Gln Gly Tyr Ala Arg Leu

195 200 205

Gly Leu Ala Asp Gly Leu Ala Leu Val Pro Arg Leu Ser Thr Leu Ala

210 215 220

Asn Leu Tyr Arg Ala Ser Gln Phe Asn Asp Ile Ser Gly Thr Ala Leu

225 230 235 240

Ile Gly Phe Glu Trp Gln Arg Gln Lys Asp Arg Phe Ser Pro Ser Ile

245 250 255

Gly Arg Thr Trp Arg Trp Tyr Gly Gly Ala Leu Tyr Ala His Thr Asp

260 265 270

Ala Val Ser Leu Asp Trp Leu His Ile Leu Gly Arg Arg Ala Gln Leu

275 280 285

Val Val Ser Gly Ser Ala Ser Lys Ala Thr Tyr Arg Arg Asn Asp Leu

290 295 300

Gln Asp Gly Ala Ile Gly Asp Leu Asn Val Ser Ile Glu Arg Ala Leu

305 310 315 320

Ser Ala Lys Ala Gly Ala Ser Ile Gly Val Ser Ile Thr Arg Gln Thr

325 330 335

Ala Arg Asp Pro Gly Tyr Ala Thr Lys Ala Ala Gly Val Ser Ala Leu

340 345 350

Gly Trp Arg Glu Leu Gly Gln Thr Thr Val Phe Val Ser Gly Gly Leu

355 360 365

Arg Arg Thr Glu Gly Asp Ala Ala Leu Phe Leu Phe Gly Asp Arg Arg

370 375 380

Arg Glu Trp Leu Met Thr Ala Arg Ala Gly Ala Thr Phe Arg Gln Leu

385 390 395 400

Lys Ile Gly Ala Phe Ser Pro Tyr Ile Arg Val Ser Tyr Glu Arg Asn

405 410 415

Ala Ser Ser Leu Gln Leu Tyr Gln Tyr Ala Arg Thr Ala Ser Glu Val

420 425 430

Gly Ile Thr Arg Ala Phe

435

<210> 581

<211> 1314

<212> DNA

<213> S. elodea SLAM 1

<400> 581

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gcccagacga ccgagcagcg ccaggtctcg gcggtcgagc tgttcactct cgccgcccgc 120

gccgagggtg tcgggcgccc ggccgacgcc gagacgatgt accgcgcgct cgccaaagac 180

cctgatgccg aggtccgcgc cgaggcgcgc tttcggctcg gccagctgct cgaacggctg 240

ggccgcaagc gcgaggcggc gaccacctat cgcgcgctgc tcgacgagaa acccgacgcc 300

gcgcgcgtcc ggctcgaact cgcccggctg ctcacccagc tgggggacga gagcgcggcg 360

cggcgggagc tgcgccaggc ccaggccggc gggctgccgc cgcaggtggc gcagatcgtc 420

gaccagttcg ccgccgcgct ccgctcgcgc aagccctggg gcgccagcct cgaggtcgcg 480

ctggtaccgg acagcaacgt caaccgcgcg accgacgcgg cgacgctcga taccgtgctt 540

gccccctcc agctctcgcg cgacgcccgc gagcaatccg gcatcggcgc gcgcatcggc 600

ggtcagctct tcgcccgcgt gccggtggcg accaacctcg cgatcgtccc gcgcctatcc 660

ggccagggcg atttctaccg ccagcgccgt ttcaacgata cctccgcctc ggcactgatc 720

ggcctggaat ggagcctcgg gcgcgatcgc ctgcgtccct cggtcggcgg cacccagcgc 780

tggtatggcg gcagccccta tgcgcgcacc gccaccgcgg cgatcgactg gcagcatccg 840

ctcggtacca gggcccagct caccaccagc gcgaccgtgg ccgacacgac ctatcgcggc 900

aacccccctgc aggacgggct gctgctgaac ggcgcgatcg cctatgaacg tgccttctcc 960

ccccgcgccg gcggaagcgt caccctgtcc gccacccgcc agacggcgaa cgatcccggc 1020

tatgccaccg ccgccggcgg cgcgaccctg ctcggctggc gcgagttcgg ccggaccacc 1080

gtctatgcca ccgccggctt gcgtcggctg gagggcgatg cccgcctgtt cctgttcgcg 1140

gaacggcgca aggactggaa cgtcagcctc ggtgtcggcg ccaccttccg ccgcatccag 1200

atccgcggct tcgcgccgat cgtgcggctg gattgggagc gcaaccgctc caccgtcggc 1260

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<210> 582

<211> 437

<212> PRT

<213> S. elodea SLAM 1

<400> 582

Met Thr Asp Arg Ser Leu Ile Ala Leu Ala Leu Ala Leu Leu Ala Pro
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20 25 30

Glu Leu Phe Thr Leu Ala Ala Arg Ala Glu Gly Val Gly Arg Pro Ala
35 40 45

Asp Ala Glu Thr Met Tyr Arg Ala Leu Ala Lys Asp Pro Asp Ala Glu
50 55 60

Val Arg Ala Glu Ala Arg Phe Arg Leu Gly Gln Leu Leu Glu Arg Leu
65 70 75 80

Gly Arg Lys Arg Glu Ala Ala Thr Thr Tyr Arg Ala Leu Leu Asp Glu
85 90 95

Lys Pro Asp Ala Ala Arg Val Arg Leu Glu Leu Ala Arg Leu Leu Thr
100 105 110

Gln Leu Gly Asp Glu Ser Ala Ala Arg Arg Glu Leu Arg Gln Ala Gln
115 120 125

Ala Gly Gly Leu Pro Pro Gln Val Ala Gln Ile Val Asp Gln Phe Ala
130 135 140

Ala Ala Leu Arg Ser Arg Lys Pro Trp Gly Ala Ser Leu Glu Val Ala
145 150 155 160

Leu Val Pro Asp Ser Asn Val Asn Arg Ala Thr Asp Ala Ala Thr Leu
165 170 175

Asp Thr Val Leu Ala Pro Leu Gln Leu Ser Arg Asp Ala Arg Glu Gln
180 185 190

Ser Gly Ile Gly Ala Arg Ile Gly Gly Gln Leu Phe Ala Arg Val Pro
195 200 205

Val Ala Thr Asn Leu Ala Ile Val Pro Arg Leu Ser Gly Gln Gly Asp
210 215 220

Phe Tyr Arg Gln Arg Arg Phe Asn Asp Thr Ser Ala Ser Ala Leu Ile
225 230 235 240

Gly Leu Glu Trp Ser Leu Gly Arg Asp Arg Leu Arg Pro Ser Val Gly
245 250 255

Gly Thr Gln Arg Trp Tyr Gly Gly Ser Pro Tyr Ala Arg Thr Ala Thr
260 265 270

Ala Ala Ile Asp Trp Gln His Pro Leu Gly Thr Arg Ala Gln Leu Thr
275 280 285

Thr Ser Ala Thr Val Ala Asp Thr Thr Tyr Arg Gly Asn Pro Leu Gln
290 295 300

Asp Gly Leu Leu Leu Asn Gly Ala Ile Ala Tyr Glu Arg Ala Phe Ser
305 310 315 320

Pro Arg Ala Gly Gly Ser Val Thr Leu Ser Ala Thr Arg Gln Thr Ala

325 330 335

Asn Asp Pro Gly Tyr Ala Thr Ala Ala Gly Gly Ala Thr Leu Leu Gly

340 345 350

Trp Arg Glu Phe Gly Arg Thr Thr Val Tyr Ala Thr Ala Gly Leu Arg

355 360 365

Arg Leu Glu Gly Asp Ala Arg Leu Phe Leu Phe Ala Glu Arg Arg Lys

370 375 380

Asp Trp Asn Val Ser Leu Gly Val Gly Ala Thr Phe Arg Arg Ile Gln

385 390 395 400

Ile Arg Gly Phe Ala Pro Ile Val Arg Leu Asp Trp Glu Arg Asn Arg

405 410 415

Ser Thr Val Gly Ile Tyr Asp Phe Thr Arg Lys Ala Ala Thr Ile Gly

420 425 430

Leu Thr Arg Ala Phe

435

<210> 583

<211> 1242

<212> DNA

<213> S. indicum SLAM 1

<400> 583

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gttgcaggca aaatcggcga tgcgaacctg attctcgatg ctctcaagca aaatgatgaa 120

ggctcgcgcg agcaaattct gctcgcaggc atcattgcgg tggctcaagg taatttgtct 180

ttggctgaag cgggcttccg aaccctccta ttgcgggatc ctcacgacac cagagtccgg 240

ctcgaacttg cacgggtact ttttttgctg caccgatatg cagctgcaga ttatcatttt 300

aggctcagcg ctgcgcgaag cccaaagtct gtgcaacata atatttcact tttccgccgc 360

gcaatacagg cacaacgaac atggcgtgtt tcggtggaag ggggaattgc cccggatacc 420

aacgtgaact cagcaggtcg tgaccgaatt gtcgatttgt tcgggttgcc ctttaacgtg 480

gacaacgatg ctcgcgaaaa atcaggggtc ggtgtttttg caaatgccga tgttgaactt 540

cggttgcggc gctctgaagc agtgggattg tccatccgcg cattcggaaa cgctcgggaa 600

taccgtcgtt cggcttttaa tgatgaggtc gcgggcatcg aaatcggacc acaatttcgg 660

tttggcaacg cgcaagtgac cgttgcggga acaggtctgt ttcggtggta tggccgagag 720

atatactcgc gagctctagg agcagcgcta cgcgttgaac tgcccatctc aacgcaatgg 780

caggtcgatc tgaagcctca attcagatca gtcaattatc tccaaaaccc aagccaaaac 840

gggccttta tgagcttgaa cggtcagatt agccgctccc tcggaagtca tgccttaggg 900

caaatcgatt ttctcgcgtc gcgacagtct gctcgcgctc ctggctacgc ttatcgagaa 960

gcagggctag gtgtgagtgc atttgctgaa cttggaaatg gaattactgt aggaggaagt 1020

atcgaggcag cgcggacggt attcgatgct ccactcttcg gctttgcaaa gacacgccgc 1080

gactggagag ccgcaacaac catttctgtt ctcaatcgga actggatttt gttaggattc 1140

tcgcctgtca cgcggctgag ttttgcacag tcgaaatcta caattagttt ttttgaatat 1200

cgtcgaacac gactggaact tgcattgcag cggccattct aa 1242

<210> 584

<211> 413

<212> PRT

<213> S. indicum SLAM 1

<400> 584

Met Leu Ser Thr Glu Gly Val Ser Ala Ser Gln Met Leu Asp Leu Gly
1 5 10 15

Glu His Leu Ala Val Ala Gly Lys Ile Gly Asp Ala Asn Leu Ile Leu
20 25 30

Asp Ala Leu Lys Gln Asn Asp Glu Gly Ser Arg Glu Gln Ile Leu Leu
35 40 45

Ala Gly Ile Ile Ala Val Ala Gln Gly Asn Leu Ser Leu Ala Glu Ala
50 55 60

Gly Phe Arg Thr Leu Leu Leu Arg Asp Pro His Asp Thr Arg Val Arg
65 70 75 80

Leu Glu Leu Ala Arg Val Leu Phe Leu Leu His Arg Tyr Ala Ala Ala
85 90 95

Asp Tyr His Phe Arg Leu Ser Ala Ala Arg Ser Pro Thr Ser Val Gln
100 105 110

His Asn Ile Ser Leu Phe Arg Arg Ala Ile Gln Ala Gln Arg Thr Trp
115 120 125

Arg Val Ser Val Glu Gly Gly Ile Ala Pro Asp Thr Asn Val Asn Ser

130 135 140

Ala Gly Arg Asp Arg Ile Val Asp Leu Phe Gly Leu Pro Phe Asn Val
145 150 155 160

Asp Asn Asp Ala Arg Glu Lys Ser Gly Val Gly Val Phe Ala Asn Ala
165 170 175

Asp Val Glu Leu Arg Leu Arg Arg Ser Glu Ala Val Gly Leu Ser Ile
180 185 190

Arg Ala Phe Gly Asn Ala Arg Glu Tyr Arg Arg Ser Ala Phe Asn Asp
195 200 205

Glu Val Ala Gly Ile Glu Ile Gly Pro Gln Phe Arg Phe Gly Asn Ala
210 215 220

Gln Val Ile Val Ala Gly Thr Gly Leu Phe Arg Trp Tyr Gly Arg Glu
225 230 235 240

Ile Tyr Ser Arg Ala Leu Gly Ala Ala Leu Arg Val Glu Leu Pro Ile
245 250 255

Ser Ala Gln Trp Gln Val Asp Leu Lys Pro Gln Phe Arg Ser Val Asn
260 265 270

Tyr Leu Gln Asn Pro Ser Gln Asn Gly Pro Phe Met Ser Leu Asn Gly
275 280 285

Gln Ile Ser Arg Ser Leu Gly Ser His Ala Leu Gly Gln Ile Asp Phe
290 295 300

Leu Ala Ser Arg Gln Ser Ala Arg Ala Pro Gly Tyr Ala Tyr Arg Glu
305 310 315 320

Ala Gly Leu Gly Val Ser Ala Phe Ala Glu Leu Gly Asn Gly Ile Thr
325 330 335

Val Gly Gly Ser Ile Glu Ala Ala Arg Thr Val Phe Asp Ala Pro Leu
340 345 350

Phe Gly Phe Ala Lys Thr Arg Arg Asp Trp Arg Ala Ala Thr Thr Ile
355 360 365

Ser Val Leu Asn Arg Asn Trp Ile Leu Leu Gly Phe Ser Pro Val Ala
370 375 380

Arg Leu Ser Phe Ala Arg Ser Lys Ser Thr Ile Ser Phe Phe Glu Tyr
385 390 395 400

Arg Arg Thr Arg Leu Glu Leu Ala Leu Gln Arg Pro Phe
405 410

<210> 585

<211> 1242

<212> DNA

<213> S. japonicum SLAM 1

<400> 585

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gttgcaggca aaatcggcga tgcgaacctg attctcgatg ctctcaagca aaatgatgaa 120

ggctcgcgcg agcaaattct gctcgcaggc atcattgcgg tggctcaagg taatttgtct 180

ttggctgaag cgggcttccg aaccctccta ttgcgggatc ctcacgacac cagagtccgg 240

ctcgaacttg cacgggtact ttttttgctg caccgatatg cagctgcaga ttatcatttt 300

aggctcagcg ctgcgcgaag cccaaagtct gtgcaacata atatttcact tttccgccgc 360

gcaatacagg cacaacgaac atggcgtgtt tcggtggaag ggggaattgc cccggatacc 420

aacgtgaact cagcaggtcg tgaccgaatt gtcgatttgt tcgggttgcc ctttaacgtg 480

gacaacgatg ctcgcgaaaa atcaggggtc ggtgtttttg caaatgccga tgttgaactt 540

cggttgcggc gctctgaagc agtgggattg tccatccgcg cattcggaaa cgctcgggaa 600

taccgtcgtt cggcttttaa tgatgaggtc gcgggcatcg aaatcggacc acaatttcgg 660

tttggcaacg cgcaagtgac cgttgcggga acaggtctgt ttcggtggta tggccgagag 720

atatactcgc gagctctagg agcagcgcta cgcgttgaac tgcccatctc aacgcaatgg 780

caggtcgatc tgaagcctca attcagatca gtcaattatc tccaaaaccc aagccaaaac 840

gggccttta tgagcttgaa cggtcagatt agccgctccc tcggaagtca tgccttaggg 900

caaatcgatt ttctcgcgtc gcgacagtct gctcgcgctc ctggctacgc ttatcgagaa 960

gcagggctag gtgtgagtgc atttgctgaa cttggaaatg gaattactgt aggaggaagt 1020

atcgaggcag cgcggacggt attcgatgct ccactcttcg gctttgcaaa gacacgccgc 1080

gactggagag ccgcaacaac catttctgtt ctcaatcgga actggatttt gttaggattc 1140

tcgcctgtca cgcggctgag ttttgcacag tcgaaatcta caattagttt ttttgaatat 1200

cgtcgaacac gactggaact tgcattgcag cggccattct aa 1242

<210> 586

<211> 413

<212> PRT

<213> S. japonicum SLAM 1

<400> 586

Met Leu Ser Thr Glu Gly Val Ser Ala Ser Gln Met Leu Asp Leu Gly
1 5 10 15

Glu His Leu Ala Val Ala Gly Lys Ile Gly Asp Ala Asn Leu Ile Leu
20 25 30

Asp Ala Leu Lys Gln Asn Asp Glu Gly Ser Arg Glu Gln Ile Leu Leu
35 40 45

Ala Gly Ile Ile Ala Val Ala Gln Gly Asn Leu Ser Leu Ala Glu Ala
50 55 60

Gly Phe Arg Thr Leu Leu Leu Arg Asp Pro His Asp Thr Arg Val Arg
65 70 75 80

Leu Glu Leu Ala Arg Val Leu Phe Leu Leu His Arg Tyr Ala Ala Ala
85 90 95

Asp Tyr His Phe Arg Leu Ser Ala Ala Arg Ser Pro Lys Ser Val Gln
100 105 110

His Asn Ile Ser Leu Phe Arg Arg Ala Ile Gln Ala Gln Arg Thr Trp
115 120 125

Arg Val Ser Val Glu Gly Gly Ile Ala Pro Asp Thr Asn Val Asn Ser
130 135 140

Ala Gly Arg Asp Arg Ile Val Asp Leu Phe Gly Leu Pro Phe Asn Val
145 150 155 160

Asp Asn Asp Ala Arg Glu Lys Ser Gly Val Gly Val Phe Ala Asn Ala
165 170 175

Asp Val Glu Leu Arg Leu Arg Arg Ser Glu Ala Val Gly Leu Ser Ile
180 185 190

Arg Ala Phe Gly Asn Ala Arg Glu Tyr Arg Arg Ser Ala Phe Asn Asp
195 200 205

Glu Val Ala Gly Ile Glu Ile Gly Pro Gln Phe Arg Phe Gly Asn Ala
210 215 220

Gln Val Thr Val Ala Gly Thr Gly Leu Phe Arg Trp Tyr Gly Arg Glu
225 230 235 240

Ile Tyr Ser Arg Ala Leu Gly Ala Ala Leu Arg Val Glu Leu Pro Ile
245 250 255
Ser Thr Gln Trp Gln Val Asp Leu Lys Pro Gln Phe Arg Ser Val Asn
260 265 270
Tyr Leu Gln Asn Pro Ser Gln Asn Gly Pro Phe Met Ser Leu Asn Gly
275 280 285
Gln Ile Ser Arg Ser Leu Gly Ser His Ala Leu Gly Gln Ile Asp Phe
290 295 300

Leu Ala Ser Arg Gln Ser Ala Arg Ala Pro Gly Tyr Ala Tyr Arg Glu
305 310 315 320
Ala Gly Leu Gly Val Ser Ala Phe Ala Glu Leu Gly Asn Gly Ile Thr
325 330 335
Val Gly Gly Ser Ile Glu Ala Ala Arg Thr Val Phe Asp Ala Pro Leu
340 345 350
Phe Gly Phe Ala Lys Thr Arg Arg Asp Trp Arg Ala Ala Thr Thr Ile
355 360 365

Ser Val Leu Asn Arg Asn Trp Ile Leu Leu Gly Phe Ser Pro Val Thr
370 375 380
Arg Leu Ser Phe Ala Gln Ser Lys Ser Thr Ile Ser Phe Phe Glu Tyr
385 390 395 400
Arg Arg Thr Arg Leu Glu Leu Ala Leu Gln Arg Pro Phe
405 410

<210> 587
<211> 1455
<212> DNA
<213> S. lithotrophicus SLAM 1
<400> 587
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tgggcgttgt ctgggctggt gctggcggcg ggcatggcac atgctcaaga cgccatcaat 120

cagaatgaaa gaatcaagac cgccgccgcg gcgggaactg ccgaatcgac gcagcagtcg 180

gcagccatcg aacggcagaa gttgctgcag gacgcagcca atctgatcaa atccggcaag 240

tcgaaagacg cctacctgtt gctggagccg gaacaatcca tacgcgccgg ggatccggat 300

tacgactatt tgctgggtat cgccgccctg gacagcggca aaccgaacga ggcgatattt 360

gcgctggagc gcgtgcttgc ggtaagaccc aaccacttgc aggcgcgcgc cgagatcgcc 420

cgggcatatc tggccgtcgg cgaaaaggca gccgcgaagc aggaattcga aacggtccag 480

agccagaatc cgcccaaaga agtgaatgcc accatccagc ggttccttga tgccatcaat 540

caggggcagg gcggtgaagc cacgatgctg agcggttatc tcgaagcgga cgtgggtagc 600

gacagcaacg tcaacagtgc gaccggcagc aaccaggttg cgatccccgc ttttggcggt 660

gcggtcgcga cattgaatgc gagcggcatt gagaccaggg ccacctttgc gaatgtcagc 720

ggtggcgcca atgtccgtca tgccctggat gccgaatggt cgatattcgg cggtgcgaac 780

gtcaaccagc gcctgaactc gaaacagtcc gttttcaaca cgcgtggcct ggacggcaat 840

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ttcgatgtcg acaacaagcg ttaccggaat ggcaccggca tgaccctgca gtggcagcat 960

gacctgagcc agagaagcag ccaggccagc ggctatttcc agtacaccaa cctgaagtat 1020

cccgggcagt cggttcgcga tgccaaccgc tatgtgcttg gtgtggccta tgccagcgtg 1080

ctgggcggcg aatatacgcc agccgtctat ttcggcgcct atgcgggcac ggaaaaggag 1140

aaacaatccg gcgtacccta tctcggccat aagctcttcg gcatgagagt cggcggcgaa 1200

atgaatatct atgcgcaggc taaactgttc ggctctttga gcgccgaatc gcgcaattac 1260

ggcggtgatg acccgttgtt cctggtcacg cgcaaagaca cccaggcaga cctgaaagtg 1320

ggcgtcaact atgagatggc caaactctgg acgctcaccc cccagatcag ctacaccaag 1380

aacaaatcca acatcgtcat caatgactac aagcgcacca tattcagtgt cggtctgcgc 1440

cgcgacttca attaa 1455

<210> 588

<211> 484

<212> PRT

<213> S. lithotrophicus SLAM 1

<400> 588

Met Leu Gln Cys Ala Val Ile Leu Gly Gly Gly Asp Met Arg Phe Ala

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Arg Leu Pro Cys Trp Ala Leu Ser Gly Leu Val Leu Ala Ala Gly Met

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Ala His Ala Gln Asp Ala Ile Asn Gln Asn Glu Arg Ile Lys Thr Ala

35 40 45

Ala Ala Ala Gly Thr Ala Glu Ser Thr Gln Gln Ser Ala Ala Ile Glu

50 55 60

Arg Gln Lys Leu Leu Gln Asp Ala Ala Asn Leu Ile Lys Ser Gly Lys

65 70 75 80

Ser Lys Asp Ala Tyr Leu Leu Leu Glu Pro Glu Gln Ser Ile Arg Ala

85 90 95

Gly Asp Pro Asp Tyr Asp Tyr Leu Leu Gly Ile Ala Ala Leu Asp Ser

100 105 110

Gly Lys Pro Asn Glu Ala Ile Phe Ala Leu Glu Arg Val Leu Ala Val

115 120 125

Arg Pro Asn His Leu Gln Ala Arg Ala Glu Ile Ala Arg Ala Tyr Leu

130 135 140

Ala Val Gly Glu Lys Ala Ala Ala Lys Gln Glu Phe Glu Thr Val Gln

145 150 155 160

Ser Gln Asn Pro Pro Lys Glu Val Asn Ala Thr Ile Gln Arg Phe Leu

165 170 175

Asp Ala Ile Asn Gln Gly Gln Gly Gly Glu Ala Thr Met Leu Ser Gly

180 185 190

Tyr Leu Glu Ala Asp Val Gly Ser Asp Ser Asn Val Asn Ser Ala Thr

195 200 205

Gly Ser Asn Gln Val Ala Ile Pro Ala Phe Gly Gly Ala Val Ala Thr

210 215 220

Leu Asn Ala Ser Gly Ile Glu Thr Arg Ala Thr Phe Ala Asn Val Ser

225 230 235 240

Gly Gly Ala Asn Val Arg His Ala Leu Asp Ala Glu Trp Ser Ile Phe

245 250 255

Gly Gly Ala Asn Val Asn Gln Arg Leu Asn Ser Lys Gln Ser Val Phe

260 265 270

Asn Thr Arg Gly Leu Asp Gly Asn Val Gly Phe Asn Leu Thr Lys Ala

275 280 285

Glu Asp Ser Tyr Ser Ala Ala Leu Gln Leu Gln Ser Phe Asp Val Asp

290 295 300

Asn Lys Arg Tyr Arg Asn Gly Thr Gly Met Thr Leu Gln Trp Gln His

305 310 315 320

Asp Leu Ser Gln Arg Ser Ser Gln Ala Ser Gly Tyr Phe Gln Tyr Thr

325 330 335

Asn Leu Lys Tyr Pro Gly Gln Ser Val Arg Asp Ala Asn Arg Tyr Val

340 345 350

Leu Gly Val Ala Tyr Ala Ser Val Leu Gly Gly Glu Tyr Thr Pro Ala

355 360 365

Val Tyr Phe Gly Ala Tyr Ala Gly Thr Glu Lys Glu Lys Gln Ser Gly

370 375 380

Val Pro Tyr Leu Gly His Lys Leu Phe Gly Met Arg Val Gly Gly Glu

385 390 395 400

Met Asn Ile Tyr Ala Gln Ala Lys Leu Phe Gly Ser Leu Ser Ala Glu

405 410 415

Ser Arg Asn Tyr Gly Gly Asp Asp Pro Leu Phe Leu Val Thr Arg Lys

420 425 430

Asp Thr Gln Ala Asp Leu Lys Val Gly Val Asn Tyr Glu Met Ala Lys

435 440 445

Leu Trp Thr Leu Thr Pro Gln Ile Ser Tyr Thr Lys Asn Lys Ser Asn

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Ile Val Ile Asn Asp Tyr Lys Arg Thr Ile Phe Ser Val Gly Leu Arg

465 470 475 480

Arg Asp Phe Asn

<210> 589

<211> 1509

<212> DNA

<213> S. lucknowense SLAM 1

<400> 589

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cggcttgacc agcaggtcga tcgccagcgc gtgaaccagg aatcccgcgc gatcgaggac 180

gctgaagcgc tcgacggtga tacatcttcg ctgaccgtag acggtcagac ttacgcggtt 240

ggcaacactg tcgatgacat cggacaagct ctctatatct cagtgacgcg caaacagtgg 300

cccgacgttc gccgtttcct cgccgcctat cagaagctgg atgggcatga tcccatgctg 360

gtcgaatatg ctcttggtgc gctcgcgcgc gagaaaggcg acctagctac cgcggaacgg 420

cattatcggg cgctgttggc gataaaggcg gattttgtcc ccggtaggct ggaactcgca 480

cgcgtccttt tcgacaatca caaggatcgt gaagctgaca gcgccttccg ggcagcgcgc 540

gatatgctgg ccgatgatgg gtcacaggcg cagggtgtga tcggcacggt cgatgcctat 600

ctgggggcgc tcaagcgccg caggagctgg cagggaagcc ttgctgtcgg gcccggatac 660

agcagcaatc tcaatcagtc gtcggcgagc tacacctgcc tgctggcgac cgacgacggc 720

acctgccttg tcgaccgaca ggttccgccc gcgatcgcgg ccgctggcgt caacttcgaa 780

gccacgctcg cgaaagatgt tccgttgagc ggacatggcg gcctccgggc gcgggcgatc 840

ctgttcggcg atgtctatcc ggaacatcat gcctattccc aggcgacggc gatcatgcgt 900

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acggtctcgc cgcggtcgct cttcaaggtt gagggaaatt accgggattt ccgttaccgc 1080

gatgcggctt ttgctccgca aaatgggccg ctcacggatg ttgctatcac aggatggtat 1140

tcgctgacgc cgactttgac cgtgttcggt ggacccgatg tcattgtgaa ggacacgcca 1200

agccttgtcg aagcctatcg ccaatggggt ggtcggctag ggatcaacaa ggctttcggc 1260

aatgtcgcga gcctcttcct catgggatca tatcgctacc gccgccaccg cgcttacagc 1320

gaattgttcg aggcgcagcg caaggatcgc caattcaacg ttatcgggat cgcccgtcta 1380

cccatcctga aagtcgggcc gctcgttccc gaaatcgttg tccagcacac ccgcgtcgag 1440

agcaacatcg actggcttta ttcctacaag cgcacgaccg cgagcgtgag gctcagctat 1500

gccttctga 1509

<210> 590

<211> 502

<212> PRT

<213> S. lucknowense SLAM 1

<400> 590

Met Asp Ile Ser Ala Phe Arg Ile Leu Ile Ser Tyr Glu Pro Leu Leu
1 5 10 15
Leu Ala Leu Ala Ala Ser Leu Trp Ala Thr Val Ala Asn Thr Gln Thr
20 25 30
Thr Ser Gly Gln Asp Thr Arg Leu Arg Leu Asp Gln Gln Val Asp Arg
35 40 45
Gln Arg Val Asn Gln Glu Ser Arg Ala Ile Glu Asp Ala Glu Ala Leu

50 55 60
Asp Gly Asp Thr Ser Ser Leu Thr Val Asp Gly Gln Thr Tyr Ala Val
65 70 75 80
Gly Asn Thr Val Asp Asp Ile Gly Gln Ala Leu Tyr Ile Ser Val Thr
85 90 95
Arg Lys Gln Trp Pro Asp Val Arg Arg Phe Leu Ala Ala Tyr Gln Lys
100 105 110
Leu Asp Gly His Asp Pro Met Leu Val Glu Tyr Ala Leu Gly Ala Leu

115 120 125
Ala Arg Glu Lys Gly Asp Leu Ala Thr Ala Glu Arg His Tyr Arg Ala
130 135 140
Leu Leu Ala Ile Lys Ala Asp Phe Val Pro Gly Arg Leu Glu Leu Ala
145 150 155 160
Arg Val Leu Phe Asp Asn His Lys Asp Arg Glu Ala Asp Ser Ala Phe
165 170 175
Arg Ala Ala Arg Asp Met Leu Ala Asp Asp Gly Ser Gln Ala Gln Gly

180 185 190
Val Ile Gly Thr Val Asp Ala Tyr Leu Gly Ala Leu Lys Arg Arg Arg
195 200 205
Ser Trp Gln Gly Ser Leu Ala Val Gly Pro Gly Tyr Ser Ser Asn Leu
210 215 220
Asn Gln Ser Ser Ala Ser Tyr Thr Cys Leu Leu Ala Thr Asp Asp Gly
225 230 235 240

Thr Cys Leu Val Asp Arg Gln Val Pro Pro Ala Ile Ala Ala Ala Gly

245 250 255

Val Asn Phe Glu Ala Thr Leu Ala Lys Asp Val Pro Leu Ser Gly His

260 265 270

Gly Gly Leu Arg Ala Arg Ala Ile Leu Phe Gly Asp Val Tyr Pro Glu

275 280 285

His His Ala Tyr Ser Gln Ala Thr Ala Ile Met Arg Leu Gly Tyr Gln

290 295 300

Tyr Gln Ala Ala Arg Asn Ala Val Ser Leu Ser Pro Ser Phe Glu Ile

305 310 315 320

Gly Ser Leu Gly Ser Ser Glu Leu Tyr Ser Ala Pro Gly Leu Asn Ala

325 330 335

Glu Trp Thr His Thr Val Ser Pro Arg Ser Leu Phe Lys Val Glu Gly

340 345 350

Asn Tyr Arg Asp Phe Arg Tyr Arg Asp Ala Ala Phe Ala Pro Gln Asn

355 360 365

Gly Pro Leu Thr Asp Val Ala Ile Thr Gly Trp Tyr Ser Leu Thr Pro

370 375 380

Thr Leu Thr Val Phe Gly Gly Pro Asp Val Ile Val Lys Asp Thr Pro

385 390 395 400

Ser Leu Val Glu Ala Tyr Arg Gln Trp Gly Gly Arg Leu Gly Ile Asn

405 410 415

Lys Ala Phe Gly Asn Val Ala Ser Leu Phe Leu Met Gly Ser Tyr Arg

420 425 430

Tyr Arg Arg His Arg Ala Tyr Ser Glu Leu Phe Glu Ala Gln Arg Lys

435 440 445

Asp Arg Gln Phe Asn Val Ile Gly Ile Ala Arg Leu Pro Ile Leu Lys

450 455 460

Val Gly Pro Leu Val Pro Glu Ile Val Val Gln His Thr Arg Val Glu

465 470 475 480

Ser Asn Ile Asp Trp Leu Tyr Ser Tyr Lys Arg Thr Thr Ala Ser Val

485 490 495

Arg Leu Ser Tyr Ala Phe

500

<210> 591

<211> 1455

<212> DNA

<213> S. maltophilia SLAM 1

<400> 591

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caggatgatc tgcgccgcgt gctcgaacag ggcagcgaac tgcgccacca gcagcaggac 120

cagcagcgcc tgcaacaggc cgaatcgcaa cggccgacgc tcaccatcga tggccagacc 180

gtgcgggtgg agcgcaccgt cgatgatctc ggccaggctc tctacttgtc attgcagcat 240

cagcagtggc cagccgccgc ggcgttcctc gccgaataca tcgagcttcc ggggcacgac 300

ccgctgctgc gccattatgc gcagggtgcg ttggcccgcg tggccggcga ccattcgcgc 360

gctgcacagg agtacgaagc gctgctggca gcgcagccgg acttcctgcc cgcccgcctg 420

gaactggcgc gtgtctatgc cgaagaccag cgcgaccgcg aggcggtggc attgttcggt 480

gctatcaagg ccggtatcga cagcaacgat ccggccaccg cgggtgtgcg cgcacgcgtg 540

gacagctatc tggtcgcgtt gcaggcacgc gggcgctgga agggtgcggt cgccgccggg 600

cctgcatgga gcgacaacat caaccgcagt tcggccagcc gcacctgcct gttcggtgtc 660

ggcaacacct gcctgatcga acgcacgctg cccgaggcgc agcgcgccac cggcctggac 720

tacgacgcca gcctggaacg gcgctgggcg ttggcaggcc atcatggcct gtacgtgcgt 780

gggctggcgt tcgggcaggc ctggcgtggc tacagcgcat acaacgagct caacgccagc 840

gtgcaggccg gctacagctg gcgcagtgca cggcacaccc tgcagctggc gccgagctat 900

gactaccagg cgctgggcaa ccacgccctg cagggcggca gtggcgtgca cggcgaatgg 960

cagtacgccc tggacgcgcg cagcctgctc aagctggagg ccgactggaa acgccagcgc 1020

taccggcagc cgggcctggc cgacaactac gatggcgaac tggccgcgct gtatgccacc 1080

tggttccgcg cgctcaaccc gcgctggacc ctgttcgcgg gcgtggacct gaccgacagc 1140

agtgcagccg accccgccaa cggctaccgc cagcacggcc tgcggctggg cgcggcacgg 1200

cagtggagtg gcaccacggc cacggtgttc gtgtcgttgc gtcaccgtga ctatggtgcc 1260

tggagtcctt tgctggaggc gcgcaggcag gacgacgaac agaacctgat cgccatcgtg 1320

cgcagcgagc ggctggcggt gggcgggctg gtgcccagcc tgagcctgcg ctacgcctgc 1380

atcgacagca acgtcggttg gctgtacagc catgaccgca gcctgctcag cctgaaatgg 1440

gagcgtgcgt tctga 1455

<210> 592

<211> 484

<212> PRT

<213> S. maltophilia SLAM 1

<400> 592

Met Arg Pro Pro Ile Phe Leu Val Phe Leu Leu Leu Val Ala Ala Asp

1 5 10 15

Val Arg Ala Gln Gln Asp Asp Leu Arg Arg Val Leu Glu Gln Gly Ser

20 25 30

Glu Leu Arg His Gln Gln Gln Asp Gln Gln Arg Leu Gln Gln Ala Glu

35 40 45

Ser Gln Arg Pro Thr Leu Thr Ile Asp Gly Gln Thr Val Arg Val Glu

50 55 60

Arg Thr Val Asp Asp Leu Gly Gln Ala Leu Tyr Leu Ser Leu Gln His

65 70 75 80

Gln Gln Trp Pro Ala Ala Ala Ala Phe Leu Ala Glu Tyr Ile Glu Leu

85 90 95

Pro Gly His Asp Pro Leu Leu Arg His Tyr Ala Gln Gly Ala Leu Ala

100 105 110

Arg Val Ala Gly Asp His Ser Arg Ala Ala Gln Glu Tyr Glu Ala Leu

115 120 125

Leu Ala Ala Gln Pro Asp Phe Leu Pro Ala Arg Leu Glu Leu Ala Arg

130 135 140

Val Tyr Ala Glu Asp Gln Arg Asp Arg Glu Ala Val Ala Leu Phe Gly

145 150 155 160

Ala Ile Lys Ala Gly Ile Asp Ser Asn Asp Pro Ala Thr Ala Gly Val

165 170 175

Arg Ala Arg Val Asp Ser Tyr Leu Val Ala Leu Gln Ala Arg Gly Arg

180 185 190

Trp Lys Gly Ala Val Ala Ala Gly Pro Ala Trp Ser Asp Asn Ile Asn

195 200 205

Arg Ser Ser Ala Ser Arg Thr Cys Leu Phe Gly Val Gly Asn Thr Cys

210 215 220

Leu Ile Glu Arg Thr Leu Pro Glu Ala Gln Arg Ala Thr Gly Leu Asp

225 230 235 240

Tyr Asp Ala Ser Leu Glu Arg Arg Trp Ala Leu Ala Gly His His Gly

245 250 255

Leu Tyr Val Arg Gly Leu Ala Phe Gly Gln Ala Trp Arg Gly Tyr Ser

260 265 270

Ala Tyr Asn Glu Leu Asn Ala Ser Val Gln Ala Gly Tyr Ser Trp Arg

275 280 285

Ser Ala Arg His Thr Leu Gln Leu Ala Pro Ser Tyr Asp Tyr Gln Ala

290 295 300

Leu Gly Asn His Ala Leu Gln Gly Gly Ser Gly Val His Gly Glu Trp

305 310 315 320

Gln Tyr Ala Leu Asp Ala Arg Ser Leu Leu Lys Leu Glu Ala Asp Trp

325 330 335

Lys Arg Gln Arg Tyr Arg Gln Pro Gly Leu Ala Asp Asn Tyr Asp Gly

340 345 350

Glu Leu Ala Ala Leu Tyr Ala Thr Trp Phe Arg Ala Leu Asn Pro Arg

355 360 365

Trp Thr Leu Phe Ala Gly Val Asp Leu Thr Asp Ser Ser Ala Ala Asp

370 375 380

Pro Ala Asn Gly Tyr Arg Gln His Gly Leu Arg Leu Gly Ala Ala Arg

385 390 395 400

Gln Trp Ser Gly Thr Thr Ala Thr Val Phe Val Ser Leu Arg His Arg

405 410 415

Asp Tyr Gly Ala Trp Ser Pro Leu Leu Glu Ala Arg Arg Gln Asp Asp

420 425 430

Glu Gln Asn Leu Ile Ala Ile Val Arg Ser Glu Arg Leu Ala Val Gly

435 440 445

Gly Leu Val Pro Ser Leu Ser Leu Arg Tyr Ala Cys Ile Asp Ser Asn

450 455 460

Val Gly Trp Leu Tyr Ser His Asp Arg Ser Leu Leu Ser Leu Lys Trp

465 470 475 480

Glu Arg Ala Phe

<210> 593

<211> 1473

<212> DNA

<213> S. melonis SLAM 1

<400> 593

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gcttccggcc agagtgcccg gagcgaggat aaccgcctgc gtctcgaccc cggtatcgat 120

cgccggacca cggcccagga ccgcgaggcg atcgaggggg gcagttcgcc ggatcgcatc 180

accatagatg gccaagtcta ttcggtcggc cataacccgg acgatctggg ccgggcgctg 240

tacctgtcgg tagcgcgcaa gaattgggcg gatgtccgcc gtttcctgcc accgtatctg 300

gcactggccc gccatgatcc gatgctggtc gcctgggcgc gcggcggcct cgcgcgcagt 360

gacgggcggc tgggcgaggc cgagcgccag taccgcgccc tgctggcgat ccagcctgac 420

ttcctgccgg ggcggctgga gctcgggcgc gtgctgttcg agaaccgcaa ggaccgagag 480

gcccgccgcc tgttccgcgc gatccgcgaa gagctggcgg ggcagggcga gcaggccgcc 540

ggggttcgcc ggacggtcga caccttcctc gccgcgctcg accggcgggg cggctggcag 600

ggcatgatcg cggcggggcc gggctatagc agcaacctca accagacgtc cgccagccag 660

acctgcctgc tggtcggggt ggacggcacc tgcctgatcg accgcaccct gccaccagcg 720

atcgcctccg tcggcctcaa cgtcgagggg agcgtcagtc gccggttcgc gctgaagggg 780

cagggcgggc tgttagcccg ggccttcgtc tatggcgatc tctggcccgg gcatggcgca 840

ttcgatcaag cgacgttgac cgcgcagatc ggctatgatc atcagactgc caggcggagc 900

ctgaccgtgt cgccgaccgt cgacctggcg agcctgggtg atcggctgct ctataccgcg 960

cccggccttc gcgccgaggc gatggtcacc ccgtcgcccg acaccgccct ccggctggag 1020

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gaggcgtccc tgaccggctg gtggtcgcgc ctgcgcagct ggacgctgtt tgccggtatc 1140

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cagcgcgatt acggggccta tagcgaattg ctggaggccg tccgccacga ccgagagacg 1320

aacctgaccg ccgtcctccg cctacccaag ctacgcctcg ccgggctgac gcccaacatc 1380

cttctccagc acaatcgggt gaagagcaat gtcgattggc tctattcctt tcatcgcacc 1440

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<210> 594

<211> 490

<212> PRT

<213> S. melonis SLAM 1

<400> 594

Met Arg His Ala Val Ser Pro Tyr Leu Leu Thr Leu Ala Thr Leu Trp
1 5 10 15

Leu Ala Ala Pro Ala Ser Gly Gln Ser Ala Arg Ser Glu Asp Asn Arg
20 25 30

Leu Arg Leu Asp Pro Gly Ile Asp Arg Arg Thr Thr Ala Gln Asp Arg
35 40 45

Glu Ala Ile Glu Gly Gly Ser Ser Pro Asp Arg Ile Thr Ile Asp Gly
50 55 60

Gln Val Tyr Ser Val Gly His Asn Pro Asp Asp Leu Gly Arg Ala Leu
65 70 75 80

Tyr Leu Ser Val Ala Arg Lys Asn Trp Ala Asp Val Arg Arg Phe Leu
85 90 95

Pro Pro Tyr Leu Ala Leu Ala Arg His Asp Pro Met Leu Val Ala Trp
100 105 110

Ala Arg Gly Gly Leu Ala Arg Ser Asp Gly Arg Leu Gly Glu Ala Glu
115 120 125

Arg Gln Tyr Arg Ala Leu Leu Ala Ile Gln Pro Asp Phe Leu Pro Gly
130 135 140

Arg Leu Glu Leu Gly Arg Val Leu Phe Glu Asn Arg Lys Asp Arg Glu
145 150 155 160

Ala Arg Arg Leu Phe Arg Ala Ile Arg Glu Glu Leu Ala Gly Gln Gly

165 170 175

Glu Gln Ala Ala Gly Val Arg Arg Thr Val Asp Thr Phe Leu Ala Ala
180 185 190
Leu Asp Arg Arg Gly Gly Trp Gln Gly Met Ile Ala Ala Gly Pro Gly
195 200 205
Tyr Ser Ser Asn Leu Asn Gln Thr Ser Ala Ser Gln Thr Cys Leu Leu
210 215 220
Val Gly Val Asp Gly Thr Cys Leu Ile Asp Arg Thr Leu Pro Pro Ala
225 230 235 240

Ile Ala Ser Val Gly Leu Asn Val Glu Gly Ser Val Ser Arg Arg Phe
245 250 255
Ala Leu Lys Gly Gln Gly Gly Leu Leu Ala Arg Ala Phe Val Tyr Gly
260 265 270
Asp Leu Trp Pro Gly His Gly Ala Phe Asp Gln Ala Thr Leu Thr Ala
275 280 285
Gln Ile Gly Tyr Asp His Gln Thr Ala Arg Arg Ser Leu Thr Val Ser
290 295 300

Pro Thr Val Asp Leu Ala Ser Leu Gly Asp Arg Leu Leu Tyr Thr Ala
305 310 315 320
Pro Gly Leu Arg Ala Glu Ala Met Val Thr Pro Ser Pro Asp Thr Ala
325 330 335
Leu Arg Leu Glu Val Ala Arg Arg Val Phe Asp Tyr Arg Arg Ser Phe
340 345 350
Asp Asp Leu Asp Gly Ala Leu Thr Glu Ala Ser Leu Thr Gly Trp Trp
355 360 365

Ser Arg Leu Arg Ser Trp Thr Leu Phe Ala Gly Ile Glu Ala Gly Asp
370 375 380
Lys Gln Ala Gly Glu Arg Ala Asn Ala Tyr Arg His Val Gly Ala Arg
385 390 395 400
Leu Gly Val Val His Gly Phe Ala Asp Trp Ala Glu Leu Thr Leu Ile
405 410 415

Gly Ser Val Arg Gln Arg Asp Tyr Gly Ala Tyr Ser Glu Leu Leu Glu
420 425 430

Ala Val Arg His Asp Arg Glu Thr Asn Leu Thr Ala Val Leu Arg Leu
435 440 445

Pro Lys Leu Arg Leu Ala Gly Leu Thr Pro Asn Ile Leu Leu Gln His
450 455 460

Asn Arg Val Lys Ser Asn Val Asp Trp Leu Tyr Ser Phe His Arg Thr
465 470 475 480

Ala Ala Ser Ile Arg Leu Glu His Ala Phe
485 490

<210> 595

<211> 1500

<212

> DNA

<213> S. muelleri SLAM 1

<400> 595

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gcgtatgcgg ctgatgtgtc caatgatgcg ccgccgtccg aacccatacc cgatacgcca 120

cctgtcgcgc cgcccgagcc tgaaacagat tttgatatta ctcaaaatca acaacgtaaa 180

accgaaaatc aacagcccga atccatacct gaaaccacac aatctgatgg cagcaaacgt 240

ttacgcttga gtaaagacga attggcaaag cagcctgaat tattatatcg cgcattgtcg 300

tcttcaattt tgctgcgaaa tgtggaaggc gtgcggacat tgctgcccat ctatcaagaa 360

caaacgcaac aacctaaaga tgaattattg attgatttgt ctgaaggcat gattgcgcgt 420

gatgatggca atgcaggcaa ggccgcgaaa cattaccaaa aagcgttgga aaaaaatcct 480

aatatggatt tggtgcgatt gaatttggcg caagtcttat ttgaagatca ccaaaatcgt 540

gaatcagata aattatttga acaaattcaa tcagaaactg aattgcccaa taatgtacgc 600

gatttaacgc aaagttaccg caaaatactt aaaaaacgca gcagaatgaa tgcgtatgct 660

catgcaaatt acacacgcaa caataatgtt aacaactcac ccaaagagcg cgttattcat 720

acccgaaatg gcgcgtggta tttgcctgaa cctgaatcgg cacaaggaat ttcttatcgt 780

gcgggtgtgg gtaaagatac accattattc aaaaattaca cgtttcgtac caatgcggat 840

ttgtggggta aattttattg ggataaccac aaatatgacg atttgagtac gcgtgccagt 900

gtgggtgtgg cgtatcaaaa tgcgcgaagt gagatggcgg tgttgcctta ttatgaacgc 960

cgttggtttg gtacggagaa atatgccact gaaaaaggca tacgtttaga atcatcgcat 1020

tggattacgc cacgacatca agctttagtc gcagccgaag ttgggcgcga tacttatgat 1080

acgcgcaaat ttctcaatgg acgtgtcagt aatttatcgg ttacttggtt acacacaccg 1140

agtaatcagc aatatttcac gttggggacg gatttttcgc gtaaatccgc gcaagatagc 1200

agtgattcgt atcgccgtca ggggattcgg gcgagttggt cgcggtcgtg gaaacgcagt 1260

ggtttgggga caactttgac ggcaaattat gggcagcgcg aatacgatac caatgatttt 1320

tttaatattg ttcgcaaaga caaagaatat tctgctacgc tatcggtttg gcataaaaaa 1380

gtgcaattgt ggggcattac gccacgtttg gtaggtgtgt attatcgtaa tgacagtaat 1440

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<210> 596

<211> 499

<212> PRT

<213> S. muelleri SLAM 1

<400> 596

Met Lys Arg Ala Tyr Gln Ile Leu Thr Val Tyr Thr Leu Ser Leu Phe
1 5 10 15

Ala Pro Met Trp Ala Tyr Ala Ala Asp Val Ser Asn Asp Ala Pro Pro
20 25 30

Ser Glu Pro Ile Pro Asp Thr Pro Pro Val Ala Pro Pro Glu Pro Glu
35 40 45

Thr Asp Phe Asp Ile Thr Gln Asn Gln Gln Arg Lys Thr Glu Asn Gln
50 55 60

Gln Pro Glu Ser Ile Pro Glu Thr Thr Gln Ser Asp Gly Ser Lys Arg
65 70 75 80

Leu Arg Leu Ser Lys Asp Glu Leu Ala Lys Gln Pro Glu Leu Leu Tyr
85 90 95

Arg Ala Leu Ser Ser Ser Ile Leu Leu Arg Asn Val Glu Gly Val Arg
100 105 110

Thr Leu Leu Pro Ile Tyr Gln Glu Gln Thr Gln Gln Pro Lys Asp Glu
115 120 125

Leu Leu Ile Asp Leu Ser Glu Gly Met Ile Ala Arg Asp Asp Gly Asn

130 135 140

Ala Gly Lys Ala Ala Lys His Tyr Gln Lys Ala Leu Glu Lys Asn Pro
145 150 155 160
Asn Met Asp Leu Val Arg Leu Asn Leu Ala Gln Val Leu Phe Glu Asp
165 170 175
His Gln Asn Arg Glu Ser Asp Lys Leu Phe Glu Gln Ile Gln Ser Glu
180 185 190
Thr Glu Leu Pro Asn Asn Val Arg Asp Leu Thr Gln Ser Tyr Arg Lys
195 200 205

Ile Leu Lys Lys Arg Ser Arg Met Asn Ala Tyr Ala His Ala Asn Tyr
210 215 220
Thr Arg Asn Asn Asn Val Asn Asn Ser Pro Lys Glu Arg Val Ile His
225 230 235 240
Thr Arg Asn Gly Ala Trp Tyr Leu Pro Glu Pro Glu Ser Ala Gln Gly
245 250 255
Ile Ser Tyr Arg Ala Gly Val Gly Lys Asp Thr Pro Leu Phe Lys Asn
260 265 270

Tyr Thr Phe Arg Thr Asn Ala Asp Leu Trp Gly Lys Phe Tyr Trp Asp
275 280 285
Asn His Lys Tyr Asp Asp Leu Ser Thr Arg Ala Ser Val Gly Val Ala
290 295 300
Tyr Gln Asn Ala Arg Ser Glu Met Ala Val Leu Pro Tyr Tyr Glu Arg
305 310 315 320
Arg Trp Phe Gly Thr Glu Lys Tyr Ala Thr Glu Lys Gly Ile Arg Leu
325 330 335

Glu Ser Ser His Trp Ile Thr Pro Arg His Gln Ala Leu Val Ala Ala
340 345 350
Glu Val Gly Arg Asp Thr Tyr Asp Thr Arg Lys Phe Leu Asn Gly Arg
355 360 365
Val Ser Asn Leu Ser Val Thr Trp Leu His Thr Pro Ser Asn Gln Gln
370 375 380

Tyr Phe Thr Leu Gly Thr Asp Phe Ser Arg Lys Ser Ala Gln Asp Ser
385 390 395 400

Ser Asp Ser Tyr Arg Arg Gln Gly Ile Arg Ala Ser Trp Ser Arg Ser
405 410 415
Trp Lys Arg Ser Gly Leu Gly Thr Thr Leu Thr Ala Asn Tyr Gly Gln
420 425 430
Arg Glu Tyr Asp Thr Asn Asp Phe Phe Asn Ile Val Arg Lys Asp Lys
435 440 445
Glu Tyr Ser Ala Thr Leu Ser Val Trp His Lys Lys Val Gln Leu Trp
450 455 460

Gly Ile Thr Pro Arg Leu Val Gly Val Tyr Tyr Arg Asn Asp Ser Asn
465 470 475 480
His Phe Met Tyr Asp Tyr Arg Lys Ala Tyr Ala Phe Ile Gln Leu Ser
485 490 495
Lys Ser Leu

<210> 597
<211> 1395
<212> DNA
<213> S. muelleri SLAM 2
<400> 597
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ttaacaaaag aatcatcata caatccctcc gtgcaatttg ctgtgccaca aaaacctata 120

cacgatgctt ataaaagtaa ggtgttcatg aattcggaag aatttttgca acacccagat 180
ttactcaaaa atgcactgga taccgccatt ttgcgagaaa atacgagtgt tgttcgtttt 240
ttgttgccac tttatgatag gttgcctgaa aatcagcgcg acaaaacatt aggtgaatat 300
gcacacgcta ttgttgccag tgccgatggt caatatgctc aagccgaaca acaattacgc 360
gcattactcg tccaaaatcc tgaatatgct ccagttcgtt tgcaattggc gcgcgttttg 420
gcgaaagatg gtcaattgcg tgatgccgcc aaagaaattg acacgctaaa acaaacacct 480
gatatgccca acgaaaccac gcaatattta gaacaatttg atcactatct tgtgaaagag 540

caagcgtgga aatttaatgc taatacctat tatattcaag atgataatgt cgggcgtgta 600

ccccagcagc gacaatatgg ctattggcgt ttttctgaac ctaaatccgc acacggtgta 660

ggttatgact tgtctgctca aaaaaacatg tctcttaaag gacattgggc gacacgtgtt 720

aatgtgtcta catcgggtaa attttattgg gacgcgcacg attatgatga tttacaaaca 780

catgctgaag tcggaacaat ttggcgcaat gcaaaacgtg agatttcagt gagtccattt 840

tatgaaagac gttggtatgg cagtaagccg tattcacaca atgcaggtgg cgtattgcgt 900

tattcagaaa ttttgtcacc caaatggcaa gtttggggcg cgtggcaatc tgcatataaa 960

aaacacgata aacgtcaatt tttagatggt gccaatcatg caggttcggt tacgctggtg 1020

tatgcgcccg atccgaagca atattttgtg atgggtggtg gtagcggtta tcaagcggca 1080

aaagacaaat cggaagcata ttcgcaaacc aatgcacgtg tgggttggca tcgtcagtgg 1140

aaaaatacat ttgatttaac aacagatttt aatttttgg tgcaatctcg gcattatcaa 1200

gcacctgatt ttttcaacat caaacgacgt gataaagagt acatgacgcg tgtgagtgtg 1260

agttcgccaa agttttcgtg gaaaggcttt gagccgcgat tgaattggac atggtcacga 1320

attaacagca accattttta ttatcgttac aagaatcatc gtgtatttat tgatgtttct 1380

aaacaattta ataa 1395

<210> 598

<211> 464

<212> PRT

<213> S. muelleri SLAM 2

<400> 598

Met Leu Thr Ser Trp Val Thr Ala Ala Pro Val Ala Thr Pro Ser Asp
1 5 10 15

Ser Ile Asp Asn Leu Thr Lys Glu Ser Ser Tyr Asn Pro Ser Val Gln
20 25 30

Phe Ala Val Pro Gln Lys Pro Ile His Asp Ala Tyr Lys Ser Lys Val
35 40 45

Phe Met Asn Ser Glu Glu Phe Leu Gln His Pro Asp Leu Leu Lys Asn
50 55 60

Ala Leu Asp Thr Ala Ile Leu Arg Glu Asn Thr Ser Val Val Arg Phe
65 70 75 80

Leu Leu Pro Leu Tyr Asp Arg Leu Pro Glu Asn Gln Arg Asp Lys Thr
85 90 95

Leu Gly Glu Tyr Ala His Ala Ile Val Ala Ser Ala Asp Gly Gln Tyr

100 105 110

Ala Gln Ala Glu Gln Gln Leu Arg Ala Leu Leu Val Gln Asn Pro Glu
115 120 125
Tyr Ala Pro Val Arg Leu Gln Leu Ala Arg Val Leu Ala Lys Asp Gly
130 135 140
Gln Leu Arg Asp Ala Ala Lys Glu Ile Asp Thr Leu Lys Gln Thr Pro
145 150 155 160
Asp Met Pro Asn Glu Thr Thr Gln Tyr Leu Glu Gln Phe Asp His Tyr
165 170 175

Leu Val Lys Glu Gln Ala Trp Lys Phe Asn Ala Asn Thr Tyr Tyr Ile
180 185 190
Gln Asp Asp Asn Val Gly Arg Val Pro Gln Gln Arg Gln Tyr Gly Tyr
195 200 205
Trp Arg Phe Ser Glu Pro Lys Ser Ala His Gly Val Gly Tyr Asp Leu
210 215 220
Ser Ala Gln Lys Asn Met Ser Leu Lys Gly His Trp Ala Thr Arg Val
225 230 235 240

Asn Val Ser Thr Ser Gly Lys Phe Tyr Trp Asp Ala His Asp Tyr Asp
245 250 255
Asp Leu Gln Thr His Ala Glu Val Gly Thr Ile Trp Arg Asn Ala Lys
260 265 270
Arg Glu Ile Ser Val Ser Pro Phe Tyr Glu Arg Arg Trp Tyr Gly Ser
275 280 285
Lys Pro Tyr Ser His Asn Ala Gly Gly Val Leu Arg Tyr Ser Glu Ile
290 295 300

Leu Ser Pro Lys Trp Gln Val Trp Gly Ala Trp Gln Ser Ala Tyr Lys
305 310 315 320
Lys His Asp Lys Arg Gln Phe Leu Asp Gly Ala Asn His Ala Gly Ser
325 330 335
Val Thr Leu Val Tyr Ala Pro Asp Pro Lys Gln Tyr Phe Val Met Gly
340 345 350

Gly Gly Ser Gly Tyr Gln Ala Ala Lys Asp Lys Ser Glu Ala Tyr Ser
355 360 365

Gln Thr Asn Ala Arg Val Gly Trp His Arg Gln Trp Lys Asn Thr Phe
370 375 380
Asp Leu Thr Thr Asp Phe Asn Phe Leu Val Gln Ser Arg His Tyr Gln
385 390 395 400
Ala Pro Asp Phe Phe Asn Ile Lys Arg Arg Asp Lys Glu Tyr Met Thr
405 410 415
Arg Val Ser Val Ser Ser Pro Lys Phe Ser Trp Lys Gly Phe Glu Pro
420 425 430

Arg Leu Asn Trp Thr Trp Ser Arg Ile Asn Ser Asn His Phe Tyr Tyr
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Arg Tyr Lys Asn His Arg Val Phe Ile Asp Val Ser Lys Gln Phe Lys
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<210> 599
<211> 1500
<212> DNA
<213> S. muelleri SLAM 3
<400> 599

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gaatcaggaa caggtttcaa ttttggtgtc aatacagaaa aaagatggtc cttacaaaat 780

gggcaatata tcggactagc aggtagtggc aatttaaaat actactggaa taatcataaa 840

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gataaattaa aatcttatac ccactcacta gggatatcaa cttctttggc ggcatggttg 1020

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cgcggtacaa aacagtattt tggttcaagt ttggatttaa tgcgccgtga tgtgggtact 1200

gaaacgaatt cgtataaacg ttatggtggg cgagtatttt ggggacagga gtggcccaaa 1260

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<210> 600

<211> 499

<212> PRT

<213> S. muelleri SLAM 3

<400> 600

Met Lys Lys Phe Ser Ser Leu Leu Cys Ala Val Ile Leu Ser Ala Gln
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Ser Ile Thr Tyr Ala Ala Glu Lys Ser Pro Asp Ile Asn Asn His Tyr
20 25 30

Leu Glu Ser Glu Thr Thr Pro Val Val Thr Gln Ser Thr Thr Pro Ser
35 40 45

Asp Asp Asp Lys Leu Arg Gly Gln Lys Ile Ser Thr Asp Val Gln Pro
50 55 60

Ala Lys Lys Met Asp Leu Thr Glu Thr Glu Trp Arg Ala Asn Pro Thr
65 70 75 80

Lys Leu Gln Gln Thr Leu Leu Phe Leu Leu Ala Thr Asn Gln Val Asn
85 90 95

His Leu Asn Asn Leu Pro Glu Leu Tyr Gly Leu Leu Pro Ala Asn Thr

100 105 110

Arg Asp Asp Ser Leu Ile Glu Trp Ala His Ala Met Arg Leu Thr Gln
115 120 125
Thr Asn Leu Arg Gln Ser Ile His Glu Tyr Arg Ile Leu Leu Gly Lys
130 135 140
Phe Pro Asp Asn Asp Phe Ile Arg Phe Gln Leu Ala Ala Leu Leu Tyr
145 150 155 160
Gln Asn Gln Glu Phe Asp Ala Ala Lys Gly Gln Phe Gln Lys Leu Arg
165 170 175

Ala Ser Pro Gln Met Thr Glu Lys Asp Met Gly Val Phe Asp Lys Tyr
180 185 190
Leu Thr Ala Ile Glu Asn Lys Asp Lys Trp His Phe Ser Leu Gly Thr
195 200 205
Ser Leu Leu Arg Asp Lys Asn Leu Thr Glu Met Ala Ala Glu Gly Thr
210 215 220
Val Met Thr Leu Pro Asn Gly Ala Thr Phe Thr Gln Ile Thr Pro Lys
225 230 235 240

Glu Ser Gly Thr Gly Phe Asn Phe Gly Val Asn Thr Glu Lys Arg Trp
245 250 255
Ser Leu Gln Asn Gly Gln Tyr Ile Gly Leu Ala Gly Ser Gly Asn Leu
260 265 270
Lys Tyr Tyr Trp Asn Asn His Lys Phe Asn Glu Leu Thr Gly Tyr Ile
275 280 285
Gly Thr Ser Tyr Gly Tyr Ala Asn Ser Asn Ile Glu Met Lys Ala Thr
290 295 300

Pro Tyr Tyr Met Lys Arg Trp Tyr Ala Gly Gly Gly Ser Asn Asp Ser
305 310 315 320
Asp Lys Leu Lys Ser Tyr Thr His Ser Leu Gly Ile Ser Thr Ser Leu
325 330 335
Ala Ala Trp Leu Thr Pro Thr Leu Lys His Ser Thr Tyr Ala Asn Tyr
340 345 350

Ser His Glu Thr Tyr Ala Asn Asp Asn Met Asp Lys Arg Tyr Gly Gly
355 360 365

Asn Ile Lys Ser Val Gly Thr Ser Leu Leu Tyr Leu Arg Gly Thr Lys
370 375 380
Gln Tyr Phe Gly Ser Ser Leu Asp Leu Met Arg Arg Asp Val Gly Thr
385 390 395 400
Glu Thr Asn Ser Tyr Lys Arg Tyr Gly Gly Arg Val Phe Trp Gly Gln
405 410 415
Glu Trp Pro Lys Gly Phe Ala Thr Gln Ala Ser Leu Ser Leu Ala Lys
420 425 430

Arg Lys Tyr Gln Ala Pro Trp Leu Gly Ile Val Arg Arg Ser Asp Lys
435 440 445
Glu Trp Asn Ala Asn Val Ser Leu Trp His Lys Ala Val His Phe Tyr
450 455 460
Gly Val Thr Pro Arg Leu Thr Phe Asn Tyr Gln Lys Thr Lys Ser Asn
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Ile Pro Ile Tyr Ser Tyr Asp Lys Asn Ile Thr Tyr Ile Glu Leu Asp
485 490 495

Lys Ser Phe

<210> 601
<211> 1452
<212> DNA
<213> S. paucimobilis SLAM 1
<400> 601
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tatgcctttt ag 1452

<210> 602

<211> 483

<212> PRT

<213> S. paucimobilis SLAM 1

<400> 602

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Ala Asp Thr Arg Leu Arg Leu Asp Gln Ser Phe Asp Arg Gln Ser Ala

20 25 30

Glu Ala Glu Arg Gln Leu Leu Glu Asp Ala Asp Asp Leu Asp Gly Thr

35 40 45

Pro Ser Thr Ile Glu Ile Asp Gly Lys Thr Tyr Ala Val Ala Asn Thr

50 55 60

Ile His Glu Val Gly Glu Ala Leu Tyr Val Ala Ile Ala Arg Arg Gln

65 70 75 80

Trp Ala Asp Val Arg Arg Phe Leu His Ala Tyr Leu Ala Phe Glu Glu

85 90 95

Arg Asp Pro Met Leu Val Ala Tyr Ala Gln Gly Ala Leu Ala Arg Thr

100 105 110

Val Gly Lys Leu Gly Glu Ala Glu Arg His Tyr Arg Thr Leu Leu Gly

115 120 125

Leu Gln Pro Asp Phe Val Pro Gly Gln Leu Glu Leu Ala Arg Val Leu

130 135 140

Phe Glu Asn Arg Lys Asp Arg Glu Ala Arg Arg Met Phe Glu Thr Ala

145 150 155 160

Arg Ala Val Leu Ala Asp Asp Gly Asp Lys Ala Ala Gly Val Leu Arg

165 170 175

Thr Ile Asp Ser Phe Thr Gln Ala Leu Asp Lys Arg Arg Gly Trp Gln

180 185 190

Gly Ser Val Ala Ile Gly Pro Gly Tyr Ser Ser Asn Leu Asn Gln Ser

195 200 205

Ser Ala Ser Tyr Thr Cys Leu Leu Ala Gly Asp Asp Gly Thr Cys Leu

210 215 220

Ile Asp Arg Lys Val Pro Asp Pro Ile Arg Ala Ala Gly Ile Asn Phe

225 230 235 240

Glu Ser Asn Val Ser Arg Arg Ile Pro Leu Arg Gly His Ser Gly Ile

245 250 255

Thr Gly Arg Ala Leu Phe Tyr Gly Asp Ile Tyr Pro Asp His Gly Arg

260 265 270

Tyr Ser Gln Thr Thr Leu Thr Thr Gln Leu Gly Tyr Asp Tyr Arg Thr

275 280 285

Ala Arg Ala Ser Val Thr Leu Ser Pro Ser Phe Asp Leu Gly Ser Leu

290 295 300

Gly Ser Asp Ile Leu Tyr Asp Ala Ile Gly Ile Arg Ala Glu Thr Met

305 310 315 320

Ile Asn Pro Ser Ala Thr Ser Ala Ile Arg Ile Glu Ala Ser Arg Arg

325 330 335

Trp Phe Asn Tyr Arg Leu Pro Ser Tyr Arg Asn Tyr Asp Gly Ala Leu

340 345 350

Thr Glu Ala Leu Leu Thr Gly Trp Lys Val Leu Pro Arg Gly Trp Ala

355 360 365

Leu Phe Ala Gly Pro Asp Phe Ala Ala Lys Glu Ala Asp Asp Pro Ile

370 375 380

Asn Ala Tyr Arg Gln Tyr Gly Leu Arg Leu Gly Val Asn Lys Gln Phe

385 390 395 400

Gly Arg Ala Val Ser Leu Leu Ala Phe Ala Ser Phe Arg Gln Arg Asp

405 410 415

Tyr Arg Ala Tyr Ser Glu Leu Leu Glu Ala Lys Arg Arg Asp Arg Glu

420 425 430

Gln Asn Tyr Ile Ala Asn Ile Arg Phe Pro Ala Leu Arg Phe Ala Asn

435 440 445

Leu Thr Pro Ser Leu Leu Val Gln His Ser Arg Val Ser Ser Asn Val

450 455 460

Asp Trp Leu Tyr Ser Tyr Arg Lys Thr Ser Val Ala Met Arg Met Asp

465 470 475 480

Tyr Ala Phe

<210> 603

<211> 1158

<212> DNA

<213> S. pontiacus SLAM 1

<400> 603

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gccacagcgt tcgagattgg cacgggcgtc gcgaccgtgc cgcgtcttac ggacgcctta 480

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cgcgaacgta tcacctatga tggcagcggt gtcggcgtgg accgaacagc aggcgctgcg 780

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<210> 604

<211> 385

<212> PRT

<213> S. pontiacus SLAM 1

<400> 604

Met Leu Glu Gly Tyr Ser Pro Lys Thr Glu Thr Glu Thr Leu Arg Arg
1 5 10 15

Met Trp Ile Leu Gly Val Ala Tyr Asn Arg Ser Gly Lys Ser Arg Gln
20 25 30

Ala Val Ala Pro Leu Ala Arg Leu Val Ile Leu Arg Pro Asp Asp Pro
35 40 45

Thr Phe Arg Leu Glu Leu Ala Asn Ala Leu Val Lys Ser Asp Gln Phe
50 55 60

Glu Arg Ala Arg Tyr His Leu Glu Leu Ala Lys Gly Ala Gly Leu Ser
65 70 75 80

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Pro Pro Val Gln Ala Lys Val Gln Ala Glu Leu Asp Arg Leu Ala Lys
                85                  90                  95

Pro Lys Lys Trp Gln Gly Tyr Phe Arg Phe Ala Ile Val Pro Glu Ser
            100                 105                 110
Asn Ala Ala Arg Arg Thr Ser Ala Glu Thr Val Asn Leu Ser Gly Phe
        115                 120                 125
Val Leu Arg Leu Asp Pro Asn Ser Arg Ala Gln Ser Ala Thr Ala Phe
    130                 135                 140
Glu Ile Gly Thr Gly Val Ala Thr Val Pro Arg Leu Thr Asp Ala Leu
145                 150                 155                 160

Arg Ala Arg Phe Ala Leu Asp Leu Asp Ala Arg Leu Phe Asp Gly Arg
                165                 170                 175
Ala Pro Asp Glu Val Thr Leu Arg Thr Ser Ala Ser Leu Leu His Phe
            180                 185                 190
Ala Asp Glu Gly Arg Leu Val Leu Ala Glu Ile Tyr Gly Ser Gln Arg
        195                 200                 205
Trp Ile Asp Asp Ala Ala Tyr Thr His Thr Leu Gly Leu Gly Leu Ser
    210                 215                 220

Tyr Thr Arg Asn Leu Gly Thr Arg Ala Arg Ala Thr Ala Val Leu Gln
225                 230                 235                 240
Arg Glu Arg Ile Thr Tyr Asp Gly Ser Gly Val Gly Val Asp Arg Thr
                245                 250                 255
Ala Gly Ala Ala Gln Phe Ala Tyr Ala Ala Ser Ser Gln Leu Val Phe
            260                 265                 270
Arg Val Gly Met Arg Ala Glu Asn Arg Ala Ser Ser Tyr Ser Pro Val
        275                 280                 285

Ala Gly His Ala Ala Gly Val Thr Ile Gly Gly Asp Tyr Ser Phe Ala
    290                 295                 300
Gly Gly Leu Arg Val Gly Leu Asp Leu Ser Phe Asp Arg Asn Glu Phe
305                 310                 315                 320
Asp Gly Val His Pro Ile Phe Gly Val Ala Arg Val Asp Lys Lys Ser
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325 330 335

Ser Val Met Leu Asn Leu Ser Asn Gln Asn Trp Ser Tyr Lys Gly Phe

340 345 350

Thr Gln Val Leu Arg Leu Gly Phe Glu Glu Gln Arg Ser Thr Ile Ser

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Ile Asn Arg Phe Arg Asn Ala Thr Ala Ser Ile Gly Leu Thr Arg Ser

370 375 380

Phe

385

<210> 605

<211> 1281

<212> DNA

<213> S. pontiacus SLAM 2

<400> 605

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gacgaacagc tgcgcgccgg attgcagacc tttatcctga acaatacctc gcgcaagccc 420

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gaaaccacgg ccgtcgcacg gttcgatgtc attcgtggcg ggcagcgggg gcggttctct 720

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gtctcgtacc aacatcggtt gacgccgacg ctcgggctgt ccttcggcct gtcgcagctg 960

cgcgagacga cacagcgcgc gcatctggat caccatgaaa ccggcgtgtc gatggggatc 1020

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agtctctcgc tcaagttctg a 1281

<210> 606

<211> 426

<212> PRT

<213> S. pontiacus SLAM 2

<400> 606

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Gln Ser Pro Gly Gln Ala Gln Ala Ala Thr Pro Gln Asp Tyr Leu Glu
20 25 30

Gln Gly Asn Tyr Asp Ala Ala Arg Ala Ser Leu Ala Gln Leu Val Lys
35 40 45

Gly Asp Pro Asn Gly Pro Leu His Gln Ala Tyr Leu Glu Gly Gln Ile
50 55 60

Leu Met Arg Gln Asn Gln Pro Ala Ala Ala Val Asp Leu Phe Arg Asp
65 70 75 80

Leu Val Arg Ile Ala Pro Asp Tyr Glu Pro Ala Arg Arg Glu Leu Thr
85 90 95

Leu Leu Leu Ala Tyr Arg Gly Asp Val Thr Ala Ala Arg Tyr His Ala
100 105 110

Glu Arg Leu Val Ala Glu Thr Ala Asp Glu Gln Leu Arg Ala Gly Leu
115 120 125

Gln Thr Phe Ile Leu Asn Asn Thr Ser Arg Lys Pro Gly Gly Phe Ala
130 135 140

Leu Arg Phe Ala Leu Leu Pro Ser Ser Asn Gln Thr Arg Gly Ser Ala
145 150 155 160

Glu Gln Glu Ile Leu Ile Gly Gly Val Pro Phe Thr Leu Asn Pro Ala
165 170 175

Ser Arg Ala Ser Ser Gly Val Gly Leu Ala Ile Gly Gly Thr Ala Trp
180 185 190

Arg Arg Trp Gln Trp Asn Glu Arg Trp Ser Gly Val Gly Thr Ala Ser
195 200 205
Leu Asp Ala Lys Phe Tyr Asp Ser Ala Leu Asn Thr Glu Thr Thr Ala
210 215 220
Val Ala Arg Phe Asp Val Ile Arg Gly Gly Gln Arg Gly Arg Phe Ser
225 230 235 240
Phe Gly Pro Ile Ala Glu Leu Ser Phe Ser Asp Ser Asp Ile Val Arg
245 250 255

Arg Arg Trp Gly Ala Glu Leu Arg Gly Ala Tyr Gln Leu Arg Pro Arg
260 265 270
Asp Leu Val Ser Gly Ala Leu Arg Phe Asp Arg Gln Thr Tyr Asp Gln
275 280 285
Ser Pro Phe Arg Asp Gly His Arg Met Arg Ala Ser Val Ser Tyr Gln
290 295 300
His Arg Leu Thr Pro Thr Leu Gly Leu Ser Phe Gly Leu Ser Gln Leu
305 310 315 320

Arg Glu Thr Thr Gln Arg Ala His Leu Asp His His Glu Thr Gly Val
325 330 335
Ser Met Gly Ile Asp Lys Gln Trp Lys Ser Gly Leu Ser Thr Gly Val
340 345 350
Ile Leu Ala Tyr Glu Gln Asp Arg Tyr Asp Gly Ile Phe Pro Gly Thr
355 360 365
Thr Thr Pro Arg Glu Asp Asp Thr Thr Ser Leu Thr Phe Thr Val Gln
370 375 380

His Asn Lys Val Gln Ile Gly Lys Tyr Val Pro Arg Ile Thr Tyr Thr
385 390 395 400
Tyr Thr Arg Ala Lys Ser Asn Val Ala Leu Phe Asp Tyr Asp Ser His
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Asp Ile Gly Ala Ser Leu Ser Leu Lys Phe

420 425

<210> 607

<211> 1473

<212> DNA

<213> S. sp. SLAM S17

<400> 607

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tacctgtcgg tttcgcgcaa ggcctgggtc gatgtccgcc gttttctgcc gcgctatgtg 300

gcgctgtccg ggcatgatcc catgctggtc gcctgggcac gcggcggtct ggcgcgcagc 360

gaggggcggc tgggcgaggc cgagcggcat tatcgcgcgc tgctggcgat ccagcccgac 420

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gtcacgcgcc ggattttcga ctatcatcgc ggtttcgacg atctcgacgg cgcattgacc 1080

gaggcgaacc tgaccggctg gctctcgctg ccgcgcggtt ggagcctgtt cgcgggcctg 1140

gatgcagggg acaagcaggc ggatgcccgc cccaatgcct atcgccatat cggtgcgcgg 1200

ctggggatgg tgcacggttt tgccgactgg gcggaactga ccctcatcgc ctccgcccgg 1260

cagcgcgatt accgcgccta tagcgaactg ctggaggcgg tccgccacga tcgcgagacc 1320

aacctgaccg ccgtcctgcg cctgcccaaa ctgcgcttcg cggggctgac gccgaacatc 1380

ctttttcagc acaaccgggt gacgagcaat gtcgactggc tctattcctt tcatcgcacc 1440

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<210> 608

<211> 490

<212> PRT

<213> S. sp. SLAM S17

<400> 608

Met Arg Tyr Phe Ala Leu Ser Ser Ile Leu Ala Leu Ile Ala Cys Pro
1 5 10 15

Leu Ala Met Pro Ala Phe Ala Gln Ser Ala Arg Ser Glu Asp Asn Arg
20 25 30

Leu Arg Leu Asp Pro Gly Ile Asp Arg Arg Thr Thr Pro Gln Glu Arg
35 40 45

Glu Ala Ile Glu Ala Ala Thr Pro Ser Asp Ser Ile Thr Ile Asp Gly
50 55 60

Glu Val Tyr Arg Val Asp Asp Thr Leu Asp Asp Leu Gly Arg Ala Ile
65 70 75 80

Tyr Leu Ser Val Ser Arg Lys Ala Trp Val Asp Val Arg Arg Phe Leu
85 90 95

Pro Arg Tyr Val Ala Leu Ser Gly His Asp Pro Met Leu Val Ala Trp
100 105 110

Ala Arg Gly Gly Leu Ala Arg Ser Glu Gly Arg Leu Gly Glu Ala Glu
115 120 125

Arg His Tyr Arg Ala Leu Leu Ala Ile Gln Pro Asp Phe Leu Pro Gly
130 135 140

Arg Leu Glu Leu Gly Arg Leu Leu Phe Glu Asn Arg Lys Asp Arg Glu
145 150 155 160

Ala Arg Arg Leu Phe Arg Ala Ile Arg Asp Glu Leu Ala Arg Gln Asp
165 170 175

Asp Arg Ala Ala Gly Val Arg Arg Asn Val Asp Ala Phe Leu Thr Ala
180 185 190

Leu Asp Arg Arg Asp Gln Trp Gln Gly Met Ile Ala Ile Gly Pro Gly
195 200 205

Tyr Ser Ser Asn Leu Asn Gln Ser Ser Ala Ser Gln Thr Cys Leu Leu

210 215 220

Thr Gly Glu Asp Gly Thr Cys Leu Ile Asp Arg Thr Leu Pro Ser Ala

225 230 235 240

Ile Ala Ser Val Gly Ile Asn Ile Glu Gly Asn Leu Ser Arg Arg Ile

245 250 255

Ala Leu Lys Gly Gln Gly Gly Leu Leu Ala Arg Ala Phe Val Tyr Gly

260 265 270

Asp Leu Trp Pro Gly His Gly Asp Phe Asp Gln Ala Thr Leu Ser Ala

275 280 285

Gln Ile Gly Tyr Asp His Gln Thr Ala Arg Arg Ser Leu Thr Leu Ser

290 295 300

Pro Thr Ile Asp Leu Ala Ser Leu Gly Asp Lys Leu Leu Tyr Ala Ala

305 310 315 320

Pro Gly Leu Arg Ala Glu Ala Met Val Thr Pro Ser Pro Asp Thr Ala

325 330 335

Leu Arg Ile Glu Val Thr Arg Arg Ile Phe Asp Tyr His Arg Gly Phe

340 345 350

Asp Asp Leu Asp Gly Ala Leu Thr Glu Ala Asn Leu Thr Gly Trp Leu

355 360 365

Ser Leu Pro Arg Gly Trp Ser Leu Phe Ala Gly Leu Asp Ala Gly Asp

370 375 380

Lys Gln Ala Asp Ala Arg Pro Asn Ala Tyr Arg His Ile Gly Ala Arg

385 390 395 400

Leu Gly Met Val His Gly Phe Ala Asp Trp Ala Glu Leu Thr Leu Ile

405 410 415

Ala Ser Ala Arg Gln Arg Asp Tyr Arg Ala Tyr Ser Glu Leu Leu Glu

420 425 430

Ala Val Arg His Asp Arg Glu Thr Asn Leu Thr Ala Val Leu Arg Leu

435 440 445

Pro Lys Leu Arg Phe Ala Gly Leu Thr Pro Asn Ile Leu Phe Gln His

450 455 460

Asn Arg Val Thr Ser Asn Val Asp Trp Leu Tyr Ser Phe His Arg Thr
465 470 475 480

Ala Ala Ser Phe Arg Leu Glu His Ala Leu
485 490

<210> 609

<211> 1386

<212> DNA

<213> S. taxi SLAM 1

<400> 609

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gagaccgagc ggctcgatcc gaccagcgtc gagatcgacg gcaccaccta tgccgtcggc 120

cgcaacgcca gcgacacggg cgcggcgctc tacgtctcga tcatgcggcg acgctgggcg 180

gacgtgcgtc gcttcctcgc cgcctatcgc gccctccccg gtcacgagga cgggctgatc 240

ctctacgccg aaggcggcct cgcgcgcgag gcgggcgaca tggcgggggc ggagcgcgcc 300

tatcgcgcgc tcgtcgcggc gcagcccgat ttcgtgcccg gccggctcga actggcgcgc 360

gtgctgttcc ttgaccgccg cgatcgcgag gcggcgcagg ccttcgccgg cgtgcgcggc 420

gcgctgctcg cgcagggcga caaggcggcg ggcgtggtgc ggacggtcga cacctttctc 480

gccgccctgc gcaaaaggcg cggcgtgcag ggcatggtgt cgttcggccc cgaatacagc 540

tccaacctca accagtcgtc ggcgagctat acctgcctga tccccggcgc ctcgggggat 600

tgcctgttcg accgcaaggt gcccgatccg atcgccgcgc gcgggatcaa tatcgagggc 660

aatgccacgc tgcgcctgcc gctcgccggc catgacggga tcggcggccg ggcgctcgcc 720

ttcggcgatc tctttcccgg ccacggccgc tacagccaga ccgcgctgtc gctgtacgcg 780

ggctacgacc gccgcaccgc cgctaccggg ctggtcctcg ccccctcgtt cgatctcggc 840

acgctggggg gccagcggct ctacgatgcc tggggtctgc acggcgaata tagccgcggg 900

ttcgggtcgc gcacgctcgt ccgggtcgag ggcaactggc gcgactatcg ctaccggcgc 960

gacggttatc gcgattacga cgggcggcag gcggatgcgt ggctgaccgg cttccacacg 1020

ctgccgcacg gctggacggt gttcggcggg ccggatctgc tcgacaagcg cgccggcgat 1080

cgggtcaacg cctatcgcca atatggcgcg cggctcgggc tcgaccggac gatcggcgcg 1140

gcggtcgacc tgctgctgac cgcctcgctc cgccgccgcg actatggcgc gttcagcccg 1200

ctgctcgacg ccagacgccg cgacgtcgag cggaattaca cgatgctcgc ccgcctcccc 1260

ggcgcgaagg tcgcgggcct cagccccagc ctgctcgtcc agcacagccg cgtcggcagc 1320

aacgtcgact ggctctattc ctaccggcgc accagcgtca gcctgaggat ggatcatgtc 1380

ttctga 1386

<210> 610

<211> 461

<212> PRT

<213> S. taxi SLAM 1

<400> 610

Met Arg Leu Asp Gln Thr Val Glu Gln Arg Lys Ala Glu Ala Glu Thr
1 5 10 15

Arg Val Arg Asp Glu Thr Glu Arg Leu Asp Pro Thr Ser Val Glu Ile
20 25 30

Asp Gly Thr Thr Tyr Ala Val Gly Arg Asn Ala Ser Asp Thr Gly Ala
35 40 45

Ala Leu Tyr Val Ser Ile Met Arg Arg Arg Trp Ala Asp Val Arg Arg
50 55 60

Phe Leu Ala Ala Tyr Arg Ala Leu Pro Gly His Glu Asp Gly Leu Ile
65 70 75 80

Leu Tyr Ala Glu Gly Gly Leu Ala Arg Glu Ala Gly Asp Met Ala Gly
85 90 95

Ala Glu Arg Ala Tyr Arg Ala Leu Val Ala Ala Gln Pro Asp Phe Val
100 105 110

Pro Gly Arg Leu Glu Leu Ala Arg Val Leu Phe Leu Asp Arg Arg Asp
115 120 125

Arg Glu Ala Ala Gln Ala Phe Ala Gly Val Arg Gly Ala Leu Leu Ala
130 135 140

Gln Gly Asp Lys Ala Ala Gly Val Val Arg Thr Val Asp Thr Phe Leu
145 150 155 160

Ala Ala Leu Arg Lys Arg Arg Gly Val Gln Gly Met Val Ser Phe Gly
165 170 175

Pro Glu Tyr Ser Ser Asn Leu Asn Gln Ser Ser Ala Ser Tyr Thr Cys
180 185 190

Leu Ile Pro Gly Ala Ser Gly Asp Cys Leu Phe Asp Arg Lys Val Pro

195 200 205

Asp Pro Ile Ala Ala Arg Gly Ile Asn Ile Glu Gly Asn Ala Thr Leu
210 215 220
Arg Leu Pro Leu Ala Gly His Asp Gly Ile Gly Gly Arg Ala Leu Ala
225 230 235 240
Phe Gly Asp Leu Phe Pro Gly His Gly Arg Tyr Ser Gln Thr Ala Leu
245 250 255
Ser Leu Tyr Ala Gly Tyr Asp Arg Arg Thr Ala Ala Thr Gly Leu Val
260 265 270

Leu Ala Pro Ser Phe Asp Leu Gly Thr Leu Gly Gly Gln Arg Leu Tyr
275 280 285
Asp Ala Trp Gly Leu His Gly Glu Tyr Ser Arg Gly Phe Gly Ser Arg
290 295 300
Thr Leu Val Arg Val Glu Gly Asn Trp Arg Asp Tyr Arg Tyr Arg Arg
305 310 315 320
Asp Gly Tyr Arg Asp Tyr Asp Gly Arg Gln Ala Asp Ala Trp Leu Thr
325 330 335

Gly Phe His Thr Leu Pro His Gly Trp Thr Val Phe Gly Gly Pro Asp
340 345 350
Leu Leu Asp Lys Arg Ala Gly Asp Arg Val Asn Ala Tyr Arg Gln Tyr
355 360 365
Gly Ala Arg Leu Gly Leu Asp Arg Thr Ile Gly Ala Ala Val Asp Leu
370 375 380
Leu Leu Thr Ala Ser Leu Arg Arg Arg Asp Tyr Gly Ala Phe Ser Pro
385 390 395 400

Leu Leu Asp Ala Arg Arg Arg Asp Val Glu Arg Asn Tyr Thr Met Leu
405 410 415
Ala Arg Leu Pro Gly Ala Lys Val Ala Gly Leu Ser Pro Ser Leu Leu
420 425 430
Val Gln His Ser Arg Val Gly Ser Asn Val Asp Trp Leu Tyr Ser Tyr
435 440 445

Arg Arg Thr Ser Val Ser Leu Arg Met Asp His Val Phe

450 455 460

<210>

611

<211> 1347

<212> DNA

<213> S. yanoikuyae SLAM 1

<400> 611

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tcggttgcca gtgcgcagca tgtcgatgcg gaacgcgcat cgacacctgc catcctgtcg 120

gccggacaga ttttcgacgt tgccgaatcc gcgcgacagg cacgcgattt cgaaaccgcc 180

caggcggcct atcgcgccct gttcgccgat gccgatcccg agttgcggat cgaagcgcgc 240

ttccggctgg ggctgatgct ggccgacgac ctgcaacgct acagcgatgc ggcggtcgag 300

ttccgggata tccttgatgt aaaaccccat gccgcccgcg tgcgcttgga actggccagg 360

gtgctggctg ccagcggtga cgtgcgggct gccggccgcg aaatgcgcgc ggcacaggcc 420

gccggcttgc cgtcacaggt cgagcagatg gtgcgcttct atgccaatgc cttgagcgca 480

cggaaggcgc tcggcggttc ggtcgaactg gcccttgcgc ccgacagcaa tgtcaatcgc 540

gcgacccgtt ccgatcggct tggaacggtg atcggcgatt tcctgctcga caaggatgcc 600

caggaaaaat caggcgtcgg gctcagtctg cgcggacagg gctattggcg ccacggcatc 660

gaaccgggcg cggatctgct ggtgcgcgcg tcggtcggcg cctcgctcta tcgcgatgcc 720

tctttcaacg acatcagtgc ggcgttgcag gtcggccccc aatatctgtc ggggtcggat 780

cgtatcaccg tggcggtcgg gccaagctgg cgctggtatg gcggccgtct ctattcgacc 840

ggctatggtg gcagcgcgaa cctgctgcac ccggtgggaa aacgtagcca acttcagctt 900

gaaggtggca tcacccatgt ccgcaaccag cgcaacgcct tgcagacatc ggatgatttt 960

accctggccg gggcatttga tcatgccttc agcgcgcggg gcggcggcgg cgttcagatg 1020

tttgccctgc gcgaagcagc gcgcgatccc ggttatagtt tcgtcagtgg tgggggcagc 1080

gtctatggct tccgcgaaat ggggcgcacg accttcgtcg cgacaatggg atacagccat 1140

ttggaggctg atgcccggct gcttctttat ccacgccggc gcatcgaaaa tcgattgagc 1200

gcgagcatcg gggcgacgtt acgcgccttg caggtcggtc cgttcgcgcc actggcgcgg 1260

ctcaaatggg aacgcaatcg ctcgaccatc gaaatctatc aatatcgccg aatttctgcc 1320

gagttcggca tcggttcggt tttctga 1347

<210> 612

<211> 448

<212> PRT

<213> S. yanoikuyae SLAM 1

<400> 612

Met Gly Asp Ser Ile Arg Phe Ala Ala Arg Leu Val Ala Ser Val Leu
1 5 10 15

Cys Val Pro Met Ser Val Ala Ser Ala Gln His Val Asp Ala Glu Arg
20 25 30

Ala Ser Thr Pro Ala Ile Leu Ser Ala Gly Gln Ile Phe Asp Val Ala
35 40 45

Glu Ser Ala Arg Gln Ala Arg Asp Phe Glu Thr Ala Gln Ala Ala Tyr
50 55 60

Arg Ala Leu Phe Ala Asp Ala Asp Pro Glu Leu Arg Ile Glu Ala Arg
65 70 75 80

Phe Arg Leu Gly Leu Met Leu Ala Asp Asp Leu Gln Arg Tyr Ser Asp
85 90 95

Ala Ala Val Glu Phe Arg Asp Ile Leu Asp Val Lys Pro His Ala Ala
100 105 110

Arg Val Arg Leu Glu Leu Ala Arg Val Leu Ala Ala Ser Gly Asp Val
115 120 125

Arg Ala Ala Gly Arg Glu Met Arg Ala Ala Gln Ala Ala Gly Leu Pro
130 135 140

Ser Gln Val Glu Gln Met Val Arg Phe Tyr Ala Asn Ala Leu Ser Ala
145 150 155 160

Arg Lys Ala Leu Gly Gly Ser Val Glu Leu Ala Leu Ala Pro Asp Ser
165 170 175

Asn Val Asn Arg Ala Thr Arg Ser Asp Arg Leu Gly Thr Val Ile Gly
180 185 190

Asp Phe Leu Leu Asp Lys Asp Ala Gln Glu Lys Ser Gly Val Gly Leu
195 200 205

Ser Leu Arg Gly Gln Gly Tyr Trp Arg His Gly Ile Glu Pro Gly Ala

210 215 220

Asp Leu Leu Val Arg Ala Ser Val Gly Ala Ser Leu Tyr Arg Asp Ala
225 230 235 240
Ser Phe Asn Asp Ile Ser Ala Ala Leu Gln Val Gly Pro Gln Tyr Leu
245 250 255
Ser Gly Ser Asp Arg Ile Thr Val Ala Val Gly Pro Ser Trp Arg Trp
260 265 270
Tyr Gly Gly Arg Leu Tyr Ser Thr Gly Tyr Gly Gly Ser Ala Asn Leu
275 280 285

Leu His Pro Val Gly Lys Arg Ser Gln Leu Gln Leu Glu Gly Gly Ile
290 295 300
Thr His Val Arg Asn Gln Arg Asn Ala Leu Gln Thr Ser Asp Asp Phe
305 310 315 320
Thr Leu Ala Gly Ala Phe Asp His Ala Phe Ser Ala Arg Gly Gly Gly
325 330 335
Gly Val Gln Met Phe Ala Leu Arg Glu Ala Ala Arg Asp Pro Gly Tyr
340 345 350

Ser Phe Val Ser Gly Gly Gly Ser Val Tyr Gly Phe Arg Glu Met Gly
355 360 365
Arg Thr Thr Phe Val Ala Thr Met Gly Tyr Ser His Leu Glu Ala Asp
370 375 380
Ala Arg Leu Leu Leu Tyr Pro Arg Arg Arg Ile Glu Asn Arg Leu Ser
385 390 395 400
Ala Ser Ile Gly Ala Thr Leu Arg Ala Leu Gln Val Gly Pro Phe Ala
405 410 415

Pro Leu Ala Arg Leu Lys Trp Glu Arg Asn Arg Ser Thr Ile Glu Ile
420 425 430
Tyr Gln Tyr Arg Arg Ile Ser Ala Glu Phe Gly Ile Gly Ser Val Phe
435 440 445
<210> 613
<211> 1508

<212> DNA

<213> S. yanoikuyae SLAM 2

<400> 613

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cgcctcgatc aacagctcga tcgacagcga gcggcacaag aggagcgttc gctcaacgag 180

gtggacgaag ggctcgatgc cccttcctcg ctcgtcatcg acggaaagac ctacgctgtc 240

ggcaacaatg tcgatgagat gggccaagcg ctgcacatcg cagtttctcg acggcaatgg 300

ggagacgctc gccgtttcct caaagcttac gaaaattttc ctgatcgtga tccgatgctc 360

atgctctttg caaacggggc agtcgcgcgc caggacggaa agctagacga ggctgaaggc 420

ttctatcgtg aaatgttggt gctggacccg ggctttgcat cgggccagct cgaactggcg 480

cgcgttctgt tcgagaatcg caaggaccgc gaagcacgcc agacttttga aagcgcgcgt 540

gcgctgctcg tggtcgacgg cgacaaggca tcaggcgtga tcgtaacgat cgatgccttc 600

ttaaatgctc tgcgccaccg gcgaggctgg caaggcaatc tggcgatagg cccgatctac 660

agcaccaaca tcaaccaatc atcggaaagc tacacatgtc tgctggcgac cgatgatggg 720

acgtgtgtgg tcgatcggaa agtgcccgac gcgataaagg gtacaggcat caacgttgaa 780

ggggcgctca gccgatatct tccactgtcc ggtcatcatg gcctacgcgg ccgcgctatt 840

ctgttcgggg aaatctaccc tgaccatcat gatttttctc aaggcgtgtt tataactcgg 900

ttgggatatc aatatcagac tggccgcaac actctcggcc tgtcgccctc attcgacctc 960

ggcacgctcg gatcatctgt tctgtatgaa gcctggggcg ccaatgcgga gtggcagcat 1020

acggcctcac gcaacgtcct attgcgcctt gaagcgaatt accgggattt tcgctatcgc 1080

cttccaggtt ccagttccca aacagggccg atggtggacg tcaatctgac ggtctggtac 1140

gccccgtcgc aggattggac cttgtttgga ggtcctgact ttaccgacaa agacacaccc 1200

agcccaacag actcctatcg ccagttcggt gcgcgtttcg gcataaacaa gacttttgga 1260

agcgacgcga gcatcctttt gctcggctcc tatcgccatc gcgagcatcg cggctttagc 1320

gctttgttcg acgccaaacg ccgcgaagac cagttcaacg cgacggccat cgcacgtttc 1380

ccagcgctga gattcgcggg gctgacaccc gagatcgtgg tccagcacaa tcaggtcaaa 1440

gcaacatcga ctggctcttt tcctacaagc gcaccaccgc gagcgtgagg ctcggctatg 1500

ccttctag 1508

<210> 614

<211> 502

<212> PRT

<213> S. yanoikuyae SLAM 2

<400> 614

Met Ile Phe Gly Ser Leu Leu Pro Arg Pro Asn Ala Pro Leu Gly Leu
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Leu Leu Leu Ile Met Ala Gly Thr Pro Ala Thr Ala Leu Ala Gln Ile
20 25 30

Asp Ser Gly Gln Asp Thr Arg Leu Arg Leu Asp Gln Gln Leu Asp Arg
35 40 45

Gln Arg Ala Ala Gln Glu Glu Arg Ser Leu Asn Glu Val Asp Glu Gly
50 55 60

Leu Asp Ala Pro Ser Ser Leu Val Ile Asp Gly Lys Thr Tyr Ala Val
65 70 75 80

Gly Asn Asn Val Asp Glu Met Gly Gln Ala Leu His Ile Ala Val Ser
85 90 95

Arg Arg Gln Trp Gly Asp Ala Arg Arg Phe Leu Lys Ala Tyr Glu Asn
100 105 110

Phe Pro Asp Arg Asp Pro Met Leu Met Leu Phe Ala Asn Gly Ala Val
115 120 125

Ala Arg Gln Asp Gly Lys Leu Asp Glu Ala Glu Gly Phe Tyr Arg Glu
130 135 140

Met Leu Val Leu Asp Pro Gly Phe Ala Ser Gly Gln Leu Glu Leu Ala
145 150 155 160

Arg Val Leu Phe Glu Asn Arg Lys Asp Arg Glu Ala Arg Gln Thr Phe
165 170 175

Glu Ser Ala Arg Ala Leu Leu Val Val Asp Gly Asp Lys Ala Ser Gly
180 185 190

Val Ile Val Thr Ile Asp Ala Phe Leu Asn Ala Leu Arg His Arg Arg
195 200 205

Gly Trp Gln Gly Asn Leu Ala Ile Gly Pro Ile Tyr Ser Thr Asn Ile
210 215 220

Asn Gln Ser Ser Glu Ser Tyr Thr Cys Leu Leu Ala Thr Asp Asp Gly

225 230 235 240

Thr Cys Val Val Asp Arg Lys Val Pro Asp Ala Ile Lys Gly Thr Gly

245 250 255

Ile Asn Val Glu Gly Ala Leu Ser Arg Tyr Leu Pro Leu Ser Gly His

260 265 270

His Gly Leu Arg Gly Arg Ala Ile Leu Phe Gly Glu Ile Tyr Pro Asp

275 280 285

His His Asp Phe Ser Gln Gly Val Phe Ile Thr Arg Leu Gly Tyr Gln

290 295 300

Tyr Gln Thr Gly Arg Asn Thr Leu Gly Leu Ser Pro Ser Phe Asp Leu

305 310 315 320

Gly Thr Leu Gly Ser Ser Val Leu Tyr Glu Ala Trp Gly Ala Asn Ala

325 330 335

Glu Trp Gln His Thr Ala Ser Arg Asn Val Leu Leu Arg Leu Glu Ala

340 345 350

Asn Tyr Arg Asp Phe Arg Tyr Arg Leu Pro Gly Ser Ser Ser Gln Thr

355 360 365

Gly Pro Met Val Asp Val Asn Leu Thr Val Trp Tyr Ala Pro Ser Gln

370 375 380

Asp Trp Thr Leu Phe Gly Gly Pro Asp Phe Thr Asp Lys Asp Thr Pro

385 390 395 400

Ser Pro Thr Asp Ser Tyr Arg Gln Phe Gly Ala Arg Phe Gly Ile Asn

405 410 415

Lys Thr Phe Gly Ser Asp Ala Ser Ile Leu Leu Leu Gly Ser Tyr Arg

420 425 430

His Arg Glu His Arg Gly Phe Ser Ala Leu Phe Asp Ala Lys Arg Arg

435 440 445

Glu Asp Gln Phe Asn Ala Thr Ala Ile Ala Arg Phe Pro Ala Leu Arg

450 455 460

Phe Ala Gly Leu Thr Pro Glu Ile Val Val Gln His Asn Gln Val Lys

465 470 475 480

Ser Asn Ile Asp Trp Leu Phe Ser Tyr Lys Arg Thr Thr Ala Ser Val

485 490 495

Arg Leu Gly Tyr Ala Phe

500

<210> 615

<211> 1326

<212> DNA

<213> Sagittula stellata E-37 SLAM 1

<400> 615

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ctggcgcttg tgtcgcaagc accggcgcag cagtctgacg tgcttgcccg tgccgaggcg 120

caggtaaatg ccggagacta tggcaccgct atctccgccc tgcagagaat ggggcctcaa 180

gcgttgcgcg aggccgagtt gcgccgtctc tgggcgctgt ccatggcgca tgtccggcag 240

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gtcacctacc gtctggaact cgccaacacg ctcgaggctg cggggcaggc agagcgcgcg 360

cgctaccact attccctggc gcgcggcgcc gcgctgcccc cgtcgctggc cgacgaggtg 420

acgcggcgca tcgaccagat tgatcgtgcc cggatctggg aaggcaattt ccgcttcgcg 480

atcgtgcccg agagtaatcc cgcgaaacga accgcggccg acaccatcat gatcggcgac 540

ctgcccttca agctcaagga cgcctcccgc gcacagcccg cccggggtgt cgaacttggc 600

ttcgggcttg ccgccctgcc cagggtggga ccggatctga ggcttcggct gggggcgtcc 660

ctcgatgcac ggctttacga agaaggtgcg cccgacgacg ttcaggcacg ggcggaactg 720

gggttgctgc acttcggcga ccgcaaccgc agactgggcg ccgggatcac tctgggaaag 780

cgctggatcg acggcgaggc atacgccaac acgcgtggca tctatctgac ctggggccag 840

tccatcgacg cccaggcccg gagcatgctt aacctgacgc tgatccgcga gcgcaccgac 900

tatgaacgcc ccggaaccga gcccgccacc cgatccgtag cagccgcatc gctcagccac 960

acggttacac cccggttgca actcagtttc ggcttgcagg tggagcggac cgaaagcgcg 1020

cttgcaaccg aagccgggca gggggggggcg gtgacgcttg gcgcgcgcta cgccttcgag 1080

ggcgggctgc tcgccgagtt gtcactggcg cttggtcggc acgaacgcga tgggcctgac 1140

cgcctgcttg gaattgtacg taaggaccag cgcgagagtc tcaccctgaa gctcacacac 1200

cgcgactggg cggtcgcggg ctttgcgccg gtactcgaac tcggagcaga gcggcaggac 1260

tcgagcaacg acctctacag ctacgagaac aaccgtgtgc tgctgggcat cacccggcgg 1320

ttctga 1326

<210> 616

<211> 441

<212> PRT

<213> Sagittula stellata E-37 SLAM 1

<400> 616

Met Met Thr Arg Leu Ala Ala Leu Gly Val Arg Arg Leu Leu Ala Gly

1 5 10 15

Leu Phe Leu Ala Leu Ala Leu Val Ser Gln Ala Pro Ala Gln Gln Ser

20 25 30

Asp Val Leu Ala Arg Ala Glu Ala Gln Val Asn Ala Gly Asp Tyr Gly

35 40 45

Thr Ala Ile Ser Ala Leu Gln Arg Met Gly Pro Gln Ala Leu Arg Glu

50 55 60

Ala Glu Leu Arg Arg Leu Trp Ala Leu Ser Met Ala His Val Arg Gln

65 70 75 80

Gly Arg Pro Arg Ala Ala Leu Pro Trp Leu Asp Arg Leu Val Ser Leu

85 90 95

Ala Pro Asp Ala Val Thr Tyr Arg Leu Glu Leu Ala Asn Thr Leu Glu

100 105 110

Ala Ala Gly Gln Ala Glu Arg Ala Arg Tyr His Tyr Ser Leu Ala Arg

115 120 125

Gly Ala Ala Leu Pro Pro Ser Leu Ala Asp Glu Val Thr Arg Arg Ile

130 135 140

Asp Gln Ile Asp Arg Ala Arg Ile Trp Glu Gly Asn Phe Arg Phe Ala

145 150 155 160

Ile Val Pro Glu Ser Asn Pro Ala Lys Arg Thr Ala Ala Asp Thr Ile

165 170 175

Met Ile Gly Asp Leu Pro Phe Lys Leu Lys Asp Ala Ser Arg Ala Gln

180 185 190

Pro Ala Arg Gly Val Glu Leu Gly Phe Gly Leu Ala Ala Leu Pro Arg

195 200 205

Val Gly Pro Asp Leu Arg Leu Arg Leu Gly Ala Ser Leu Asp Ala Arg

210 215 220

Leu Tyr Glu Glu Gly Ala Pro Asp Asp Val Gln Ala Arg Ala Glu Leu

225 230 235 240

Gly Leu Leu His Phe Gly Asp Arg Asn Arg Arg Leu Gly Ala Gly Ile

245 250 255

Thr Leu Gly Lys Arg Trp Ile Asp Gly Glu Ala Tyr Ala Asn Thr Arg

260 265 270

Gly Ile Tyr Leu Thr Trp Gly Gln Ser Ile Asp Ala Gln Ala Arg Ser

275 280 285

Met Leu Asn Leu Thr Leu Ile Arg Glu Arg Thr Asp Tyr Glu Arg Pro

290 295 300

Gly Thr Glu Pro Ala Thr Arg Ser Val Ala Ala Ala Ser Leu Ser His

305 310 315 320

Thr Val Thr Pro Arg Leu Gln Leu Ser Phe Gly Leu Gln Val Glu Arg

325 330 335

Thr Glu Ser Ala Leu Ala Thr Glu Ala Gly Gln Gly Gly Ala Val Thr

340 345 350

Leu Gly Ala Arg Tyr Ala Phe Glu Gly Gly Leu Leu Ala Glu Leu Ser

355 360 365

Leu Ala Leu Gly Arg His Glu Arg Asp Gly Pro Asp Arg Leu Leu Gly

370 375 380

Ile Val Arg Lys Asp Gln Arg Glu Ser Leu Thr Leu Lys Leu Thr His

385 390 395 400

Arg Asp Trp Ala Val Ala Gly Phe Ala Pro Val Leu Glu Leu Gly Ala

405 410 415

Glu Arg Gln Asp Ser Ser Asn Asp Leu Tyr Ser Tyr Glu Asn Asn Arg

420 425 430

Val Leu Leu Gly Ile Thr Arg Arg Phe

435 440

<210> 617

<211> 1344

<212> DNA

<213> Salmonella enterica subsp diarizonae SLAM 1

<400> 617

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atatttctcc tgttttccac ctttacatca gcaaaagaac aaactctgga gacgggaaat 120

ctaaacaaca aattaactca ctatttaatt agcaataatt ctgtggcagt aaaaaacata 180

ctacagacct gtggagaatg ttcacagttc attgacccac ttttgctcga atgggctaat 240

ggcattcttg ctcgtcagga aaaaaactac gccgaatcaa tacggcatta cagaaaagtc 300

atctctgtac atcctgactg gtacagtgcc agattacaac tggccacagt attgtacctg 360

aataaagata tactgtccgc tgaagctcag ttacgtaaat tacgcagtga atctttacct 420

gaagaagcag ccgtactgat tgactccttc attgcaaaaa tacaaaagac agacaactgg 480

gcatttcgtg gcggattcac ttatctgaat gaaaaaaaca tcaataacgc gccagcatcc 540

ggtcgttcca tcggtcgatg gaaatctgag aaaccacaat caggaaaagg tgtgatgttt 600

tggggagagg cagaaaaaac attctctttg ccggataatc tttttggtat cacacgatta 660

gccacctcag ggaaagtata caaaaataac cactcttatg atgagcttga tggtagtatc 720

ggactgggtt ttggttatcg caatattgat actacgattc ttctccttcc attttatgaa 780

aaaagttatt atggcggagg caaaaaatca gaaaaaggtc tgaaacctta ttctgatacc 840

cgtgggttcg gagtagaaac cacgctccag ctttcaaacc gctggcgttt atactcagac 900

gttaaactgg gtaaaaatga atataaaaaa aagacttacc ttaacggata ccgctactca 960

cttaatgaaa ctctgattta tttcccagat tcacgccagt atatttctgc aggtcttgga 1020

tacagtatgc tcagaactga agaaaaagac agttctttca ataaggcagc attccggacc 1080

ggatggatgt acgaatggaa tggaggtgta tcaacgctat tacaggctgc ttatggtcat 1140

aaaaaatacc tggccggaga cttctgggga ataaagcaaa ttaatcatga atacaatact 1200

tctgtcacgg tatggcaccg cgatatttat ttttttggca taacaccaaa aatcacatgg 1260

agttatcagc gaactgacag taatcatcct tttcacgaca cggagaggaa tcgtcttttg 1320

ctgagtttca gcaaatactt ctga 1344

<210> 618

<211> 447

<212> PRT

<213> Salmonella enterica subsp diarizonae SLAM 1

<400> 618

Met Lys Ile Ile Thr Phe Met Arg Leu Lys Pro Gly Lys Pro Pro Ala
1 5 10 15

Met Val Ser Phe Ile Phe Leu Leu Phe Ser Thr Phe Thr Ser Ala Lys
20 25 30

Glu Gln Thr Leu Glu Thr Gly Asn Leu Asn Asn Lys Leu Thr His Tyr
35 40 45

Leu Ile Ser Asn Asn Ser Val Ala Val Lys Asn Ile Leu Gln Thr Cys
50 55 60

Gly Glu Cys Ser Gln Phe Ile Asp Pro Leu Leu Leu Glu Trp Ala Asn
65 70 75 80

Gly Ile Leu Ala Arg Gln Glu Lys Asn Tyr Ala Glu Ser Ile Arg His
85 90 95

Tyr Arg Lys Val Ile Ser Val His Pro Asp Trp Tyr Ser Ala Arg Leu
100 105 110

Gln Leu Ala Thr Val Leu Tyr Leu Asn Lys Asp Ile Leu Ser Ala Glu
115 120 125

Ala Gln Leu Arg Lys Leu Arg Ser Glu Ser Leu Pro Glu Glu Ala Ala
130 135 140

Val Leu Ile Asp Ser Phe Ile Ala Lys Ile Gln Lys Thr Asp Asn Trp
145 150 155 160

Ala Phe Arg Gly Gly Phe Thr Tyr Leu Asn Glu Lys Asn Ile Asn Asn
165 170 175

Ala Pro Ala Ser Gly Arg Ser Ile Gly Arg Trp Lys Ser Glu Lys Pro
180 185 190

Gln Ser Gly Lys Gly Val Met Phe Trp Gly Glu Ala Glu Lys Thr Phe
195 200 205

Ser Leu Pro Asp Asn Leu Phe Gly Ile Thr Arg Leu Ala Thr Ser Gly
210 215 220

Lys Val Tyr Lys Asn Asn His Ser Tyr Asp Glu Leu Asp Gly Ser Ile
225 230 235 240
Gly Leu Gly Phe Gly Tyr Arg Asn Ile Asp Thr Thr Ile Leu Leu Leu
245 250 255
Pro Phe Tyr Glu Lys Ser Tyr Tyr Gly Gly Gly Lys Lys Ser Glu Lys
260 265 270
Gly Leu Lys Pro Tyr Ser Asp Thr Arg Gly Phe Gly Val Glu Thr Thr
275 280 285

Leu Gln Leu Ser Asn Arg Trp Arg Leu Tyr Ser Asp Val Lys Leu Gly
290 295 300
Lys Asn Glu Tyr Lys Lys Lys Thr Tyr Leu Asn Gly Tyr Arg Tyr Ser
305 310 315 320
Leu Asn Glu Thr Leu Ile Tyr Phe Pro Asp Ser Arg Gln Tyr Ile Ser
325 330 335
Ala Gly Leu Gly Tyr Ser Met Leu Arg Thr Glu Glu Lys Asp Ser Ser
340 345 350

Phe Asn Lys Ala Ala Phe Arg Thr Gly Trp Met Tyr Glu Trp Asn Gly
355 360 365
Gly Val Ser Thr Leu Leu Gln Ala Ala Tyr Gly His Lys Lys Tyr Leu
370 375 380
Ala Gly Asp Phe Trp Gly Ile Lys Gln Ile Asn His Glu Tyr Asn Thr
385 390 395 400
Ser Val Thr Val Trp His Arg Asp Ile Tyr Phe Phe Gly Ile Thr Pro
405 410 415

Lys Ile Thr Trp Ser Tyr Gln Arg Thr Asp Ser Asn His Pro Phe His
420 425 430
Asp Thr Glu Arg Asn Arg Leu Leu Leu Ser Phe Ser Lys Tyr Phe
435 440 445

<210> 619
<211> 1239
<212> DNA
<213> Sphingobium baderi LL03 SLAM 1

<400> 619

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ttcgcggcag ccgagacggc ctatcgcgcg ctccagtccg accctgatct tgagattcga 120

acagaggcgc gtttccgtct cgggatgatg ctggctgacg atctgcgccg ttatagcgac 180

gcggcaatcg agtttcgtca catccttgac gaccaaccca aagcagcacg ggtacggctg 240

gaactggcgc gcgtactggc cctgatgggc catcttggta gcgcggaacg cgagtttcgc 300

gcagccgagg ccgctggcct gcctcctgaa gtcgagcgca tggtccgctt cttcgccaat 360

gctctgaacg cgcgaaaaac cttcggcggg tcggtcgaag tggcgctcgc gccggatagc 420

aatatcaacc gtgcaacgcg ctcggacacg ctcggcacag tgattgggga cttcacactc 480

gacaaaaacg ccaaagcgaa gtccgggatt ggacttgaac tgcgtggtca ggcctactgg 540

cgcaacaggc tggagcatga cgccgacttg ctggtgcgcg gatcagttgg cggcagcttt 600

tatggcgaca ccagtttcaa cgacatctcc gcgagcctgc aagtgggacc gcaatacaca 660

tcgggcaaag accgcatcac gttgtccaca ggccccgtct ggcgctggta tggccagcag 720

ccctatagtg tcggcctgag cggcacggcg aactggcaac atcccacggg caaaagaagc 780

cagatgtctc tggaaggcag cgctgcgcac gtcaccaaca aacgtaacag cctgcaaacg 840

gcagacacct tcacggtaag cgccagcctc gatcgcgcct tcagcgcgcg ttttggaggc 900

ggcatgcaaa tctacggctt tcgggagaag gcgcgcgatc cgggttactc gctcgcgagc 960

ggcggtacga gcgcctacct gttccgcgag atgggccgcg ccacgctcgt cggcaatatc 1020

agctacagcc atcttgaaac cgatacacgg cttttcctct atccacgccg tcgcatcgaa 1080

gatcgttacg ccgccagcct cgccgccacg ctgcgcactc ttcgcgtagg ccccctcgcg 1140

ccgttggtcc gcgtcaagtg ggagcgtaac cgctcttcta tcgaggtcta tgactataaa 1200

cgtttttctg ccgaacttgg tgtgagttcg gctttttga 1239

<210> 620

<211> 412

<212> PRT

<213> Sphingobium baderi LL03 SLAM 1

<400> 620

Met Arg Leu Ser Ala Ala Gln Val Phe Thr Leu Ala Asp Ala Ala Arg

1 5 10 15

Ala Gly Gly Asp Phe Ala Ala Ala Glu Thr Ala Tyr Arg Ala Leu Gln

20 25 30

Ser Asp Pro Asp Leu Glu Ile Arg Thr Glu Ala Arg Phe Arg Leu Gly
35 40 45
Met Met Leu Ala Asp Asp Leu Arg Arg Tyr Ser Asp Ala Ala Ile Glu
50 55 60
Phe Arg His Ile Leu Asp Asp Gln Pro Lys Ala Ala Arg Val Arg Leu
65 70 75 80

Glu Leu Ala Arg Val Leu Ala Leu Met Gly His Leu Gly Ser Ala Glu
85 90 95
Arg Glu Phe Arg Ala Ala Glu Ala Ala Gly Leu Pro Pro Glu Val Glu
100 105 110
Arg Met Val Arg Phe Phe Ala Asn Ala Leu Asn Ala Arg Lys Thr Phe
115 120 125
Gly Gly Ser Val Glu Val Ala Leu Ala Pro Asp Ser Asn Ile Asn Arg
130 135 140

Ala Thr Arg Ser Asp Thr Leu Gly Thr Val Ile Gly Asp Phe Thr Leu
145 150 155 160
Asp Lys Asn Ala Lys Ala Lys Ser Gly Ile Gly Leu Glu Leu Arg Gly
165 170 175
Gln Ala Tyr Trp Arg Asn Arg Leu Glu His Asp Ala Asp Leu Leu Val
180 185 190
Arg Gly Ser Val Gly Gly Ser Phe Tyr Gly Asp Thr Ser Phe Asn Asp
195 200 205

Ile Ser Ala Ser Leu Gln Val Gly Pro Gln Tyr Thr Ser Gly Lys Asp
210 215 220
Arg Ile Thr Leu Ser Thr Gly Pro Val Trp Arg Trp Tyr Gly Gln Gln
225 230 235 240
Pro Tyr Ser Val Gly Leu Ser Gly Thr Ala Asn Trp Gln His Pro Thr
245 250 255
Gly Lys Arg Ser Gln Met Ser Leu Glu Gly Ser Ala Ala His Val Thr
260 265 270

Asn Lys Arg Asn Ser Leu Gln Thr Ala Asp Thr Phe Thr Val Ser Ala

275 280 285

Ser Leu Asp Arg Ala Phe Ser Ala Arg Phe Gly Gly Gly Met Gln Ile

290 295 300

Tyr Gly Phe Arg Glu Lys Ala Arg Asp Pro Gly Tyr Ser Leu Ala Ser

305 310 315 320

Gly Gly Thr Ser Ala Tyr Leu Phe Arg Glu Met Gly Arg Ala Thr Leu

325 330 335

Val Gly Asn Ile Ser Tyr Ser His Leu Glu Thr Asp Thr Arg Leu Phe

340 345 350

Leu Tyr Pro Arg Arg Arg Ile Glu Asp Arg Tyr Ala Ala Ser Leu Ala

355 360 365

Ala Thr Leu Arg Thr Leu Arg Val Gly Pro Leu Ala Pro Leu Val Arg

370 375 380

Val Lys Trp Glu Arg Asn Arg Ser Ser Ile Glu Val Tyr Asp Tyr Lys

385 390 395 400

Arg Phe Ser Ala Glu Leu Gly Val Ser Ser Ala Phe

405 410

<210> 621

<211> 1509

<212> DNA

<213> Sphingobium sp. HDIP04 SLAM 1

<400> 621

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cggcttgacc agcaggtcga tcgccagcgc gtgaaccagg aatcccgcgc gatcgaggac 180

gctgaagcgc tcgacggtga tacatcttcg ctgaccgtag acggtcagac ttacgcggtt 240

ggcaacactg tcgatgacat cggacaagct ctctatatct cagtgacgcg caaacagtgg 300

cccgacgttc gccgtttcct cgccgcctat cagaagctgg atgggcatga tcccatgctg 360

gtcgaatatg ctcttggtgc gctcgcgcgc gagaaaggcg acctagctac cgcggaacgg 420

cattatcggg cgctgttggc gataaaggcg gattttgtcc ccggtaggct ggaactcgca 480

cgcgtccttt tcgacaatca caaggatcgt gaagctgaca gcgccttccg ggcagcgcgc 540

gatatgctgg ccgatgatgg gtcacaggcg cagggtgtga tcggcacggt cgatgcctat 600

ctgggggcgc tcaagcgccg caggagctgg cagggaagcc ttgctgtcgg gcccggatac 660

agcagcaatc tcaatcagtc gtcggcgagc tacacctgcc tgctggcgac cgacgacggc 720

acctgccttg tcgaccgaca ggttccgccc gcgatcgcgg ccgctggcgt caacttcgaa 780

gccacgctcg cgaaagatgt tccgttgagc ggacatggcg gcctccgggc gcgggcgatc 840

ctgttcggcg atgtctatcc ggaacatcat gcctattccc aggcgacggc gatcatgcgt 900

ctaggctatc aatatcaggc cgcccgcaac gccgtctccc tctcgccctc attcgagatc 960

ggttcgctcg gatcgtcgga gctctacagt gcgccaggtc tgaacgcgga atggacgcac 1020

acggtctcgc cgcggtcgct cttcaaggtt gagggaaatt accgggattt ccgttaccgc 1080

gatgcggctt ttgctccgca aaatgggccg ctcacggatg ttgctatcac aggatggtat 1140

tcgctgacgc cgactttgac cgtgttcggt ggacccgatg tcattgtgaa ggacacgcca 1200

agccttgtcg aagcctatcg ccaatggggt ggtcggctag ggatcaacaa ggctttcggc 1260

aatgtcgcga gcctcttcct catgggatca tatcgctacc gccgccaccg cgcttacagc 1320

gaattgttcg aggcgcagcg caaggatcgc caattcaacg ttatcgggat cgcccgtcta 1380

cccatcctga aagtcgggcc gctcgttccc gaaatcgttg tccagcacac ccgcgtcgag 1440

agcaacatcg actggcttta ttcctacaag cgcacgaccg cgagcgtgag gctcagctat 1500

gccttctga 1509

<210> 622

<211> 502

<212> PRT

<213> Sphingobium sp. HDIP04 SLAM 1

<400> 622

Met Asp Ile Ser Ala Phe Arg Ile Leu Ile Ser Tyr Glu Pro Leu Leu

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Leu Ala Leu Ala Ala Ser Leu Trp Ala Thr Val Ala Asn Thr Gln Thr

20 25 30

Thr Ser Gly Gln Asp Thr Arg Leu Arg Leu Asp Gln Gln Val Asp Arg

35 40 45

Gln Arg Val Asn Gln Glu Ser Arg Ala Ile Glu Asp Ala Glu Ala Leu

50 55 60

Asp Gly Asp Thr Ser Ser Leu Thr Val Asp Gly Gln Thr Tyr Ala Val

65 70 75 80

Gly Asn Thr Val Asp Asp Ile Gly Gln Ala Leu Tyr Ile Ser Val Thr
85 90 95
Arg Lys Gln Trp Pro Asp Val Arg Arg Phe Leu Ala Ala Tyr Gln Lys
100 105 110
Leu Asp Gly His Asp Pro Met Leu Val Glu Tyr Ala Leu Gly Ala Leu

115 120 125
Ala Arg Glu Lys Gly Asp Leu Ala Thr Ala Glu Arg His Tyr Arg Ala
130 135 140
Leu Leu Ala Ile Lys Ala Asp Phe Val Pro Gly Arg Leu Glu Leu Ala
145 150 155 160
Arg Val Leu Phe Asp Asn His Lys Asp Arg Glu Ala Asp Ser Ala Phe
165 170 175
Arg Ala Ala Arg Asp Met Leu Ala Asp Asp Gly Ser Gln Ala Gln Gly

180 185 190
Val Ile Gly Thr Val Asp Ala Tyr Leu Gly Ala Leu Lys Arg Arg Arg
195 200 205
Ser Trp Gln Gly Ser Leu Ala Val Gly Pro Gly Tyr Ser Ser Asn Leu
210 215 220
Asn Gln Ser Ser Ala Ser Tyr Thr Cys Leu Leu Ala Thr Asp Asp Gly
225 230 235 240
Thr Cys Leu Val Asp Arg Gln Val Pro Pro Ala Ile Ala Ala Ala Gly

245 250 255
Val Asn Phe Glu Ala Thr Leu Ala Lys Asp Val Pro Leu Ser Gly His
260 265 270
Gly Gly Leu Arg Ala Arg Ala Ile Leu Phe Gly Asp Val Tyr Pro Glu
275 280 285
His His Ala Tyr Ser Gln Ala Thr Ala Ile Met Arg Leu Gly Tyr Gln
290 295 300
Tyr Gln Ala Ala Arg Asn Ala Val Ser Leu Ser Pro Ser Phe Glu Ile

305 310 315 320
Gly Ser Leu Gly Ser Ser Glu Leu Tyr Ser Ala Pro Gly Leu Asn Ala

325 330 335

Glu Trp Thr His Thr Val Ser Pro Arg Ser Leu Phe Lys Val Glu Gly

340 345 350

Asn Tyr Arg Asp Phe Arg Tyr Arg Asp Ala Ala Phe Ala Pro Gln Asn

355 360 365

Gly Pro Leu Thr Asp Val Ala Ile Thr Gly Trp Tyr Ser Leu Thr Pro

370 375 380

Thr Leu Thr Val Phe Gly Gly Pro Asp Val Ile Val Lys Asp Thr Pro

385 390 395 400

Ser Leu Val Glu Ala Tyr Arg Gln Trp Gly Gly Arg Leu Gly Ile Asn

405 410 415

Lys Ala Phe Gly Asn Val Ala Ser Leu Phe Leu Met Gly Ser Tyr Arg

420 425 430

Tyr Arg Arg His Arg Ala Tyr Ser Glu Leu Phe Glu Ala Gln Arg Lys

435 440 445

Asp Arg Gln Phe Asn Val Ile Gly Ile Ala Arg Leu Pro Ile Leu Lys

450 455 460

Val Gly Pro Leu Val Pro Glu Ile Val Val Gln His Thr Arg Val Glu

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Ser Asn Ile Asp Trp Leu Tyr Ser Tyr Lys Arg Thr Thr Ala Ser Val

485 490 495

Arg Leu Ser Tyr Ala Phe

500

<210> 623

<211> 1404

<212> DNA

<213> Sphingobium sp. SYK-6 SLAM 1

<400> 623

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gccgccggcc ccgcccacgc tcaggcggag agcgaagctg ccccggatcg ccccgaggcc 120

agcacgcctg cgccgacacc gcgcgtcacg caggacggcg cggcactcag cggactgagc 180

gcggcgcagc ttttcgacat tgccgatcag gcgcgcgttg ccggacgcct tgccgatgcc 240

gaagccatct atgccgcgct tgcgcgagac ccggatggcg aagtgcgggc tgaggcgcgc 300

ttccggctcg gcatgatgca ggccgaccag ggccgcaacg ccgacgcagc cctcacattc 360

cgcgccttgc tggacgagcg ccccaaggcc gcccgtgtcc ggctggagct tgcccgcgtg 420

cttgccgcga tgggcgagga aggtcgggcg cgccagcagc ttcgccaggc gcaagccagc 480

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cagcagtccg gcataggcct gcacctgacc ggccaggtct tcgcgcgcct cggcctgaca 720

ccacgcctga cgctggtgcc gcgcctctcc ggcgatggga ccttctatgg caagagccag 780

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gccacggcgg atctgcgcct gacacagcgc gtcggccgcc gcgcgcagag cgaagtcggc 960

ttctcctatg gccggacgca ttatctgttc aacgagatgc aggatggtga cctgttcaac 1020

ctgagcgcgg ggatcgagcg cgcgctctct ccccgcaccg gaatcggcgt gacgctgagc 1080

ggcacccgcc agacggcccg cgaccccggc ttctcgaccg cggcgggcgg cgtgacgctg 1140

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gcggccggcg cgacgttccg ccagattgag gtggcgggct tctcgccggt ggtgcgactc 1320

gcctacgagc gcaacatctc gaccgtcggc atctacgact atcgccgcac caccatcgac 1380

ctcggcatta cgcgcgcctt ctga 1404

<210> 624

<211> 467

<212> PRT

<213> Sphingobium sp. SYK-6 SLAM 1

<400> 624

Met Arg Arg Arg Val Ala Ala Gly Leu Gly Met Met Ser Ala Val Ile
1 5 10 15

Ala Leu Ala Ser Ala Ala Gly Pro Ala His Ala Gln Ala Glu Ser Glu
20 25 30

Ala Ala Pro Asp Arg Pro Glu Ala Ser Thr Pro Ala Pro Thr Pro Arg
35 40 45

Val Thr Gln Asp Gly Ala Ala Leu Ser Gly Leu Ser Ala Ala Gln Leu
50 55 60
Phe Asp Ile Ala Asp Gln Ala Arg Val Ala Gly Arg Leu Ala Asp Ala
65 70 75 80

Glu Ala Ile Tyr Ala Ala Leu Ala Arg Asp Pro Asp Gly Glu Val Arg
85 90 95
Ala Glu Ala Arg Phe Arg Leu Gly Met Met Gln Ala Asp Gln Gly Arg
100 105 110
Asn Ala Asp Ala Ala Leu Thr Phe Arg Ala Leu Leu Asp Glu Arg Pro
115 120 125
Lys Ala Ala Arg Val Arg Leu Glu Leu Ala Arg Val Leu Ala Ala Met
130 135 140

Gly Glu Glu Gly Arg Ala Arg Gln Gln Leu Arg Gln Ala Gln Ala Ser
145 150 155 160
Gly Leu Pro Pro Asp Val Ala Gln Val Val Asp Arg Phe Ala Thr Ala
165 170 175
Leu Arg Ser Asn Arg Arg Phe Gly Gly Asn Phe Glu Leu Ala Met Ala
180 185 190
Pro Asp Ser Asn Val Asn Arg Ala Thr Asp Ala Arg Glu Leu Asp Thr
195 200 205

Val Ile Ala Pro Leu Asn Leu Ser Asp Asp Ala Arg Gln Gln Ser Gly
210 215 220
Ile Gly Leu His Leu Thr Gly Gln Val Phe Ala Arg Leu Gly Leu Thr
225 230 235 240
Pro Arg Leu Thr Leu Val Pro Arg Leu Ser Gly Asp Gly Thr Phe Tyr
245 250 255
Gly Lys Ser Gln Phe Asn Asp Leu Ser Gly Ser Ala Leu Leu Gly Phe
260 265 270

Glu Trp Gln Ala Gly Gly Thr Arg Leu Met Pro Ser Phe Gly Ala Thr
275 280 285
Trp Arg Thr Tyr Gly Gly Arg Ala Tyr Ala Arg Thr Ala Thr Ala Asp

290 295 300

Leu Arg Leu Thr Gln Arg Val Gly Arg Arg Ala Gln Ser Glu Val Gly
305 310 315 320

Phe Ser Tyr Gly Arg Thr His Tyr Leu Phe Asn Glu Met Gln Asp Gly
325 330 335

Asp Leu Phe Asn Leu Ser Ala Gly Ile Glu Arg Ala Leu Ser Pro Arg
340 345 350

Thr Gly Ile Gly Val Thr Leu Ser Gly Thr Arg Gln Thr Ala Arg Asp
355 360 365

Pro Gly Phe Ser Thr Ala Ala Gly Gly Val Thr Leu Leu Gly Trp Arg
370 375 380

Asp Met Gly Arg Met Thr Val Phe Gly His Val Thr Ala Arg Arg Leu
385 390 395 400

Glu Ser Asp Ala Arg Leu Phe Pro Phe Thr Glu Arg Arg Lys Glu Trp
405 410 415

Phe Leu Arg Gly Ala Ala Gly Ala Thr Phe Arg Gln Ile Glu Val Ala
420 425 430

Gly Phe Ser Pro Val Val Arg Leu Ala Tyr Glu Arg Asn Ile Ser Thr
435 440 445

Val Gly Ile Tyr Asp Tyr Arg Arg Thr Thr Ile Asp Leu Gly Ile Thr
450 455 460

Arg Ala Phe
465

<210> 625

<211> 1374

<212> DNA

<213> Sphingomonas sp. LH128 SLAM 1

<400> 625

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gggcccccga cgtcgctgga gatcgacggc aagacttacg cggtaggcga taatgtcgat 120

gagatgggac aggccctcta tattgcgatc cggcgccgca tatggagcga gggtcgccgt 180

tttctgacgg cctatgaggg atacacagat cgtgatccca aactcgtgct tttcgccaag 240

ggcgcgcttg cgcgccagga tcgcaagctg ggtgaagccg aacggcatta tcgtgcactg 300

gtggagctcg accccgatct catgtcgggc caactcgaac tggcgcgggt cttgttcgaa 360

aaccgcaagg accgtgaagc gcagggcgcc ttccggcagg tgcgtgaacg cctggttgtc 420

gatggcgaca gatcgacggg ggtggtccgt accgtagacg cctttctcct ggcgttgaga 480

cagcggcggg gctggcaagg caatatcgcc ataggcccca gctacagcac caatctcaat 540

caatcgtccg aaagctacac ctgcctgctg gcgaccagcg acggcagttg cctgttcgac 600

cggcagttgc ccgatgcggt aaaggccatg gggatcagtt tcgaaggctc gctcaaccgc 660

agcattccga tatcgggcca tcacggtttg cgcgcccgcg cgctcctttt cggcgatgtg 720

tacccaagtg aacatgatta ctcgcaagcc agcctcatca tgcggcttgg ctaccaatat 780

cagtctgcgc gtgacacgtt ctcgctgtcg ccatcctttg acattgggac gttaggttca 840

tccgtcctct acgatgcctg gggcgcaaat gccgagtggc agcataccct gtcccgtaaa 900

gtactgctcc ggcttgaggg caattatcgc gactatcgct accggcagcg cggtttcagt 960

tcccaggatg gcccgctcat cgataccagc ctgaccgcgt ggtatacgcc ggcgccggga 1020

tggacggtgt ttggcggccc ggatcttgcc gtgaaggaca ctccggcggc caccaacgcc 1080

taccggcaat ggggcgggcg cttggggatc ggcaggacgc taggcaaaag cgccagcctt 1140

cttcttctcg gttcctaccg gcatcgcgat aaccgcgcct atagcgccgt cttcgccgcc 1200

aagcggagcg atgaccagtt caatgccacg gcgatcgcgc gcttccccgg tttcgctttc 1260

gccgggctga cgcctgaggt tgtgttccag cacaatcgcg tcgaaagcaa catcgactgg 1320

ctctattcct acaagcgcac caccgccagc gtgaggctga gccgtgcgtt ctag 1374

<210> 626

<211> 457

<212> PRT

<213> Sphingomonas sp. LH128 SLAM 1

<400> 626

Met Gln Gly Gln Glu Arg Lys Thr Glu Ser Arg Leu Leu Glu Asp Ala

1 5 10 15

Asp Ala Leu Asp Gly Pro Pro Thr Ser Leu Glu Ile Asp Gly Lys Thr

20 25 30

Tyr Ala Val Gly Asp Asn Val Asp Glu Met Gly Gln Ala Leu Tyr Ile

35 40 45

Ala Ile Arg Arg Arg Ile Trp Ser Glu Gly Arg Arg Phe Leu Thr Ala

50 55 60

Tyr Glu Gly Tyr Thr Asp Arg Asp Pro Lys Leu Val Leu Phe Ala Lys

65 70 75 80

Gly Ala Leu Ala Arg Gln Asp Arg Lys Leu Gly Glu Ala Glu Arg His

85 90 95

Tyr Arg Ala Leu Val Glu Leu Asp Pro Asp Leu Met Ser Gly Gln Leu

100 105 110

Glu Leu Ala Arg Val Leu Phe Glu Asn Arg Lys Asp Arg Glu Ala Gln

115 120 125

Gly Ala Phe Arg Gln Val Arg Glu Arg Leu Val Val Asp Gly Asp Arg

130 135 140

Ser Thr Gly Val Val Arg Thr Val Asp Ala Phe Leu Leu Ala Leu Arg

145 150 155 160

Gln Arg Arg Gly Trp Gln Gly Asn Ile Ala Ile Gly Pro Ser Tyr Ser

165 170 175

Thr Asn Leu Asn Gln Ser Ser Glu Ser Tyr Thr Cys Leu Leu Ala Thr

180 185 190

Ser Asp Gly Ser Cys Leu Phe Asp Arg Gln Leu Pro Asp Ala Val Lys

195 200 205

Ala Met Gly Ile Ser Phe Glu Gly Ser Leu Asn Arg Ser Ile Pro Ile

210 215 220

Ser Gly His His Gly Leu Arg Ala Arg Ala Leu Leu Phe Gly Asp Val

225 230 235 240

Tyr Pro Ser Glu His Asp Tyr Ser Gln Ala Ser Leu Ile Met Arg Leu

245 250 255

Gly Tyr Gln Tyr Gln Ser Ala Arg Asp Thr Phe Ser Leu Ser Pro Ser

260 265 270

Phe Asp Ile Gly Thr Leu Gly Ser Ser Val Leu Tyr Asp Ala Trp Gly

275 280 285

Ala Asn Ala Glu Trp Gln His Thr Leu Ser Arg Lys Val Leu Leu Arg

290 295 300

Leu Glu Gly Asn Tyr Arg Asp Tyr Arg Tyr Arg Gln Arg Gly Phe Ser
305 310 315 320
Ser Gln Asp Gly Pro Leu Ile Asp Thr Ser Leu Thr Ala Trp Tyr Thr
325 330 335
Pro Ala Pro Gly Trp Thr Val Phe Gly Gly Pro Asp Leu Ala Val Lys

340 345 350
Asp Thr Pro Ala Ala Thr Asn Ala Tyr Arg Gln Trp Gly Gly Arg Leu
355 360 365
Gly Ile Gly Arg Thr Leu Gly Lys Ser Ala Ser Leu Leu Leu Leu Gly
370 375 380
Ser Tyr Arg His Arg Asp Asn Arg Ala Tyr Ser Ala Val Phe Ala Ala
385 390 395 400
Lys Arg Ser Asp Asp Gln Phe Asn Ala Thr Ala Ile Ala Arg Phe Pro

405 410 415
Gly Phe Ala Phe Ala Gly Leu Thr Pro Glu Val Val Phe Gln His Asn
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Arg Val Glu Ser Asn Ile Asp Trp Leu Tyr Ser Tyr Lys Arg Thr Thr
435 440 445
Ala Ser Val Arg Leu Ser Arg Ala Phe
450 455

<210> 627
<211> 1364
<212> DNA
<213> Sphingomonas sp. URHD0057 SLAM 1
<400> 627
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gcgctcaccc aggatccaca tccggagtta cgcgccgagg cgaggtttcg gctcgccgcc 240
gtccgcgaaa agctcggcga cctcaagggc gcggttcagg ccctccgcca gcttctggcc 300
gagcagccca acgcgaaccc ggcccggctc gagctcgcgc ggatcctgtc gcggctcggc 360
cagaccgaag aagcaaaaaa gcaagtcgcg gcggccgaag cctggggctt gccgccggag 420

gttgagcaga atgtccgccg cttcgccagc acgctgcgga cgaccaaacg ccgcgggctc 480

accgtggaag tgaccgcggg cccggattcg aacgtcaacc gatcgacgtc gagcctgttc 540

atcgacacca tcatcgcgcc gttcgagctc gaccccgatg cgcggcgcca gcccgcgctt 600

ggcttcaccg gcagcctgcg cggttattcg cgcgaccgga tcggcgggat caccttgctg 660

tccgatgccg ggcttcgcgc ggatctttcg accaagccgc gcttcaacga cgtccagctt 720

gcgctcgaca gcgggccgga gttccttctc ggcaaggtgc aggtccgtcc cgccgcgctc 780

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gacgtggcaa agaattcggg acaggacggc tggcggaccg ccctcggagc cgacctgaca 960

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cgcgtgaacc ccgaaagcct gcgccaggca ggcgccgggc ttctgcttgc gcaccagtcg 1080

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aatcgcgccg ccgtcgccgg cttcacgccg ctgatgcgcg tcacgcacag cgacagccgc 1260

gccaacatcg cgctgttcga ttaccgccgc actcgcctcg atttcggcgt cacgcggagc 1320

ttttagatgg ggacccaagc ggtgcgcgaa gccgagttgc gccg 1364

<210> 628

<211> 441

<212> PRT

<213> Sphingomonas sp. URHD0057 SLAM 1

<400> 628

Met Leu Thr Leu Leu Ser Ala Ala Ala Ser Leu Ala Ala Gly Pro Pro
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Ser Ser Thr Ala Ala Pro Asp Pro Cys Ala Gly Gln Gln Asn Cys Gln
20 25 30

Gln Leu Thr Ala Ala Gln Leu Phe Ala Ala Ala Asp Glu Leu Ala Gly
35 40 45

Lys Gly Asp Leu Ala Gly Ala Ala Gln Leu Leu Glu Ala Leu Thr Gln
50 55 60

Asp Pro His Pro Glu Leu Arg Ala Glu Ala Arg Phe Arg Leu Ala Ala
65 70 75 80

Val Arg Glu Lys Leu Gly Asp Leu Lys Gly Ala Val Gln Ala Leu Arg
85 90 95
Gln Leu Leu Ala Glu Gln Pro Asn Ala Asn Pro Ala Arg Leu Glu Leu
100 105 110

Ala Arg Ile Leu Ser Arg Leu Gly Gln Thr Glu Glu Ala Lys Lys Gln
115 120 125
Val Ala Ala Ala Glu Ala Trp Gly Leu Pro Pro Glu Val Glu Gln Asn
130 135 140
Val Arg Arg Phe Ala Ser Thr Leu Arg Thr Thr Lys Arg Arg Gly Leu
145 150 155 160
Thr Val Glu Val Thr Ala Gly Pro Asp Ser Asn Val Asn Arg Ser Thr
165 170 175

Ser Ser Leu Phe Ile Asp Thr Ile Ile Ala Pro Phe Glu Leu Asp Pro
180 185 190
Asp Ala Arg Arg Gln Pro Ala Leu Gly Phe Thr Gly Ser Leu Arg Gly
195 200 205
Tyr Ser Arg Asp Arg Ile Gly Gly Ile Thr Leu Leu Ser Asp Ala Gly
210 215 220
Leu Arg Ala Asp Leu Ser Thr Lys Pro Arg Phe Asn Asp Val Gln Leu
225 230 235 240

Ala Leu Asp Ser Gly Pro Glu Phe Leu Leu Gly Lys Val Gln Val Arg
245 250 255
Pro Ala Ala Leu Tyr Glu Arg Arg Trp Phe Gly Gly Asp Leu Phe Ser
260 265 270
Ser Gly Ile Gly Gly Gln Ile Glu Leu Leu Ala Pro Leu Gly Pro Lys
275 280 285
Ala Gln Ile Ser Leu Thr Gly Ser His Leu His Gln Asp Val Ala Lys
290 295 300

Asn Ser Gly Gln Asp Gly Trp Arg Thr Ala Leu Gly Ala Asp Leu Thr
305 310 315 320
Arg Ala Leu Ser Ala Ala Thr Thr Ala Arg Val Thr Leu Arg Tyr Ala

325 330 335

Ser Leu Asn Ala Arg Val Asn Pro Glu Ser Leu Arg Gln Ala Gly Ala

340 345 350

Gly Leu Leu Leu Ala His Gln Ser Arg Ser Leu Thr Leu Phe Gly Glu

355 360 365

Ala Asp Tyr Thr Arg Thr Arg Gly Ile Glu Pro Gln Phe Leu Phe Gly

370 375 380

Lys Thr Arg Arg Asp His Arg Trp Asp Leu Thr Ala Gly Ala Ile Phe

385 390 395 400

Asn Arg Ala Ala Val Ala Gly Phe Thr Pro Leu Met Arg Val Thr His

405 410 415

Ser Asp Ser Arg Ala Asn Ile Ala Leu Phe Asp Tyr Arg Arg Thr Arg

420 425 430

Leu Asp Phe Gly Val Thr Arg Ser Phe

435 440

<210> 629

<211> 1461

<212> DNA

<213> Stenotrophomonas sp. RIT309 SLAM 1

<400> 629

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gcgcagcagg atgacctgcg ccgtgtgctc gaacagggca gcgagctgcg tcatcagcag 120

caggaccagc agcgcctgcg ccaggccgaa cacgagcgac cgaccatcac cctcgacggc 180

cagcagtacc gcgtggagcg cactgtcgac gacctcggcc aggcgctcta tctcgcgctg 240

cagcaccagc aatggcaggc cgcggccgcc ttccttgccg agtacatcga actgcctggc 300

cacgatccgc tgctgcgcca ctacgcgcag ggtgcgctgg cgcgcgtggg tggccagcac 360

ggcaaggccg cggccgaata cgaggccgtg ctcgccacgc agccggactt cctgccggcg 420

cggctggaac tggcgcgtgt gtatgccgaa gaccagcgcg accgcgatgc catcgccctg 480

ttcgaggcga tcgcagccgg catcgctggc ggcgaccctg caacggcggg cgtgcgtacg 540

cgggtggacg gctacctgca ggccctgcat gcacgccagc gctggaaggg tggcatcgcc 600

gccggccccg cctggagcga caacgtcaac cgcagttcgg ccagccgcac ctgcctgttt 660

ggtgacggca ccacctgctt catcgaacgc cggttgcccg atgcacaggc agcgttcggc 720

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agctacgatt accagggact cggcaaccac gcgctgcagg gcggtgccgg catgcatggc 960
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gacagcagcg ccgccgatcc cgccaatggc taccggcaac gcggcctgcg cctgggcgca 1200
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aaatgggaac gggcgttctg a 1461

<210> 630
<211> 486
<212> PRT
<213> Stenotrophomonas sp. RIT309 SLAM 1

<400> 630

Met Arg His Leu Leu Phe Leu Val Val Leu Leu Leu Ala Trp Pro Leu
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Asn Val Ala His Ala Gln Gln Asp Asp Leu Arg Arg Val Leu Glu Gln
20 25 30
Gly Ser Glu Leu Arg His Gln Gln Gln Asp Gln Gln Arg Leu Arg Gln
35 40 45
Ala Glu His Glu Arg Pro Thr Ile Thr Leu Asp Gly Gln Gln Tyr Arg
50 55 60

Val Glu Arg Thr Val Asp Asp Leu Gly Gln Ala Leu Tyr Leu Ala Leu
65 70 75 80
Gln His Gln Gln Trp Gln Ala Ala Ala Ala Phe Leu Ala Glu Tyr Ile
85 90 95

Glu Leu Pro Gly His Asp Pro Leu Leu Arg His Tyr Ala Gln Gly Ala
100 105 110
Leu Ala Arg Val Gly Gly Gln His Gly Lys Ala Ala Ala Glu Tyr Glu
115 120 125

Ala Val Leu Ala Thr Gln Pro Asp Phe Leu Pro Ala Arg Leu Glu Leu
130 135 140
Ala Arg Val Tyr Ala Glu Asp Gln Arg Asp Arg Asp Ala Ile Ala Leu
145 150 155 160
Phe Glu Ala Ile Ala Ala Gly Ile Ala Gly Gly Asp Pro Ala Thr Ala
165 170 175
Gly Val Arg Thr Arg Val Asp Gly Tyr Leu Gln Ala Leu His Ala Arg
180 185 190

Gln Arg Trp Lys Gly Gly Ile Ala Ala Gly Pro Ala Trp Ser Asp Asn
195 200 205
Val Asn Arg Ser Ser Ala Ser Arg Thr Cys Leu Phe Gly Asp Gly Thr
210 215 220
Thr Cys Phe Ile Glu Arg Arg Leu Pro Asp Ala Gln Ala Ala Phe Gly
225 230 235 240
Leu Asp Tyr Asp Gly Ser Leu Glu Arg Arg Leu Pro Leu Ala Gly His
245 250 255

His Gly Leu Tyr Leu Arg Gly Leu Ala Phe Gly Gln Ala Trp Arg Gly
260 265 270
His Ser Asp Tyr Asn Glu Leu Asn Ala Ser Val Gln Ala Gly Tyr Ser
275 280 285
Trp Arg Ser Ala Arg His Thr Leu Leu Leu Ala Pro Ser Tyr Asp Tyr
290 295 300
Gln Gly Leu Gly Asn His Ala Leu Gln Gly Gly Ala Gly Met His Gly
305 310 315 320

Glu Trp Gln Phe Ala Ala Asp Ala Arg Ser Leu Leu Lys Leu Glu Ala
325 330 335
Asp Trp Lys Arg Gln Arg Tyr Arg Gln Gln Gly Val Ala Ser Asn Tyr

340 345 350

Asp Gly Glu Leu Ala Ala Ile Tyr Ala Thr Trp Phe Arg Ala Leu Asn

355 360 365

Pro Arg Trp Thr Val Phe Ala Gly Val Asp Leu Ser Asp Ser Ser Ala

370 375 380

Ala Asp Pro Ala Asn Gly Tyr Arg Gln Arg Gly Leu Arg Leu Gly Ala

385 390 395 400

Ala Arg Gln Trp Ser Gly Thr Thr Ala Thr Val Phe Val Ser Leu Arg

405 410 415

Glu Arg Asp Tyr Asp Ala Trp Ser Pro Leu Leu Glu Ala Arg Arg Gln

420 425 430

Asp Ser Glu Gln Asn Leu Ile Ala Ile Val Arg Ser Glu Arg Leu Ala

435 440 445

Val Ala Gly Leu Ile Pro Ser Leu Ser Leu Arg Tyr Ala Arg Ile Asp

450 455 460

Ser Asn Val Asp Trp Leu Tyr Ser His Asp Arg Ser Leu Leu Ser Leu

465 470 475 480

Lys Trp Glu Arg Ala Phe

485

<210> 631

<211> 1455

<212> DNA

<213> Stenotrophomonas sp. SKA14 SLAM 1

<400> 631

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cagcagcgcc tgcggcaggc cgagtcggag cggccgacca tcaccatcga cggccagacc 180

ctgcgcgtgg agcgcaccgt ggatgacctc ggccaggccc tttacctgtc gctgcagcat 240

cagcaatggc aggcagcagc ggccttcctc gacgagtaca tcgaactgcc ggggcatgat 300

ccattgctgc gccactatgc acagggcgcg ctggcgcggg tcagtggcga tcatcggcgc 360

gcggcgaagg agtacgaagc gctgctggcc gtgcagccgg atttcctgcc ggcccgcctc 420

gaactggcgc gtgtctacgc cgaagaccag cgcgatcgcg atgccgtcgc gttgttcacg 480

gccatcgccg ccggcatcaa tagcgacgaa ccggccacgg ccggtgtccg cgcccgcgtg 540

gacggctacc tgagcgcgct gcaggcccgc cagcgctgga agggcgccct ggccgccggt 600
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atcgacagca atgtcggctg gctgtacagc cacgaccgca gcctgctcag cctgaagtgg 1440
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<210> 632
<211> 484
<212> PRT
<213> Stenotrophomonas sp. SKA14 SLAM 1
<400> 632

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Val Arg Ala Gln Gln Asp Asp Leu Arg Arg Val Leu Glu Gln Gly Ser
20 25 30

Glu Leu Arg His Gln Gln Gln Asp Gln Gln Arg Leu Arg Gln Ala Glu
35 40 45
Ser Glu Arg Pro Thr Ile Thr Ile Asp Gly Gln Thr Leu Arg Val Glu
50 55 60
Arg Thr Val Asp Asp Leu Gly Gln Ala Leu Tyr Leu Ser Leu Gln His

65 70 75 80

Gln Gln Trp Gln Ala Ala Ala Ala Phe Leu Asp Glu Tyr Ile Glu Leu

85 90 95

Pro Gly His Asp Pro Leu Leu Arg His Tyr Ala Gln Gly Ala Leu Ala

100 105 110

Arg Val Ser Gly Asp His Arg Arg Ala Ala Lys Glu Tyr Glu Ala Leu

115 120 125

Leu Ala Val Gln Pro Asp Phe Leu Pro Ala Arg Leu Glu Leu Ala Arg

130 135 140

Val Tyr Ala Glu Asp Gln Arg Asp Arg Asp Ala Val Ala Leu Phe Thr

145 150 155 160

Ala Ile Ala Ala Gly Ile Asn Ser Asp Glu Pro Ala Thr Ala Gly Val

165 170 175

Arg Ala Arg Val Asp Gly Tyr Leu Ser Ala Leu Gln Ala Arg Gln Arg

180 185 190

Trp Lys Gly Ala Leu Ala Ala Gly Pro Ala Trp Ser Asp Asn Ile Asn

195 200 205

Arg Ser Ser Ala Ser Arg Thr Cys Leu Phe Gly Val Gly Glu Thr Cys

210 215 220

Leu Ile Glu Arg Thr Leu Pro Asp Ala Gln Arg Ala Thr Gly Leu Asp

225 230 235 240

Tyr Asp Gly Asn Leu Glu Arg Arg Trp Ala Leu Ala Gly His His Gly

245 250 255

Leu Tyr Val Arg Gly Leu Ala Phe Gly Gln Ala Trp Arg Gly Tyr Ser

260 265 270

Ala Tyr Asn Glu Leu Asn Ala Ser Leu Gln Ala Gly Tyr Ser Trp Arg

275 280 285

Ser Ala Arg His Thr Val Leu Leu Ala Pro Ser Tyr Asp Tyr Gln Ala

290 295 300

Leu Gly Asn His Ala Leu Gln Gly Gly Ser Gly Val His Gly Glu Trp

305 310 315 320

Gln Tyr Ala Leu Asp Ala Arg Ser Leu Leu Lys Leu Glu Ala Asp Trp
325 330 335
Lys Arg Gln Arg Tyr Arg Gln Pro Gly Leu Ala Ser Asn Tyr Asp Gly
340 345 350

Glu Leu Ala Ala Leu Tyr Ala Thr Trp Phe Arg Ala Leu Asn Pro Arg
355 360 365
Trp Thr Val Phe Ala Gly Leu Asp Val Thr Thr Ser Arg Ala Asp Asp
370 375 380
Gln Ala Asn Gly Tyr Arg Gln Arg Gly Leu Arg Leu Gly Ala Ala Arg
385 390 395 400
Gln Trp Pro Gly Thr Thr Ala Thr Val Phe Val Ser Leu Arg Glu Arg
405 410 415

Asp Tyr Asp Ala Trp Ser Pro Leu Leu Glu Ala Arg Arg Glu Asp Ser
420 425 430
Glu Gln Asn Leu Ile Ala Ile Val Arg Ser Glu Arg Leu Ala Val Ala
435 440 445
Gly Leu Val Pro Ser Leu Ser Leu Arg Tyr Ala Arg Ile Asp Ser Asn
450 455 460
Val Gly Trp Leu Tyr Ser His Asp Arg Ser Leu Leu Ser Leu Lys Trp
465 470 475 480

Glu Arg Ala Phe

<210> 633
<211> 1158
<212> DNA
<213> Sulfitobacter sp. CB2047 SLAM 1
<400> 633
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cagggctatt tccgttttgc cattgtgccc gaaagcaatg ccgcccgccg gacctctgca 360
gagacggtga acctcagcgg ctttgtgctg cggctggacc cgaattcccg cgcccaatcc 420
gccacggcgt tcgagattgg cacgggcgtt gcgaccgtgc cgcgtcttac ggacgcctta 480
cgcgcccggt tcgcactgga tctggatgcc cggcttttcg acgggcgtgc acccgatgaa 540
gtgacccttc ggaccagtgc atccctgctg catttcgccg atgaggggcg tcttgtctcg 600
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cgcgaacgta tcacctatga tggcagcggt gtcgacgtgg accgaacagc tggtgcagcg 780
caattcgctt atgcggcatc gtcgcagctt gtgtttcgcg taggtatgcg cgcggaaaac 840
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<210> 634
<211> 385
<212> PRT
<213> Sulfitobacter sp. CB2047 SLAM 1
<400> 634

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Met Trp Ile Leu Gly Val Ala Tyr Asn Arg Ser Gly Lys Ser His Gln
20 25 30
Ala Val Ala Pro Leu Ala Arg Leu Val Ile Leu Arg Pro Asp Asp Pro
35 40 45

Thr Phe Arg Leu Glu Leu Ala Asn Ala Leu Val Lys Ser Asp Gln Ile
50 55 60
Glu Arg Ala Arg Tyr His Leu Glu Leu Ala Lys Gly Ala Gly Leu Ser
65 70 75 80

Pro Ser Val Gln Ala Lys Val Gln Ala Glu Leu Asp Arg Leu Ala Lys
85 90 95
Pro Lys Lys Trp Gln Gly Tyr Phe Arg Phe Ala Ile Val Pro Glu Ser
100 105 110

Asn Ala Ala Arg Arg Thr Ser Ala Glu Thr Val Asn Leu Ser Gly Phe
115 120 125
Val Leu Arg Leu Asp Pro Asn Ser Arg Ala Gln Ser Ala Thr Ala Phe
130 135 140
Glu Ile Gly Thr Gly Val Ala Thr Val Pro Arg Leu Thr Asp Ala Leu
145 150 155 160
Arg Ala Arg Phe Ala Leu Asp Leu Asp Ala Arg Leu Phe Asp Gly Arg
165 170 175

Ala Pro Asp Glu Val Thr Leu Arg Thr Ser Ala Ser Leu Leu His Phe
180 185 190
Ala Asp Glu Gly Arg Leu Val Ser Ala Glu Ile Tyr Gly Ser Gln Arg
195 200 205
Trp Ile Asp Asp Val Ala Tyr Ala His Thr Tyr Gly Leu Gly Leu Ser
210 215 220
Tyr Thr Arg Asn Leu Gly Thr Arg Ala Arg Ala Thr Ala Val Leu Gln
225 230 235 240

Arg Glu Arg Ile Thr Tyr Asp Gly Ser Gly Val Asp Val Asp Arg Thr
245 250 255
Ala Gly Ala Ala Gln Phe Ala Tyr Ala Ala Ser Ser Gln Leu Val Phe
260 265 270
Arg Val Gly Met Arg Ala Glu Asn Arg Ala Ser Ser Tyr Ser Pro Val
275 280 285
Ala Gly His Ala Ala Gly Val Thr Ile Gly Gly Asp Tyr Ser Phe Ala
290 295 300

Gly Gly Leu Arg Val Gly Leu Asp Leu Ser Phe Asp Arg Asn Glu Phe
305 310 315 320
Asp Gly Val His Pro Ile Phe Gly Val Ala Arg Val Asp Lys Lys Ser

325 330 335

Ser Val Met Leu Asn Leu Ser Asn Gln Asn Trp Ser Tyr Lys Gly Phe

340 345 350

Thr Gln Val Leu Arg Leu Gly Phe Glu Glu Gln Arg Ser Thr Ile Ser

355 360 365

Ile Asn Arg Phe Arg Asn Ala Thr Ala Ser Ile Gly Leu Thr Arg Ser

370 375 380

Phe

385

<210> 635

<211> 1281

<212> DNA

<213> Sulfitobacter sp. CB2047 SLAM 2

<400> 635

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gccagtctgg cgcagttggt caaggggggat ccgaacgggc cgctgcatca ggcctatctg 180

gaaggtcaaa tcctgatgcg ccagaaccag cctgcggcgg cggttgatct gtttcgcgat 240

ctggtacgca tcgcgcccga ttatgaaccc gcaagacgag agctgaccct gctgctggcc 300

tatcgcggtg atgtgaccgc ggcgcgctat catgcggaac ggttggtcgc ggaaaccgcc 360

gacgaacagc tgcgcgccgg attgcagacc tttatcctga acaacacctc gcgcaagccc 420

ggcggctttg ccctgcggtt cgcgctgttg ccgtcgtcga accagacccg cggcagtgcc 480

gagcaggaga tcctgattgg cggggtgccg ttcacgttga accctgcgtc gcgcgcgtct 540

tccggggtgg gactggcgat tggcggcacc gcgtggcggc gctggcaatg gaatgaaaga 600

tggtccggcg tgggcaccgc cagtctggat gcgaaattct acgattccgc gctgaacacg 660

gaaaccacgg ccgtcgcacg gttcgatgtc attcgtggcg ggcagcgggg gcggttctct 720

ttcgggccga ttgccgagct gagcttttct gattcagaca tcgtgcgacg ccggtggggg 780

gcggagctgc gcggcgccta tcagctgcgt ccgcgtgatc tggtgtcggg tgcgcttcgg 840

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gtctcgtacc aacatcggtt gacgccgacg ctcgggctat ccttcggcct gtcgcagctg 960

cgcgagacga cacagcgcgc gcatctggat caccatgaaa ccggcgtgtc gatggggatc 1020

gacaaacagt ggaaatcggg cctctcgacc ggagcgatac tggcatacga acaggacaga 1080

tacgacggca tcttccccgg caccacgacc ccgcgcgagg atgacaccac cagcctcacc 1140

ttcaccgtgc agcacaacaa ggtgcagatc gggaaatatg tgccgcgcat cacctatacc 1200

tacacgcggg cgaaatcgaa tgtggcgttg ttcgactatg acagccacga catcggggcg 1260

agtctctcgc tcaagttctg a 1281

<210> 636

<211> 426

<212> PRT

<213> Sulfitobacter sp. CB2047 SLAM 2

<400> 636

Met Lys His Leu Leu Phe Ala Ala Leu Met Gly Val Leu Leu Ala Cys
1 5 10 15

Gln Ser Pro Gly Gln Ala Gln Ala Ala Thr Pro Gln Asp Tyr Leu Glu
20 25 30

Gln Gly Asn Tyr Asp Ala Ala Arg Ala Ser Leu Ala Gln Leu Val Lys
35 40 45

Gly Asp Pro Asn Gly Pro Leu His Gln Ala Tyr Leu Glu Gly Gln Ile
50 55 60

Leu Met Arg Gln Asn Gln Pro Ala Ala Ala Val Asp Leu Phe Arg Asp
65 70 75 80

Leu Val Arg Ile Ala Pro Asp Tyr Glu Pro Ala Arg Arg Glu Leu Thr
85 90 95

Leu Leu Leu Ala Tyr Arg Gly Asp Val Thr Ala Ala Arg Tyr His Ala
100 105 110

Glu Arg Leu Val Ala Glu Thr Ala Asp Glu Gln Leu Arg Ala Gly Leu
115 120 125

Gln Thr Phe Ile Leu Asn Asn Thr Ser Arg Lys Pro Gly Gly Phe Ala
130 135 140

Leu Arg Phe Ala Leu Leu Pro Ser Ser Asn Gln Thr Arg Gly Ser Ala
145 150 155 160

Glu Gln Glu Ile Leu Ile Gly Gly Val Pro Phe Thr Leu Asn Pro Ala

165 170 175

Ser Arg Ala Ser Ser Gly Val Gly Leu Ala Ile Gly Gly Thr Ala Trp

180 185 190

Arg Arg Trp Gln Trp Asn Glu Arg Trp Ser Gly Val Gly Thr Ala Ser

195 200 205

Leu Asp Ala Lys Phe Tyr Asp Ser Ala Leu Asn Thr Glu Thr Thr Ala

210 215 220

Val Ala Arg Phe Asp Val Ile Arg Gly Gly Gln Arg Gly Arg Phe Ser

225 230 235 240

Phe Gly Pro Ile Ala Glu Leu Ser Phe Ser Asp Ser Asp Ile Val Arg

245 250 255

Arg Arg Trp Gly Ala Glu Leu Arg Gly Ala Tyr Gln Leu Arg Pro Arg

260 265 270

Asp Leu Val Ser Gly Ala Leu Arg Phe Asp Arg Gln Thr Tyr Asp Gln

275 280 285

Ser Pro Phe Arg Asp Gly His Arg Met Arg Ala Ser Val Ser Tyr Gln

290 295 300

His Arg Leu Thr Pro Thr Leu Gly Leu Ser Phe Gly Leu Ser Gln Leu

305 310 315 320

Arg Glu Thr Thr Gln Arg Ala His Leu Asp His His Glu Thr Gly Val

325 330 335

Ser Met Gly Ile Asp Lys Gln Trp Lys Ser Gly Leu Ser Thr Gly Ala

340 345 350

Ile Leu Ala Tyr Glu Gln Asp Arg Tyr Asp Gly Ile Phe Pro Gly Thr

355 360 365

Thr Thr Pro Arg Glu Asp Asp Thr Thr Ser Leu Thr Phe Thr Val Gln

370 375 380

His Asn Lys Val Gln Ile Gly Lys Tyr Val Pro Arg Ile Thr Tyr Thr

385 390 395 400

Tyr Thr Arg Ala Lys Ser Asn Val Ala Leu Phe Asp Tyr Asp Ser His

405 410 415

Asp Ile Gly Ala Ser Leu Ser Leu Lys Phe

420 425

<210> 637

<211> 1110

<212> DNA

<213> Sulfitobacter sp. NAS-14.1 SLAM 1

<400> 637

atgtggattc taggggtcgc ctacaaccgt tcgggaaaat cacaccaagc cgttgccccg 60

ctggcgcggc ttgtgatctt gcggccagac gatcccacgt tccggcttga actggcgaac 120

gcattggtga aaagcgacca gatcgaacgg gcgcgatatc accttgaact ggccaagggc 180

gcgggtttgt cgccccctgt ccaggcaaaa gtgcaggcgg agcttgaccg tttggccaaa 240

ccgaaaaaat ggcagggcta tttccgtttt gccattgtgc ccgaaagcaa tgccgcccgc 300

cggacctctg cagagacggt gaacctcagc ggctttgtgc tgcggctgga cccgaattcg 360

cgcgcccaat ccgccacagc gttcgagatt ggcacgggcg tcgcgaccgt gccgcgtctt 420

acggacgcct tacgcgcccg gttcgcactg gatctggatg cccggctttt cgacgggcgt 480

gcgcccgatg aagtgaccct tcggaccagt gcatccctgc tgcatttcgc cgatgagggg 540

cgtcttgtct cggccgagat ttatggatcg cagcgctgga ttgatgacgc ggcctatgcg 600

catacctatg gccttggcct gtcctatacg cgcaacctcg gcacccgcgc ccgcgccacg 660

gcggtgcttc agcgcgaacg catcacctat gatggcagcg gtgttggcgt gaaccgaaca 720

gcaggtgctg cgcaattcgc ttatgcggca tcgtcgcagc ttgtgtttcg cgtaggcttg 780

cgcgcggaaa gccgtaccag ttcttacagc cccgtcgcgg gccatgcggc gggcgtcacc 840

atcggcggcg attattcctt tgccggcggt cttcgggtcg ggctggatct gtcgtttgac 900

cggaacgaat ttgacggcat gcatcccatc ttcggcgttg cccgcgtcga caagaaatca 960

agcgtcatgc tgaacctgtc caaccagaac tggagctaca agggatttac ccaggttctg 1020

aggctcgggt ttgaagagca acgctccacc atctcgatca acaggtttcg caacgccact 1080

gccagcatcg gcctcacacg atcgttttga 1110

<210> 638

<211> 369

<212> PRT

<213> Sulfitobacter sp. NAS-14.1 SLAM 1

<400> 638

Met Trp Ile Leu Gly Val Ala Tyr Asn Arg Ser Gly Lys Ser His Gln

1 5 10 15

Ala Val Ala Pro Leu Ala Arg Leu Val Ile Leu Arg Pro Asp Asp Pro

20 25 30

Thr Phe Arg Leu Glu Leu Ala Asn Ala Leu Val Lys Ser Asp Gln Ile

35 40 45

Glu Arg Ala Arg Tyr His Leu Glu Leu Ala Lys Gly Ala Gly Leu Ser

50 55 60

Pro Pro Val Gln Ala Lys Val Gln Ala Glu Leu Asp Arg Leu Ala Lys

65 70 75 80

Pro Lys Lys Trp Gln Gly Tyr Phe Arg Phe Ala Ile Val Pro Glu Ser

85 90 95

Asn Ala Ala Arg Arg Thr Ser Ala Glu Thr Val Asn Leu Ser Gly Phe

100 105 110

Val Leu Arg Leu Asp Pro Asn Ser Arg Ala Gln Ser Ala Thr Ala Phe

115 120 125

Glu Ile Gly Thr Gly Val Ala Thr Val Pro Arg Leu Thr Asp Ala Leu

130 135 140

Arg Ala Arg Phe Ala Leu Asp Leu Asp Ala Arg Leu Phe Asp Gly Arg

145 150 155 160

Ala Pro Asp Glu Val Thr Leu Arg Thr Ser Ala Ser Leu Leu His Phe

165 170 175

Ala Asp Glu Gly Arg Leu Val Ser Ala Glu Ile Tyr Gly Ser Gln Arg

180 185 190

Trp Ile Asp Asp Ala Ala Tyr Ala His Thr Tyr Gly Leu Gly Leu Ser

195 200 205

Tyr Thr Arg Asn Leu Gly Thr Arg Ala Arg Ala Thr Ala Val Leu Gln

210 215 220

Arg Glu Arg Ile Thr Tyr Asp Gly Ser Gly Val Gly Val Asn Arg Thr

225 230 235 240

Ala Gly Ala Ala Gln Phe Ala Tyr Ala Ala Ser Ser Gln Leu Val Phe

245 250 255

Arg Val Gly Leu Arg Ala Glu Ser Arg Thr Ser Ser Tyr Ser Pro Val
260 265 270
Ala Gly His Ala Ala Gly Val Thr Ile Gly Gly Asp Tyr Ser Phe Ala
275 280 285

Gly Gly Leu Arg Val Gly Leu Asp Leu Ser Phe Asp Arg Asn Glu Phe
290 295 300
Asp Gly Met His Pro Ile Phe Gly Val Ala Arg Val Asp Lys Lys Ser
305 310 315 320
Ser Val Met Leu Asn Leu Ser Asn Gln Asn Trp Ser Tyr Lys Gly Phe
325 330 335
Thr Gln Val Leu Arg Leu Gly Phe Glu Glu Gln Arg Ser Thr Ile Ser
340 345 350

Ile Asn Arg Phe Arg Asn Ala Thr Ala Ser Ile Gly Leu Thr Arg Ser
355 360 365
Phe

<210> 639
<211> 1281
<212> DNA
<213> Sulfitobacter sp. NAS-14.1 SLAM 2
<400> 639
atgaaacatc ttctttttgc cgccctgatg ggcgttcttt tggcgtgcca atcgcccgga 60
caggcgcagg ccgcgacacc acaggactat ctggaacagg gaaactatga tgccgcgcgg 120
gccagtctgg cgcagttggt caaggggggat ccgaacgggc cgttgcatca ggcctatctg 180
gaaggtcaga tcctgatgcg ccagaaccag cccgcggcgg cggttgatct gtttcgcgat 240

ctggtacgca tcgcgcccga ttatgaaccc gccagacgcg agttgaccct gctgttggcc 300
tatcgcggtg atgtgaccgc tgcgcgctat catgcggaac ggttggtcgc ggaaaccgcc 360
gacgaacagc tgcgcgccgg gttgcagacc tttatcctga acaacacctc gcgcaagccc 420
ggcggctttg ccctgcggtt cgcgctgttg ccgtcgtcga accagacccg cggcagtgcc 480
gagcaggaga ttctgattgg cggggtgccg ttcacgctga accctgcgtc gcgggcatct 540
tccggggtgg ggctggcgat tggcggcacc gcatggcggc gctggcagtg gaatgaaaga 600

tggtcgggcg tgggcacggc cagtctggat gcgaaattct acgattccgc gctgaacacg 660

gaaaccacgg ccatcacacg cttcgatgtc attcgcggcg gccagcgggg gcggttctct 720

ttcgggccga ttgccgagct gagcttttcc ggttcagaca tcgtgcgacg acggtggggg 780

gcggagctgc gcggcgccta tcagctgcgt ccgcgtgatc tggtgtcggg tgcgctgcgg 840

tttgaccggc agacctatga ccaaagcccg tttcgggacg ggcaccggat gcgggcctcg 900

gtctcgtacc aacatcggtt gacgccgacg ctcgggcttt ccttcggcct gtcgcagctg 960

cgcgaaacga cacagcgcgc gcatctggat caccatgaaa ccggcgtgtc gatggggatc 1020

gacaaacagt ggaaatcggg tctctcgacc ggcatgatac tggcatacga acaggacaaa 1080

tacgacggca tcttccccgg caccacgacc ccgcgcgagg atgacaccac cagcctcacc 1140

ttcaccgtgc agcacaacaa ggtgcagatc gggaaatatg tgccgcgcat cacctatacc 1200

tacacgcggg cgaaatcgaa tgtggcgttg ttcgactatg acagccacga catcggggcg 1260

agtctctcgc tcaagttctg a 1281

<210> 640

<211> 426

<212> PRT

<213> Sulfitobacter sp. NAS-14.1 SLAM 2

<400> 640

Met Lys His Leu Leu Phe Ala Ala Leu Met Gly Val Leu Leu Ala Cys
1 5 10 15

Gln Ser Pro Gly Gln Ala Gln Ala Ala Thr Pro Gln Asp Tyr Leu Glu
20 25 30

Gln Gly Asn Tyr Asp Ala Ala Arg Ala Ser Leu Ala Gln Leu Val Lys
35 40 45

Gly Asp Pro Asn Gly Pro Leu His Gln Ala Tyr Leu Glu Gly Gln Ile
50 55 60

Leu Met Arg Gln Asn Gln Pro Ala Ala Ala Val Asp Leu Phe Arg Asp
65 70 75 80

Leu Val Arg Ile Ala Pro Asp Tyr Glu Pro Ala Arg Arg Glu Leu Thr
85 90 95

Leu Leu Leu Ala Tyr Arg Gly Asp Val Thr Ala Ala Arg Tyr His Ala
100 105 110

Glu Arg Leu Val Ala Glu Thr Ala Asp Glu Gln Leu Arg Ala Gly Leu
115 120 125
Gln Thr Phe Ile Leu Asn Asn Thr Ser Arg Lys Pro Gly Gly Phe Ala
130 135 140

Leu Arg Phe Ala Leu Leu Pro Ser Ser Asn Gln Thr Arg Gly Ser Ala
145 150 155 160
Glu Gln Glu Ile Leu Ile Gly Gly Val Pro Phe Thr Leu Asn Pro Ala
165 170 175
Ser Arg Ala Ser Ser Gly Val Gly Leu Ala Ile Gly Gly Thr Ala Trp
180 185 190
Arg Arg Trp Gln Trp Asn Glu Arg Trp Ser Gly Val Gly Thr Ala Ser
195 200 205

Leu Asp Ala Lys Phe Tyr Asp Ser Ala Leu Asn Thr Glu Thr Thr Ala
210 215 220
Ile Thr Arg Phe Asp Val Ile Arg Gly Gly Gln Arg Gly Arg Phe Ser
225 230 235 240
Phe Gly Pro Ile Ala Glu Leu Ser Phe Ser Gly Ser Asp Ile Val Arg
245 250 255
Arg Arg Trp Gly Ala Glu Leu Arg Gly Ala Tyr Gln Leu Arg Pro Arg
260 265 270

Asp Leu Val Ser Gly Ala Leu Arg Phe Asp Arg Gln Thr Tyr Asp Gln
275 280 285
Ser Pro Phe Arg Asp Gly His Arg Met Arg Ala Ser Val Ser Tyr Gln
290 295 300
His Arg Leu Thr Pro Thr Leu Gly Leu Ser Phe Gly Leu Ser Gln Leu
305 310 315 320
Arg Glu Thr Thr Gln Arg Ala His Leu Asp His His Glu Thr Gly Val
325 330 335

Ser Met Gly Ile Asp Lys Gln Trp Lys Ser Gly Leu Ser Thr Gly Met
340 345 350
Ile Leu Ala Tyr Glu Gln Asp Lys Tyr Asp Gly Ile Phe Pro Gly Thr

355 360 365

Thr Thr Pro Arg Glu Asp Asp Thr Thr Ser Leu Thr Phe Thr Val Gln

370 375 380

His Asn Lys Val Gln Ile Gly Lys Tyr Val Pro Arg Ile Thr Tyr Thr

385 390 395 400

Tyr Thr Arg Ala Lys Ser Asn Val Ala Leu Phe Asp Tyr Asp Ser His

405 410 415

Asp Ile Gly Ala Ser Leu Ser Leu Lys Phe

420 425

<210> 641

<211> 1380

<212> DNA

<213> T. equigenitalis SLAM 1

<400> 641

atggtttttg ctagtttcaa ttatgcttat gcaatagatg accatgtcta tatcccagaa 60

catgtcgaga aaaaaatatt agaaaaccct cttaaagagc aacaaacaac ggttgaagtc 120

acttcaaaag agattgcttc aaatcctgac cttatcgtta gggcaatgct atatgcactt 180

ataaacaata atatcgatga tattgttttc ctgtatccat actacgaggc attgccacca 240

gaagcaaaag agccagttgt gcactcgtgg gccaggggtg tatatggagt gtattcaaac 300

aaagtgcatg agggcatttc agatttaaga gaagtcatta gtcagcgacc cgatattgtg 360

caagctagaa ttcaacttgc aatggcacta tatttagata atcaatatat tgcatccaaa 420

gatcagttcc aaaaacttaa gggtgaggga ggtgagaatt cggggctagt acaactaagc 480

gatacattta tagaacgcat tgagaataaa agcgattttg agttcacgct aaacgcaagg 540

tatatcgtgg acgataacct aaatcaggct ccagaaaatc cagatttggg gggcggttgg 600

aaagcagaac ctgcgaaatc cgataggggg ctggggctga gcgtgaacat tgccaaacga 660

tttgtcatag cggataattt ttttgcagac attaatttaa atagcaatgg aaagttttat 720

aaaaaatacg ggcgacaaaa tgaactaaat aatcgcctaa gcctaactat tggacattct 780

gaagcaaagt ggagtctgtt tactggacca atcttcgggc ttgatttaaa cggtcaaaat 840

caagagcaaa aaaaattaga taaatattct cggtctttgg ggatgagcat caatggcaat 900

tattggctta ctaaaaatat tcgtagcttt gcatatgtcg agcattcacg tctttaccat 960

acgcaacgaa aacatctaaa tggtcgtcaa tcgtttgcat ctttagggct ttcatatttt 1020

ccaaatgcac gacacaacat ttatttactg gcggactttt tgagatataa agctaaattt 1080

aaagacgatt cgtatgttcg aaaagggctt agactggggc tcataaagga gtggaatgga 1140

ggtctttcaa ctcaattaga agcctcaaaa cacctaaaaa cttttgatgg aattggattc 1200

tttaacaagg tccagaccaa tcatgattat gaattaggtg tcacgatatg gcatagaaac 1260

ttacacttcg caggtcttac accgcgtatt aattacacct atcataagac aaagagcaat 1320

gtcgcccttt atgcttacaa caagcataat gtatatttct cagtaagtaa gagtttttaa 1380

<210> 642

<211> 1488

<212> DNA

<213> T. equigenitalis SLAM 1

<400> 642

atgaaatcca agtttttttct ttactgtact ttatatgtaa tcagtataaa ttgccaatca 60

attgaaactc acaacgagat ttcaaatgat tttaacgtcc aaactaaaaa ctttatatcc 120

aatacaaatg aaaattcgct tttggataca tcattgattt ctcaaacaca aaacgcaacc 180

tatataacaa ttaatggttc tacttactta gttccacata ccgaacatga tttaagatta 240

gctatttatc atgcgattaa tgcaaatctt tggggcgatt tatcggaatt aatagaaata 300

tatcagacat tgccaaacca tcagaaacaa ctggtttata tggcacaggg gttgttggaa 360

cgtagccggg gatatattaa taaagcctta actcatatgc aaagggcata tgatattaat 420

aaggaggatt tgagggttca acttgagtta gcaagacttt attttgaaga ctacaacaat 480

agacaatcta agaaaatatt taattcatta gctcaaagtt atgaattacc gaattatacg 540

aaggggttga ttaatgaata ccaatcagcc attaattccc agtataaatg gcaaggtaat 600

attgggttgt ctattggtta tgattctaat attaaccaag gtaatggtat aagacagtgt 660

gtgtttaatt ttatggacac ctgtgttatt tatagaaatt tacctccccc cataggttca 720

tcatatttgg gtttaaattt tgacttatcc aaaagatatg ccttgtctga taataatgac 780

ttggaaatat cagcaagatt tcagggagct aagtattcta agacagattc taaagcctta 840

tttttaacgg actatagtaa tttctcttcc tctgcaaaaa tatcttatat ttatagggac 900

agcgttaaga aagtaatgct ttatccagaa tttgaaatat tgcacaaaaa caaatctact 960

tattatcaat cgccaagcat taatttaaat actgaaattc aattatcacg tcgtttaaat 1020

ctgaacagca atttctcttt taaatggatt aattacgagg gagaaaacaa aaagtatttt 1080

gaagattata aacaagttaa tgtgggatta gggcttgtat ttgaacctag taaaaataca 1140

tttctttata caaattttga tttttatcgt aatctttatt taactaatta ttccagcagt 1200

aaagagcaat ctataagaat cggagcttat aaatacttat catcaggtgt ctatttgcat 1260

gcattggcta tgtatcgaga cactaaaaat gatgtggcaa attttctgtc atttgaacca 1320
aggcatgata atactaaaat tgcaatctta agtataggtt tgcctaaaat ttcatttaaa 1380
ggtgtagtgc cagaattaag gtttaaatac atacaaaata aaagcaatat tgatttttat 1440
atctatacgc aaagggaaat tagtttaaat ttaaattata gtttttaa 1488

<210> 643
<211> 459
<212> PRT
<213> T. equigenitalis SLAM 1
<400> 643

Met Val Phe Ala Ser Phe Asn Tyr Ala Tyr Ala Ile Asp Asp His Val
1 5 10 15

Tyr Ile Pro Glu His Val Glu Lys Lys Ile Leu Glu Asn Pro Leu Lys
20 25 30
Glu Gln Gln Thr Thr Val Glu Val Thr Ser Lys Glu Ile Ala Ser Asn
35 40 45
Pro Asp Leu Ile Val Arg Ala Met Leu Tyr Ala Leu Ile Asn Asn Asn
50 55 60
Ile Asp Asp Ile Val Phe Leu Tyr Pro Tyr Tyr Glu Ala Leu Pro Pro
65 70 75 80

Glu Ala Lys Glu Pro Val Val His Ser Trp Ala Arg Gly Val Tyr Gly
85 90 95
Val Tyr Ser Asn Lys Val His Glu Gly Ile Ser Asp Leu Arg Glu Val
100 105 110
Ile Ser Gln Arg Pro Asp Ile Val Gln Ala Arg Ile Gln Leu Ala Met
115 120 125
Ala Leu Tyr Leu Asp Asn Gln Tyr Ile Ala Ser Lys Asp Gln Phe Gln
130 135 140

Lys Leu Lys Gly Glu Gly Gly Glu Asn Ser Gly Leu Val Gln Leu Ser
145 150 155 160
Asp Thr Phe Ile Glu Arg Ile Glu Asn Lys Ser Asp Phe Glu Phe Thr

165 170 175

Leu Asn Ala Arg Tyr Ile Val Asp Asp Asn Leu Asn Gln Ala Pro Glu

180 185 190

Asn Pro Asp Leu Gly Gly Gly Trp Lys Ala Glu Pro Ala Lys Ser Asp

195 200 205

Arg Gly Leu Gly Leu Ser Val Asn Ile Ala Lys Arg Phe Val Ile Ala

210 215 220

Asp Asn Phe Phe Ala Asp Ile Asn Leu Asn Ser Asn Gly Lys Phe Tyr

225 230 235 240

Lys Lys Tyr Gly Arg Gln Asn Glu Leu Asn Asn Arg Leu Ser Leu Thr

245 250 255

Ile Gly His Ser Glu Ala Lys Trp Ser Leu Phe Thr Gly Pro Ile Phe

260 265 270

Gly Leu Asp Leu Asn Gly Gln Asn Gln Glu Gln Lys Lys Leu Asp Lys

275 280 285

Tyr Ser Arg Ser Leu Gly Met Ser Ile Asn Gly Asn Tyr Trp Leu Thr

290 295 300

Lys Asn Ile Arg Ser Phe Ala Tyr Val Glu His Ser Arg Leu Tyr His

305 310 315 320

Thr Gln Arg Lys His Leu Asn Gly Arg Gln Ser Phe Ala Ser Leu Gly

325 330 335

Leu Ser Tyr Phe Pro Asn Ala Arg His Asn Ile Tyr Leu Leu Ala Asp

340 345 350

Phe Leu Arg Tyr Lys Ala Lys Phe Lys Asp Asp Ser Tyr Val Arg Lys

355 360 365

Gly Leu Arg Leu Gly Leu Ile Lys Glu Trp Asn Gly Gly Leu Ser Thr

370 375 380

Gln Leu Glu Ala Ser Lys His Leu Lys Thr Phe Asp Gly Ile Gly Phe

385 390 395 400

Phe Asn Lys Val Gln Thr Asn His Asp Tyr Glu Leu Gly Val Thr Ile

405 410 415

Trp His Arg Asn Leu His Phe Ala Gly Leu Thr Pro Arg Ile Asn Tyr
420 425 430

Thr Tyr His Lys Thr Lys Ser Asn Val Ala Leu Tyr Ala Tyr Asn Lys
435 440 445

His Asn Val Tyr Phe Ser Val Ser Lys Ser Phe
450 455

<210> 644

<211> 495

<212> PRT

<213> T. equigenitalis SLAM 1

<400> 644

Met Lys Ser Lys Phe Phe Leu Tyr Cys Thr Leu Tyr Val Ile Ser Ile
1 5 10 15

Asn Cys Gln Ser Ile Glu Thr His Asn Glu Ile Ser Asn Asp Phe Asn
20 25 30

Val Gln Thr Lys Asn Phe Ile Ser Asn Thr Asn Glu Asn Ser Leu Leu
35 40 45

Asp Thr Ser Leu Ile Ser Gln Thr Gln Asn Ala Thr Tyr Ile Thr Ile
50 55 60

Asn Gly Ser Thr Tyr Leu Val Pro His Thr Glu His Asp Leu Arg Leu
65 70 75 80

Ala Ile Tyr His Ala Ile Asn Ala Asn Leu Trp Gly Asp Leu Ser Glu
85 90 95

Leu Ile Glu Ile Tyr Gln Thr Leu Pro Asn His Gln Lys Gln Leu Val
100 105 110

Tyr Met Ala Gln Gly Leu Leu Glu Arg Ser Arg Gly Tyr Ile Asn Lys
115 120 125

Ala Leu Thr His Met Gln Arg Ala Tyr Asp Ile Asn Lys Glu Asp Leu
130 135 140

Arg Val Gln Leu Glu Leu Ala Arg Leu Tyr Phe Glu Asp Tyr Asn Asn
145 150 155 160

Arg Gln Ser Lys Lys Ile Phe Asn Ser Leu Ala Gln Ser Tyr Glu Leu

165 170 175

Pro Asn Tyr Thr Lys Gly Leu Ile Asn Glu Tyr Gln Ser Ala Ile Asn

180 185 190

Ser Gln Tyr Lys Trp Gln Gly Asn Ile Gly Leu Ser Ile Gly Tyr Asp

195 200 205

Ser Asn Ile Asn Gln Gly Asn Gly Ile Arg Gln Cys Val Phe Asn Phe

210 215 220

Met Asp Thr Cys Val Ile Tyr Arg Asn Leu Pro Pro Pro Ile Gly Ser

225 230 235 240

Ser Tyr Leu Gly Leu Asn Phe Asp Leu Ser Lys Arg Tyr Ala Leu Ser

245 250 255

Asp Asn Asn Asp Leu Glu Ile Ser Ala Arg Phe Gln Gly Ala Lys Tyr

260 265 270

Ser Lys Thr Asp Ser Lys Ala Leu Phe Leu Thr Asp Tyr Ser Asn Phe

275 280 285

Ser Ser Ser Ala Lys Ile Ser Tyr Ile Tyr Arg Asp Ser Val Lys Lys

290 295 300

Val Met Leu Tyr Pro Glu Phe Glu Ile Leu His Lys Asn Lys Ser Thr

305 310 315 320

Tyr Tyr Gln Ser Pro Ser Ile Asn Leu Asn Thr Glu Ile Gln Leu Ser

325 330 335

Arg Arg Leu Asn Leu Asn Ser Asn Phe Ser Phe Lys Trp Ile Asn Tyr

340 345 350

Glu Gly Glu Asn Lys Lys Tyr Phe Glu Asp Tyr Lys Gln Val Asn Val

355 360 365

Gly Leu Gly Leu Val Phe Glu Pro Ser Lys Asn Thr Phe Leu Tyr Thr

370 375 380

Asn Phe Asp Phe Tyr Arg Asn Leu Tyr Leu Thr Asn Tyr Ser Ser Ser

385 390 395 400

Lys Glu Gln Ser Ile Arg Ile Gly Ala Tyr Lys Tyr Leu Ser Ser Gly

405 410 415

Val Tyr Leu His Ala Leu Ala Met Tyr Arg Asp Thr Lys Asn Asp Val

420 425 430

Ala Asn Phe Leu Ser Phe Glu Pro Arg His Asp Asn Thr Lys Ile Ala

435 440 445

Ile Leu Ser Ile Gly Leu Pro Lys Ile Ser Phe Lys Gly Val Val Pro

450 455 460

Glu Leu Arg Phe Lys Tyr Ile Gln Asn Lys Ser Asn Ile Asp Phe Tyr

465 470 475 480

Ile Tyr Thr Gln Arg Glu Ile Ser Leu Asn Leu Asn Tyr Ser Phe

485 490 495

<210> 645

<211> 1412

<212> DNA

<213> T. linaloolentis SLAM 1

<400> 645

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gcctgggccg acgatgacga cacccgcttc ctgcaggaac agacgcagcg cgccgccgag 120

cagaaagcgc aggccgaaca ggccctggcc gcgccgccgg gctcgctgct gtacgaaggc 180

aaggtctatc aggtcggcaa cacgctggag gaactggaac cggccctcta cgtcgccatc 240

aacaccgggc aatggacccg cctgcccgat ttcatctccc gctaccgcct gctgcgcggg 300

caccgcccgg ccctggtcgc gatggccgac agcctgctgg cgcgcttcca cggcgactac 360

ccgaccgccg tgcagcgcat gcaggacgcc aacgcccacg agcccggcga cgcccgcatc 420

cgcctcgaac tggcccgcct gctgttcgag gataaccagg acaagcgcgc acgcacaggc 480

tttgcccacg cactcgaagc cggcctgccg cccaatgccc ggatgctggt gcaacagtat 540

gagcaggccc tggacctccg cgccggctgg cacggcacgg ccgcgctggg ctggggctac 600

aacgacaaca tcaaccaggc caacggctac cgcagttgcg aaagctacgt cccgatatgg 660

aacgtctgcg ccttcgaacg gatcatgccc gaggccatcg gctcacagat ggtgaattac 720

gaactgtcca tgcagcgccg cttcaacctg tcgggcaacc ataacctgca tgtgcgcccg 780

ctcagctacg gcaactacta cgcgcgcacc aacccttcgg acacggccag catccgggac 840

tacagcacca acctggcgat ccttcaggcg ggctaccagt atctggatgc gcgcgacaac 900

gtcacgctga ccccgtacct ggagcactac taccgcaacc gccacagcga gtacctggcc 960

cacggcctgc aactggagtg gcgccattcg ctgagccggc agtggcagat cggtaccagc 1020

ctggatgcca agcgctacga atacacctcg aaagggctgc gggtcggcat ggactacaag 1080

cagtatcagt ggggcgtgac ggcgagcttc tccccccagc cagccaccgc gctgtacggt 1140

gggctggacc tgacgcgcaa gcaatacgaa gtggcgcagg ccagcagcaa ggattgggcg 1200

ctgcgcgccg gcatctacca ccagtttgcc ggcgaggcgg gcctgttcat gaacgtgctg 1260

ggcatctacc gtgcgctgcg caacgacgcc ttcgatggct ttctcggcgc gcggcggcac 1320

gacaggcagc aggtctacat cgtcagcctg ggcgccaacg gctggaagat cgccgggctg 1380

gtgccggaac tgcgcgtgcg ccacagccgc aa 1412

<210> 646

<211> 470

<212> PRT

<213> T. linaloolentis SLAM 1

<400> 646

Met Phe His Arg Phe Lys Ala Leu Gly Phe Val Leu Ala Ala Ala Phe

1 5 10 15

Val Leu Pro Ala Ala Trp Ala Asp Asp Asp Asp Thr Arg Phe Leu Gln

20 25 30

Glu Gln Thr Gln Arg Ala Ala Glu Gln Lys Ala Gln Ala Glu Gln Ala

35 40 45

Leu Ala Ala Pro Pro Gly Ser Leu Leu Tyr Glu Gly Lys Val Tyr Gln

50 55 60

Val Gly Asn Thr Leu Glu Glu Leu Glu Pro Ala Leu Tyr Val Ala Ile

65 70 75 80

Asn Thr Gly Gln Trp Thr Arg Leu Pro Asp Phe Ile Ser Arg Tyr Arg

85 90 95

Leu Leu Arg Gly His Arg Pro Ala Leu Val Ala Met Ala Asp Ser Leu

100 105 110

Leu Ala Arg Phe His Gly Asp Tyr Pro Thr Ala Val Gln Arg Met Gln

115 120 125

Asp Ala Asn Ala His Glu Pro Gly Asp Ala Arg Ile Arg Leu Glu Leu

130 135 140

Ala Arg Leu Leu Phe Glu Asp Asn Gln Asp Lys Arg Ala Arg Thr Gly

145 150 155 160

Phe Ala His Ala Leu Glu Ala Gly Leu Pro Pro Asn Ala Arg Met Leu

165 170 175

Val Gln Gln Tyr Glu Gln Ala Leu Asp Leu Arg Ala Gly Trp His Gly

180 185 190

Thr Ala Ala Leu Gly Trp Gly Tyr Asn Asp Asn Ile Asn Gln Ala Asn

195 200 205

Gly Tyr Arg Ser Cys Glu Ser Tyr Val Pro Ile Trp Asn Val Cys Ala

210 215 220

Phe Glu Arg Ile Met Pro Glu Ala Ile Gly Ser Gln Met Val Asn Tyr

225 230 235 240

Glu Leu Ser Met Gln Arg Arg Phe Asn Leu Ser Gly Asn His Asn Leu

245 250 255

His Val Arg Pro Leu Ser Tyr Gly Asn Tyr Tyr Ala Arg Thr Asn Pro

260 265 270

Ser Asp Thr Ala Ser Ile Arg Asp Tyr Ser Thr Asn Leu Ala Ile Leu

275 280 285

Gln Ala Gly Tyr Gln Tyr Leu Asp Ala Arg Asp Asn Val Thr Leu Thr

290 295 300

Pro Tyr Leu Glu His Tyr Tyr Arg Asn Arg His Ser Glu Tyr Leu Ala

305 310 315 320

His Gly Leu Gln Leu Glu Trp Arg His Ser Leu Ser Arg Gln Trp Gln

325 330 335

Ile Gly Thr Ser Leu Asp Ala Lys Arg Tyr Glu Tyr Thr Ser Lys Gly

340 345 350

Leu Arg Val Gly Met Asp Tyr Lys Gln Tyr Gln Trp Gly Val Thr Ala

355 360 365

Ser Phe Ser Pro Gln Pro Ala Thr Ala Leu Tyr Gly Gly Leu Asp Leu

370 375 380

Thr Arg Lys Gln Tyr Glu Val Ala Gln Ala Ser Ser Lys Asp Trp Ala

385 390 395 400

Leu Arg Ala Gly Ile Tyr His Gln Phe Ala Gly Glu Ala Gly Leu Phe

405 410 415

Met Asn Val Leu Gly Ile Tyr Arg Ala Leu Arg Asn Asp Ala Phe Asp

420 425 430

Gly Phe Leu Gly Ala Arg Arg His Asp Arg Gln Gln Val Tyr Ile Val

435 440 445

Ser Leu Gly Ala Asn Gly Trp Lys Ile Ala Gly Leu Val Pro Glu Leu

450 455 460

Arg Val Arg His Ser Arg

465 470

<210> 647

<211> 1497

<212> DNA

<213> T. linaloolentis SLAM 2

<400> 647

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ctggctgacg atgacgatac ccgcctgctg cttaacaaga tcgatcgcag cacggcggta 120

agggaacgct ctcacttagt ggaggatacg ccgcctggca tcgatccggg atccttgatc 180

accattggcg agacgactta tcacgtcgag aatacgctgg aagatttggg gccggccatt 240

tatgtttcga tgaacctgcg gcagtggcac aaggtggggc agtttgtaga aaagtaccgc 300

agtttgtccg ggcatgagga agggctcgtg ctattagccg aaggaatgct ggaccgagag 360

aacagagact atcgcgcagc cagcgacaag ctcaatgccg cattggcggc caagccggat 420

ttcgcgcgtg ccaggctgga actggcacgt gtctacttcg aggatcacaa gtcgcaagaa 480

gccagggatt tgttcgacca ggtttccacc agcggtattc cggatgaggt tcgtcccgtc 540

atcgaaggtt ttcagcgggc cttgcgcgac cgcgatactt ggcatggttc gctggccctg 600

gggctcggct acagtagcaa cgtcaaccag gctaacggca aggtgctggt ttcggaaacc 660

tgcattccgg tcttcggctg cgcgatcacc aggcgtcgca tggacgagcc gatcgaatcc 720

tccatgttta cctatgattt gacattgaac cgtcgttatc agatttccgg ccaccacaac 780

gcattgctgc gggcgatcag ctacggcaag ctgcccaatg agcacaagga cacaaccgca 840

acgttagcca gcacttacta tgacgaaagc accagcatcg tctacgcggg ctacaactac 900

atgagtgcat tgaatgattt ttcggtgatg ccgctgttcg aacatcatta cggcaaccgc 960

cacgtccgct atcaggccgt gggtttgcgt ctggactgga agcacaatcc aaggccggat 1020

acccaggtcg gcgtcaatgc gcagcgaaag cactttcgct ttcagggtcg cgaacggcag 1080

tatttcgaca attacgacga aaatcagttt ggcttctatg cttcgaatgt gctcgacgcc 1140

aagacaatga tttacggcgg tctgaacttt acccgcaagc tgtttccaca agctgttgcc 1200

agcagcaagg aatacatggc caacctgggg gcatacagaa tgttcgatgc gggcttcacc 1260

atcaacgcca ccgcgctttt tcgccatatc cgcaacgacg agggcagcca actcatgggc 1320

gggcgccgcg aggacgacca gcagatctac atcgtcaatc tcggcatgcc gcgcttcgcg 1380

ttcaaaggca taacgcccaa tctgtatctc aagcgcacgg tcaacgacag cagcatcgac 1440

tgggcttacg aataccgcca gaccgaagta gtgctgaagc tcgagaaaaa tttttga 1497

<210> 648

<211> 498

<212> PRT

<213> T. linaloolentis SLAM 2

<400> 648

Met Phe Gln Arg Pro Ile Met Ala Ile Phe Phe Leu Ala Val Met Leu

1 5 10 15

Pro Ile His Ala Leu Ala Asp Asp Asp Asp Thr Arg Leu Leu Leu Asn

20 25 30

Lys Ile Asp Arg Ser Thr Ala Val Arg Glu Arg Ser His Leu Val Glu

35 40 45

Asp Thr Pro Pro Gly Ile Asp Pro Gly Ser Leu Ile Thr Ile Gly Glu

50 55 60

Thr Thr Tyr His Val Glu Asn Thr Leu Glu Asp Leu Gly Pro Ala Ile

65 70 75 80

Tyr Val Ser Met Asn Leu Arg Gln Trp His Lys Val Gly Gln Phe Val

85 90 95

Glu Lys Tyr Arg Ser Leu Ser Gly His Glu Glu Gly Leu Val Leu Leu

100 105 110

Ala Glu Gly Met Leu Asp Arg Glu Asn Arg Asp Tyr Arg Ala Ala Ser

115 120 125

Asp Lys Leu Asn Ala Ala Leu Ala Ala Lys Pro Asp Phe Ala Arg Ala

130 135 140

Arg Leu Glu Leu Ala Arg Val Tyr Phe Glu Asp His Lys Ser Gln Glu
145 150 155 160
Ala Arg Asp Leu Phe Asp Gln Val Ser Thr Ser Gly Ile Pro Asp Glu
165 170 175
Val Arg Pro Val Ile Glu Gly Phe Gln Arg Ala Leu Arg Asp Arg Asp
180 185 190
Thr Trp His Gly Ser Leu Ala Leu Gly Leu Gly Tyr Ser Ser Asn Val

195 200 205

Asn Gln Ala Asn Gly Lys Val Leu Val Ser Glu Thr Cys Ile Pro Val
210 215 220
Phe Gly Cys Ala Ile Thr Arg Arg Arg Met Asp Glu Pro Ile Glu Ser
225 230 235 240
Ser Met Phe Thr Tyr Asp Leu Thr Leu Asn Arg Arg Tyr Gln Ile Ser
245 250 255
Gly His His Asn Ala Leu Leu Arg Ala Ile Ser Tyr Gly Lys Leu Pro

260 265 270

Asn Glu His Lys Asp Thr Thr Ala Thr Leu Ala Ser Thr Tyr Tyr Asp
275 280 285
Glu Ser Thr Ser Ile Val Tyr Ala Gly Tyr Asn Tyr Met Ser Ala Leu
290 295 300
Asn Asp Phe Ser Val Met Pro Leu Phe Glu His His Tyr Gly Asn Arg
305 310 315 320
His Val Arg Tyr Gln Ala Val Gly Leu Arg Leu Asp Trp Lys His Asn

325 330 335

Pro Arg Pro Asp Thr Gln Val Gly Val Asn Ala Gln Arg Lys His Phe
340 345 350
Arg Phe Gln Gly Arg Glu Arg Gln Tyr Phe Asp Asn Tyr Asp Glu Asn
355 360 365
Gln Phe Gly Phe Tyr Ala Ser Asn Val Leu Asp Ala Lys Thr Met Ile

370 375 380

Tyr Gly Gly Leu Asn Phe Thr Arg Lys Leu Phe Pro Gln Ala Val Ala

385 390 395 400

Ser Ser Lys Glu Tyr Met Ala Asn Leu Gly Ala Tyr Arg Met Phe Asp

405 410 415

Ala Gly Phe Thr Ile Asn Ala Thr Ala Leu Phe Arg His Ile Arg Asn

420 425 430

Asp Glu Gly Ser Gln Leu Met Gly Gly Arg Arg Glu Asp Asp Gln Gln

435 440 445

Ile Tyr Ile Val Asn Leu Gly Met Pro Arg Phe Ala Phe Lys Gly Ile

450 455 460

Thr Pro Asn Leu Tyr Leu Lys Arg Thr Val Asn Asp Ser Ser Ile Asp

465 470 475 480

Trp Ala Tyr Glu Tyr Arg Gln Thr Glu Val Val Leu Lys Leu Glu Lys

485 490 495

Asn Phe

<210> 649

<211> 1479

<212> DNA

<213> V. coralliilyticus SLAM 1

<400> 649

atgaaaatcg accgtaactt tattcttggc tcactgttaa tggtgagcgt tagctattcc 60

tttttctctt acgcggatca ggataccgat ttacgtatcc agcaacgcga cgcgctatct 120

tcccgtcaaa acgaaaatgc tcttattgaa gaagagctgg aaaaagaacg cctagctgaa 180

cagtcggcgt caggctcaga atcgagtgta gcgaacaccg cagatgagct tggaccggca 240

ttgcatgtcg cggttcggca gcgtcaatgg gcactggcag agagtctgct ggaaaggtat 300

atggcgttgg cggattttga tcctatgttg gtgcactacg catcgggggc attggcacgc 360

aatgcgcgtg attataatca ggcagaaacg cactactcgg cattgcttga gatgcaggaa 420

aacttttgc ccgcagagct ggagttagct cgcgtctggt ttgaagacag agaaaacagc 480

gcttctttgt cgttgtttaa tgacatcctc acccgcttac ctgctgataa cccgagatcg 540

gcgggagtcc ggaatacggt agaaagtttt gttagtgcac tggagtatcg tgatgattgg 600

caaggcgcgt tttcctttgg gccgacctac aatgacaacc tcaatttgtc ctcgaaacat 660

tatgaatgtc tggtctattt caccaatggt cagtgttttt tagagcgcag cgcgcccaag 720

gttaaatctg cctatggtat tgactacgac gccagtttaa atcgacgttt ttcgcttagt 780

ggtcatcatg gcttgcagct acgcagcttt gcctatggca ccaattatca gaaccacaaa 840

gaacataacg agcagacgtt aaacgtgacc tttggttaca gctatcagac tgccaaacat 900

cagatcagta ttgcaccgca gtttgaatat cgcgccttag cgaatcaggc gttgtttgct 960

tcgggcggct tcaaggcgga ttggttcacc aatcttagcc agacttctgc tatgaaactc 1020

gaagtggaag gggaatacct cgattatcgt aatcaggcct ttcgttacca atccgactgg 1080

caatggtctg tctttggcac ttactggcat cagttacccg acaaatggtt agtgtttggt 1140

ggtgtagact ggacactgaa acaaaaccga caggcggtgc atgagtacga tttgtgggga 1200

ggtcgattgg gcgtgaataa aaccttcaca tcgctgaata ctgacgtggc cttattcgct 1260

tcgttgcggc aacgtattta tggtgacttc aatgcggtgc tcggtgagcg gcgtgacgat 1320

actgagcaaa attatacctt agtggtgacc ttgccagagc tgtttgccgg gtttaaaccg 1380

ctcatcgaag tcaaagccaa tcagaccaag agtaatgttg attgggcata cagctacaag 1440

cagcatcaat acagtataaa actagaaaaa agattctga 1479

<210> 650

<211> 492

<212> PRT

<213> V. coralliilyticus SLAM 1

<400> 650

Met Lys Ile Asp Arg Asn Phe Ile Leu Gly Ser Leu Leu Met Val Ser

1 5 10 15

Val Ser Tyr Ser Phe Phe Ser Tyr Ala Asp Gln Asp Thr Asp Leu Arg

20 25 30

Ile Gln Gln Arg Asp Ala Leu Ser Ser Arg Gln Asn Glu Asn Ala Leu

35 40 45

Ile Glu Glu Glu Leu Glu Lys Glu Arg Leu Ala Glu Gln Ser Ala Ser

50 55 60

Gly Ser Glu Ser Ser Val Ala Asn Thr Ala Asp Glu Leu Gly Pro Ala

65 70 75 80

Leu His Val Ala Val Arg Gln Arg Gln Trp Ala Leu Ala Glu Ser Leu

85 90 95

Leu Glu Arg Tyr Met Ala Leu Ala Asp Phe Asp Pro Met Leu Val His

100 105 110

Tyr Ala Ser Gly Ala Leu Ala Arg Asn Ala Arg Asp Tyr Asn Gln Ala

115 120 125

Glu Thr His Tyr Ser Ala Leu Leu Glu Met Gln Glu Asn Phe Leu Pro

130 135 140

Ala Glu Leu Glu Leu Ala Arg Val Trp Phe Glu Asp Arg Glu Asn Ser

145 150 155 160

Ala Ser Leu Ser Leu Phe Asn Asp Ile Leu Thr Arg Leu Pro Ala Asp

165 170 175

Asn Pro Arg Ser Ala Gly Val Arg Asn Thr Val Glu Ser Phe Val Ser

180 185 190

Ala Leu Glu Tyr Arg Asp Asp Trp Gln Gly Ala Phe Ser Phe Gly Pro

195 200 205

Thr Tyr Asn Asp Asn Leu Asn Leu Ser Ser Lys His Tyr Glu Cys Leu

210 215 220

Val Tyr Phe Thr Asn Gly Gln Cys Phe Leu Glu Arg Ser Ala Pro Lys

225 230 235 240

Val Lys Ser Ala Tyr Gly Ile Asp Tyr Asp Ala Ser Leu Asn Arg Arg

245 250 255

Phe Ser Leu Ser Gly His His Gly Leu Gln Leu Arg Ser Phe Ala Tyr

260 265 270

Gly Thr Asn Tyr Gln Asn His Lys Glu His Asn Glu Gln Thr Leu Asn

275 280 285

Val Thr Phe Gly Tyr Ser Tyr Gln Thr Ala Lys His Gln Ile Ser Ile

290 295 300

Ala Pro Gln Phe Glu Tyr Arg Ala Leu Ala Asn Gln Ala Leu Phe Ala

305 310 315 320

Ser Gly Gly Phe Lys Ala Asp Trp Phe Thr Asn Leu Ser Gln Thr Ser

325 330 335

Ala Met Lys Leu Glu Val Glu Gly Glu Tyr Leu Asp Tyr Arg Asn Gln

340 345 350

Ala Phe Arg Tyr Gln Ser Asp Trp Gln Trp Ser Val Phe Gly Thr Tyr

355 360 365

Trp His Gln Leu Pro Asp Lys Trp Leu Val Phe Gly Gly Val Asp Trp

370 375 380

Thr Leu Lys Gln Asn Arg Gln Ala Val His Glu Tyr Asp Leu Trp Gly

385 390 395 400

Gly Arg Leu Gly Val Asn Lys Thr Phe Thr Ser Leu Asn Thr Asp Val

405 410 415

Ala Leu Phe Ala Ser Leu Arg Gln Arg Ile Tyr Gly Asp Phe Asn Ala

420 425 430

Val Leu Gly Glu Arg Arg Asp Asp Thr Glu Gln Asn Tyr Thr Leu Val

435 440 445

Val Thr Leu Pro Glu Leu Phe Ala Gly Phe Lys Pro Leu Ile Glu Val

450 455 460

Lys Ala Asn Gln Thr Lys Ser Asn Val Asp Trp Ala Tyr Ser Tyr Lys

465 470 475 480

Gln His Gln Tyr Ser Ile Lys Leu Glu Lys Arg Phe

485 490

<210> 651

<211> 1482

<212> DNA

<213> V. fortis SLAM 1

<400> 651

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cctctttctt ggtctcaaga cacggatacg cagtttcgta ttgaacaacg agacgccctg 120

tcggctcaaa acaaagaaca agcaatactt gaagaagaga accagcgcga agcaagctcc 180

ccaaaaccag cccaaactgg ataccagatc gacacaaacg atgtgagtca agtcgcgaaa 240

gctcttcatc ttgctgttcg ttatcgtcaa tgggtgcaag ctaaccagtt actggaaatc 300

tatcgacagt ttgaacagcc tgacccactg ttacttaaat acgctgacgg cgcaatctct 360

cgagctaaag gttatctgga acacgcccaa ctcgcattcg aagacgcatt agccttacaa 420

cccaatttta tgcccgcgca gttagagcta gcacgagtct tgtttgaaag taaccaaaac 480

cgagatgcgc tcaatctgtt caatcaaatc aaatcaaaaa taccctcaca aaatccgaga 540

gctgctgggg tgattcgaac catcgacagc tttacccaag cgcttattgc tcgcgacagc 600

tggaacgggt ctgtggcgat tggcggttct tttaatgata acttaaacag ctcttctgaa 660

tcctatacct gcctagtgac atccaacaca ggtcagtgtc tctttgaccg tgttacgcct 720

aaaaaagaaa aagcatatgg gatcgatttt gaggcgagta tcaataaacg tttctctttg 780

tctcgacacc acggtattca tttacaaggc ctaacttatg gcactaacta cgggaacaac 840

agtgattaca atgaacatac ctctcgaatc ggctttggat acagttttca tgatcgcctc 900

aacaaagtat caatcggccc ctcttttgaa ctaagtcgtt acgcgaacag ctctgtttat 960

ttcagctcag gagtcaagtt agactggctt agaacaacca gccaaaacag tgcccttaaa 1020

ttcgagttca aagccgacta tcaagactac atcccaagtg tactcagcta tcaaacagac 1080

tggcagctgg cttcgtatct tacttattgg taccaattta atcatgacct attgttattc 1140

ggtggcatag actggacagg taaacagaac aaagaacaag tccatgctta cgagttatat 1200

ggcggtaaaa ttggcttgaa ttcagatgtg attccttggg ttgatctgac acttttgga 1260

tcgtttagac atcgtgacta ccaaggcttc aatagcattc tgagcgaaac gcgtagagat 1320

aaagagcaaa attacgcgat ctctgcttcg ctaaaagata tcaagttatt cggtgttacc 1380

ccttcattgg tttggaatca taaaagaata aaaagcaatg ttgattggct ctacacctac 1440

cagcaaagtg agatcactat caagttcact aggcgttttt aa 1482

<210> 652

<211> 493

<212> PRT

<213> V. fortis SLAM 1

<400> 652

Met Asn Ser Asn Thr Thr Pro Leu Ile Arg Cys Leu Leu Leu Ser Cys
1 5 10 15

Val Phe Ser Ser Pro Leu Ser Trp Ser Gln Asp Thr Asp Thr Gln Phe
20 25 30

Arg Ile Glu Gln Arg Asp Ala Leu Ser Ala Gln Asn Lys Glu Gln Ala
35 40 45

Ile Leu Glu Glu Glu Asn Gln Arg Glu Ala Ser Ser Pro Lys Pro Ala

50 55 60

Gln Thr Gly Tyr Gln Ile Asp Thr Asn Asp Val Ser Gln Val Ala Lys
65 70 75 80
Ala Leu His Leu Ala Val Arg Tyr Arg Gln Trp Val Gln Ala Asn Gln
85 90 95
Leu Leu Glu Ile Tyr Arg Gln Phe Glu Gln Pro Asp Pro Leu Leu Leu
100 105 110
Lys Tyr Ala Asp Gly Ala Ile Ser Arg Ala Lys Gly Tyr Leu Glu His

115 120 125

Ala Gln Leu Ala Phe Glu Asp Ala Leu Ala Leu Gln Pro Asn Phe Met
130 135 140
Pro Ala Gln Leu Glu Leu Ala Arg Val Leu Phe Glu Ser Asn Gln Asn
145 150 155 160
Arg Asp Ala Leu Asn Leu Phe Asn Gln Ile Lys Ser Lys Ile Pro Ser
165 170 175
Gln Asn Pro Arg Ala Ala Gly Val Ile Arg Thr Ile Asp Ser Phe Thr

180 185 190

Gln Ala Leu Ile Ala Arg Asp Ser Trp Asn Gly Ser Val Ala Ile Gly
195 200 205
Gly Ser Phe Asn Asp Asn Leu Asn Ser Ser Ser Glu Ser Tyr Thr Cys
210 215 220
Leu Val Thr Ser Asn Thr Gly Gln Cys Leu Phe Asp Arg Val Thr Pro
225 230 235 240
Lys Lys Glu Lys Ala Tyr Gly Ile Asp Phe Glu Ala Ser Ile Asn Lys

245 250 255

Arg Phe Ser Leu Ser Arg His His Gly Ile His Leu Gln Gly Leu Thr
260 265 270
Tyr Gly Thr Asn Tyr Gly Asn Asn Ser Asp Tyr Asn Glu His Thr Ser
275 280 285
Arg Ile Gly Phe Gly Tyr Ser Phe His Asp Arg Leu Asn Lys Val Ser

290 295 300

Ile Gly Pro Ser Phe Glu Leu Ser Arg Tyr Ala Asn Ser Ser Val Tyr

305 310 315 320

Phe Ser Ser Gly Val Lys Leu Asp Trp Leu Arg Thr Thr Ser Gln Asn

325 330 335

Ser Ala Leu Lys Phe Glu Phe Lys Ala Asp Tyr Gln Asp Tyr Ile Pro

340 345 350

Ser Val Leu Ser Tyr Gln Thr Asp Trp Gln Leu Ala Ser Tyr Leu Thr

355 360 365

Tyr Trp Tyr Gln Phe Asn His Asp Leu Leu Leu Phe Gly Gly Ile Asp

370 375 380

Trp Thr Gly Lys Gln Asn Lys Glu Gln Val His Ala Tyr Glu Leu Tyr

385 390 395 400

Gly Gly Lys Ile Gly Leu Asn Ser Asp Val Ile Pro Trp Val Asp Leu

405 410 415

Thr Leu Phe Gly Ser Phe Arg His Arg Asp Tyr Gln Gly Phe Asn Ser

420 425 430

Ile Leu Ser Glu Thr Arg Arg Asp Lys Glu Gln Asn Tyr Ala Ile Ser

435 440 445

Ala Ser Leu Lys Asp Ile Lys Leu Phe Gly Val Thr Pro Ser Leu Val

450 455 460

Trp Asn His Lys Arg Ile Lys Ser Asn Val Asp Trp Leu Tyr Thr Tyr

465 470 475 480

Gln Gln Ser Glu Ile Thr Ile Lys Phe Thr Arg Arg Phe

485 490

<210> 653

<211> 917

<212> DNA

<213> V. harveyi SLAM 1

<400> 653

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tttcccgttg tagccaatga ccaagatacg aatcttcgca ttcagcaaag agatgcgcta 120

tcagcacaag aaaaagaaaa gcgtctcctg caagaagaaa aagaactcga attacagagg 180

tcgaagcaag ctcaggaaca aagctcgtca gatcaaagca acgacaactt agggcaagcg 240

ctttacctag cagttaaagg aaagcaatgg tcacaagtag aagtactatt gaaccagtat 300

caatcttcac cctatgcaga tcctttactt atccattatg cccaaggcgg tctatcacgc 360

tatttaggtc gtttaagtga tgcagaggca gagtaccgat cgcttttatc cttatatccg 420

aattttcttc ccgctcagtt agagcttgct cgcgttttgt ttgagcgtaa gaaaaaccaa 480

gacgcacaca ccctttctc acaaatcaaa tctactctcc ctactgataa cccaagggct 540

gatggtgtca gacgtactct caatgccttt atatcagcac tagagcacag agatgcatgg 600

caaggtgcga tcagttttgg tccaactttc aatgacaatc tcaatagcag ctcagaaacc 660

tatacttgct tagtccgtca tgagacagga aagtgtttat ttgatcgagt cacaccggaa 720

aaacagagag cagcagggtt aacttttaac gcaagtgcga ataagcgcat tagcttcaaa 780

ggtcatcatg gtatgagttt gcaagcgctg acgtatggtt ctcgttacaa caatcacagt 840

gaatacaacg agcaaacagc gaatgttagc ttgggttaca gctttcaaga ccagcgtcat 900

agtatcttgg ttgcgcc 917

<210> 654

<211> 306

<212> PRT

<213> V. harveyi SLAM 1

<400> 654

Met Ala Val Arg Thr Ser Tyr Thr Ile Ala Leu Thr Ser Leu Leu Val
1 5 10 15

Pro Leu Phe Ser Phe Pro Val Val Ala Asn Asp Gln Asp Thr Asn Leu
20 25 30

Arg Ile Gln Gln Arg Asp Ala Leu Ser Ala Gln Glu Lys Glu Lys Arg
35 40 45

Leu Leu Gln Glu Glu Lys Glu Leu Glu Leu Gln Arg Ser Lys Gln Ala
50 55 60

Gln Glu Gln Ser Ser Ser Asp Gln Ser Asn Asp Asn Leu Gly Gln Ala
65 70 75 80

Leu Tyr Leu Ala Val Lys Gly Lys Gln Trp Ser Gln Val Glu Val Leu
85 90 95

Leu Asn Gln Tyr Gln Ser Ser Pro Tyr Ala Asp Pro Leu Leu Ile His

100 105 110

Tyr Ala Gln Gly Gly Leu Ser Arg Tyr Leu Gly Arg Leu Ser Asp Ala

115 120 125

Glu Ala Glu Tyr Arg Ser Leu Leu Ser Leu Tyr Pro Asn Phe Leu Pro

130 135 140

Ala Gln Leu Glu Leu Ala Arg Val Leu Phe Glu Arg Lys Lys Asn Gln

145 150 155 160

Asp Ala His Thr Leu Phe Ser Gln Ile Lys Ser Thr Leu Pro Thr Asp

165 170 175

Asn Pro Arg Ala Asp Gly Val Arg Arg Thr Leu Asn Ala Phe Ile Ser

180 185 190

Ala Leu Glu His Arg Asp Ala Trp Gln Gly Ala Ile Ser Phe Gly Pro

195 200 205

Thr Phe Asn Asp Asn Leu Asn Ser Ser Ser Glu Thr Tyr Thr Cys Leu

210 215 220

Val Arg His Glu Thr Gly Lys Cys Leu Phe Asp Arg Val Thr Pro Glu

225 230 235 240

Lys Gln Arg Ala Ala Gly Leu Thr Phe Asn Ala Ser Ala Asn Lys Arg

245 250 255

Ile Ser Phe Lys Gly His His Gly Met Ser Leu Gln Ala Leu Thr Tyr

260 265 270

Gly Ser Arg Tyr Asn Asn His Ser Glu Tyr Asn Glu Gln Thr Ala Asn

275 280 285

Val Ser Leu Gly Tyr Ser Phe Gln Asp Gln Arg His Ser Ile Leu Val

290 295 300

Ala Pro

305

<210> 655

<211> 1479

<212> DNA

<213> V. nigripulchritudo SLAM 1

<400> 655

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ttcagtgcac atacattagc cgatcaagac aaaaatcagc gtctgcagca acgggacgcc 120

ctttctgcgc tggaaaaaga gcaggaactg ttgaaagaag aacgggaaag agaagctgct 180

ttaactgtag atggtgtcac ctatgaagtg agcgacacat tagatgagct cggtcctgcc 240

ctgcatatcg cggtaaaaac aaggcaatgg gaacaagctc agggtttcct aatccgttat 300

aaagcgctgg aaggatacga tcccttgctg gtgcactacg ctcagggtgc gcttttcaga 360

attgagggaa aattaacaga atcggaagaa gaatatcagt ctcttcttgt cctcgctccg 420

gaattcatgc cagccaagct agagctggct agggtacagt ttgaaaacca aaaaaaccga 480

gattctctga atctgttccg agagatcaaa aacaacattc cacaggataa cccaagagca 540

gcaggtgtta tccggaccat tgatacgttc agcgaagcgc tcgaagtccg tgatagctgg 600

caaggggctt ttagctttgg tccttcttac agtgacaacc tgaatcgcac ctcggaaagc 660

tcggtatgcc tggcaacgct acctaacggg caatgctgga taagtcagac gacacccgac 720

aaagaatctg gctttgggat ggattatgac gccagcttaa acaaacgctt ctcgctgtcc 780

ggtcaccacg gcgtcaaatt taacgcattg gcgtatggat tgctgaatga cggcaagaaa 840

aagttcaacc aacacaccct gattaccggg ctcagttaca gctatcaaag cgccaagttt 900

cagttttcta tcggtccgca agccgaatac aacaactctg gcgatcgcac gctttacgtc 960

tctcccggat taaaactgga tggcttctac agcatcaata ataaaagcgc cgcaaaagta 1020

gaactgaaag ccgaatatca ggattacaaa gatccggatc tagaccacaa cagcgactgg 1080

ctatggacgg cttctggcac ttactggtat caattaccca aaagatggct tgtgtttggt 1140

ggcatagact ggaacaagaa gcaaagtgaa atagaactct ttgcctatga gtccctaggt 1200

gggcgactgg gtgtaaaccg cgctttcttt gacggctggg acatcagcgt attttcgtcg 1260

gtgaaagagc gaaagcacga cggattcaac aaagttctca acggaaaaag agaagacaaa 1320

gagcaaaacc acaccttgct cgtcactgca aaaccgctgg agttttgggg gctgacaccc 1380

acatttacct ggcaatacca aaaagtcgac agcacattgg atgcgatata cagctacagc 1440

caaaatgaat acagcattaa gctagagaaa cgtttttaa 1479

<210> 656

<211> 492

<212> PRT

<213> V. nigripulchritudo SLAM 1

<400> 656

Met Val Ile Pro Leu Leu Lys Ser Phe Leu Thr Leu Ser Pro Ile Ala
1 5 10 15
Leu Ala Phe Leu Phe Ser Ala His Thr Leu Ala Asp Gln Asp Lys Asn
20 25 30
Gln Arg Leu Gln Gln Arg Asp Ala Leu Ser Ala Leu Glu Lys Glu Gln
35 40 45
Glu Leu Leu Lys Glu Glu Arg Glu Arg Glu Ala Ala Leu Thr Val Asp
50 55 60

Gly Val Thr Tyr Glu Val Ser Asp Thr Leu Asp Glu Leu Gly Pro Ala
65 70 75 80
Leu His Ile Ala Val Lys Thr Arg Gln Trp Glu Gln Ala Gln Gly Phe
85 90 95
Leu Ile Arg Tyr Lys Ala Leu Glu Gly Tyr Asp Pro Leu Leu Val His
100 105 110
Tyr Ala Gln Gly Ala Leu Phe Arg Ile Glu Gly Lys Leu Thr Glu Ser
115 120 125

Glu Glu Glu Tyr Gln Ser Leu Leu Val Leu Ala Pro Glu Phe Met Pro
130 135 140
Ala Lys Leu Glu Leu Ala Arg Val Gln Phe Glu Asn Gln Lys Asn Arg
145 150 155 160
Asp Ser Leu Asn Leu Phe Arg Glu Ile Lys Asn Asn Ile Pro Gln Asp
165 170 175
Asn Pro Arg Ala Ala Gly Val Ile Arg Thr Ile Asp Thr Phe Ser Glu
180 185 190

Ala Leu Glu Val Arg Asp Ser Trp Gln Gly Ala Phe Ser Phe Gly Pro
195 200 205
Ser Tyr Ser Asp Asn Leu Asn Arg Thr Ser Glu Ser Ser Val Cys Leu
210 215 220
Ala Thr Leu Pro Asn Gly Gln Cys Trp Ile Ser Gln Thr Thr Pro Asp
225 230 235 240
Lys Glu Ser Gly Phe Gly Met Asp Tyr Asp Ala Ser Leu Asn Lys Arg

245 250 255

Phe Ser Leu Ser Gly His His Gly Val Lys Phe Asn Ala Leu Ala Tyr
260 265 270
Gly Leu Leu Asn Asp Gly Lys Lys Lys Phe Asn Gln His Thr Leu Ile
275 280 285
Thr Gly Leu Ser Tyr Ser Tyr Gln Ser Ala Lys Phe Gln Phe Ser Ile
290 295 300
Gly Pro Gln Ala Glu Tyr Asn Asn Ser Gly Asp Arg Thr Leu Tyr Val
305 310 315 320

Ser Pro Gly Leu Lys Leu Asp Gly Phe Tyr Ser Ile Asn Asn Lys Ser
325 330 335
Ala Ala Lys Val Glu Leu Lys Ala Glu Tyr Gln Asp Tyr Lys Asp Pro
340 345 350
Asp Leu Asp His Asn Ser Asp Trp Leu Trp Thr Ala Ser Gly Thr Tyr
355 360 365
Trp Tyr Gln Leu Pro Lys Arg Trp Leu Val Phe Gly Gly Ile Asp Trp
370 375 380

Asn Lys Lys Gln Ser Glu Ile Glu Leu Phe Ala Tyr Glu Ser Leu Gly
385 390 395 400
Gly Arg Leu Gly Val Asn Arg Ala Phe Phe Asp Gly Trp Asp Ile Ser
405 410 415
Val Phe Ser Ser Val Lys Glu Arg Lys His Asp Gly Phe Asn Lys Val
420 425 430
Leu Asn Gly Lys Arg Glu Asp Lys Glu Gln Asn His Thr Leu Leu Val
435 440 445

Thr Ala Lys Pro Leu Glu Phe Trp Gly Leu Thr Pro Thr Phe Thr Trp
450 455 460
Gln Tyr Gln Lys Val Asp Ser Thr Leu Asp Ala Ile Tyr Ser Tyr Ser
465 470 475 480
Gln Asn Glu Tyr Ser Ile Lys Leu Glu Lys Arg Phe
485 490

<210> 657

<211> 1473

<212> DNA

<213> V. sinaloensis SLAM 1

<400> 657

atgactcgcc actacaccac ttcactgctt atgttatgca gtattccctt ttcaactcac 60

ctttacgcag acgcgcaaga tactcgctta agaattgagc agcaagatgc cttaaccgcg 120

caaaaaaaag aaagcaaaat acttgaagaa gaacgagaaa aggaacaagc taacacccag 180

ccagcgaccc ctttaaatat cgacctcaat gacccaaatc aagtcgctca agccctctat 240

ctatccgtca agaatcaaca gtgggattct gttgaagacc ttcttgacct atatcgtcaa 300

tttgaacacg ccgatccgtt acttgtgcat tacgctcaag gtggtgttta ccgcgtcaaa 360

ggtgagctaa ccaaagctga gcaagagtac acggcattac ttgtctatca agccgacttt 420

ttacctgcaa aactagagct cgctcgagtc ttgtttgaaa acaacaaaaa ctctgatgcg 480

caaagcctgt ttgacgaaat agcgctcgca ctacccgctg ataacccacg ttctgaaggt 540

gtacgaaaaa ccattgatgc cttcacttta gcgctaaaca ctcgagatgc ttggagcggc 600

tcattcagcc taggcccttc ttttaacgac aacctaaaca gttcatccga aagctacact 660

tgcctgctgc gcgacaacgt cggtcaatgc attatcgata gagtgactcc agacaaagag 720

cgagcatacg gacttgatta tgaggccagc ttaaacaaac gcttctcctt atccgggcac 780

cacggcattg ttgtacaagg acaaacctac ggcagccagt accgtcacca tgaagattac 840

aacgaaaaca cctcacgtat cgctctcggt tacagctatc acagtcaagc tcatcgcatt 900

tcgctctcac ctcagttcga atacaacggg tttggaggca agactctcta tttgggttcg 960

gccgtcaaag tcgattggct cgcgacgctc aatcgccaaa gtgcgataaa atttgagaca 1020

aaagcagagt atcaagacta tttacctaag caacttcact atcaatcaga ttggcaattt 1080

tcttcccttg cgaccatttg gtatcagaca tcgaataagt ggctactttt tggaggtgta 1140

gactggacag acaaacgcaa caagcaaagc gtccacgcgt atcaggttgt tggcgctcgc 1200

gttggtgtca acaaatccat tgactcacta atagatgcca gtctttttgc gtctttcaga 1260

gaccgacgtt accaagcgtt tagcgccctc ttagatgaga agcgtcatga ccaagaacag 1320

aattacacct taattttgtc ctctcccgtg ttcaatttct atggcatcac accttcatta 1380

agttggaccc acaagcgagt agaaagtaac gtagactggc tttacaccta ccagcaaaat 1440

gaagtgtcac ttaagctggt caaaagattt taa 1473

<210> 658

<211> 490

<212> PRT

<213> V. sinaloensis SLAM 1

<400> 658

Met Thr Arg His Tyr Thr Thr Ser Leu Leu Met Leu Cys Ser Ile Pro
1 5 10 15

Phe Ser Thr His Leu Tyr Ala Asp Ala Gln Asp Thr Arg Leu Arg Ile
20 25 30

Glu Gln Gln Asp Ala Leu Thr Ala Gln Lys Lys Glu Ser Lys Ile Leu
35 40 45

Glu Glu Glu Arg Glu Lys Glu Gln Ala Asn Thr Gln Pro Ala Thr Pro
50 55 60

Leu Asn Ile Asp Leu Asn Asp Pro Asn Gln Val Ala Gln Ala Leu Tyr
65 70 75 80

Leu Ser Val Lys Asn Gln Gln Trp Asp Ser Val Glu Asp Leu Leu Asp
85 90 95

Leu Tyr Arg Gln Phe Glu His Ala Asp Pro Leu Leu Val His Tyr Ala
100 105 110

Gln Gly Gly Val Tyr Arg Val Lys Gly Glu Leu Thr Lys Ala Glu Gln
115 120 125

Glu Tyr Thr Ala Leu Leu Val Tyr Gln Ala Asp Phe Leu Pro Ala Lys
130 135 140

Leu Glu Leu Ala Arg Val Leu Phe Glu Asn Asn Lys Asn Ser Asp Ala
145 150 155 160

Gln Ser Leu Phe Asp Glu Ile Ala Leu Ala Leu Pro Ala Asp Asn Pro
165 170 175

Arg Ser Glu Gly Val Arg Lys Thr Ile Asp Ala Phe Thr Leu Ala Leu
180 185 190

Asn Thr Arg Asp Ala Trp Ser Gly Ser Phe Ser Leu Gly Pro Ser Phe
195 200 205

Asn Asp Asn Leu Asn Ser Ser Ser Glu Ser Tyr Thr Cys Leu Leu Arg

210 215 220

Asp Asn Val Gly Gln Cys Ile Ile Asp Arg Val Thr Pro Asp Lys Glu

225 230 235 240

Arg Ala Tyr Gly Leu Asp Tyr Glu Ala Ser Leu Asn Lys Arg Phe Ser

245 250 255

Leu Ser Gly His His Gly Ile Val Val Gln Gly Gln Thr Tyr Gly Ser

260 265 270

Gln Tyr Arg His His Glu Asp Tyr Asn Glu Asn Thr Ser Arg Ile Ala

275 280 285

Leu Gly Tyr Ser Tyr His Ser Gln Ala His Arg Ile Ser Leu Ser Pro

290 295 300

Gln Phe Glu Tyr Asn Gly Phe Gly Gly Lys Thr Leu Tyr Leu Gly Ser

305 310 315 320

Ala Val Lys Val Asp Trp Leu Ala Thr Leu Asn Arg Gln Ser Ala Ile

325 330 335

Lys Phe Glu Thr Lys Ala Glu Tyr Gln Asp Tyr Leu Pro Lys Gln Leu

340 345 350

His Tyr Gln Ser Asp Trp Gln Phe Ser Ser Leu Ala Thr Ile Trp Tyr

355 360 365

Gln Thr Ser Asn Lys Trp Leu Leu Phe Gly Gly Val Asp Trp Thr Asp

370 375 380

Lys Arg Asn Lys Gln Ser Val His Ala Tyr Gln Val Val Gly Ala Arg

385 390 395 400

Val Gly Val Asn Lys Ser Ile Asp Ser Leu Ile Asp Ala Ser Leu Phe

405 410 415

Ala Ser Phe Arg Asp Arg Arg Tyr Gln Ala Phe Ser Ala Leu Leu Asp

420 425 430

Glu Lys Arg His Asp Gln Glu Gln Asn Tyr Thr Leu Ile Leu Ser Ser

435 440 445

Pro Val Phe Asn Phe Tyr Gly Ile Thr Pro Ser Leu Ser Trp Thr His

450 455 460

Lys Arg Val Glu Ser Asn Val Asp Trp Leu Tyr Thr Tyr Gln Gln Asn

465 470 475 480

Glu Val Ser Leu Lys Leu Val Lys Arg Phe

485 490

<210> 659

<211> 1539

<212> DNA

<213> V. splendidus SLAM 1

<400> 659

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agcgcattag tcagtttgcc gagcgtggca tctaaccctg atactagcct tcgaattgaa 120

caacaagatg cgctatcggc agtcgaaaaa gaaaacgcta ttttagctga agaaatgcaa 180

gatgaagaac agcgacaaaa cgcgcagcaa tcatcttcta atttaattga cccttcaata 240

gcggatcctg agtcaacgtt cagcatagat ctttcggatt caaaccaagt cgcccaagcc 300

ttgcaccttt ctgctcagca gcataattgg ggcttagctc agcaactact cagccattat 360

cagctattcg ataacgcaga cccgctgctt attcattatg tgcgtggtgg tatttatcgt 420

tcacaaggtg acctaaaacg tgcacaagag gaatacactc agttaatcac gttacaaccc 480

aactttatgc cagcgcaatt agaactagca cgcgttctat tcgaaaacca caacaactca 540

gagtcattag aattattcaa acaaattgaa gcttcactcc catctaacaa ccctcgaact 600

caaggtattc aacgaaccat agatgtattt tcaagtgcgc ttaaagctcg tgatgactgg 660

ggcggttcca ttagtttcgg gccatcgttt aatgacaatc taaacagctc ttccgaaagc 720

tacacatgtt tagttcatag cgatattggg caatgcatca tcgatagagt caccccaaaa 780

aagcaacagg cttttggtat cgattatgaa gcgagcttaa ataaacgaac ctcactcact 840

ggtcatcatg gcgtttcttt tagtgggctt acctacggca ctcgttattc aggtcatgac 900

gaatatgatg agcaaaccgt aaaagcgagc tttgggtaca gttatcagag ccaaagagat 960

cgcgtgtcct tcgcaccaca atttgagttc aatacgtttg caggaaaaag cctgtattta 1020

agttctggaa tcaaactgga ttggttcaaa accgtaaaca aacaaagtgc atttaaattc 1080

gaaaccaaag ctgattatca aaactatcaa ccaggaaaac tggattatca gtctgattgg 1140

caattctcaa ccttgttcac ttattggtat caattacctg aaaaatggtt gttatttgga 1200

ggcttggact ggacagataa acgaaatgat caacaagttc atgcttatac tttgtctggc 1260

gttcgacttg gggttaataa aaacgtcagc ccatggttag atatcagtct atttgcttct 1320

ttgagagatc gccgatatca agatttcagt gctttacttg gagataagcg acatgacaga 1380

gaacaaaatt acaccttagt cattcactca ccaagtattg agtatttagg cgtgtctccc 1440

acccttagct ggactcataa acgagtgaaa agcaatattg actggcttta tacttaccaa 1500

cagaatgaaa tcggcttaaa gctcactaaa cgcttctag 1539

<210> 660

<211> 512

<212> PRT

<213> V. splendidus SLAM 1

<400> 660

Met Lys Leu Asn Leu Pro Gln Arg Leu Phe Leu Pro Leu Ile Ser Phe
1 5 10 15

Val Ala Ile Pro Ser Ala Leu Val Ser Leu Pro Ser Val Ala Ser Asn
20 25 30

Pro Asp Thr Ser Leu Arg Ile Glu Gln Gln Asp Ala Leu Ser Ala Val
35 40 45

Glu Lys Glu Asn Ala Ile Leu Ala Glu Glu Met Gln Asp Glu Glu Gln
50 55 60

Arg Gln Asn Ala Gln Gln Ser Ser Ser Asn Leu Ile Asp Pro Ser Ile
65 70 75 80

Ala Asp Pro Glu Ser Thr Phe Ser Ile Asp Leu Ser Asp Ser Asn Gln
85 90 95

Val Ala Gln Ala Leu His Leu Ser Ala Gln Gln His Asn Trp Gly Leu
100 105 110

Ala Gln Gln Leu Leu Ser His Tyr Gln Leu Phe Asp Asn Ala Asp Pro
115 120 125

Leu Leu Ile His Tyr Val Arg Gly Gly Ile Tyr Arg Ser Gln Gly Asp
130 135 140

Leu Lys Arg Ala Gln Glu Glu Tyr Thr Gln Leu Ile Thr Leu Gln Pro
145 150 155 160

Asn Phe Met Pro Ala Gln Leu Glu Leu Ala Arg Val Leu Phe Glu Asn
165 170 175

His Asn Asn Ser Glu Ser Leu Glu Leu Phe Lys Gln Ile Glu Ala Ser
180 185 190
Leu Pro Ser Asn Asn Pro Arg Thr Gln Gly Ile Gln Arg Thr Ile Asp
195 200 205
Val Phe Ser Ser Ala Leu Lys Ala Arg Asp Asp Trp Gly Gly Ser Ile
210 215 220
Ser Phe Gly Pro Ser Phe Asn Asp Asn Leu Asn Ser Ser Ser Glu Ser
225 230 235 240

Tyr Thr Cys Leu Val His Ser Asp Ile Gly Gln Cys Ile Ile Asp Arg
245 250 255
Val Thr Pro Lys Lys Gln Gln Ala Phe Gly Ile Asp Tyr Glu Ala Ser
260 265 270
Leu Asn Lys Arg Thr Ser Leu Thr Gly His His Gly Val Ser Phe Ser
275 280 285
Gly Leu Thr Tyr Gly Thr Arg Tyr Ser Gly His Asp Glu Tyr Asp Glu
290 295 300

Gln Thr Val Lys Ala Ser Phe Gly Tyr Ser Tyr Gln Ser Gln Arg Asp
305 310 315 320
Arg Val Ser Phe Ala Pro Gln Phe Glu Phe Asn Thr Phe Ala Gly Lys
325 330 335
Ser Leu Tyr Leu Ser Ser Gly Ile Lys Leu Asp Trp Phe Lys Thr Val
340 345 350
Asn Lys Gln Ser Ala Phe Lys Phe Glu Thr Lys Ala Asp Tyr Gln Asn
355 360 365

Tyr Gln Pro Gly Lys Leu Asp Tyr Gln Ser Asp Trp Gln Phe Ser Thr
370 375 380
Leu Phe Thr Tyr Trp Tyr Gln Leu Pro Glu Lys Trp Leu Leu Phe Gly
385 390 395 400
Gly Leu Asp Trp Thr Asp Lys Arg Asn Asp Gln Gln Val His Ala Tyr
405 410 415
Thr Leu Ser Gly Val Arg Leu Gly Val Asn Lys Asn Val Ser Pro Trp

420 425 430

Leu Asp Ile Ser Leu Phe Ala Ser Leu Arg Asp Arg Arg Tyr Gln Asp
435 440 445
Phe Ser Ala Leu Leu Gly Asp Lys Arg His Asp Arg Glu Gln Asn Tyr
450 455 460
Thr Leu Val Ile His Ser Pro Ser Ile Glu Tyr Leu Gly Val Ser Pro
465 470 475 480
Thr Leu Ser Trp Thr His Lys Arg Val Lys Ser Asn Ile Asp Trp Leu
485 490 495

Tyr Thr Tyr Gln Gln Asn Glu Ile Gly Leu Lys Leu Thr Lys Arg Phe
500 505 510

<210> 661
<211> 1176
<212> DNA
<213> Vibrio cholerae MZO-3 SLAM 1
<400> 661

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gttctttttgg cttgtcaacc tgtggtatgc aaagagaaga atgagcttga tgatacagta 120
cttaatgctc aaagatatct tgttgagaat aatattaagg ccgcactttc tattctggaa 180
aatgctatat taaaatatcc taaaaataac gtgctaagac ttcagtttgc tattgcttta 240

tataaaaata aatcttatga ggattctctt aaccaattgt ttaaattaaa gtctatggag 300
gaggactctc aggttttaga aaaaatagat atgtatatag ataggattaa taatattaaa 360
agaacaacat acgattttca tttttcatac gaagtagatg ataatgtttt taattatcct 420
agggggggaat ttaatggttg gcatttttct gaacccaaaa aggataatta tattaattat 480
ttttttttcat tggaaaatat taatcctatt tttaaaaatg ttagttttaa aaacaatctt 540
ttaatttatg gaagagagta caaagatatc aaagagaaaa attatgtttc atttaaatta 600
aaatcaggtt tacactatgc agattttaat attgcttact cgatacaacc tttagttgag 660

tttaaagata gttaccaaga aaatattttt ttcttaggtg cttatgtata cttttcaact 720
gtttttgata gaaataaaaa gtttaatatc catatggaga aaaaatggga tatcgagcat 780
catgataatt ccaatctgtt aaattttggt tatttgcaaa atatatcgcc atggagttat 840
atttatcttg attttggtag gagttatttt gttggtaata atgtaatagg ttctaatgat 900

tattttagat tggggtggag ttatgattgg gatattggaa tatctacact tatgagttgt 960

ggcttttcat atagaaaatc taatactata gatattttta aagttaaacc aaaatcatat 1020

gaatatgaac ctgagcttgt tgtatggtat cgcccattat ccttgtatgg catagtgcca 1080

aaaataaaag tttcctttat aaaaagtaag agtaatcatc ctgcgtttaa cttttcaaaa 1140

agaaatattt ctctttttat tacaaaaaca ttttaa 1176

<210> 662

<211> 388

<212> PRT

<213> Vibrio cholerae MZO-3 SLAM 1

<400> 662

Met Val Val Asn Ile Met Lys Gly Lys Cys Ile Leu Ile Val Phe Thr
1 5 10 15

Leu Val Leu Leu Ala Cys Gln Pro Val Val Cys Lys Glu Lys Asn Glu
20 25 30

Leu Asp Asp Thr Val Leu Asn Ala Gln Arg Tyr Leu Val Glu Asn Asn
35 40 45

Ile Lys Ala Ala Leu Ser Ile Leu Glu Asn Ala Ile Leu Lys Tyr Pro
50 55 60

Lys Asn Asn Val Leu Arg Leu Gln Phe Ala Ile Ala Leu Tyr Lys Asn
65 70 75 80

Lys Ser Tyr Glu Asp Ser Leu Asn Gln Leu Phe Lys Leu Lys Ser Met
85 90 95

Glu Glu Asp Ser Gln Val Leu Glu Lys Ile Asp Met Tyr Ile Asp Arg
100 105 110

Ile Asn Asn Ile Lys Arg Thr Thr Tyr Asp Phe His Phe Ser Tyr Glu
115 120 125

Val Asp Asp Asn Val Phe Asn Tyr Pro Arg Gly Glu Phe Asn Gly Trp
130 135 140

His Phe Ser Glu Pro Lys Lys Asp Asn Tyr Ile Asn Tyr Phe Phe Ser
145 150 155 160

Leu Glu Asn Ile Asn Pro Ile Phe Lys Asn Val Ser Phe Lys Asn Asn

165 170 175

Leu Leu Ile Tyr Gly Arg Glu Tyr Lys Asp Ile Lys Glu Lys Asn Tyr

180 185 190

Val Ser Phe Lys Leu Lys Ser Gly Leu His Tyr Ala Asp Phe Asn Ile

195 200 205

Ala Tyr Ser Ile Gln Pro Leu Val Glu Phe Lys Asp Ser Tyr Gln Glu

210 215 220

Asn Ile Phe Phe Leu Gly Ala Tyr Val Tyr Phe Ser Thr Val Phe Asp

225 230 235 240

Arg Asn Lys Lys Phe Asn Ile His Met Glu Lys Lys Trp Asp Ile Glu

245 250 255

His His Asp Asn Ser Asn Leu Leu Asn Phe Gly Tyr Leu Gln Asn Ile

260 265 270

Ser Pro Trp Ser Tyr Ile Tyr Leu Asp Phe Gly Arg Ser Tyr Phe Val

275 280 285

Gly Asn Asn Val Ile Gly Ser Asn Asp Tyr Phe Arg Leu Gly Trp Ser

290 295 300

Tyr Asp Trp Asp Ile Gly Ile Ser Thr Leu Met Ser Cys Gly Phe Ser

305 310 315 320

Tyr Arg Lys Ser Asn Thr Ile Asp Ile Phe Lys Val Lys Pro Lys Ser

325 330 335

Tyr Glu Tyr Glu Pro Glu Leu Val Val Trp Tyr Arg Pro Leu Ser Leu

340 345 350

Tyr Gly Ile Val Pro Lys Ile Lys Val Ser Phe Ile Lys Ser Lys Ser

355 360 365

Asn His Pro Ala Phe Asn Phe Ser Lys Arg Asn Ile Ser Leu Phe Ile

370 375 380

Thr Lys Thr Phe

385

<210> 663

<211> 1479

<212> DNA

<213> Vibrio sp. B183 SLAM 1

<400> 663

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tctttctctt acgcggatca ggataccgat ttgcgtatcc agcaacgtga cgcgttatcc 120

tcccgtcaga acgaaaatgc tcttattgaa gaagagttgg aaaaagaacg cctagccgag 180

caatcggcgt caggctcaga atcgatcgta gcgaataccg cagatgagct tggaccggca 240

ttgcatgtcg cggttcggca gcgtcaatgg gcactggcag agagtctgct ggaaaggtat 300

atggcgttgg cggattttga tcctatgttg gtgcactacg catcgggggc attggcacgc 360

aatgcgcgtg attatgatcg ggcagaaacg cactacgcga cattgcttga gatgcaggaa 420

aacttttac ccgcagagtt agagttagct cgcgtctggt ttgaagacag agaaaacagc 480

gcctctatat cattatttca tgacatcctc agtcgcttac ctgctgataa cccgagagcg 540

gcgggagtcc ggaatactgt agaaagtttt gttagtgcac tggagtatcg tgatgagtgg 600

caaggtgcat tttcatttgg gccgacttac aacgacaacc tgaatttgtc ctcgaaacac 660

tatgaatgtc tggtctattt caccaatggt cagtgctttt tagagcgtag cgcgcccaag 720

gttaaatctg cctatggtat tgactacgac gccagtttaa atcgacgctt ttcgcttagt 780

ggtcatcatg gcttgcagct acgcagcttt gcctatggca ccaattacca gaaccgcaaa 840

gaacataacg agcagacgtt aaacgtgacc tttggttaca gctatcagac cgctaaacat 900

cagctcagta ttgcgccgca gtttgaatat cgcgccttag cgaatcaggc gttgtttgct 960

tcgggcggct tcaaggcgga ttggtttgcc aatcttagcc agacttctgc tatgaaactc 1020

gaagtggaag gggaatatct cgattatcgt aatcagacct ttcgctatca atccgactgg 1080

caatggtctg tctttggcac ttactggcat cagttacccg acaaatggtt agtgtttggt 1140

ggtgtagact ggacactgaa acaaaaccga caggcggtgc atgagtacga tttgtgggga 1200

ggtcgattgg gcgtgaataa aaccttcaca tcgctgaata ctgacgtgac cttattcgct 1260

tcgttgcggc aacgtattta tggtgacttc aatgcggtgc tcggtgagcg gcgtgatgat 1320

actgagcaaa attatacctt agtggtgact ctgccagagc tgtttgccgg gtttaaaccg 1380

ctcatcgaag tcaaagccaa tcagaccaag agtaatgttg attgggcata cagctacaag 1440

cagcatcaat acagcgtaaa actagaaaaa agattctga 1479

<210> 664

<211> 492

<212> PRT

<213> Vibrio sp. B183 SLAM 1

<400> 664

Met Lys Ile Asp Arg Asn Phe Ile Leu Gly Ser Leu Leu Met Val Ser
1 5 10 15

Val Ser Tyr Ser Ser Phe Ser Tyr Ala Asp Gln Asp Thr Asp Leu Arg
20 25 30

Ile Gln Gln Arg Asp Ala Leu Ser Ser Arg Gln Asn Glu Asn Ala Leu
35 40 45

Ile Glu Glu Glu Leu Glu Lys Glu Arg Leu Ala Glu Gln Ser Ala Ser
50 55 60

Gly Ser Glu Ser Ile Val Ala Asn Thr Ala Asp Glu Leu Gly Pro Ala
65 70 75 80

Leu His Val Ala Val Arg Gln Arg Gln Trp Ala Leu Ala Glu Ser Leu
85 90 95

Leu Glu Arg Tyr Met Ala Leu Ala Asp Phe Asp Pro Met Leu Val His
100 105 110

Tyr Ala Ser Gly Ala Leu Ala Arg Asn Ala Arg Asp Tyr Asp Arg Ala
115 120 125

Glu Thr His Tyr Ala Thr Leu Leu Glu Met Gln Glu Asn Phe Leu Pro
130 135 140

Ala Glu Leu Glu Leu Ala Arg Val Trp Phe Glu Asp Arg Glu Asn Ser
145 150 155 160

Ala Ser Ile Ser Leu Phe His Asp Ile Leu Ser Arg Leu Pro Ala Asp
165 170 175

Asn Pro Arg Ala Ala Gly Val Arg Asn Thr Val Glu Ser Phe Val Ser
180 185 190

Ala Leu Glu Tyr Arg Asp Glu Trp Gln Gly Ala Phe Ser Phe Gly Pro
195 200 205

Thr Tyr Asn Asp Asn Leu Asn Leu Ser Ser Lys His Tyr Glu Cys Leu
210 215 220

Val Tyr Phe Thr Asn Gly Gln Cys Phe Leu Glu Arg Ser Ala Pro Lys
225 230 235 240

Val Lys Ser Ala Tyr Gly Ile Asp Tyr Asp Ala Ser Leu Asn Arg Arg
245 250 255

Phe Ser Leu Ser Gly His His Gly Leu Gln Leu Arg Ser Phe Ala Tyr
260 265 270

Gly Thr Asn Tyr Gln Asn Arg Lys Glu His Asn Glu Gln Thr Leu Asn
275 280 285

Val Thr Phe Gly Tyr Ser Tyr Gln Thr Ala Lys His Gln Leu Ser Ile
290 295 300

Ala Pro Gln Phe Glu Tyr Arg Ala Leu Ala Asn Gln Ala Leu Phe Ala
305 310 315 320

Ser Gly Gly Phe Lys Ala Asp Trp Phe Ala Asn Leu Ser Gln Thr Ser
325 330 335

Ala Met Lys Leu Glu Val Glu Gly Glu Tyr Leu Asp Tyr Arg Asn Gln
340 345 350

Thr Phe Arg Tyr Gln Ser Asp Trp Gln Trp Ser Val Phe Gly Thr Tyr
355 360 365

Trp His Gln Leu Pro Asp Lys Trp Leu Val Phe Gly Gly Val Asp Trp
370 375 380

Thr Leu Lys Gln Asn Arg Gln Ala Val His Glu Tyr Asp Leu Trp Gly
385 390 395 400

Gly Arg Leu Gly Val Asn Lys Thr Phe Thr Ser Leu Asn Thr Asp Val
405 410 415

Thr Leu Phe Ala Ser Leu Arg Gln Arg Ile Tyr Gly Asp Phe Asn Ala
420 425 430

Val Leu Gly Glu Arg Arg Asp Asp Thr Glu Gln Asn Tyr Thr Leu Val
435 440 445

Val Thr Leu Pro Glu Leu Phe Ala Gly Phe Lys Pro Leu Ile Glu Val
450 455 460

Lys Ala Asn Gln Thr Lys Ser Asn Val Asp Trp Ala Tyr Ser Tyr Lys
465 470 475 480

Gln His Gln Tyr Ser Val Lys Leu Glu Lys Arg Phe
485 490

<210> 665

<

211> 1479

<212> DNA

<213> Vibrio sp. HENC-01 SLAM 1

<400> 665

atggcggtta gaacctctta caccatcgct ctgacatccc tgttagtgcc gttgttttct 60

tttcccgttg tagccaatga ccaagatacg aatcttcgca ttcagcaaag agatgcgcta 120

tcagcacaag aaaaagaaaa gcgtctcctg caagaagaaa aagaactcga attacagagg 180

tcgaagcaag ctcaggaaca aagctcgtca gatcaaagca acgacaactt agggcaagcg 240

ctttacctag cagttaaagg aaagcaatgg tcacaagtag aagtactatt gaaccagtat 300

caatcttcac cctatgcaga tcctttactt atccattatg cccaaggcgg tctatcacgc 360

tatttaggtc gtttaagtga tgcagaggca gagtaccgat cgcttttatc cttatatccg 420

aattttcttc ccgctcagtt agagcttgct cgcgttttgt ttgagcgtaa gaaaaaccaa 480

gacgcacaca ccctttctc acaaatcaaa tctactctcc ctactgataa cccaagggct 540

gatggtgtca gacgtactct cgatgctttt atatcagcac tagaacacag agatgcatgg 600

caaggtgcga tcagttttgg tccaactttc aatgacaatc tcaatagcag ctcagaaacc 660

tatacttgct tagtccgtca tgagacagga aagtgtttat ttgatcgagt cacaccggaa 720

aaacagagag cagcagggtt aacttttaac gcaagtgcga ataagcgcat tagcttcaaa 780

ggtcatcatg gtatgagttt gcaagcgctg acgtatggtt ctcgttacaa caatcacagt 840

gaatacaacg agcaaacagc gaatgttagc ttgggttaca gctttcaaga ccagcgtcat 900

agtatcttgg ttgcgtcgtt gatcgagtac agcacatacg cggataagag tttgtattgg 960

tcaacaggtc taaagttgaa tggattccat agcttagact cgaaaagcgc attgagatgg 1020

gaactaaaag gcgaatacca atattaccgt ccaacaaagc tcgactatca atcagattgg 1080

caatggaatg caagcatcaa ctattggcac cagttgccac aacaatggct cgcattcggt 1140

ggcatagact ggacgcataa acaaaatgat caagatgtac atgcttacca gctctatggt 1200

ggtcgaatcg gagtcgtgaa aagcgtcgaa ggttggcttg acgctaacct gtttgcatca 1260

ctgcgagaaa ggcaatacga gggatataac gccctactcg atgcaaagag aagagacaca 1320

gagcaaaact atactgtcac attttcctct ccaaagttgg ttttttggac gttgacaccc 1380

attctagagt ggactcataa acgggtaaac agcaacgttg attggctgta cacctatcag 1440

cagaatgagg tgagcgtaaa atttgaaaag cgtttttga 1479

<210> 666

<211> 492

<212> PRT

<213> Vibrio sp. HENC-01 SLAM 1

<400> 666

Met Ala Val Arg Thr Ser Tyr Thr Ile Ala Leu Thr Ser Leu Leu Val

1 5 10 15

Pro Leu Phe Ser Phe Pro Val Val Ala Asn Asp Gln Asp Thr Asn Leu

20 25 30

Arg Ile Gln Gln Arg Asp Ala Leu Ser Ala Gln Glu Lys Glu Lys Arg

35 40 45

Leu Leu Gln Glu Glu Lys Glu Leu Glu Leu Gln Arg Ser Lys Gln Ala

50 55 60

Gln Glu Gln Ser Ser Ser Asp Gln Ser Asn Asp Asn Leu Gly Gln Ala

65 70 75 80

Leu Tyr Leu Ala Val Lys Gly Lys Gln Trp Ser Gln Val Glu Val Leu

85 90 95

Leu Asn Gln Tyr Gln Ser Ser Pro Tyr Ala Asp Pro Leu Leu Ile His

100 105 110

Tyr Ala Gln Gly Gly Leu Ser Arg Tyr Leu Gly Arg Leu Ser Asp Ala

115 120 125

Glu Ala Glu Tyr Arg Ser Leu Leu Ser Leu Tyr Pro Asn Phe Leu Pro

130 135 140

Ala Gln Leu Glu Leu Ala Arg Val Leu Phe Glu Arg Lys Lys Asn Gln

145 150 155 160

Asp Ala His Thr Leu Phe Ser Gln Ile Lys Ser Thr Leu Pro Thr Asp

165 170 175

Asn Pro Arg Ala Asp Gly Val Arg Arg Thr Leu Asp Ala Phe Ile Ser

180 185 190

Ala Leu Glu His Arg Asp Ala Trp Gln Gly Ala Ile Ser Phe Gly Pro

195 200 205

Thr Phe Asn Asp Asn Leu Asn Ser Ser Ser Glu Thr Tyr Thr Cys Leu

210 215 220

Val Arg His Glu Thr Gly Lys Cys Leu Phe Asp Arg Val Thr Pro Glu

225 230 235 240

Lys Gln Arg Ala Ala Gly Leu Thr Phe Asn Ala Ser Ala Asn Lys Arg

245 250 255

Ile Ser Phe Lys Gly His His Gly Met Ser Leu Gln Ala Leu Thr Tyr

260 265 270

Gly Ser Arg Tyr Asn Asn His Ser Glu Tyr Asn Glu Gln Thr Ala Asn

275 280 285

Val Ser Leu Gly Tyr Ser Phe Gln Asp Gln Arg His Ser Ile Leu Val

290 295 300

Ala Ser Leu Ile Glu Tyr Ser Thr Tyr Ala Asp Lys Ser Leu Tyr Trp

305 310 315 320

Ser Thr Gly Leu Lys Leu Asn Gly Phe His Ser Leu Asp Ser Lys Ser

325 330 335

Ala Leu Arg Trp Glu Leu Lys Gly Glu Tyr Gln Tyr Tyr Arg Pro Thr

340 345 350

Lys Leu Asp Tyr Gln Ser Asp Trp Gln Trp Asn Ala Ser Ile Asn Tyr

355 360 365

Trp His Gln Leu Pro Gln Gln Trp Leu Ala Phe Gly Gly Ile Asp Trp

370 375 380

Thr His Lys Gln Asn Asp Gln Asp Val His Ala Tyr Gln Leu Tyr Gly

385 390 395 400

Gly Arg Ile Gly Val Val Lys Ser Val Glu Gly Trp Leu Asp Ala Asn

405 410 415

Leu Phe Ala Ser Leu Arg Glu Arg Gln Tyr Glu Gly Tyr Asn Ala Leu

420 425 430

Leu Asp Ala Lys Arg Arg Asp Thr Glu Gln Asn Tyr Thr Val Thr Phe

435 440 445

Ser Ser Pro Lys Leu Val Phe Trp Thr Leu Thr Pro Ile Leu Glu Trp

450 455 460

Thr His Lys Arg Val Asn Ser Asn Val Asp Trp Leu Tyr Thr Tyr Gln

465 470 475 480

Gln Asn Glu Val Ser Val Lys Phe Glu Lys Arg Phe

485 490

<210> 667

<211> 687

<212> DNA

<213> Vibrio sp. HENC-02 SLAM 1

<400> 667

atgagtttgc aagcgctgac gtatggttct cgttacaaca atcacagtga atacaacgag 60

caaacagcga atgttagctt tggttatagc tttcaagacc agcgtcatag tatcttggtt 120

gcgccgttga tcgagtacag ctcatacgcg gataagagtt tgtattggtc aacaggtcta 180

aagttgaatg gattccatag cttagactcg aaaagcgcat tgagatggga actaaaaggc 240

gaataccaag attaccgtcc aacaaagctc gactatcaat cagattggca atggaatgca 300

agcatcaact attggcacca gttgccacaa caatggctcg cattcggtgg catagactgg 360

acgcataaac aaaatgatca agatgtacat gcttaccagc tctatggtgg tcgaatcgga 420

gtcgtgaaaa gcgtcgaagg ttggcttgac gctaacctgt ttgcatcact gcgagaaagg 480

caatacgagg gatataacgc cctactcgat gcaaagagaa gagacacaga gcaaaactat 540

actgtcacat tttcctctcc aaagttggtt ttttggacgt tgacacccat tctagagtgg 600

actcataaac gggtaaacag caacgttgat tggctgtaca cctatcagca aaatgaggtg 660

agcgtaaaat ttgaaaagcg tttttga 687

<210> 668

<211> 228

<212> PRT

<213> Vibrio sp. HENC-02 SLAM 1

<400> 668

Met Ser Leu Gln Ala Leu Thr Tyr Gly Ser Arg Tyr Asn Asn His Ser

1 5 10 15

Glu Tyr Asn Glu Gln Thr Ala Asn Val Ser Phe Gly Tyr Ser Phe Gln

20 25 30

Asp Gln Arg His Ser Ile Leu Val Ala Pro Leu Ile Glu Tyr Ser Ser

35 40 45

Tyr Ala Asp Lys Ser Leu Tyr Trp Ser Thr Gly Leu Lys Leu Asn Gly

50 55 60

Phe His Ser Leu Asp Ser Lys Ser Ala Leu Arg Trp Glu Leu Lys Gly

65 70 75 80

Glu Tyr Gln Asp Tyr Arg Pro Thr Lys Leu Asp Tyr Gln Ser Asp Trp

85 90 95

Gln Trp Asn Ala Ser Ile Asn Tyr Trp His Gln Leu Pro Gln Gln Trp

100 105 110

Leu Ala Phe Gly Gly Ile Asp Trp Thr His Lys Gln Asn Asp Gln Asp

115 120 125

Val His Ala Tyr Gln Leu Tyr Gly Gly Arg Ile Gly Val Val Lys Ser

130 135 140

Val Glu Gly Trp Leu Asp Ala Asn Leu Phe Ala Ser Leu Arg Glu Arg

145 150 155 160

Gln Tyr Glu Gly Tyr Asn Ala Leu Leu Asp Ala Lys Arg Arg Asp Thr

165 170 175

Glu Gln Asn Tyr Thr Val Thr Phe Ser Ser Pro Lys Leu Val Phe Trp

180 185 190

Thr Leu Thr Pro Ile Leu Glu Trp Thr His Lys Arg Val Asn Ser Asn

195 200 205

Val Asp Trp Leu Tyr Thr Tyr Gln Gln Asn Glu Val Ser Val Lys Phe

210 215 220

Glu Lys Arg Phe

225

<210> 669

<211> 1473

<212> DNA

<213> X. bovienii SLAM 1

<400> 669

atgtctgaca atataacaac cccaatatta ttaacggcac tgatggcctt atgtctctcc 60

ctgccggttt atgctgatga agataccaac cgcaaaatct ggcaggaggc gcagcacaat 120

caacaagaaa atgaagctga tctgataacg ccagagccta tttttattga ggatggtgct 180

tcatcgatag tcattaacgg acagacattt caggtagaaa acaacctcga taacatcggt 240

caggcactat accttgccac taaccatcga cagtggccgg acgtcagacg ttttctgacg 300

gcttatcaaa aactatccgg gcatgatgtc atgctggcct cttttgccca gggcggcctg 360

gcgcgttttg aaggcgattt ggatctcgcc gcctatcatt atcaaaagct cctgaaccaa 420

caacccgact tcacacgcat caagctggaa ctggcccgtg tttattttga aaatcataaa 480

aatcgggaag ccgagcaact gtttgtagga ttgagtgaac agaacctctt accggaaacg 540

gtcttgaaaa atatcaacag ctatttgaaa gcgatagcat tgagaagtga ctggcgtggc 600

tctttttcgg taggttatgc ctataacgat aatgtcaata tgtctccgga tcaggaatca 660

acctgccttg aatataaccc tgatgggagt tgccaggagg aacgccggat accaaaagcc 720

attaaaaagt gggggatgtc ttatgacgcc acattaagcc gacgttacca actttccggt 780

catcacggca tttttggacg tggcctgatt tatggcgaaa actaccgtga ttaccacgct 840

gaaaatgaaa ataccgtcct gctggtcagc ggatacaact acaaaagcag aaatcacgat 900

ttctcttttg gccccctgtt tgaatataaa catcgggcgg gtgataccta ttaccgcgcc 960

acaggtgtca aaacggaatg gagacaaaca ttcagcccta aaacagctct caatatcgaa 1020

ctggagcata aacaactgcg gcatcagcag cgttaccact ggaaaaatgg cgacctctcc 1080

tcatcctatc tcactctttc ccatgccatc agcaaagaat ttgtcatatt tggtggcggt 1140

gactgggtct atcggaacaa tccgcaaccg gcggatcgct atcaacaatg gggaattcgg 1200

gcaggcgtat ccggacagat ctaccccggt attaatggct cactgtctgc cacactgcga 1260

gagcggcgct ttggtgctta cagcccgata ctgctcgcca gacgtcagga tgatgaacag 1320

atctatactg ccgtcattaa agtccctgcc gctgaaatat tgggtatgac cccctctatc 1380

actttccgcc atcgacgcaa tcacagcagt gtgaattggc tgtacaacta taacaaaaac 1440

gaagtactgc tgaggctgga aaaatatttt taa 1473

<210> 670

<211> 490

<212> PRT

<213> X. bovienii SLAM 1

<400> 670

Met Ser Asp Asn Ile Thr Thr Pro Ile Leu Leu Thr Ala Leu Met Ala

1 5 10 15

Leu Cys Leu Ser Leu Pro Val Tyr Ala Asp Glu Asp Thr Asn Arg Lys

20 25 30

Ile Trp Gln Glu Ala Gln His Asn Gln Gln Glu Asn Glu Ala Asp Leu
35 40 45
Ile Thr Pro Glu Pro Ile Phe Ile Glu Asp Gly Ala Ser Ser Ile Val
50 55 60

Ile Asn Gly Gln Thr Phe Gln Val Glu Asn Asn Leu Asp Asn Ile Gly
65 70 75 80
Gln Ala Leu Tyr Leu Ala Thr Asn His Arg Gln Trp Pro Asp Val Arg
85 90 95
Arg Phe Leu Thr Ala Tyr Gln Lys Leu Ser Gly His Asp Val Met Leu
100 105 110
Ala Ser Phe Ala Gln Gly Gly Leu Ala Arg Phe Glu Gly Asp Leu Asp
115 120 125

Leu Ala Ala Tyr His Tyr Gln Lys Leu Leu Asn Gln Gln Pro Asp Phe
130 135 140
Thr Arg Ile Lys Leu Glu Leu Ala Arg Val Tyr Phe Glu Asn His Lys
145 150 155 160
Asn Arg Glu Ala Glu Gln Leu Phe Val Gly Leu Ser Glu Gln Asn Leu
165 170 175
Leu Pro Glu Thr Val Leu Lys Asn Ile Asn Ser Tyr Leu Lys Ala Ile
180 185 190

Ala Leu Arg Ser Asp Trp Arg Gly Ser Phe Ser Val Gly Tyr Ala Tyr
195 200 205
Asn Asp Asn Val Asn Met Ser Pro Asp Gln Glu Ser Thr Cys Leu Glu
210 215 220
Tyr Asn Pro Asp Gly Ser Cys Gln Glu Glu Arg Arg Ile Pro Lys Ala
225 230 235 240
Ile Lys Lys Trp Gly Met Ser Tyr Asp Ala Thr Leu Ser Arg Arg Tyr
245 250 255

Gln Leu Ser Gly His His Gly Ile Phe Gly Arg Gly Leu Ile Tyr Gly
260 265 270
Glu Asn Tyr Arg Asp Tyr His Ala Glu Asn Glu Asn Thr Val Leu Leu

275 280 285

Val Ser Gly Tyr Asn Tyr Lys Ser Arg Asn His Asp Phe Ser Phe Gly

290 295 300

Pro Leu Phe Glu Tyr Lys His Arg Ala Gly Asp Thr Tyr Tyr Arg Ala

305 310 315 320

Thr Gly Val Lys Thr Glu Trp Arg Gln Thr Phe Ser Pro Lys Thr Ala

325 330 335

Leu Asn Ile Glu Leu Glu His Lys Gln Leu Arg His Gln Gln Arg Tyr

340 345 350

His Trp Lys Asn Gly Asp Leu Ser Ser Ser Tyr Leu Thr Leu Ser His

355 360 365

Ala Ile Ser Lys Glu Phe Val Ile Phe Gly Gly Gly Asp Trp Val Tyr

370 375 380

Arg Asn Asn Pro Gln Pro Ala Asp Arg Tyr Gln Gln Trp Gly Ile Arg

385 390 395 400

Ala Gly Val Ser Gly Gln Ile Tyr Pro Gly Ile Asn Gly Ser Leu Ser

405 410 415

Ala Thr Leu Arg Glu Arg Arg Phe Gly Ala Tyr Ser Pro Ile Leu Leu

420 425 430

Ala Arg Arg Gln Asp Asp Glu Gln Ile Tyr Thr Ala Val Ile Lys Val

435 440 445

Pro Ala Ala Glu Ile Leu Gly Met Thr Pro Ser Ile Thr Phe Arg His

450 455 460

Arg Arg Asn His Ser Ser Val Asn Trp Leu Tyr Asn Tyr Asn Lys Asn

465 470 475 480

Glu Val Leu Leu Arg Leu Glu Lys Tyr Phe

485 490

<210> 671

<211> 1476

<212> DNA

<213> X. cabanillasii SLAM 1

<400> 671

atgtctgaca atagaaaaac gccaatatta ttaacgtcat tgatagcctt atgcttctct 60

ttacccattt atgctgatga cgaagatact tcacgcaaaa tctggcaaga agcacagcat 120

aaccaacagg agaaagaaac taatctgatt acgccagatc ctgttttcat tgaaaataac 180

tcatcattga ttgtcattaa tgggcaacct tttcaggtcg aaaataatat taatgatatc 240

ggtcaggcac tcttcctcgc cgttaaccat caacaatggt cagacgtcag gcgttttctg 300

gcagcatacc tgaaattgcc ggaacacgat gttatgttgg tgaattttgc ccaaggtgga 360

ctggcccgcc ttgacggaaa tttagatctc gctgcctatc attatcaaca aatcctgaac 420

caacaacccg attttcctcg catcaagctg gaattggccc gtgcctattt tgaggatcat 480

aagaatcggg aagcagagga attgtttact gaattgtatg aagcaaaaaa gctaccagaa 540

gtagtgctga aaaatatcaa tagctatctg gaagcaataa gcttaagaaa tagctggcgc 600

ggctctttct ctgctggtta tgcctataac gacaatgtga atatgtcctc caatcagagg 660

ggaacctgcc tgtacaatat ctctgccgat aaatgtctca aacgacaagt tccaaaagct 720

attaaagcat ggggaatgtc ttatgacgca acattaagcc gacgctacca acttatcggc 780

catcacggta tttttggccg cggcctgatt tatggtgaaa actaccgtga ctaccatgat 840

gagaacgaaa acactttcca gctaatcggt ggctacagtt ataaaaacag gaagcacgat 900

atctcttttg gccctgtgtt tgaatataaa caacatgctg gtgatacttt ttatcgtgcc 960

acaggtctca aaactgagtg gagatggggc attacttctc aaactgccct taatgttgaa 1020

cttgaacaca aacaattgcg ccatcaacgg cattatcgca ggaaagacgg tgaactcacc 1080

tcttcttacc tcactttatc ccacgccatc aacaaagaat ttatcctgtt tggcggtggt 1140

gactgggttt atcgggataa cgacctgtat cccgtagacc gttatcaaca atggggtgcc 1200

cgtgcgggga ttgccgggca aatctacccc ggcatcaatg gatcactgtt tgccacactg 1260

cgggatcggc gctttggtgc ttacagcccg atgcttagag ccagacgtca ggatacggag 1320

cagatttata ccgccgttat caaagttcct gccgctgaaa tattgggcat gacccctct 1380

gtgactttcc gccaccgacg caatcatagc aatgtagatt ggctatacag ctttaacaaa 1440

aacgaagtgc tgatccggct ggaaaagtat ttttaa 1476

<210> 672

<211> 491

<212> PRT

<213> X. cabanillasii SLAM 1

<400> 672

Met Ser Asp Asn Arg Lys Thr Pro Ile Leu Leu Thr Ser Leu Ile Ala

1 5 10 15

Leu Cys Phe Ser Leu Pro Ile Tyr Ala Asp Asp Glu Asp Thr Ser Arg

20 25 30

Lys Ile Trp Gln Glu Ala Gln His Asn Gln Gln Glu Lys Glu Thr Asn

35 40 45

Leu Ile Thr Pro Asp Pro Val Phe Ile Glu Asn Asn Ser Ser Leu Ile

50 55 60

Val Ile Asn Gly Gln Pro Phe Gln Val Glu Asn Asn Ile Asn Asp Ile

65 70 75 80

Gly Gln Ala Leu Phe Leu Ala Val Asn His Gln Gln Trp Ser Asp Val

85 90 95

Arg Arg Phe Leu Ala Ala Tyr Leu Lys Leu Pro Glu His Asp Val Met

100 105 110

Leu Val Asn Phe Ala Gln Gly Gly Leu Ala Arg Leu Asp Gly Asn Leu

115 120 125

Asp Leu Ala Ala Tyr His Tyr Gln Gln Ile Leu Asn Gln Gln Pro Asp

130 135 140

Phe Pro Arg Ile Lys Leu Glu Leu Ala Arg Ala Tyr Phe Glu Asp His

145 150 155 160

Lys Asn Arg Glu Ala Glu Glu Leu Phe Thr Glu Leu Tyr Glu Ala Lys

165 170 175

Lys Leu Pro Glu Val Val Leu Lys Asn Ile Asn Ser Tyr Leu Glu Ala

180 185 190

Ile Ser Leu Arg Asn Ser Trp Arg Gly Ser Phe Ser Ala Gly Tyr Ala

195 200 205

Tyr Asn Asp Asn Val Asn Met Ser Ser Asn Gln Arg Gly Thr Cys Leu

210 215 220

Tyr Asn Ile Ser Ala Asp Lys Cys Leu Lys Arg Gln Val Pro Lys Ala

225 230 235 240

Ile Lys Ala Trp Gly Met Ser Tyr Asp Ala Thr Leu Ser Arg Arg Tyr

245 250 255

Gln Leu Ile Gly His His Gly Ile Phe Gly Arg Gly Leu Ile Tyr Gly
260 265 270
Glu Asn Tyr Arg Asp Tyr His Asp Glu Asn Glu Asn Thr Phe Gln Leu
275 280 285
Ile Gly Gly Tyr Ser Tyr Lys Asn Arg Lys His Asp Ile Ser Phe Gly

290 295 300
Pro Val Phe Glu Tyr Lys Gln His Ala Gly Asp Thr Phe Tyr Arg Ala
305 310 315 320
Thr Gly Leu Lys Thr Glu Trp Arg Trp Gly Ile Thr Ser Gln Thr Ala
325 330 335
Leu Asn Val Glu Leu Glu His Lys Gln Leu Arg His Gln Arg His Tyr
340 345 350
Arg Arg Lys Asp Gly Glu Leu Thr Ser Ser Tyr Leu Thr Leu Ser His

355 360 365
Ala Ile Asn Lys Glu Phe Ile Leu Phe Gly Gly Gly Asp Trp Val Tyr
370 375 380
Arg Asp Asn Asp Leu Tyr Pro Val Asp Arg Tyr Gln Gln Trp Gly Ala
385 390 395 400
Arg Ala Gly Ile Ala Gly Gln Ile Tyr Pro Gly Ile Asn Gly Ser Leu
405 410 415
Phe Ala Thr Leu Arg Asp Arg Arg Phe Gly Ala Tyr Ser Pro Met Leu

420 425 430
Arg Ala Arg Arg Gln Asp Thr Glu Gln Ile Tyr Thr Ala Val Ile Lys
435 440 445
Val Pro Ala Ala Glu Ile Leu Gly Met Thr Pro Ser Val Thr Phe Arg
450 455 460
His Arg Arg Asn His Ser Asn Val Asp Trp Leu Tyr Ser Phe Asn Lys
465 470 475 480
Asn Glu Val Leu Ile Arg Leu Glu Lys Tyr Phe
485 490

<210> 673

<211> 1383

<212> DNA

<213> X. cabanillasii SLAM 2

<400> 673

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tcaacaggct acgccaatga tatatcaaat gagatttcac caaagattca tgggcaagaa 120

tttaaggtta aaaacaatct taaggatatc ggtcaagcac tgtaccttgc cattaattat 180

cagcaatggt cagatgtaag acgctttttg tcggtttatc aaaaattgcc ggggcatgat 240

gttatgctgg tcaattttgc cctgggtggg ctggcacgtc gtgaggggaa tttaactctc 300

gcagcttccc tctatcaaaa aatcctgcgt caaaaaccga atttcacccg catcaaattg 360

gaattggccc gtgtctattt tgaagatcat aaaaatcggg aagccaaaca gttaatggat 420

gaattaagta aacagcatca attacccgca accgttttga agaacatcga cggttatata 480

aaagcaatca cccaaagaaa ccgctggcgc agttcgtttt cactcagtta tatctataac 540

gataatataa atatgtctcc aaatatgaaa ccggactgtc tgcttatttt aaaaggagaa 600

tgtaaaattg aacgggaaat accaaaagcg atcaaagaat ggggaagcgc ttatcatgtt 660

acattaagcc ggcgttacca gcttgttggc caccacggca tttttggtcg cggaatgatt 720

gatggtgaaa tctatcctca tttccataac ggaaacgaaa acacgttttt gctgatcagt 780

ggctacaatt ttaaaagcag gaataatgac ttatcctttg ctcctttgtt tgaatataaa 840

caacaagccg gaataaccga ataccatgct gtcgctgcca aaatagaatg gcaatgggct 900

atctctgatc aaaccttcct cagcgctgaa tttgaacata agcgattcag ttatcagcct 960

ctttatcatt ggaaaaatgg cgaactttcc tcatcttatt tcaatctctc ccatgctatc 1020

ggcaacgatt ttattctgtt tggcggcact ggctggagct atcgaaacaa tcaacaaccg 1080

gcagctcgct atcaacaatg gggagttact gcggggatag ccgggccact ttattccggc 1140

attgatggct cgctgtttgc cacactgaaa acgcaacgtt ttggcgccta cagcgcatta 1200

ctgggtgcca aacgtcaaga taatgaacag atctataccg cttccgttaa atttcctgcc 1260

agcaaaatct gggggatgac accttctgtc actttccgcc acttgcacaa tcgtagcaat 1320

gtaaactggc aatacagtta cgataaaaac gaaatacaaa tacagctaga aaaatatttt 1380

tag 1383

<210> 674

<211> 460

<212> PRT

<213> X. cabanillasii SLAM 2

<400> 674

Met Thr Gly Lys Arg Asn Val Ala Val Leu Leu Ala Ser Leu Leu Thr
1 5 10 15

Ser Leu Leu Phe Ser Thr Gly Tyr Ala Asn Asp Ile Ser Asn Glu Ile
20 25 30

Ser Pro Lys Ile His Gly Gln Glu Phe Lys Val Lys Asn Asn Leu Lys
35 40 45

Asp Ile Gly Gln Ala Leu Tyr Leu Ala Ile Asn Tyr Gln Gln Trp Ser
50 55 60

Asp Val Arg Arg Phe Leu Ser Val Tyr Gln Lys Leu Pro Gly His Asp
65 70 75 80

Val Met Leu Val Asn Phe Ala Leu Gly Gly Leu Ala Arg Arg Glu Gly
85 90 95

Asn Leu Thr Leu Ala Ala Ser Leu Tyr Gln Lys Ile Leu Arg Gln Lys
100 105 110

Pro Asn Phe Thr Arg Ile Lys Leu Glu Leu Ala Arg Val Tyr Phe Glu
115 120 125

Asp His Lys Asn Arg Glu Ala Lys Gln Leu Met Asp Glu Leu Ser Lys
130 135 140

Gln His Gln Leu Pro Ala Thr Val Leu Lys Asn Ile Asp Gly Tyr Ile
145 150 155 160

Lys Ala Ile Thr Gln Arg Asn Arg Trp Arg Ser Ser Phe Ser Leu Ser
165 170 175

Tyr Ile Tyr Asn Asp Asn Ile Asn Met Ser Pro Asn Met Lys Pro Asp
180 185 190

Cys Leu Leu Ile Leu Lys Gly Glu Cys Lys Ile Glu Arg Glu Ile Pro
195 200 205

Lys Ala Ile Lys Glu Trp Gly Ser Ala Tyr His Val Thr Leu Ser Arg
210 215 220

Arg Tyr Gln Leu Val Gly His His Gly Ile Phe Gly Arg Gly Met Ile
225 230 235 240

Asp Gly Glu Ile Tyr Pro His Phe His Asn Gly Asn Glu Asn Thr Phe
245 250 255
Leu Leu Ile Ser Gly Tyr Asn Phe Lys Ser Arg Asn Asn Asp Leu Ser
260 265 270

Phe Ala Pro Leu Phe Glu Tyr Lys Gln Gln Ala Gly Ile Thr Glu Tyr
275 280 285
His Ala Val Ala Ala Lys Ile Glu Trp Gln Trp Ala Ile Ser Asp Gln
290 295 300
Thr Phe Leu Ser Ala Glu Phe Glu His Lys Arg Phe Ser Tyr Gln Pro
305 310 315 320
Leu Tyr His Trp Lys Asn Gly Glu Leu Ser Ser Ser Tyr Phe Asn Leu
325 330 335

Ser His Ala Ile Gly Asn Asp Phe Ile Leu Phe Gly Gly Thr Gly Trp
340 345 350
Ser Tyr Arg Asn Asn Gln Gln Pro Ala Ala Arg Tyr Gln Gln Trp Gly
355 360 365
Val Thr Ala Gly Ile Ala Gly Pro Leu Tyr Ser Gly Ile Asp Gly Ser
370 375 380
Leu Phe Ala Thr Leu Lys Thr Gln Arg Phe Gly Ala Tyr Ser Ala Leu
385 390 395 400

Leu Gly Ala Lys Arg Gln Asp Asn Glu Gln Ile Tyr Thr Ala Ser Val
405 410 415
Lys Phe Pro Ala Ser Lys Ile Trp Gly Met Thr Pro Ser Val Thr Phe
420 425 430
Arg His Leu His Asn Arg Ser Asn Val Asn Trp Gln Tyr Ser Tyr Asp
435 440 445
Lys Asn Glu Ile Gln Ile Gln Leu Glu Lys Tyr Phe
450 455 460
<210> 675
<
211> 1473
<212> DNA

<213> X. doucetiae SLAM 1

<400> 675

atgtctgaca atcgaacacc ctctatatta ttcaccgcag tggtggcctt atgcctgtcc 60

ctgccaggct atgccgatga cgataccagc caaaaaatct ggcaggaggc acaacataat 120

caacgagaaa atgaagccag cctgattaca cccgaccccg tttttactga gaatggttca 180

tcgttaattg tgattaacgg gcaaaccttt caggtagaaa ataatattaa tgatatcggc 240

caggcattat ttcttgccat taaccatcaa caatggccgg atgtcaggcg cttcctcacg 300

gcttatctaa aattgccgga gcatgatgtg atgctggtta attttgccca aggtggactg 360

gcgcgtttag acggggactt ggatctcgcc gccgatcatt accaacaaat cctgcatcaa 420

cagcccgatt ttccccgtat cacactggaa ctggcccggg tctattttga ggatcataaa 480

aaccgggaag ccgaacaact gtttaccgga ttgtatcagg cgcaaaacct cccggaagcc 540

gtactgaaaa atattaacag ctatctggaa gcgatagcgc tgagaaacag ttggcgcggc 600

tctttctcgg ccggttacgc ctataacgat aacgtcaata tgtctcctga tcaggggcca 660

gtctgtaggc aatacgtggg agataaatgt aatattgaac agcgaatacc aaaagccgtc 720

aaagcctggg gcatgtctta tgacgccaca ttaagccgac gctatcagct taccggtcat 780

catggcattt ttggccgtag cctgatttat ggcgaaaatt accgtgatta ccacgatgaa 840

aacgaaaata cgttgctgct ggtgggtggc tataactata aaagcaagcg tcatgatttc 900

tcgtttggcc cgttgtttga atataaacaa cgggcagacg atgccggtta ccgtgccacc 960

ggggctaaaa ccgaatggcg atgggccttc actgccaaaa ccgccctgaa tgtggagctt 1020

gagcataaac agctacgtta ccaacaaccg ttccgccgga aagatggcag cttttcctca 1080

acctatctca ccctattcca ttccatcaat aaagacgttg ttctgtttgg cggcggcgac 1140

tgggtttacc gcgacaacaa gcagtatgcc gtggatcgct atcagcaatg gggtgttcgg 1200

gcggggattg ccggacagat ctatcccggc attaacggtt ccctgtttgc cacactgaaa 1260

cagcgccatt ttggggcaag tcacccaatg acaaagaccc ggcgtcagga taacgaacag 1320

atttacagcg cggtgattaa agtgccggcc gcagaaattt ggggcatgac accgtctgtg 1380

acgttccgcc atcggcgcaa tcacagcaac gtggcctggc tgtacagcta taacaaaaac 1440

gaaatcctta tcaggctgga aaagtatttt taa 1473

<210> 676

<211> 490

<212> PRT

<213> X. doucetiae SLAM 1

<400> 676

Met Ser Asp Asn Arg Thr Pro Ser Ile Leu Phe Thr Ala Val Val Ala

1 5 10 15

Leu Cys Leu Ser Leu Pro Gly Tyr Ala Asp Asp Asp Thr Ser Gln Lys

20 25 30

Ile Trp Gln Glu Ala Gln His Asn Gln Arg Glu Asn Glu Ala Ser Leu

35 40 45

Ile Thr Pro Asp Pro Val Phe Thr Glu Asn Gly Ser Ser Leu Ile Val

50 55 60

Ile Asn Gly Gln Thr Phe Gln Val Glu Asn Asn Ile Asn Asp Ile Gly

65 70 75 80

Gln Ala Leu Phe Leu Ala Ile Asn His Gln Gln Trp Pro Asp Val Arg

85 90 95

Arg Phe Leu Thr Ala Tyr Leu Lys Leu Pro Glu His Asp Val Met Leu

100 105 110

Val Asn Phe Ala Gln Gly Gly Leu Ala Arg Leu Asp Gly Asp Leu Asp

115 120 125

Leu Ala Ala Asp His Tyr Gln Gln Ile Leu His Gln Gln Pro Asp Phe

130 135 140

Pro Arg Ile Thr Leu Glu Leu Ala Arg Val Tyr Phe Glu Asp His Lys

145 150 155 160

Asn Arg Glu Ala Glu Gln Leu Phe Thr Gly Leu Tyr Gln Ala Gln Asn

165 170 175

Leu Pro Glu Ala Val Leu Lys Asn Ile Asn Ser Tyr Leu Glu Ala Ile

180 185 190

Ala Leu Arg Asn Ser Trp Arg Gly Ser Phe Ser Ala Gly Tyr Ala Tyr

195 200 205

Asn Asp Asn Val Asn Met Ser Pro Asp Gln Gly Pro Val Cys Arg Gln

210 215 220

Tyr Val Gly Asp Lys Cys Asn Ile Glu Gln Arg Ile Pro Lys Ala Val

225 230 235 240

Lys Ala Trp Gly Met Ser Tyr Asp Ala Thr Leu Ser Arg Arg Tyr Gln

245 250 255

Leu Thr Gly His His Gly Ile Phe Gly Arg Ser Leu Ile Tyr Gly Glu

260 265 270

Asn Tyr Arg Asp Tyr His Asp Glu Asn Glu Asn Thr Leu Leu Leu Val

275 280 285

Gly Gly Tyr Asn Tyr Lys Ser Lys Arg His Asp Phe Ser Phe Gly Pro

290 295 300

Leu Phe Glu Tyr Lys Gln Arg Ala Asp Asp Ala Gly Tyr Arg Ala Thr

305 310 315 320

Gly Ala Lys Thr Glu Trp Arg Trp Ala Phe Thr Ala Lys Thr Ala Leu

325 330 335

Asn Val Glu Leu Glu His Lys Gln Leu Arg Tyr Gln Gln Pro Phe Arg

340 345 350

Arg Lys Asp Gly Ser Phe Ser Ser Thr Tyr Leu Thr Leu Phe His Ser

355 360 365

Ile Asn Lys Asp Val Val Leu Phe Gly Gly Gly Asp Trp Val Tyr Arg

370 375 380

Asp Asn Lys Gln Tyr Ala Val Asp Arg Tyr Gln Gln Trp Gly Val Arg

385 390 395 400

Ala Gly Ile Ala Gly Gln Ile Tyr Pro Gly Ile Asn Gly Ser Leu Phe

405 410 415

Ala Thr Leu Lys Gln Arg His Phe Gly Ala Ser His Pro Met Thr Lys

420 425 430

Thr Arg Arg Gln Asp Asn Glu Gln Ile Tyr Ser Ala Val Ile Lys Val

435 440 445

Pro Ala Ala Glu Ile Trp Gly Met Thr Pro Ser Val Thr Phe Arg His

450 455 460

Arg Arg Asn His Ser Asn Val Ala Trp Leu Tyr Ser Tyr Asn Lys Asn

465 470 475 480

Glu Ile Leu Ile Arg Leu Glu Lys Tyr Phe

485 490

<210> 677

<211> 1434

<212> DNA

<213> X. doucetiae SLAM 2

<400> 677

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ttgacttcat ttctctcacc agcaatttgt gccaatgaag atcatttgat ggcaccaaac 120

ccccttttctg ccaaacatga ttccttatta aatattatcc gtagacaaaa aattaaggtt 180

agcaacaatc tcaacgatat cggtcaggca ctgtactttg ccattaatta tcggcagtgg 240

cgagacgtca gacgtctttt gctggcttat caaaagctcc ctggttacga tccgtttctc 300

atcgattttg ctcagggccg gctagcctat cgtgaaggaa atttagcact cgctacctct 360

tattatcaaa agatcttgcg ccaaaaaccg aatttcacgc gcatcaaact ggaactggct 420

cgtgtttatt ttgaagatca aaaaaaccgt gaatccaagc agttatttga aggaataagc 480

caacagcagc aattacccga aatggtctta aataatatcg gcagttatct ggcagaaata 540

gccctaagaa atggctggca aagttcactt tcattcggct atacctatga cgataatatc 600

aatatgtcgc caaatcagaa acccatctgc ctggtttccg agaagggaaa gtgcatcatt 660

aaacggcaag tgccgaaacc tgtcacggca tggggtggaa cttataacgc aacattaaac 720

cgacgttacc aactggttgg tcatcacggc attttcggtc gtggtctgat ttatggagaa 780

aattattccc attaccataa cgaaaacgaa aacaggttcc tgctggtcag tggctacaac 840

tataaaaacc ggttccatga tttctctttt ggccccctct ttgaatatca acagagtgca 900

gggaaaaccg aataccatgc catcggtgcc aaaatggaat ggcaatgggc tattaccaag 960

caaacctccc tcaatgtcga actggaacat aagaaattga gttatccacc gatttaccgc 1020

gggaaagaca acgtgctttc ctcatcctat ttcagcctgt ctcatgccat cagtgaaaaa 1080

ttaatattgt ttggcggcgg taattggcgc tatggaaact atcaagatcc cgcagattgc 1140

tatcagcaat ggggggtaag tgcaggaata gcggggcagc tctatccccg cattaatggt 1200

tctctgtctt tcactttaag gaaacagcgc ttcagcgcct acagcgcatt attgggtgcc 1260

agacgtcaag ataatgaaca gatctatacg gctgccatta aatttcctgc tgccaaggta 1320

ttgggcatga caccctcttt aactttccgc catcactaca atcacagtaa cgtgaactgg 1380

ttgtacagtt atgataaaaa cgaaatccag atacagttag aaaaatattt ctaa 1434

<210> 678

<211> 477

<212> PRT

<213> X. doucetiae SLAM 2

<400> 678

Met Ser Asp Lys Lys Glu Gly Ser Gly Lys Arg Lys Tyr Leu Leu Leu
1 5 10 15

Leu Ile Phe Leu Leu Thr Ser Phe Leu Ser Pro Ala Ile Cys Ala Asn
20 25 30

Glu Asp His Leu Met Ala Pro Asn Pro Leu Ser Ala Lys His Asp Ser
35 40 45

Leu Leu Asn Ile Ile Arg Arg Gln Lys Ile Lys Val Ser Asn Asn Leu
50 55 60

Asn Asp Ile Gly Gln Ala Leu Tyr Phe Ala Ile Asn Tyr Arg Gln Trp
65 70 75 80

Arg Asp Val Arg Arg Leu Leu Leu Ala Tyr Gln Lys Leu Pro Gly Tyr
85 90 95

Asp Pro Phe Leu Ile Asp Phe Ala Gln Gly Arg Leu Ala Tyr Arg Glu
100 105 110

Gly Asn Leu Ala Leu Ala Thr Ser Tyr Tyr Gln Lys Ile Leu Arg Gln
115 120 125

Lys Pro Asn Phe Thr Arg Ile Lys Leu Glu Leu Ala Arg Val Tyr Phe
130 135 140

Glu Asp Gln Lys Asn Arg Glu Ser Lys Gln Leu Phe Glu Gly Ile Ser
145 150 155 160

Gln Gln Gln Gln Leu Pro Glu Met Val Leu Asn Asn Ile Gly Ser Tyr
165 170 175

Leu Ala Glu Ile Ala Leu Arg Asn Gly Trp Gln Ser Ser Leu Ser Phe
180 185 190

Gly Tyr Thr Tyr Asp Asp Asn Ile Asn Met Ser Pro Asn Gln Lys Pro
195 200 205

Ile Cys Leu Val Ser Glu Lys Gly Lys Cys Ile Ile Lys Arg Gln Val
210 215 220

Pro Lys Pro Val Thr Ala Trp Gly Gly Thr Tyr Asn Ala Thr Leu Asn

225 230 235 240

Arg Arg Tyr Gln Leu Val Gly His His Gly Ile Phe Gly Arg Gly Leu
245 250 255
Ile Tyr Gly Glu Asn Tyr Ser His Tyr His Asn Glu Asn Glu Asn Arg
260 265 270
Phe Leu Leu Val Ser Gly Tyr Asn Tyr Lys Asn Arg Phe His Asp Phe
275 280 285
Ser Phe Gly Pro Leu Phe Glu Tyr Gln Gln Ser Ala Gly Lys Thr Glu
290 295 300

Tyr His Ala Ile Gly Ala Lys Met Glu Trp Gln Trp Ala Ile Thr Lys
305 310 315 320
Gln Thr Ser Leu Asn Val Glu Leu Glu His Lys Lys Leu Ser Tyr Pro
325 330 335
Pro Ile Tyr Arg Gly Lys Asp Asn Val Leu Ser Ser Ser Tyr Phe Ser
340 345 350
Leu Ser His Ala Ile Ser Glu Lys Leu Ile Leu Phe Gly Gly Gly Asn
355 360 365

Trp Arg Tyr Gly Asn Tyr Gln Asp Pro Ala Asp Cys Tyr Gln Gln Trp
370 375 380
Gly Val Ser Ala Gly Ile Ala Gly Gln Leu Tyr Pro Arg Ile Asn Gly
385 390 395 400
Ser Leu Ser Phe Thr Leu Arg Lys Gln Arg Phe Ser Ala Tyr Ser Ala
405 410 415
Leu Leu Gly Ala Arg Arg Gln Asp Asn Glu Gln Ile Tyr Thr Ala Ala
420 425 430

Ile Lys Phe Pro Ala Ala Lys Val Leu Gly Met Thr Pro Ser Leu Thr
435 440 445
Phe Arg His His Tyr Asn His Ser Asn Val Asn Trp Leu Tyr Ser Tyr
450 455 460
Asp Lys Asn Glu Ile Gln Ile Gln Leu Glu Lys Tyr Phe
465 470 475

<210> 679

<211> 1476

<212> DNA

<213> X. nematophila SLAM 1

<400> 679

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ctgtccgttt atgccgatga ggatacttcc cgtaatatct ggctggacgc tcaacataac 120

caacaagaaa atgaaactaa cctaattacg ccagatccca tttttatggg aagtaactcg 180

tcatttattg tgattaacgg acagactttt caggttggca acaatattaa tgatctcggg 240

caggctttat tccttgccat taaccaccaa caatggccgg atgtcaggcg ctttcttgcg 300

gcttaccaaa aactgccgga gcatgatgcc atgctggtga attttgccca aggcgggttg 360

gctcgccttg aaggtgattt agatctcgcg acctatcatt atcaacaaat cctgcatcaa 420

caacctgact ttccccgtat cgagctggaa ttggcccgta tctattttga agatcaccag 480

aatcgggaag ccaagcaact ctttactgga ttgaatgaaa aacaacagct gccagccgct 540

gtcctgaaga atattaacag ctatctggaa gcgatagagc tgagaacagg ctggcggggc 600

tctttttcgg caggttatgc ctataacgat aacgtcaata tgtcctctaa tcatggcccc 660

atctgcttaa gctactctat gggtatatgc acaaagaagc agcaagttcc caaagcgatc 720

aaagcatggg gaatgtctta cgatgcaacg ttaagccggc gttatcagct ttctgaccat 780

cacggcattt ttggccgagg tctgatgtat ggagaaaact accgcaatta tcacgatggg 840

aatgagaata cattcctgct ggtcggtgga tataacttta aaaacagaaa tcacgatttc 900

tcctttggcc ccctgtttga atataaacag cgcacagatg acaccactta ccgcgccatc 960

ggtgctaaaa cagagtggag atgggcattc accaataaga ccaccctgaa tattgagctt 1020

gaacataaac aactgcggca tcaggagcaa cgttatcgca gaaaagatgg cgaactttct 1080

tcaacctacc tcacgttatc ccatgccatt aacaaaaacg ttgtcctgtt tggcggcggt 1140

gactggctgt accgaaacaa cgaccattat cgcgaagaca gctatcagca atggggaatt 1200

cgggcaggga tcgccgggga actttattcc ggcatcactg gctcactgtt tgccacgttg 1260

aaagagcggc gctttggtgc ttacaccccg atgctgaacg ccacacgtca ggatactgaa 1320

caaatttaca cagcggttat caaagtaccc gctgccgaaa tactgggcat gacgccttct 1380

cttactttcc gccaccgacg taaccacagc aatgtggatt ggttatacag ctataacaaa 1440

aacgaagtgc tgattaggct ggagaagtat ttttaa 1476

<210> 680

<211> 491

<212> PRT

<213> X. nematophila SLAM 1

<400> 680

Met Ser Asp Asn Arg Thr Thr Pro Ile Leu Ala Ala Ala Leu Ile Ala
1 5 10 15
Leu Cys Leu Ser Leu Ser Val Tyr Ala Asp Glu Asp Thr Ser Arg Asn

20 25 30
Ile Trp Leu Asp Ala Gln His Asn Gln Gln Glu Asn Glu Thr Asn Leu
35 40 45
Ile Thr Pro Asp Pro Ile Phe Met Gly Ser Asn Ser Ser Phe Ile Val
50 55 60
Ile Asn Gly Gln Thr Phe Gln Val Gly Asn Asn Ile Asn Asp Leu Gly
65 70 75 80
Gln Ala Leu Phe Leu Ala Ile Asn His Gln Gln Trp Pro Asp Val Arg

85 90 95
Arg Phe Leu Ala Ala Tyr Gln Lys Leu Pro Glu His Asp Ala Met Leu
100 105 110
Val Asn Phe Ala Gln Gly Gly Leu Ala Arg Leu Glu Gly Asp Leu Asp
115 120 125
Leu Ala Thr Tyr His Tyr Gln Gln Ile Leu His Gln Gln Pro Asp Phe
130 135 140
Pro Arg Ile Glu Leu Glu Leu Ala Arg Ile Tyr Phe Glu Asp His Gln

145 150 155 160
Asn Arg Glu Ala Lys Gln Leu Phe Thr Gly Leu Asn Glu Lys Gln Gln
165 170 175
Leu Pro Ala Ala Val Leu Lys Asn Ile Asn Ser Tyr Leu Glu Ala Ile
180 185 190
Glu Leu Arg Thr Gly Trp Arg Gly Ser Phe Ser Ala Gly Tyr Ala Tyr
195 200 205
Asn Asp Asn Val Asn Met Ser Ser Asn His Gly Pro Ile Cys Leu Ser

210 215 220

Tyr Ser Met Gly Ile Cys Thr Lys Lys Gln Gln Val Pro Lys Ala Ile

225 230 235 240

Lys Ala Trp Gly Met Ser Tyr Asp Ala Thr Leu Ser Arg Arg Tyr Gln

245 250 255

Leu Ser Asp His His Gly Ile Phe Gly Arg Gly Leu Met Tyr Gly Glu

260 265 270

Asn Tyr Arg Asn Tyr His Asp Gly Asn Glu Asn Thr Phe Leu Leu Val

275 280 285

Gly Gly Tyr Asn Phe Lys Asn Arg Asn His Asp Phe Ser Phe Gly Pro

290 295 300

Leu Phe Glu Tyr Lys Gln Arg Thr Asp Asp Thr Thr Tyr Arg Ala Ile

305 310 315 320

Gly Ala Lys Thr Glu Trp Arg Trp Ala Phe Thr Asn Lys Thr Thr Leu

325 330 335

Asn Ile Glu Leu Glu His Lys Gln Leu Arg His Gln Glu Gln Arg Tyr

340 345 350

Arg Arg Lys Asp Gly Glu Leu Ser Ser Thr Tyr Leu Thr Leu Ser His

355 360 365

Ala Ile Asn Lys Asn Val Val Leu Phe Gly Gly Gly Asp Trp Leu Tyr

370 375 380

Arg Asn Asn Asp His Tyr Arg Glu Asp Ser Tyr Gln Gln Trp Gly Ile

385 390 395 400

Arg Ala Gly Ile Ala Gly Glu Leu Tyr Ser Gly Ile Thr Gly Ser Leu

405 410 415

Phe Ala Thr Leu Lys Glu Arg Arg Phe Gly Ala Tyr Thr Pro Met Leu

420 425 430

Asn Ala Thr Arg Gln Asp Thr Glu Gln Ile Tyr Thr Ala Val Ile Lys

435 440 445

Val Pro Ala Ala Glu Ile Leu Gly Met Thr Pro Ser Leu Thr Phe Arg

450 455 460

His Arg Arg Asn His Ser Asn Val Asp Trp Leu Tyr Ser Tyr Asn Lys

465 470 475 480

Asn Glu Val Leu Ile Arg Leu Glu Lys Tyr Phe

485 490

<210> 681

<211> 1401

<212> DNA

<213> X. nematophila SLAM 2

<400> 681

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aacgtcgtaa tagccgaaga aataaaacct cagaatcaaa acgtatatac ggaagacgaa 120

atattaaggc aacctagatt acttgaaaat gcaattctct ttttaattca tgaacaaaat 180

gataacctag agaaagtact tagcctttat aaaaagtcgc atagtcaaga tccttacctg 240

attctttggg ctgaggcgaa aatcctcatg aaaaaaagag aataccatca ggctattaat 300

aagttagaac aatttgtcaa tcagtatgat aacccaaccg ctaaatttga tttggccata 360

ctttacttac tcaataaaaa atacaatcaa tccgaaaata ttttcaacaa tttactgctt 420

accacccgta atcaacagga taaggaaagt ataaataatt atatagaata cattaaaaag 480

aaaaaggaaa ttaaatttaa tacatatttt tcattcaaaa gagattcaaa catctcaaaa 540

atcactgata aaaaagtata tggatgggat ccaaataaaa ggataaaaga tgtgggattg 600

tcttttaccc cacgcattag caaaaagtat ttttttgact ctggtttatt ctctgaattt 660

gatattgatg ctcatggaat taagtatctg aaagaaaaaa gatatgattt cttaagcacc 720

agaataggca ataaaatcgg gtttgaagat tactccaatt atttctactt aaaacctttt 780

tatataaagt cattttatgg tggcggttcg acatcatcat ctaaagaaat aggttttaaa 840

ccttttttatg atgcaattgg gtttaactta tttaaattat cagatataaa tgaaaatctt 900

aaatatgcca ttttctatga aaataaaaat gaatattata acaagaaaaa acatcttaat 960

ggagacatta actttgttag cggttcatta atatttatcc catttaatga tttatatatg 1020

tccttatctg gaagttatag tgtaaccgat agaagatcta aagaggatag tcatcatgac 1080

aaagggatga cttttctaat cagcaaacgc tttttagatg attatttagt agagctaaac 1140

tatcaaaaga taaaaactga ctatataggt aaaaccacta tatactcc agctcatatc 1200

tttattcgag atttaccccc cattaaaata aaaagagaag atattactga ttccgtctcg 1260

ctttcactct caaatgagag tattaattta tttggttttt acccgacact ctcttttcc 1320

tatacaaaaa acaaaagcag caatcttttt tattcttata ctgaaaaaga tatttttctg 1380

gacttcaagc gtaatttta a 1401

<210> 682

<211> 466

<212> PRT

<213> X. nematophila SLAM 2

<400> 682

Met Lys Lys Ile Lys Ser Ile Val Ile Thr Val Val Thr Thr Leu Leu
1 5 10 15

Ile Pro Ile Ser Asn Val Val Ile Ala Glu Glu Ile Lys Pro Gln Asn
20 25 30

Gln Asn Val Tyr Thr Glu Asp Glu Ile Leu Arg Gln Pro Arg Leu Leu
35 40 45

Glu Asn Ala Ile Leu Phe Leu Ile His Glu Gln Asn Asp Asn Leu Glu
50 55 60

Lys Val Leu Ser Leu Tyr Lys Lys Ser His Ser Gln Asp Pro Tyr Leu
65 70 75 80

Ile Leu Trp Ala Glu Ala Lys Ile Leu Met Lys Lys Arg Glu Tyr His
85 90 95

Gln Ala Ile Asn Lys Leu Glu Gln Phe Val Asn Gln Tyr Asp Asn Pro
100 105 110

Thr Ala Lys Phe Asp Leu Ala Ile Leu Tyr Leu Leu Asn Lys Lys Tyr
115 120 125

Asn Gln Ser Glu Asn Ile Phe Asn Asn Leu Leu Leu Thr Thr Arg Asn
130 135 140

Gln Gln Asp Lys Glu Ser Ile Asn Asn Tyr Ile Glu Tyr Ile Lys Lys
145 150 155 160

Lys Lys Glu Ile Lys Phe Asn Thr Tyr Phe Ser Phe Lys Arg Asp Ser
165 170 175

Asn Ile Ser Lys Ile Thr Asp Lys Lys Val Tyr Gly Trp Asp Pro Asn
180 185 190

Lys Arg Ile Lys Asp Val Gly Leu Ser Phe Thr Pro Arg Ile Ser Lys
195 200 205

Lys Tyr Phe Phe Asp Ser Gly Leu Phe Ser Glu Phe Asp Ile Asp Ala
210 215 220

His Gly Ile Lys Tyr Leu Lys Glu Lys Arg Tyr Asp Phe Leu Ser Thr
225 230 235 240

Arg Ile Gly Asn Lys Ile Gly Phe Glu Asp Tyr Ser Asn Tyr Phe Tyr
245 250 255

Leu Lys Pro Phe Tyr Ile Lys Ser Phe Tyr Gly Gly Gly Ser Thr Ser
260 265 270

Ser Ser Lys Glu Ile Gly Phe Lys Pro Phe Tyr Asp Ala Ile Gly Phe
275 280 285

Asn Leu Phe Lys Leu Ser Asp Ile Asn Glu Asn Leu Lys Tyr Ala Ile
290 295 300

Phe Tyr Glu Asn Lys Asn Glu Tyr Tyr Asn Lys Lys Lys His Leu Asn
305 310 315 320

Gly Asp Ile Asn Phe Val Ser Gly Ser Leu Ile Phe Ile Pro Phe Asn
325 330 335

Asp Leu Tyr Met Ser Leu Ser Gly Ser Tyr Ser Val Thr Asp Arg Arg
340 345 350

Ser Lys Glu Asp Ser His His Asp Lys Gly Met Thr Phe Leu Ile Ser
355 360 365

Lys Arg Phe Leu Asp Asp Tyr Leu Val Glu Leu Asn Tyr Gln Lys Ile
370 375 380

Lys Thr Asp Tyr Ile Gly Lys Thr Thr Ile Tyr Thr Pro Ala His Ile
385 390 395 400

Phe Ile Arg Asp Leu Pro Pro Ile Lys Ile Lys Arg Glu Asp Ile Thr
405 410 415

Asp Ser Val Ser Leu Ser Leu Ser Asn Glu Ser Ile Asn Leu Phe Gly
420 425 430

Phe Tyr Pro Thr Leu Ser Phe Ser Tyr Thr Lys Asn Lys Ser Ser Asn

435 440 445

Leu Phe Tyr Ser Tyr Thr Glu Lys Asp Ile Phe Leu Asp Phe Lys Arg

450 455 460

Asn Phe

465

<210> 683

<211> 1464

<212> DNA

<213> X. poinarii SLAM 1

<400> 683

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ctgcctgttt atgccgatga agatacgccc cgaaaaatct ggcaggaagc acaacataac 120

caacaagaga atgaaacaaa cctgattgcg tcagagcctg tttttactga ggataatacg 180

tcactgattg tcattaatgg gcaaacattt caggttgaaa ataatattaa tgatattggt 240

caagcgcttt tcctcgccat aaaccaccaa caatggtcgg atgtcagacg cttcctcgcg 300

gcttatctga aattgccgga tcatgatgca atgttagtca attttgccca agggggtctg 360

gcacgccttg aaggcgattt ggatctcgct acctatcatt accaacagat cctgagccaa 420

caacctgatt ttacccgtat caaactggaa ctcgcccggg tctattttga ggatcataaa 480

actcgggaag ccgaacaact atttactgaa ttaaatgaac aacagctatt accaaaaacc 540

gtattgaaga acattcacag ttacctggaa gcgatagcgc tgagaaatgg ctggcgcgga 600

tctttttcta tgggttatgc ctataatgat aacgtcaata tgtcgtctga tcagaagaca 660

gtaaaaaatc tgataaacca aatagtagag cagaaaacat ccaaagccat caaagcttgg 720

ggcatgtctt atgacgcaac attaagccga cgttatcaac tttttggtca ccatggtatt 780

tttggtcgtg ggctgattta tggcgaaaat taccgtgatc accacaatga aaacgaaaac 840

acgttcctgc tggttggtgg ttacaactat aaaagcaaac gtcacgatgt ctcttttggc 900

ccattatttg aatataaaca acgtgcggac gataccttt accacgccgc cgggatcaaa 960

acggaatggc gatggggatt cacgcctcac acagccctaa atatagaact tgaatataag 1020

aaactgcgac atcaacaact ttaccgtaga aaagatggtg aattatcttc cacttacctc 1080

accttgtccc atgttatcaa caaagatttc gttctgtttg gtggcggtga ttggctttat 1140

cgcggcaacg acgactatcc tgtcgatcgt tatcagcaat ggggcattcg gacggggatt 1200

gccgggcaga tttatcccgg aatcaacggt tcactgtttg ctacgttgaa aaaacgccag 1260

tttggcgctt acaaccccat gctcaatgcc cgacgtcagg ataccgagca aatttacacc 1320

gcagtgataa aaataccagc cgccgaaata ttcagcatga caccatccct aacttttcgc 1380

caccgacaca atcgcagcaa tgtggattgg ctgtacagct ataacaaaaa tgaagtgttg 1440

ataagactgg aaaaatattt ttaa 1464

<210> 684

<211> 487

<212> PRT

<213> X. poinarii SLAM 1

<400> 684

Met Ser Asp Asn Lys Thr Thr Pro Val Leu Leu Ala Ala Leu Met Ala

1 5 10 15

Leu Cys Leu Ser Leu Pro Val Tyr Ala Asp Glu Asp Thr Pro Arg Lys

20 25 30

Ile Trp Gln Glu Ala Gln His Asn Gln Gln Glu Asn Glu Thr Asn Leu

35 40 45

Ile Ala Ser Glu Pro Val Phe Thr Glu Asp Asn Thr Ser Leu Ile Val

50 55 60

Ile Asn Gly Gln Thr Phe Gln Val Glu Asn Asn Ile Asn Asp Ile Gly

65 70 75 80

Gln Ala Leu Phe Leu Ala Ile Asn His Gln Gln Trp Ser Asp Val Arg

85 90 95

Arg Phe Leu Ala Ala Tyr Leu Lys Leu Pro Asp His Asp Ala Met Leu

100 105 110

Val Asn Phe Ala Gln Gly Gly Leu Ala Arg Leu Glu Gly Asp Leu Asp

115 120 125

Leu Ala Thr Tyr His Tyr Gln Gln Ile Leu Ser Gln Gln Pro Asp Phe

130 135 140

Thr Arg Ile Lys Leu Glu Leu Ala Arg Val Tyr Phe Glu Asp His Lys

145 150 155 160

Thr Arg Glu Ala Glu Gln Leu Phe Thr Glu Leu Asn Glu Gln Gln Leu

165 170 175

Leu Pro Lys Thr Val Leu Lys Asn Ile His Ser Tyr Leu Glu Ala Ile

180 185 190

Ala Leu Arg Asn Gly Trp Arg Gly Ser Phe Ser Met Gly Tyr Ala Tyr

195 200 205

Asn Asp Asn Val Asn Met Ser Ser Asp Gln Lys Thr Val Lys Asn Leu

210 215 220

Ile Asn Gln Ile Val Glu Gln Lys Thr Ser Lys Ala Ile Lys Ala Trp

225 230 235 240

Gly Met Ser Tyr Asp Ala Thr Leu Ser Arg Arg Tyr Gln Leu Phe Gly

245 250 255

His His Gly Ile Phe Gly Arg Gly Leu Ile Tyr Gly Glu Asn Tyr Arg

260 265 270

Asp His His Asn Glu Asn Glu Asn Thr Phe Leu Leu Val Gly Gly Tyr

275 280 285

Asn Tyr Lys Ser Lys Arg His Asp Val Ser Phe Gly Pro Leu Phe Glu

290 295 300

Tyr Lys Gln Arg Ala Asp Asp Thr Phe Tyr His Ala Ala Gly Ile Lys

305 310 315 320

Thr Glu Trp Arg Trp Gly Phe Thr Pro His Thr Ala Leu Asn Ile Glu

325 330 335

Leu Glu Tyr Lys Lys Leu Arg His Gln Gln Leu Tyr Arg Arg Lys Asp

340 345 350

Gly Glu Leu Ser Ser Thr Tyr Leu Thr Leu Ser His Val Ile Asn Lys

355 360 365

Asp Phe Val Leu Phe Gly Gly Gly Asp Trp Leu Tyr Arg Gly Asn Asp

370 375 380

Asp Tyr Pro Val Asp Arg Tyr Gln Gln Trp Gly Ile Arg Thr Gly Ile

385 390 395 400

Ala Gly Gln Ile Tyr Pro Gly Ile Asn Gly Ser Leu Phe Ala Thr Leu

405 410 415

Lys Lys Arg Gln Phe Gly Ala Tyr Asn Pro Met Leu Asn Ala Arg Arg

420 425 430

Gln Asp Thr Glu Gln Ile Tyr Thr Ala Val Ile Lys Ile Pro Ala Ala

435 440 445

Glu Ile Phe Ser Met Thr Pro Ser Leu Thr Phe Arg His Arg His Asn

450 455 460

Arg Ser Asn Val Asp Trp Leu Tyr Ser Tyr Asn Lys Asn Glu Val Leu

465 470 475 480

Ile Arg Leu Glu Lys Tyr Phe

485

<210> 685

<211> 1485

<212> DNA

<213> X. poinarii SLAM 2

<400> 685

atgtctgata aaagaaaagc gactgtctta ctgacaccac tgctgatctc agtcctctct 60

ctggacgtcc atgccagtca tgaagatatt caccagaaaa tctggcaaga agcacgatac 120

caccgacaac ataatcaaca acagaatgaa gcggatttaa caatgccgga gacccтttca 180

acccagaagg gtgtttcatg gctcgtcatt cacgggcaaa aattaaagat aagaaacaat 240

attaacgaca tcggccaggc actgtacctc gcgattaacg atcagcaatg gcaagaggtc 300

agctatttcc tggccattta tcaaaaaatg cctgcgcacg atccattact tgtctatctt 360

gctaaaggcg cgctggcacg tattcaaggc aatttggcac tcgcaatagc ttattatcaa 420

aagatcctgc accaacaacc caacttcacc cgcgccaaac tggaactggc ccgtctttat 480

tttgaagatc agaacaatcg ggcatctgaa acattattta aagagatcag gcaacagcat 540

caattaccca acatggtctt aaagaatatc gatcgttatc tgcaagcaat aaaccaaaga 600

gacggctggc acggttcctt ctcattcggt tatgcctatg atgataatat caacatgtct 660

ccaaatcaga aggcgagttg tctggtattc aaaagcggaa agtgtgtgtt agaacggcac 720

atcccgaaac ctatcaaaga agggggggaa acatataacg cgacattaag ctggcattat 780

caacttgttg gtcaccacgg tatttttggt cgtagcctga tttatggtga acattatccc 840

cattaccacg atgaaaacga aaatacgttt ctgctgatcg gcggttacaa ctataaaaac 900

agaacccagg atttttcctt tggtcctgag tttgaatata aacatcatgc cggcaatacc 960

gaataccatg ccatcggtgc caaaatagag tggtactgga acatcaccga tcaaaccgcc 1020

ctgaatgttg aacttgggca taagaaatta acttttcagc cgctttacca ctggaaagaa 1080

ggttcgcttt tttcatccta tttcagactc tctcatgcca tcagtgatag cactgttctg 1140

tttggcggtg gcaactggga ttaccgccat gctcaacaac ccacggttcg ctatcaacaa 1200

tggggagtca ataccggcat aaccgggcag ctctattccg gcatacatgg ctcgctgttt 1260

atcacgctga gaaaacaaca aatggggaga tatgaccctt tattgaacgc cagacgtcaa 1320

gataatgaac tgatctctac ggcttcggtt acatttcctg gcactaaaat cggcggaatg 1380

acccccctcca tcacgttcaa gcatcgacat aatcgcagta atgtgaactg gttatacagt 1440

tatgataaaa acgaagtaca aatccaacta gagaactatt tttaa 1485

<210> 686

<211> 494

<212> PRT

<213> X. poinarii SLAM 2

<400> 686

Met Ser Asp Lys Arg Lys Ala Thr Val Leu Leu Thr Pro Leu Leu Ile
1 5 10 15

Ser Val Leu Ser Leu Asp Val His Ala Ser His Glu Asp Ile His Gln
20 25 30

Lys Ile Trp Gln Glu Ala Arg Tyr His Arg Gln His Asn Gln Gln Gln
35 40 45

Asn Glu Ala Asp Leu Thr Met Pro Glu Thr Leu Ser Thr Gln Lys Gly
50 55 60

Val Ser Trp Leu Val Ile His Gly Gln Lys Leu Lys Ile Arg Asn Asn
65 70 75 80

Ile Asn Asp Ile Gly Gln Ala Leu Tyr Leu Ala Ile Asn Asp Gln Gln
85 90 95

Trp Gln Glu Val Ser Tyr Phe Leu Ala Ile Tyr Gln Lys Met Pro Ala
100 105 110

His Asp Pro Leu Leu Val Tyr Leu Ala Lys Gly Ala Leu Ala Arg Ile
115 120 125

Gln Gly Asn Leu Ala Leu Ala Ile Ala Tyr Tyr Gln Lys Ile Leu His
130 135 140

Gln Gln Pro Asn Phe Thr Arg Ala Lys Leu Glu Leu Ala Arg Leu Tyr

145 150 155 160

Phe Glu Asp Gln Asn Asn Arg Ala Ser Glu Thr Leu Phe Lys Glu Ile
165 170 175
Arg Gln Gln His Gln Leu Pro Asn Met Val Leu Lys Asn Ile Asp Arg
180 185 190
Tyr Leu Gln Ala Ile Asn Gln Arg Asp Gly Trp His Gly Ser Phe Ser
195 200 205
Phe Gly Tyr Ala Tyr Asp Asp Asn Ile Asn Met Ser Pro Asn Gln Lys
210 215 220

Ala Ser Cys Leu Val Phe Lys Ser Gly Lys Cys Val Leu Glu Arg His
225 230 235 240
Ile Pro Lys Pro Ile Lys Glu Gly Gly Glu Thr Tyr Asn Ala Thr Leu
245 250 255
Ser Trp His Tyr Gln Leu Val Gly His His Gly Ile Phe Gly Arg Ser
260 265 270
Leu Ile Tyr Gly Glu His Tyr Pro His Tyr His Asp Glu Asn Glu Asn
275 280 285

Thr Phe Leu Leu Ile Gly Gly Tyr Asn Tyr Lys Asn Arg Thr Gln Asp
290 295 300
Phe Ser Phe Gly Pro Glu Phe Glu Tyr Lys His His Ala Gly Asn Thr
305 310 315 320
Glu Tyr His Ala Ile Gly Ala Lys Ile Glu Trp Tyr Trp Asn Ile Thr
325 330 335
Asp Gln Thr Ala Leu Asn Val Glu Leu Gly His Lys Lys Leu Thr Phe
340 345 350

Gln Pro Leu Tyr His Trp Lys Glu Gly Ser Leu Phe Ser Ser Tyr Phe
355 360 365
Arg Leu Ser His Ala Ile Ser Asp Ser Thr Val Leu Phe Gly Gly Gly
370 375 380
Asn Trp Asp Tyr Arg His Ala Gln Gln Pro Thr Val Arg Tyr Gln Gln
385 390 395 400

Trp Gly Val Asn Thr Gly Ile Thr Gly Gln Leu Tyr Ser Gly Ile His
405 410 415

Gly Ser Leu Phe Ile Thr Leu Arg Lys Gln Gln Met Gly Arg Tyr Asp
420 425 430

Pro Leu Leu Asn Ala Arg Arg Gln Asp Asn Glu Leu Ile Ser Thr Ala
435 440 445

Ser Val Thr Phe Pro Gly Thr Lys Ile Gly Gly Met Thr Pro Ser Ile
450 455 460

Thr Phe Lys His Arg His Asn Arg Ser Asn Val Asn Trp Leu Tyr Ser
465 470 475 480

Tyr Asp Lys Asn Glu Val Gln Ile Gln Leu Glu Asn Tyr Phe
485 490

<210> 687

<211> 1467

<212> DNA

<213> X. szentirmaii SLAM 1

<400> 687

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ctgacggctc atgccgatga agatatttca cggaaaatct ggcaggaagc acaacataac 120

cagcaggaaa atgaaaacaa tctggtcacg ccagaccctg tttttatcga agatgacgct 180

tcattgattg tgattgatgg gcaaccgttt aaggtagaaa ataatctgag cgatatggga 240

caagcacttt accttgccac taaccatcgg cagtggccgg atgtcaggcg ttttctcgct 300

gcttaccaaa aattatccgg gcatgatgag atgttgcttc attttgccca aggcggattg 360

gcccgttttg aagaaaattt tgatcttgcc gcctatcact atcagcagat tttaaaccaa 420

caacctgatt tcacccgcat caaactggag ctggcccgcg tttattttga ggatcataag 480

actcgggaag ccagacagct gttttctgtg ttgagtgaac aaagtcaact accggaaacc 540

gtcttaaaaa atatcaacag ctatctggaa gctatagcgc tgagaaacag ttggcgcggc 600

tctttctctg cgggttatgg ctataacgat aatgtgaata tgtcttctga tagtggcgca 660

atccggtatt gcggcgaaaa aagctgtgta ttggttcaag taccaaaagc cgttaaagcg 720

tggggtttgt cttatgacgc catcctgaac cgccgttatc agtttgtcgg ccatcacggc 780

atttttggcc gtggtctgat gtatggggaa aattaccggc attaccatga cggggatgaa 840

aatacgctgt tgctggtcgg gggatataac tataaaagca ggcatcacga tgtttctttg 900

ggtcccttgt ttgaatataa gcaacttgca ggtgatattt tttatcgtgc aaacggtgcc 960

aaaacagaat ggcgatgggc tttgacctcc caaacagcct tcaatgcaga aattgaacat 1020

aaacgactgc gccatcaaca acaacttcag cggaaagacg gcacactttc atcaacttac 1080

tttactttat cccatgccct taatcgcgac atggttctgt ttggcggcgg ggattggctc 1140

tatcgcagca atgataaata cgacatggac agctaccggc aatggggagc tcgggcaggt 1200

attgccgggc aactctaccc cgggatcacc ggatcactgt ttgccacggt gaagaaacgg 1260

caatttgatg ccaaacaccc catgctgaac atcctccgtg aggataatga acaaatttat 1320

actgctgtca ttaaagtgcc tgccgctgaa atcgggggca tgacccctc tctgacgttc 1380

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<210> 688

<211> 488

<212> PRT

<213> X. szentirmaii SLAM 1

<400> 688

Met Pro Asp Asn Lys Thr Arg Pro Thr Leu Ser Ala Ala Leu Ala Val
1 5 10 15

Leu Cys Leu Ser Leu Thr Ala His Ala Asp Glu Asp Ile Ser Arg Lys
20 25 30

Ile Trp Gln Glu Ala Gln His Asn Gln Gln Glu Asn Glu Asn Asn Leu
35 40 45

Val Thr Pro Asp Pro Val Phe Ile Glu Asp Asp Ala Ser Leu Ile Val
50 55 60

Ile Asp Gly Gln Pro Phe Lys Val Glu Asn Asn Leu Ser Asp Met Gly
65 70 75 80

Gln Ala Leu Tyr Leu Ala Thr Asn His Arg Gln Trp Pro Asp Val Arg
85 90 95

Arg Phe Leu Ala Ala Tyr Gln Lys Leu Ser Gly His Asp Glu Met Leu
100 105 110

Leu His Phe Ala Gln Gly Gly Leu Ala Arg Phe Glu Glu Asn Phe Asp

115 120 125

Leu Ala Ala Tyr His Tyr Gln Gln Ile Leu Asn Gln Gln Pro Asp Phe
130 135 140
Thr Arg Ile Lys Leu Glu Leu Ala Arg Val Tyr Phe Glu Asp His Lys
145 150 155 160
Thr Arg Glu Ala Arg Gln Leu Phe Ser Val Leu Ser Glu Gln Ser Gln
165 170 175
Leu Pro Glu Thr Val Leu Lys Asn Ile Asn Ser Tyr Leu Glu Ala Ile
180 185 190

Ala Leu Arg Asn Ser Trp Arg Gly Ser Phe Ser Ala Gly Tyr Gly Tyr
195 200 205
Asn Asp Asn Val Asn Met Ser Ser Asp Ser Gly Ala Ile Arg Tyr Cys
210 215 220
Gly Glu Lys Ser Cys Val Leu Val Gln Val Pro Lys Ala Val Lys Ala
225 230 235 240
Trp Gly Leu Ser Tyr Asp Ala Ile Leu Asn Arg Arg Tyr Gln Phe Val
245 250 255

Gly His His Gly Ile Phe Gly Arg Gly Leu Met Tyr Gly Glu Asn Tyr
260 265 270
Arg His Tyr His Asp Gly Asp Glu Asn Thr Leu Leu Leu Val Gly Gly
275 280 285
Tyr Asn Tyr Lys Ser Arg His His Asp Val Ser Leu Gly Pro Leu Phe
290 295 300
Glu Tyr Lys Gln Leu Ala Gly Asp Ile Phe Tyr Arg Ala Asn Gly Ala
305 310 315 320

Lys Thr Glu Trp Arg Trp Ala Leu Thr Ser Gln Thr Ala Phe Asn Ala
325 330 335
Glu Ile Glu His Lys Arg Leu Arg His Gln Gln Gln Leu Gln Arg Lys
340 345 350
Asp Gly Thr Leu Ser Ser Thr Tyr Phe Thr Leu Ser His Ala Leu Asn
355 360 365

Arg Asp Met Val Leu Phe Gly Gly Gly Asp Trp Leu Tyr Arg Ser Asn
370 375 380

Asp Lys Tyr Asp Met Asp Ser Tyr Arg Gln Trp Gly Ala Arg Ala Gly
385 390 395 400
Ile Ala Gly Gln Leu Tyr Pro Gly Ile Thr Gly Ser Leu Phe Ala Thr
405 410 415
Val Lys Lys Arg Gln Phe Asp Ala Lys His Pro Met Leu Asn Ile Leu
420 425 430
Arg Glu Asp Asn Glu Gln Ile Tyr Thr Ala Val Ile Lys Val Pro Ala
435 440 445

Ala Glu Ile Gly Gly Met Thr Pro Ser Leu Thr Phe Arg His Arg Arg
450 455 460
Asn His Ser Asn Val Ala Trp Leu Tyr Ser Tyr Asn Lys Asn Glu Val
465 470 475 480
Leu Phe Arg Leu Glu Lys Tyr Phe
485

<210> 689
<211> 1551
<212> DNA
<213> X. szentirmaii SLAM 2
<400> 689
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gcatcactgg ccttatttca ctctccggca gcctattccc atcaagatgg tagtcatgaa 120

gcgtttacaa gtgaagaaag tacccattgg atctggaaag aaatacggca caatcaacag 180
caaaaccaac aaaaacatga agcgggcctg agtataccgg ctgttgtttc gacggaagag 240
gatgaatcaa aagagggtaa atcgtcgggc acaggtcatg ggcaaccctt tgagattgaa 300
aataatcctg aaaacctggc gaaggcactg tattttgcta ttaactatca acgctggtca 360
gaagttaaac gcttgctggc ggtttatcag aaaatacctg agagcaatcc gttactcgtc 420
gattttgctc agggcgggct ggcccgcatc gaaggaaagt tggcactttc tgccgctcat 480
tatcaaaaga tactgagtca acaacctaat tcaacacgca taaagctgga actggcccgt 540

gtctattttg aagattacaa caatcgggaa gctgaaaaat tatttagtga attaagagaa 600

cagcatcagt taccgaaaat agttctggag aatattgacc gttacctcca cgcaattccc 660

ctgagaagcc gttggcacag ttcattttcc atcagttctg tctatgatga taatttaaat 720

atgacgccaa atcaggaagc ccaatgtctg cttattctgg aaggacattg cctcatgcaa 780

cgaaaattac ccaaaatcat caaagagtgg gggagtacat atactgcgac attgagccgg 840

cgctattcat ttgctggtca tcacggtgtt tttggccgtg ccctgattta cggggaaaat 900

tacccacact atcatgacgc aaatgaaaac atattcttgc tggtcaatgg ctacaattat 960

aaaaacagga ctcatgactt atcctttggt cccttgtttg aatataaaca gagtgcagga 1020

aagacggaat attacgcgct cggcgctaaa ctcgagtggc aatgggcaat gactgcccag 1080

actggcctga atgtggaaat atcaaataag cggctgaatt atcagcaaaa tgacagtgtt 1140

aaaaatggct cactttcctc atcctatttc agcttatccc acttcatcaa cgacaaagtt 1200

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cagcaatggg ggataactgc cgggattgca ggacaaattt actctggcat taatggctcg 1320

ttggttgcca cactaaggca gctgcgtttt gcagcctaca acgccgtatt ggaggccaga 1380

cgccaagata atgagcaaat ttatacagcg tccattaaat ttccaaaagc caagatcgtg 1440

ggcatgaccc cctctttaat tttccggcat cgacataatc gcagtaatgt ggactggctt 1500

tacagctatg ataaaaacca agtgcaaata caactggaga aatattttta a 1551

<210> 690

<211> 516

<212> PRT

<213> X. szentirmaii SLAM 2

<400> 690

Met Asp Phe Ala Ala Met Thr Cys Lys Lys Lys Thr Ala Val Ser Thr

1 5 10 15

Leu Leu Phe Met Ala Ser Leu Ala Leu Phe His Ser Pro Ala Ala Tyr

20 25 30

Ser His Gln Asp Gly Ser His Glu Ala Phe Thr Ser Glu Glu Ser Thr

35 40 45

His Trp Ile Trp Lys Glu Ile Arg His Asn Gln Gln Gln Asn Gln Gln

50 55 60

Lys His Glu Ala Gly Leu Ser Ile Pro Ala Val Val Ser Thr Glu Glu

65 70 75 80

Asp Glu Ser Lys Glu Gly Lys Ser Ser Gly Thr Gly His Gly Gln Pro

85 90 95

Phe Glu Ile Glu Asn Asn Pro Glu Asn Leu Ala Lys Ala Leu Tyr Phe

100 105 110

Ala Ile Asn Tyr Gln Arg Trp Ser Glu Val Lys Arg Leu Leu Ala Val

115 120 125

Tyr Gln Lys Ile Pro Glu Ser Asn Pro Leu Leu Val Asp Phe Ala Gln

130 135 140

Gly Gly Leu Ala Arg Ile Glu Gly Lys Leu Ala Leu Ser Ala Ala His

145 150 155 160

Tyr Gln Lys Ile Leu Ser Gln Gln Pro Asn Ser Thr Arg Ile Lys Leu

165 170 175

Glu Leu Ala Arg Val Tyr Phe Glu Asp Tyr Asn Asn Arg Glu Ala Glu

180 185 190

Lys Leu Phe Ser Glu Leu Arg Glu Gln His Gln Leu Pro Lys Ile Val

195 200 205

Leu Glu Asn Ile Asp Arg Tyr Leu His Ala Ile Pro Leu Arg Ser Arg

210 215 220

Trp His Ser Ser Phe Ser Ile Ser Ser Val Tyr Asp Asp Asn Leu Asn

225 230 235 240

Met Thr Pro Asn Gln Glu Ala Gln Cys Leu Leu Ile Leu Glu Gly His

245 250 255

Cys Leu Met Gln Arg Lys Leu Pro Lys Ile Ile Lys Glu Trp Gly Ser

260 265 270

Thr Tyr Thr Ala Thr Leu Ser Arg Arg Tyr Ser Phe Ala Gly His His

275 280 285

Gly Val Phe Gly Arg Ala Leu Ile Tyr Gly Glu Asn Tyr Pro His Tyr

290 295 300

His Asp Ala Asn Glu Asn Ile Phe Leu Leu Val Asn Gly Tyr Asn Tyr

305 310 315 320

Lys Asn Arg Thr His Asp Leu Ser Phe Gly Pro Leu Phe Glu Tyr Lys

325 330 335

Gln Ser Ala Gly Lys Thr Glu Tyr Tyr Ala Leu Gly Ala Lys Leu Glu

340 345 350

Trp Gln Trp Ala Met Thr Ala Gln Thr Gly Leu Asn Val Glu Ile Ser

355 360 365

Asn Lys Arg Leu Asn Tyr Gln Gln Asn Asp Ser Val Lys Asn Gly Ser

370 375 380

Leu Ser Ser Ser Tyr Phe Ser Leu Ser His Phe Ile Asn Asp Lys Val

385 390 395 400

Ile Leu Phe Gly Gly Gly Gln Trp Ser Tyr Gln Asp Ser Gln Arg Pro

405 410 415

Ser Ser Arg Tyr Gln Gln Trp Gly Ile Thr Ala Gly Ile Ala Gly Gln

420 425 430

Ile Tyr Ser Gly Ile Asn Gly Ser Leu Val Ala Thr Leu Arg Gln Leu

435 440 445

Arg Phe Ala Ala Tyr Asn Ala Val Leu Glu Ala Arg Arg Gln Asp Asn

450 455 460

Glu Gln Ile Tyr Thr Ala Ser Ile Lys Phe Pro Lys Ala Lys Ile Val

465 470 475 480

Gly Met Thr Pro Ser Leu Ile Phe Arg His Arg His Asn Arg Ser Asn

485 490 495

Val Asp Trp Leu Tyr Ser Tyr Asp Lys Asn Gln Val Gln Ile Gln Leu

500 505 510

Glu Lys Tyr Phe

515

<210> 691

<211> 1413

<212> DNA

<213> Xanthomonas sp. SHU199 SLAM 1

<400> 691

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ctcgaacgcg aacgcgcgct ggtgcaggag ccggccaccg gcgagcgacc gagcatcgtc 120

gtcgacggca tgtcctacgt cgtcgcgccg accgccaacg acgtcggccg cgcgctgtac 180

ctgtcgcttc agaacaaaca atggccggcc gtgcagcggt tcctcgccga atacctgacc 240

ctgcccgagc gcgacccgct gctggtgcat tacgcgcagg gcgcggtggc gcgcaaccgc 300

ggccgctacg gcgacgccga gcgggagtac cgcgcgctgc tgaagttgca gccggacttc 360

ctgcccgggc gtctggaact ggcgcgggtg ctgttcgagg accagcagga ccgcgaggcc 420

gaacaggcgt tcgcagccat tgccgcctcg atcgacgctg gcgatcccag gaccgagggt 480

gtgcgcaaca ccatcgccgg cttccgccag gccttggcca accggcgcga ctggaacggc 540

accttcgcgc tgggaccggc ctggagcgac aacgtcaatc gcacctcggc cagttccatc 600

tgcctgctgc cgctggaagg gcgctgctac ttcagccgca gcacgcccac ggcgatcgtc 660

gccttcggcg ccgactacga tgccagcgcc gaacggcgcc tgccgctgcg cggtcaccat 720

gggctgtacc tgcgcacgct gctgttcggc cagagctatc gcgacaacgg cgcctacaac 780

gaactcaccg cgctgaccca ggccggttac agctatcgca gcggccgcca cagcctggcg 840

ctggcgccct cgttcgatta ctacgcgctg ggcaaccagg cgctgtatgg cgcctggggc 900

gtgcatgcgg aatggagttg gagcctgtcg ccgcggtcgc tggtcaagct ggaaggcgac 960

tggaaggaca tgcgctaccg ccgccgcgct tacgccgcca gctacgacgc gatcgtgcgc 1020

ggcgcctcgg ccacctattt ccgcagcctg gatgcgcgct ggaccgtgtt cgccggggtc 1080

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acctacaccc tggtgctgcg cgcgccgcgc ctggcggtcg gcggcttcgt gccgctgctg 1320

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accatcaacc tgaaactgga gcgcgccctg tga 1413

<210> 692

<211> 477

<212> PRT

<213> Xanthomonas sp. SHU199 SLAM 1

<400> 692

Met Ala Ala Ala Pro Cys Ala Met Ala Gln Ala Gln Asp Asp Thr Arg

1 5 10 15

Arg Leu Leu Glu Gln Arg Asp Gln Gly Gln Ala Leu Glu Arg Glu Arg

20 25 30

Ala Leu Val Gln Glu Pro Ala Thr Gly Glu Arg Pro Ser Ile Val Val

35 40 45

Asp Gly Met Ser Tyr Val Val Ala Pro Thr Ala Asn Asp Val Gly Arg

50 55 60

Ala Leu Tyr Leu Ser Leu Gln Asn Lys Gln Trp Pro Ala Val Gln Arg

65 70 75 80

Phe Leu Ala Glu Tyr Leu Thr Leu Pro Glu Arg Asp Pro Leu Leu Val

85 90 95

His Tyr Ala Gln Gly Ala Val Ala Arg Asn Arg Gly Arg Tyr Gly Asp

100 105 110

Ala Glu Arg Glu Tyr Arg Ala Leu Leu Lys Leu Gln Pro Asp Phe Leu

115 120 125

Pro Gly Arg Leu Glu Leu Ala Arg Val Leu Phe Glu Asp Gln Gln Asp

130 135 140

Arg Glu Ala Glu Gln Ala Phe Ala Ala Ile Ala Ala Ser Ile Asp Ala

145 150 155 160

Gly Asp Pro Arg Thr Glu Gly Val Arg Asn Thr Ile Ala Gly Phe Arg

165 170 175

Gln Ala Leu Ala Asn Arg Arg Asp Trp Asn Gly Thr Phe Ala Leu Gly

180 185 190

Pro Ala Trp Ser Asp Asn Val Asn Arg Thr Ser Ala Ser Ser Ile Cys

195 200 205

Leu Leu Pro Leu Glu Gly Arg Cys Tyr Phe Ser Arg Ser Thr Pro Thr

210 215 220

Ala Ile Val Ala Phe Gly Ala Asp Tyr Asp Ala Ser Ala Glu Arg Arg

225 230 235 240

Leu Pro Leu Arg Gly His His Gly Leu Tyr Leu Arg Thr Leu Leu Phe

245 250 255

Gly Gln Ser Tyr Arg Asp Asn Gly Ala Tyr Asn Glu Leu Thr Ala Leu

260 265 270

Thr Gln Ala Gly Tyr Ser Tyr Arg Ser Gly Arg His Ser Leu Ala Leu

275 280 285

Ala Pro Ser Phe Asp Tyr Tyr Ala Leu Gly Asn Gln Ala Leu Tyr Gly

290 295 300

Ala Trp Gly Val His Ala Glu Trp Ser Trp Ser Leu Ser Pro Arg Ser

305 310 315 320

Leu Val Lys Leu Glu Gly Asp Trp Lys Asp Met Arg Tyr Arg Arg Arg

325 330 335

Ala Tyr Ala Ala Ser Tyr Asp Ala Ile Val Arg Gly Ala Ser Ala Thr

340 345 350

Tyr Phe Arg Ser Leu Asp Ala Arg Trp Thr Val Phe Ala Gly Val Asp

355 360 365

Ala Ser Asp Thr Ala Ala Val Gln Asp Thr Glu Ala Tyr Leu Gln Arg

370 375 380

Gly Val Arg Leu Gly Gly Ser Arg Gln Trp Pro Gly Gly Ile Asp Ala

385 390 395 400

Thr Val Phe Ala Ser Tyr Arg Leu Arg Asp Tyr Gly Ala Tyr Ser Ala

405 410 415

Val Leu Arg Ala Arg Arg His Asp Ala Glu Arg Thr Tyr Thr Leu Val

420 425 430

Leu Arg Ala Pro Arg Leu Ala Val Gly Gly Phe Val Pro Leu Leu Thr

435 440 445

Leu Arg His Asn Arg Val Arg Ser Asn Val Asp Trp Leu Tyr Gly Tyr

450 455 460

Glu Arg Asn Thr Ile Asn Leu Lys Leu Glu Arg Ala Leu

465 470 475

<210> 693

<211> 1413

<212> DNA

<213> Xanthomonas sp. SHU308 SLAM 1

<400> 693

atggcgcagg cgcaggacga tacccgacgc ctgctcgaac agcgcgacca gggccaggcg 60

ctcgaacgcg aacgcgcgct ggtgcaggag ccggccaccg gcgagcgacc gagcatcgtc 120

gtcgacggca tgtcctacgt cgtcgcgccg accgccaacg acgtcggccg cgcgctgtac 180

ctgtcgcttc agaacaaaca atggccggcc gtgcagcggt tcctcgccga atacctgacc 240

ctgcccgagc gcgacccgct gctggtgcat tacgcgcagg gcgcggtggc gcgcaaccgc 300

ggccgctacg gcgacgccga gcgggagtac cgcgcgctgc tgacgttgca gccggacttc 360

ctgcccgggc gtctggaact ggcgcgggtg ctgttcgagg accagcagga ccgcgaggcc 420

gaacaggcgt tcgcagccat tgccgcctcg atcgacgctg gcgatcccag gaccgagggt 480

gtgcgcaaca ccatcgccgg cttccgccag gccttggcca accggcgcga ctggaacggc 540

accttcgcgc tgggaccggc ctggagcgac aacgtcaatc gcacctcggc cagttccatc 600

tgcctgctgc cgctggaagg gcgctgctac ttcagccgca gcacgcccac ggcgatcgtc 660

gccttcggcg ccgactacga tgccagcgcc gaacggcgcc tgccgctgcg cggtcaccat 720

gggctgtacc tgcgcacgct gctgttcggc cagagctatc gcgacaacgg cgcctacaac 780

gaacttaccg cgctgaccca ggccggttac agctatcgca gcggccgcca cagcctggcg 840

ctggcgccct cgttcgatta ctacgcgctg ggcaaccagg cgctgtatgg cgcctggggc 900

gtgcatgcgg aatggagttg gagcctgtcg ccgcggtcgc tggtcaagct ggaaggcgac 960

tggaaggaca tgcgctaccg ccgccgcgct tacgccgcca gctacgacgc gatcatgcgc 1020

ggcgcctcgg ccacctattt ccgcagcctg gatgcgcgct ggaccgtgtt cgccggggtc 1080

gacgccagcg acactgccgc cgtgcaggac accgaggcgt acctgcagcg cggcgtccgc 1140

ctgggcggtt cgcggcaatg gccgggaggc atcgacgcca ccgtgttcgc ctcctaccgg 1200

ctgcgcgact acggcgccta cagcgcggtc ctgcgcgcac gccgccacga tgccgagcgc 1260

acctacaccc tggtgctgcg cgcgccgcgc ctggcggtcg gcggcttcgt gccgctgctg 1320

acgctgcgcc acaaccgcgt gcgcagcaac gtcgactggc tgtacggcta cgagcgcaac 1380

accatcaacc tgaaactgga gcgcgccctg tga 1413

<210> 694

<211> 477

<212> PRT

<213> Xanthomonas sp. SHU308 SLAM 1

<400> 694

Met Ala Ala Ala Pro Cys Ala Met Ala Gln Ala Gln Asp Asp Thr Arg

1 5 10 15

Arg Leu Leu Glu Gln Arg Asp Gln Gly Gln Ala Leu Glu Arg Glu Arg

20 25 30

Ala Leu Val Gln Glu Pro Ala Thr Gly Glu Arg Pro Ser Ile Val Val

35 40 45

Asp Gly Met Ser Tyr Val Val Ala Pro Thr Ala Asn Asp Val Gly Arg

50 55 60

Ala Leu Tyr Leu Ser Leu Gln Asn Lys Gln Trp Pro Ala Val Gln Arg

65 70 75 80

Phe Leu Ala Glu Tyr Leu Thr Leu Pro Glu Arg Asp Pro Leu Leu Val

85 90 95

His Tyr Ala Gln Gly Ala Val Ala Arg Asn Arg Gly Arg Tyr Gly Asp

100 105 110

Ala Glu Arg Glu Tyr Arg Ala Leu Leu Thr Leu Gln Pro Asp Phe Leu

115 120 125

Pro Gly Arg Leu Glu Leu Ala Arg Val Leu Phe Glu Asp Gln Gln Asp

130 135 140

Arg Glu Ala Glu Gln Ala Phe Ala Ala Ile Ala Ala Ser Ile Asp Ala

145 150 155 160

Gly Asp Pro Arg Thr Glu Gly Val Arg Asn Thr Ile Ala Gly Phe Arg

165 170 175

Gln Ala Leu Ala Asn Arg Arg Asp Trp Asn Gly Thr Phe Ala Leu Gly

180 185 190

Pro Ala Trp Ser Asp Asn Val Asn Arg Thr Ser Ala Ser Ser Ile Cys

195 200 205

Leu Leu Pro Leu Glu Gly Arg Cys Tyr Phe Ser Arg Ser Thr Pro Thr

210 215 220

Ala Ile Val Ala Phe Gly Ala Asp Tyr Asp Ala Ser Ala Glu Arg Arg

225 230 235 240

Leu Pro Leu Arg Gly His His Gly Leu Tyr Leu Arg Thr Leu Leu Phe

245 250 255

Gly Gln Ser Tyr Arg Asp Asn Gly Ala Tyr Asn Glu Leu Thr Ala Leu

260 265 270

Thr Gln Ala Gly Tyr Ser Tyr Arg Ser Gly Arg His Ser Leu Ala Leu

275 280 285

Ala Pro Ser Phe Asp Tyr Tyr Ala Leu Gly Asn Gln Ala Leu Tyr Gly

290 295 300

Ala Trp Gly Val His Ala Glu Trp Ser Trp Ser Leu Ser Pro Arg Ser

305 310 315 320

Leu Val Lys Leu Glu Gly Asp Trp Lys Asp Met Arg Tyr Arg Arg Arg

325 330 335

Ala Tyr Ala Ala Ser Tyr Asp Ala Ile Met Arg Gly Ala Ser Ala Thr

340 345 350

Tyr Phe Arg Ser Leu Asp Ala Arg Trp Thr Val Phe Ala Gly Val Asp

355 360 365

Ala Ser Asp Thr Ala Ala Val Gln Asp Thr Glu Ala Tyr Leu Gln Arg

370 375 380

Gly Val Arg Leu Gly Gly Ser Arg Gln Trp Pro Gly Gly Ile Asp Ala

385 390 395 400

Thr Val Phe Ala Ser Tyr Arg Leu Arg Asp Tyr Gly Ala Tyr Ser Ala

405 410 415

Val Leu Arg Ala Arg Arg His Asp Ala Glu Arg Thr Tyr Thr Leu Val

420 425 430

Leu Arg Ala Pro Arg Leu Ala Val Gly Gly Phe Val Pro Leu Leu Thr

435 440 445

Leu Arg His Asn Arg Val Arg Ser Asn Val Asp Trp Leu Tyr Gly Tyr

450 455 460

Glu Arg Asn Thr Ile Asn Leu Lys Leu Glu Arg Ala Leu

465 470 475

<210> 695

<211> 762

<212> DNA

<213> A. actinomycetemcomitans SLP 1a

<400> 695

atgagtaatt ttaaacactc aatttcaaaa ttgagtctta ttgtattaac atcattaacc 60

gttgcagctt gcggaagtgg cggcggtggt tccggtactc cgacacctgt agttaatact 120

ggcgctgtat tttcagtttc agaaaaaggt gctgtatcaa aaacttcaat aaatagtaat 180

tcaaatctaa aagcgttaga tattgctgga cataaaatta atctacttga agattctgat 240

agttatagtt ttataggcga gaacaatagc ctttatcaat atggttattt atcttctaag 300

acagaagatt tccctaatga tcaagtattt tacaatggag aaattgctaa aaatattcct 360

aatgcgggtg aagtccgcta ttccggtagt gtagttatag gtggtcagaa gagtgatggc 420

gcccctatcg gagctagtga gcaattaaca aaaggtaaag cagaaattag agctgatttt 480

gggtcaaaaa aattagatgg taaatttatt tttaagcctg atactttaga gcgtacagga 540

gaattatctg aacaagtggt tcaaatgaac gcaactattt ctaataacag ttttgaggga 600

aaagctacat ctaagcattt atctggcgag gctaccgtgg agggtaaatt ctatggtaat 660

aatgccgaag cattggctgg cgcatttcat agatcaggag acaaaccttg gtatggtgcg 720

tttggtgcaa aaaaagatga cagtgctaaa cctaatccat ag 762

<210> 696

<211> 253

<212> PRT

<213> A. actinomycetemcomitans SLP 1a

<400> 696

Met Ser Asn Phe Lys His Ser Ile Ser Lys Leu Ser Leu Ile Val Leu
1 5 10 15

Thr Ser Leu Thr Val Ala Ala Cys Gly Ser Gly Gly Gly Gly Ser Gly
20 25 30

Thr Pro Thr Pro Val Val Asn Thr Gly Ala Val Phe Ser Val Ser Glu
35 40 45

Lys Gly Ala Val Ser Lys Thr Ser Ile Asn Ser Asn Ser Asn Leu Lys
50 55 60

Ala Leu Asp Ile Ala Gly His Lys Ile Asn Leu Leu Glu Asp Ser Asp
65 70 75 80

Ser Tyr Ser Phe Ile Gly Glu Asn Asn Ser Leu Tyr Gln Tyr Gly Tyr
85 90 95

Leu Ser Ser Lys Thr Glu Asp Phe Pro Asn Asp Gln Val Phe Tyr Asn

100 105 110

Gly Glu Ile Ala Lys Asn Ile Pro Asn Ala Gly Glu Val Arg Tyr Ser
115 120 125
Gly Ser Val Val Ile Gly Gly Gln Lys Ser Asp Gly Ala Pro Ile Gly
130 135 140
Ala Ser Glu Gln Leu Thr Lys Gly Lys Ala Glu Ile Arg Ala Asp Phe
145 150 155 160
Gly Ser Lys Lys Leu Asp Gly Lys Phe Ile Phe Lys Pro Asp Thr Leu
165 170 175

Glu Arg Thr Gly Glu Leu Ser Glu Gln Val Val Gln Met Asn Ala Thr
180 185 190
Ile Ser Asn Asn Ser Phe Glu Gly Lys Ala Thr Ser Lys His Leu Ser
195 200 205
Gly Glu Ala Thr Val Glu Gly Lys Phe Tyr Gly Asn Asn Ala Glu Ala
210 215 220
Leu Ala Gly Ala Phe His Arg Ser Gly Asp Lys Pro Trp Tyr Gly Ala
225 230 235 240

Phe Gly Ala Lys Lys Asp Asp Ser Ala Lys Pro Asn Pro
245 250

<210> 697
<211> 792
<212> DNA
<213> A. baumannii SLP 1a
<400> 697
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gcaattgaag gcgcttcaag caatgaagca aatatcaaag tcggtgcggc agcaaatgcc 120
agtcatagcg gtggaacagc tgccgtttca gtagaggcgg caggtgcacc ttataatgca 180
ttcaccggtt ttagttcact caaaggtcta gcgcaggcat ttgctgcaca aggaaccagc 240
aatagcaatg taactgtggg tagcaagagc tttaatatct ctcacattcc tgtctctgca 300

atgccgcctt cacatagcgc tttaggtaat tttaactttg gccaggtcgg cacacaggaa 360
gtttatttcg gtgaatggtg gaaagcaggt gatacgcctg ccagcgcaag ccatacggtt 420

tattacgcag gtgacaatac caataccaca gtacctaccg cagggacggc aacctatacc 480

gttgcaggga ttaatggctt ggtagccaat ctgttaactg gtaatttcac tgcaaacttc 540

ggtgcaggca cgctcgaagg atcattaacc ggaaccggta ctagcgtttc aaacttaaca 600

ctggatggcg tgacctttaa tccgggttcg gctgcattta gcggttttgc aattgcaaat 660

ggtaccgccg gcttaaatga ttccggagct gttcagggac atttctttgg cgcaaatgcg 720

gctgctttag cgggtatcgc gaaatttgac aatgtgtctt ataacacggc atttggcggt 780

gcgaaaaact aa 792

<210> 698

<211> 263

<212> PRT

<213> A. baumannii SLP 1a

<400> 698

Met Lys Ile Ser Gln Leu Phe Ile Ala Leu Val Ala Cys Ser Ala Val
1 5 10 15

Phe Ser His Ala Ala Ile Glu Gly Ala Ser Ser Asn Glu Ala Asn Ile
20 25 30

Lys Val Gly Ala Ala Ala Asn Ala Ser His Ser Gly Gly Thr Ala Ala
35 40 45

Val Ser Val Glu Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Ala Ala Gln Gly Thr Ser
65 70 75 80

Asn Ser Asn Val Thr Val Gly Ser Lys Ser Phe Asn Ile Ser His Ile
85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn
100 105 110

Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys
115 120 125

Ala Gly Asp Thr Pro Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly
130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ala Gly Thr Ala Thr Tyr Thr
145 150 155 160

Val Ala Gly Ile Asn Gly Leu Val Ala Asn Leu Leu Thr Gly Asn Phe

165 170 175

Thr Ala Asn Phe Gly Ala Gly Thr Leu Glu Gly Ser Leu Thr Gly Thr

180 185 190

Gly Thr Ser Val Ser Asn Leu Thr Leu Asp Gly Val Thr Phe Asn Pro

195 200 205

Gly Ser Ala Ala Phe Ser Gly Phe Ala Ile Ala Asn Gly Thr Ala Gly

210 215 220

Leu Asn Asp Ser Gly Ala Val Gln Gly His Phe Phe Gly Ala Asn Ala

225 230 235 240

Ala Ala Leu Ala Gly Ile Ala Lys Phe Asp Asn Val Ser Tyr Asn Thr

245 250 255

Ala Phe Gly Gly Ala Lys Asn

260

<210> 699

<211> 759

<212> DNA

<213> A. bereziniae SLP 1a

<400> 699

atgaaacttc aatctatctc actggctgtt ttactatcta ttggtttagt cggtgctgct 60

caggcagcta tagtcggtga gtcgagtgat gttagtaaaa tcgaggtcgc agctacaggt 120

tcactggggc caaaccatcc aaactcgggt gtaggtttcg gaatcaaaga cttttataac 180

ggcgcagttg ttgcattctc gggttttaac ggttatgcag atggcaatgg ggtagtgcgt 240

ttgaacccgt atttaccagg tcttccgcca acacatgctg ctatcggtta tgccaactat 300

aaacaagtgc ctacgcaaga cgtttggttt ggtgagtgga atgccgaagc caaagatgcc 360

agtggaaacc gtctaggtac agttgatcca acaacacata ctgtttatta caatggtaaa 420

gatgcggata ccagcgtacc gtctacaggt actgcaaatt atagcgttca aggtgtcaat 480

aattataatg gctctaattt gttgtcaggt acgtttactg caaactttgc aaccaaacag 540

ttaactggtt cattgagcga tagttcacgt acctttaatt taggtactgc aacaattaat 600

aatgacgcta cgattagtgg ttcaaatgca tcttggacag gtggaccttc tggtggtgat 660

gtttcaggtc agttttataa tagccaaagc agcttagcag gcattgcaac atttgtaggt 720

aacaatacat atgatgttgc attcggcggt aagaaataa 759

<210> 700

<211> 252

<212> PRT

<213> A. bereziniae SLP 1a

<400> 700

Met Lys Leu Gln Ser Ile Ser Leu Ala Val Leu Leu Ser Ile Gly Leu
1 5 10 15

Val Gly Ala Ala Gln Ala Ala Ile Val Gly Glu Ser Ser Asp Val Ser
20 25 30

Lys Ile Glu Val Ala Ala Thr Gly Ser Leu Gly Pro Asn His Pro Asn
35 40 45

Ser Gly Val Gly Phe Gly Ile Lys Asp Phe Tyr Asn Gly Ala Val Val
50 55 60

Ala Phe Ser Gly Phe Asn Gly Tyr Ala Asp Gly Asn Gly Val Val Arg
65 70 75 80

Leu Asn Pro Tyr Leu Pro Gly Leu Pro Pro Thr His Ala Ala Ile Gly
85 90 95

Tyr Ala Asn Tyr Lys Gln Val Pro Thr Gln Asp Val Trp Phe Gly Glu
100 105 110

Trp Asn Ala Glu Ala Lys Asp Ala Ser Gly Asn Arg Leu Gly Thr Val
115 120 125

Asp Pro Thr Thr His Thr Val Tyr Tyr Asn Gly Lys Asp Ala Asp Thr
130 135 140

Ser Val Pro Ser Thr Gly Thr Ala Asn Tyr Ser Val Gln Gly Val Asn
145 150 155 160

Asn Tyr Asn Gly Ser Asn Leu Leu Ser Gly Thr Phe Thr Ala Asn Phe
165 170 175

Ala Thr Lys Gln Leu Thr Gly Ser Leu Ser Asp Ser Ser Arg Thr Phe
180 185 190

Asn Leu Gly Thr Ala Thr Ile Asn Asn Asp Ala Thr Ile Ser Gly Ser
195 200 205

Asn Ala Ser Trp Thr Gly Gly Pro Ser Gly Gly Asp Val Ser Gly Gln
210 215 220

Phe Tyr Asn Ser Gln Ser Ser Leu Ala Gly Ile Ala Thr Phe Val Gly
225 230 235 240
Asn Asn Thr Tyr Asp Val Ala Phe Gly Gly Lys Lys
245 250

<210> 701
<211> 1245
<212> DNA
<213> A. capsulatus SLP 2a
<400> 701

atgaaaaata ttttaaataa acaagtatta aatacggcag caacaatttt gttatctatc 60
gtagtaacgg cgtgttcatc aggaggaagt gatcagcccg gaattgatca aagtacacgc 120
ttaagccaag tggcggtaca aaatttatta gaagataaat tacaagctca agaacacctt 180

gaagtaataa aaaaggcatt ggttgatctt caattagctt tagttaaagc acaatcggct 240
aattcgacat cagatgcaca acaagtatta aaagatgcca atagcttatt agaaaaagcg 300
aaattggcag ccgaaaatgc taaaaatgaa gctaaaaatg ccgcttcacg ggtctcaaat 360
gcaagtgcgc aactatctac tgctgtagat gaagcgaata atgtaatgaa cattgcgaat 420
caggcaaata gcgtgttatt agaggcaact aacaccttta atcaaattca gtcggtgctt 480
gctgatttaa ctcaaaaaga ggtgacaaaa gccgaagagc agacgaaaaa aatcgcacaa 540
gaaaagcaaa ttgcgacaaa taaagcgatt actactgcaa tatcttataa caaccttgat 600

tcgattgtgc atgattatag taatagtgaa gcacgagaag tattattagc aaaattacaa 660
aaacaaggtt caaatgcgcc ggcatcttgt agtaatgcaa aaacgtcaac ttgctataaa 720
gaagtggcaa gaggtagtgt catagtcaat tacaaccaag cttactcaag ttatgcggtt 780
attcgtgaga cttacaataa tgaaaactta cagccgagta atgcttttat tgtattagcg 840
aaggagagtg atttaactac agagcgtgcg gcggttgtaa atgcgaccta tacgggtaaa 900
gcgtcttata gtgcgaaaaa tgtgcctgct gtaatgacac gagacttcac cttaaaagtg 960
gaaaatgaca aggtcagcgg ctcggttttc caaaaaacga ttaattcgaa aggtatagaa 1020

aaagtaacgg aaaatgtagc gttaaatgaa ggaaagatca gggttgagaa cggcgtagta 1080
ggctttagtg gctcagcaaa attcggggcg attgcaagca atgccgaagg ttcttataaa 1140
ggcgtattcg taggcaaaaa tgcggaagaa gtgatcggta cttttgaaac aaatagcaca 1200

gaaaaagcct cttcggcgca aggtgctttt gcaggaaaaa aataa 1245

<210> 702

<211> 414

<212> PRT

<213> A. capsulatus SLP 2a

<400> 702

Met Lys Asn Ile Leu Asn Lys Gln Val Leu Asn Thr Ala Ala Thr Ile
1 5 10 15

Leu Leu Ser Ile Val Val Thr Ala Cys Ser Ser Gly Gly Ser Asp Gln
20 25 30

Pro Gly Ile Asp Gln Ser Thr Arg Leu Ser Gln Val Ala Val Gln Asn
35 40 45

Leu Leu Glu Asp Lys Leu Gln Ala Gln Glu His Leu Glu Val Ile Lys
50 55 60

Lys Ala Leu Val Asp Leu Gln Leu Ala Leu Val Lys Ala Gln Ser Ala
65 70 75 80

Asn Ser Thr Ser Asp Ala Gln Gln Val Leu Lys Asp Ala Asn Ser Leu
85 90 95

Leu Glu Lys Ala Lys Leu Ala Ala Glu Asn Ala Lys Asn Glu Ala Lys
100 105 110

Asn Ala Ala Ser Arg Val Ser Asn Ala Ser Ala Gln Leu Ser Thr Ala
115 120 125

Val Asp Glu Ala Asn Asn Val Met Asn Ile Ala Asn Gln Ala Asn Ser
130 135 140

Val Leu Leu Glu Ala Thr Asn Thr Phe Asn Gln Ile Gln Ser Val Leu
145 150 155 160

Ala Asp Leu Thr Gln Lys Glu Val Thr Lys Ala Glu Glu Gln Thr Lys
165 170 175

Lys Ile Ala Gln Glu Lys Gln Ile Ala Thr Asn Lys Ala Ile Thr Thr
180 185 190

Ala Ile Ser Tyr Asn Asn Leu Asp Ser Ile Val His Asp Tyr Ser Asn

195 200 205

Ser Glu Ala Arg Glu Val Leu Leu Ala Lys Leu Gln Lys Gln Gly Ser
210 215 220
Asn Ala Pro Ala Ser Cys Ser Asn Ala Lys Thr Ser Thr Cys Tyr Lys
225 230 235 240
Glu Val Ala Arg Gly Ser Val Ile Val Asn Tyr Asn Gln Ala Tyr Ser
245 250 255
Ser Tyr Ala Val Ile Arg Glu Thr Tyr Asn Asn Glu Asn Leu Gln Pro
260 265 270

Ser Asn Ala Phe Ile Val Leu Ala Lys Glu Ser Asp Leu Thr Thr Glu
275 280 285
Arg Ala Ala Val Val Asn Ala Thr Tyr Thr Gly Lys Ala Ser Tyr Ser
290 295 300
Ala Lys Asn Val Pro Ala Val Met Thr Arg Asp Phe Thr Leu Lys Val
305 310 315 320
Glu Asn Asp Lys Val Ser Gly Ser Val Phe Gln Lys Thr Ile Asn Ser
325 330 335

Lys Gly Ile Glu Lys Val Thr Glu Asn Val Ala Leu Asn Glu Gly Lys
340 345 350
Ile Arg Val Glu Asn Gly Val Val Gly Phe Ser Gly Ser Ala Lys Phe
355 360 365
Gly Ala Ile Ala Ser Asn Ala Glu Gly Ser Tyr Lys Gly Val Phe Val
370 375 380
Gly Lys Asn Ala Glu Glu Val Ile Gly Thr Phe Glu Thr Asn Ser Thr
385 390 395 400

Glu Lys Ala Ser Ser Ala Gln Gly Ala Phe Ala Gly Lys Lys
405 410

<210> 703
<211> 792
<212> DNA
<213> A. gyllenbergii SLP 1a

<400> 703

atgaaaatct ctcaactgtt catcggtctt gttgcatgtt ctgctgtgtt tgcacatgca 60

ggtattgatg gtgcttcaag taatgaaaac aatatcatta ttggtgctgc tgcaaatgcc 120

agccacccag gtggtgcagc agccgtttct gtacaagcgg ctggtgcacc ctacaatgca 180

tttacaggtt ttagctcgtt aaaaggtttg gcacaagcgt tcactgcacg cggtgcaagc 240

aatactgatg ttactgtcgg tagcaaaact tttaatatct cccatattcc tgtttcggca 300

atgccacctt cacatagtgc cttaggtaat ttcaattttg gtcaggtggg ctcacaggaa 360

gtctattttg gtgaatggtg gaaagcgggt gatacagcag caagtgcaag tcatactgtt 420

tattacgcag gtgacaatac caatactaca gtaccaacct ctggtacggc gacttatacc 480

gttgcaggga ttaatggttc agcaaccaat ctgctaagtg gtaatttaac tgctaacttt 540

ggtgcaggta ctttagaagg atcattaact ggaacaggga ctgctgtttc aagcttaagc 600

ttaaatggtg tgacatttaa tccaggtact gcggcattca gtggcggcgc tagtgcaaat 660

ggtacggctg ggctaaataa ttcaggtatt gttcaaggac acttctttgg tgcaaatgcc 720

gcagctttag cgggtattgc cgagtttaac aatgctgctt ataacactgc ctttggtggt 780

gcgaaaaact aa 792

<210> 704

<211> 263

<212> PRT

<213> A. gyllenbergii SLP 1a

<400> 704

Met Lys Ile Ser Gln Leu Phe Ile Gly Leu Val Ala Cys Ser Ala Val
1 5 10 15

Phe Ala His Ala Gly Ile Asp Gly Ala Ser Ser Asn Glu Asn Asn Ile
20 25 30

Ile Ile Gly Ala Ala Ala Asn Ala Ser His Pro Gly Gly Ala Ala Ala
35 40 45

Val Ser Val Gln Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Thr Ala Arg Gly Ala Ser
65 70 75 80

Asn Thr Asp Val Thr Val Gly Ser Lys Thr Phe Asn Ile Ser His Ile
85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn

100 105 110

Phe Gly Gln Val Gly Ser Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys

115 120 125

Ala Gly Asp Thr Ala Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly

130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ser Gly Thr Ala Thr Tyr Thr

145 150 155 160

Val Ala Gly Ile Asn Gly Ser Ala Thr Asn Leu Leu Ser Gly Asn Leu

165 170 175

Thr Ala Asn Phe Gly Ala Gly Thr Leu Glu Gly Ser Leu Thr Gly Thr

180 185 190

Gly Thr Ala Val Ser Ser Leu Ser Leu Asn Gly Val Thr Phe Asn Pro

195 200 205

Gly Thr Ala Ala Phe Ser Gly Gly Ala Ser Ala Asn Gly Thr Ala Gly

210 215 220

Leu Asn Asn Ser Gly Ile Val Gln Gly His Phe Phe Gly Ala Asn Ala

225 230 235 240

Ala Ala Leu Ala Gly Ile Ala Glu Phe Asn Asn Ala Ala Tyr Asn Thr

245 250 255

Ala Phe Gly Gly Ala Lys Asn

260

<210> 705

<211> 792

<212> DNA

<213> A. haemolyticus SLP 1a

<400> 705

atgaaaatct ctcaactgtt catcggtctt gttgcatgtt ctgctgtgtt tgctcatgca 60

ggtattgaag gtgcttcaag taacgaagca aatataaaaa ttggtgctgc ggcaaatgca 120

agtcatcctg gtggcgctgc tgcggtttct gtacaagcag cgggtgcgcc atataatgct 180

ttcacaggct ttagttcatt gaaaggcttg gcacaagcat ttgccgcaca aggtacaagc 240

aataccaatg tcactgtggg tactaagacc tttaatatct ctcatattcc tgtatcggcg 300

atgccacctt cacatagtgc tttaggtaat tttaatttcg gtcaggtggg tacacaggaa 360

gtttatttcg gtgaatggtg gaaagcaggt gatacacctg ctagtgcaag ccatacagtg 420

tattacgcag gcgataatac caataccaca gtaccaactg caggtactgc aacttatacc 480

gttgctggga ttaatggatc cgcgacgaat ctgttaactg gtaatttcac tgcgaacttt 540

ggaacaggta ctttggaagg ttcattaaca ggaacaggca ctgctgtttc aagtttaacc 600

ttgaatgggg tggcatttaa tcctggtact gctgaatttg gtggtgcagc aactgcaaat 660

ggtacagctg gagtcaataa ctctggtgct gttcaggggc atttctttgg tgcaaatgct 720

gctgctttag caggtatcgc gcaatttgat aatgcttctt ataacactgc atttggcggt 780

gctaagaatt aa 792

<210> 706

<211> 263

<212> PRT

<213> A. haemolyticus SLP 1a

<400> 706

Met Lys Ile Ser Gln Leu Phe Ile Gly Leu Val Ala Cys Ser Ala Val
1 5 10 15

Phe Ala His Ala Gly Ile Glu Gly Ala Ser Ser Asn Glu Ala Asn Ile
20 25 30

Lys Ile Gly Ala Ala Ala Asn Ala Ser His Pro Gly Gly Ala Ala Ala
35 40 45

Val Ser Val Gln Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Ala Ala Gln Gly Thr Ser
65 70 75 80

Asn Thr Asn Val Thr Val Gly Thr Lys Thr Phe Asn Ile Ser His Ile
85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn
100 105 110

Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys
115 120 125

Ala Gly Asp Thr Pro Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly

130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ala Gly Thr Ala Thr Tyr Thr
145 150 155 160
Val Ala Gly Ile Asn Gly Ser Ala Thr Asn Leu Leu Thr Gly Asn Phe
165 170 175
Thr Ala Asn Phe Gly Thr Gly Thr Leu Glu Gly Ser Leu Thr Gly Thr
180 185 190
Gly Thr Ala Val Ser Ser Leu Thr Leu Asn Gly Val Ala Phe Asn Pro
195 200 205

Gly Thr Ala Glu Phe Gly Gly Ala Ala Thr Ala Asn Gly Thr Ala Gly
210 215 220
Val Asn Asn Ser Gly Ala Val Gln Gly His Phe Phe Gly Ala Asn Ala
225 230 235 240
Ala Ala Leu Ala Gly Ile Ala Gln Phe Asp Asn Ala Ser Tyr Asn Thr
245 250 255
Ala Phe Gly Gly Ala Lys Asn
260

<210> 707
<211> 776
<212> DNA
<213> A. minor SLP 1a

<400> 707
cgaaagcaga aaccttagcg gaacaagcga aagctcaaca agatgtagaa aaagcaaaag 60
ccgaattagc aaaattacaa gaaaaacaac tttatttgga ttctatttgg cgttatttag 120
ggagagatga tcctagttct ccccaacgag caacagctgg tagaagttca atgaagatag 180
atctttctca atatccagaa gaagatgaga tgagagaagc tgtcgttgtt gatagtaata 240
atgcaaaatt aggaacggca tattttatta accaagccta ttctagttat gagcaatttg 300
ttcctgaaaa tgtatctttt gatgcaccat atttctcaaa caatgatttt gtatttatcc 360
caactgatgt aacaaaatct tctaccattc aaaataaaat gacagctacc tatagtggtt 420

tagctttaga tcgtaattat cacaatgatg aagatcgtag cggttgggta actaaagcta 480
aattttcttt aactgctgat tttgctcaaa atacggtaga aggagctatt actgaacgtg 540

aaaacaaagc gcctgatatt aagttagaac aaggagctat tgcttcgtca gtaaccaatc 600

aaaatatcaa tatgccatat atgggattta gcggtaatgc tacattaact agaaaaaatg 660

gttcggttag aacaggggaa tatatcggct tctttgccgg tcctgatgct gaagaagtgg 720

taggttctgt taataacctt ggaggacaaa catcttttgg tggcaaacgc caataa 776

<210> 708

<211> 257

<212> PRT

<213> A. minor SLP 1a

<400> 708

Lys Ala Glu Thr Leu Ala Glu Gln Ala Lys Ala Gln Gln Asp Val Glu
1 5 10 15

Lys Ala Lys Ala Glu Leu Ala Lys Leu Gln Glu Lys Gln Leu Tyr Leu
20 25 30

Asp Ser Ile Trp Arg Tyr Leu Gly Arg Asp Asp Pro Ser Ser Pro Gln
35 40 45

Arg Ala Thr Ala Gly Arg Ser Ser Met Lys Ile Asp Leu Ser Gln Tyr
50 55 60

Pro Glu Glu Asp Glu Met Arg Glu Ala Val Val Val Asp Ser Asn Asn
65 70 75 80

Ala Lys Leu Gly Thr Ala Tyr Phe Ile Asn Gln Ala Tyr Ser Ser Tyr
85 90 95

Glu Gln Phe Val Pro Glu Asn Val Ser Phe Asp Ala Pro Tyr Phe Ser
100 105 110

Asn Asn Asp Phe Val Phe Ile Pro Thr Asp Val Thr Lys Ser Ser Thr
115 120 125

Ile Gln Asn Lys Met Thr Ala Thr Tyr Ser Gly Leu Ala Leu Asp Arg
130 135 140

Asn Tyr His Asn Asp Glu Asp Arg Ser Gly Trp Val Thr Lys Ala Lys
145 150 155 160

Phe Ser Leu Thr Ala Asp Phe Ala Gln Asn Thr Val Glu Gly Ala Ile
165 170 175

Thr Glu Arg Glu Asn Lys Ala Pro Asp Ile Lys Leu Glu Gln Gly Ala

180 185 190

Ile Ala Ser Ser Val Thr Asn Gln Asn Ile Asn Met Pro Tyr Met Gly
195 200 205

Phe Ser Gly Asn Ala Thr Leu Thr Arg Lys Asn Gly Ser Val Arg Thr
210 215 220

Gly Glu Tyr Ile Gly Phe Phe Ala Gly Pro Asp Ala Glu Glu Val Val
225 230 235 240

Gly Ser Val Asn Asn Leu Gly Gly Gln Thr Ser Phe Gly Gly Lys Arg
245 250 255

Gln

<210> 709

<211> 1344

<212> DNA

<213> A. minor SLP 2a

<400> 709

atgaaatttc aagttaagac aacagcatta gcaattttag tttcttcagg tgtggtgggg 60

tgtaaatcta acgatacgcc taaccaagtt gttgaaccaa caccggcaaa tcaagcatca 120

aaaacagatg cggagaagaa agccgaagca gatgcaaagg caaaagcaac cgctgaagcg 180

aaagctaaag cagaagcaga ggctaaagca aaagctgagg aagcaaaacg tttagaagaa 240

gaacgtaaaa aggctgaagc agaagcgaaa aaattaacgg atgccaaagc aaaagcggaa 300

gcagaagcga aggcaaaagc agccgctgaa gcgaaagcta aagcagaagc tgcagagaaa 360

cttaaaccag taaatctgtt agataaaaat ggagttgcat ggcgaattat taatattcgt 420

caaaatggtc caagcaatga tacaacagaa tatcgctatg gtggtcgtaa tagctcgttg 480

agcagtgatt tgtactacgt aggaaaacct gaaagctttt ttgagctact tggagtcaat 540

gcaataacga atcttaattt caatgaatta agtgagaaag atggcaagcc attccttgga 600

gttcatcaag ggaaaaaaga agatcctgat ttcagcggaa aaattgtaac taaagttaaa 660

cgtgatggcc atcttatcaa ggttgctgaa ctagaggatg ccaaagcatt taattatctc 720

tatgtaaatc aaccttattc gacttatggc gctctcttta ccaacggaca cgatgtgaaa 780

ttcttctcag tggcacaaag cgcaggtaaa gccggatatt cccatattta tcctgtatgg 840

agagaggaag ttgtggagcg taacgggcaa tctgttaaaa ccggtaaaat tatttggaat 900

gatgcggtag ccggagaggc aacttataaa ggacaagtaa ttgcaagcgt aataaaatcg 960

gatatagagg gttataacag gactggtatc cgttctgaac ctgtccttga tggtacggta 1020

acattaaaag ccaaatttga taaagatcct gagcgtaact ctattgaggg tgaaattgat 1080

agtaacctaa taggtaaaat cgttttagag aaaaatcttg atcaatcggg gacttttcgt 1140

ctaggtaggg cgacaaatga aacgatgaac atcaaagaag catctgggag aggcacgtac 1200

gaagttaagt tctacggtaa agatttaaat gatgccgtag gaaaagtaaa tttaaatagt 1260

gacgacgcat atactagata taaagaaact ggcgatgtaa ttcaatacga cgccgtcttc 1320

ggtgcaacca aacaacctaa ataa 1344

<210> 710

<211> 447

<212> PRT

<213> A. minor SLP 2a

<400> 710

Met Lys Phe Gln Val Lys Thr Thr Ala Leu Ala Ile Leu Val Ser Ser
1 5 10 15

Gly Val Val Gly Cys Lys Ser Asn Asp Thr Pro Asn Gln Val Val Glu
20 25 30

Pro Thr Pro Ala Asn Gln Ala Ser Lys Thr Asp Ala Glu Lys Lys Ala
35 40 45

Glu Ala Asp Ala Lys Ala Lys Ala Thr Ala Glu Ala Lys Ala Lys Ala
50 55 60

Glu Ala Glu Ala Lys Ala Lys Ala Glu Glu Ala Lys Arg Leu Glu Glu
65 70 75 80

Glu Arg Lys Lys Ala Glu Ala Glu Ala Lys Lys Leu Thr Asp Ala Lys
85 90 95

Ala Lys Ala Glu Ala Glu Ala Lys Ala Lys Ala Ala Ala Glu Ala Lys
100 105 110

Ala Lys Ala Glu Ala Ala Glu Lys Leu Lys Pro Val Asn Leu Leu Asp
115 120 125

Lys Asn Gly Val Ala Trp Arg Ile Ile Asn Ile Arg Gln Asn Gly Pro
130 135 140

Ser Asn Asp Thr Thr Glu Tyr Arg Tyr Gly Gly Arg Asn Ser Ser Leu

145 150 155 160

Ser Ser Asp Leu Tyr Tyr Val Gly Lys Pro Glu Ser Phe Phe Glu Leu
165 170 175
Leu Gly Val Asn Ala Ile Thr Asn Leu Asn Phe Asn Glu Leu Ser Glu
180 185 190
Lys Asp Gly Lys Pro Phe Leu Gly Val His Gln Gly Lys Lys Glu Asp
195 200 205
Pro Asp Phe Ser Gly Lys Ile Val Thr Lys Val Lys Arg Asp Gly His
210 215 220

Leu Ile Lys Val Ala Glu Leu Glu Asp Ala Lys Ala Phe Asn Tyr Leu
225 230 235 240
Tyr Val Asn Gln Pro Tyr Ser Thr Tyr Gly Ala Leu Phe Thr Asn Gly
245 250 255
His Asp Val Lys Phe Phe Ser Val Ala Gln Ser Ala Gly Lys Ala Gly
260 265 270
Tyr Ser His Ile Tyr Pro Val Trp Arg Glu Glu Val Val Glu Arg Asn
275 280 285

Gly Gln Ser Val Lys Thr Gly Lys Ile Ile Trp Asn Asp Ala Val Ala
290 295 300
Gly Glu Ala Thr Tyr Lys Gly Gln Val Ile Ala Ser Val Ile Lys Ser
305 310 315 320
Asp Ile Glu Gly Tyr Asn Arg Thr Gly Ile Arg Ser Glu Pro Val Leu
325 330 335
Asp Gly Thr Val Thr Leu Lys Ala Lys Phe Asp Lys Asp Pro Glu Arg
340 345 350

Asn Ser Ile Glu Gly Glu Ile Asp Ser Asn Leu Ile Gly Lys Ile Val
355 360 365
Leu Glu Lys Asn Leu Asp Gln Ser Gly Thr Phe Arg Leu Gly Arg Ala
370 375 380
Thr Asn Glu Thr Met Asn Ile Lys Glu Ala Ser Gly Arg Gly Thr Tyr
385 390 395 400

Glu Val Lys Phe Tyr Gly Lys Asp Leu Asn Asp Ala Val Gly Lys Val
405 410 415

Asn Leu Asn Ser Asp Asp Ala Tyr Thr Arg Tyr Lys Glu Thr Gly Asp
420 425 430

Val Ile Gln Tyr Asp Ala Val Phe Gly Ala Thr Lys Gln Pro Lys
435 440 445

<210> 711

<211> 603

<212> DNA

<213> A. minor SLP 3a

<400> 711

atgaaaaaat tacttctttc tgcaattttg gctggattat taaccgcttg tagtggcggc 60

ggtggtggta gcggtacagc aacaacaccg gataattcta acgttgattt aaccaacagc 120

ccgaaagggg atgtcggtgc taaaactact gatggagaac tgtatggtca aaacagcaat 180

gactctttct atggtatttg gttaaacgat agcaaaacgc taaaagaagt tcgctatcaa 240

ggaacagcag caacaaattt accttctggt agcgcaactt acttaggcga tgcttattgg 300

gtaagtggca caacaggaca accatccaaa ggtggtaaaa ctacattaaa cgtagatttt 360

gatcagaaaa cggtagatgg taaagttgaa tttagcctat taaccgatgg tcgtgcacaa 420

gatattacct tgcacaaaac ccaattaaac ggtaccactt tcagcggcaa agcaaccacc 480

ctattacagg aaggcactta tgaaggtggc ttgttcggta atggagcaaa agaagcagca 540

ggtattgcaa ctttcagtgg tgataacagc tacaatactt cattcggtgg tattcgttac 600

taa 603

<210> 712

<211> 200

<212> PRT

<213> A. minor SLP 3a

<400> 712

Met Lys Lys Leu Leu Leu Ser Ala Ile Leu Ala Gly Leu Leu Thr Ala
1 5 10 15

Cys Ser Gly Gly Gly Gly Gly Ser Gly Thr Ala Thr Thr Pro Asp Asn
20 25 30

Ser Asn Val Asp Leu Thr Asn Ser Pro Lys Gly Asp Val Gly Ala Lys

35 40 45

Thr Thr Asp Gly Glu Leu Tyr Gly Gln Asn Ser Asn Asp Ser Phe Tyr
50 55 60
Gly Ile Trp Leu Asn Asp Ser Lys Thr Leu Lys Glu Val Arg Tyr Gln
65 70 75 80
Gly Thr Ala Ala Thr Asn Leu Pro Ser Gly Ser Ala Thr Tyr Leu Gly
85 90 95
Asp Ala Tyr Trp Val Ser Gly Thr Thr Gly Gln Pro Ser Lys Gly Gly
100 105 110

Lys Thr Thr Leu Asn Val Asp Phe Asp Gln Lys Thr Val Asp Gly Lys
115 120 125
Val Glu Phe Ser Leu Leu Thr Asp Gly Arg Ala Gln Asp Ile Thr Leu
130 135 140
His Lys Thr Gln Leu Asn Gly Thr Thr Phe Ser Gly Lys Ala Thr Thr
145 150 155 160
Leu Leu Gln Glu Gly Thr Tyr Glu Gly Gly Leu Phe Gly Asn Gly Ala
165 170 175

Lys Glu Ala Ala Gly Ile Ala Thr Phe Ser Gly Asp Asn Ser Tyr Asn
180 185 190
Thr Ser Phe Gly Gly Ile Arg Tyr
195 200

<210> 713
<211> 792
<212> DNA
<213> A. oleivorans SLP 1a
<400> 713
atgaaaatct ctcaattgtt cttgggtctc gttgcttgtt caactgcatt tgcttatgca 60
ggaattgatg gtatttcgag taatgaaagt aacatcaaaa tcggtgctgc tgccaatgca 120
aaccatccgg gtggtgtagc agcggtgtcg gttcaagctg ccggtgcacc atataacgct 180

tttacaggtt ttagttcgtt aaaaggtttg gctcaggctt ttgctgcgca gggaacgagt 240
aataccaatg taacggttgg cagcaaaacc tttaatattt cgcatattcc agtgtctgca 300

atgccacctt cacacagtgc cttaggtaat tttaactttg gtcaggtggg cacacaggaa 360

gtctattttg gtgaatggtg gaaagcgggc gacacaccgg caagcgcgag ccataccgtt 420

tactacgcgg gtgataacac caataccacg gttccaaccg caggtactgc aacttatacc 480

gttgcaggga ttaatggttc tggaagcaat ctgttaagtg gtacgttcac ggcaaattat 540

ggcgcgggta cacttgaagg aacgcttacc ggaacaggta cggctgtttc atcattaagc 600

ctagatggtg tggcatttaa cccgggtact gctgcgtttg caggtttggc aacggctaac 660

ggtacggctg gtgtcgacaa ctctggtgta gttcaaggtc aattcttcgg tgcaaatgct 720

tcggctttag cgggtattgc ccagtttgat aacgtgtctt acaacactgc atttggcggt 780

gctaaaaatt aa 792

<210> 714

<211> 263

<212> PRT

<213> A. oleivorans SLP 1a

<400> 714

Met Lys Ile Ser Gln Leu Phe Leu Gly Leu Val Ala Cys Ser Thr Ala
1 5 10 15

Phe Ala Tyr Ala Gly Ile Asp Gly Ile Ser Ser Asn Glu Ser Asn Ile
20 25 30

Lys Ile Gly Ala Ala Ala Asn Ala Asn His Pro Gly Gly Val Ala Ala
35 40 45

Val Ser Val Gln Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Ala Ala Gln Gly Thr Ser
65 70 75 80

Asn Thr Asn Val Thr Val Gly Ser Lys Thr Phe Asn Ile Ser His Ile
85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn
100 105 110

Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys
115 120 125

Ala Gly Asp Thr Pro Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly

130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ala Gly Thr Ala Thr Tyr Thr
145 150 155 160
Val Ala Gly Ile Asn Gly Ser Gly Ser Asn Leu Leu Ser Gly Thr Phe
165 170 175
Thr Ala Asn Tyr Gly Ala Gly Thr Leu Glu Gly Thr Leu Thr Gly Thr
180 185 190
Gly Thr Ala Val Ser Ser Leu Ser Leu Asp Gly Val Ala Phe Asn Pro
195 200 205

Gly Thr Ala Ala Phe Ala Gly Leu Ala Thr Ala Asn Gly Thr Ala Gly
210 215 220
Val Asp Asn Ser Gly Val Val Gln Gly Gln Phe Phe Gly Ala Asn Ala
225 230 235 240
Ser Ala Leu Ala Gly Ile Ala Gln Phe Asp Asn Val Ser Tyr Asn Thr
245 250 255
Ala Phe Gly Gly Ala Lys Asn
260

<210> 715
<211> 792
<212> DNA
<213> A. pittii SLP 1a

<400> 715
atgaaaatct ctcaattgtt cttgggtctc gttgcttgtt caactgcatt tgcttatgca 60
ggaattgatg gtatttcgag taatgaaagt aacatcaaaa tcggtgctgc tgccaatgca 120
agccatccgg gtggtgtagc agcggtgtcg gttcaagctg cgggtgcacc atataacgct 180
tttacaggtt ttagttcgtt aaaaggtttg gctcaggctt ttgctgctca gggaacgagt 240
aacaccaatg taacggttgg cagcaaaacc tttaatattt cacatattcc agtgtctgca 300
atgccacctt cacacagtgc attaggtaat tttaactttg gtcaggtggg cacacaggaa 360
gtctattttg gtgaatggtg gaaagcgggc gacacgccgg caagcgcgag ccataccgtt 420

tactacgcgg gtgataacac caataccact gttccaaccg cgggtactgc aacctatacc 480
gttgcaggga ttaacggttc tggaagcaat ctgttaagtg gtacgttcac ggcaaattat 540

ggcgctggta cacttgaagg aacgcttaca ggaactggta cggctgtttc atcattaagc 600

ctagatggtg tggcatttaa cccaggtact gctgcgtttg caggtttggc aacggctaat 660

ggtacggctg gtgtcgacaa ctctggtgta gttcaaggtc aattcttcgg tgcaaatgct 720

tcggctttag cgggtattgc ccagtttgat aacgtgtctt acaacactgc atttggcggt 780

gctaaaaatt aa 792

<210> 716

<211> 263

<212> PRT

<213> A. pittii SLP 1a

<400> 716

Met Lys Ile Ser Gln Leu Phe Leu Gly Leu Val Ala Cys Ser Thr Ala

1 5 10 15

Phe Ala Tyr Ala Gly Ile Asp Gly Ile Ser Ser Asn Glu Ser Asn Ile

20 25 30

Lys Ile Gly Ala Ala Ala Asn Ala Ser His Pro Gly Gly Val Ala Ala

35 40 45

Val Ser Val Gln Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe

50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Ala Ala Gln Gly Thr Ser

65 70 75 80

Asn Thr Asn Val Thr Val Gly Ser Lys Thr Phe Asn Ile Ser His Ile

85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn

100 105 110

Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys

115 120 125

Ala Gly Asp Thr Pro Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly

130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ala Gly Thr Ala Thr Tyr Thr

145 150 155 160

Val Ala Gly Ile Asn Gly Ser Gly Ser Asn Leu Leu Ser Gly Thr Phe

165 170 175

Thr Ala Asn Tyr Gly Ala Gly Thr Leu Glu Gly Thr Leu Thr Gly Thr

180 185 190

Gly Thr Ala Val Ser Ser Leu Ser Leu Asp Gly Val Ala Phe Asn Pro

195 200 205

Gly Thr Ala Ala Phe Ala Gly Leu Ala Thr Ala Asn Gly Thr Ala Gly

210 215 220

Val Asp Asn Ser Gly Val Val Gln Gly Gln Phe Phe Gly Ala Asn Ala

225 230 235 240

Ser Ala Leu Ala Gly Ile Ala Gln Phe Asp Asn Val Ser Tyr Asn Thr

245 250 255

Ala Phe Gly Gly Ala Lys Asn

260

<210> 717

<211> 1116

<212> DNA

<213> A. pleuropneumoniae SLP 3a

<400> 717

gtgtacttag ttggtctgcc gccttattct tacggctggg gacaggcttg cttctacggg 60

tttcctttat ggtatgtaga tgtcggagcc ggaaatgtcg cacgtagcct cggttacgtg 120

ttttacgtca cagccgtact ttgtaccact tacttaatcg gcttattgtt attaaccaaa 180

gccaaaccgt ttctaagcga gtcctgtatc aaacttgttc gcgccaccat cttatgtgcg 240

cttgccactt tacctatttt gattatcagc acgttactta acggtaaaat ttatcaacaa 300

gcggtaattt cttatttctg tgcggtactc ttatttatta tcgcattacg taacgtgatt 360

aatcgccata tcagcaatat caatatttat tcggcaattc aatttttcca aagtcataaa 420

agtaacgtac tgatctttac ttatgtgtat ttcgtgatct ttgcctttat ggtcggttat 480

ttacgtccgc atttcaaaac acgcttcgat atgatcgaaa ttaatgccca aatgtattat 540

gtgctcgcca aatacaacaa aacctttatc ttgtcgaaag aactaaaaat agataatgat 600

gaattttatc tgtatgaact aaatccgaat cagcttggtc atatccaaat cgtcgatgcg 660

catcatccgt ttgggttaca ggtggcattt gattctcaca gccaaggaac acttacttat 720

aatgtagatt ttgctaagaa aacaggacaa ggaagtattg aagggttaga gcatataggt 780

cgtttaacac ttgatcaagg tgaaatttat aaatcggctt cctctggcgg tatgcgagca 840

agaggcagaa ttagtgcgga tgaatggaaa aatgtaagag atactagtgg agattaccaa 900

ttaggattct atggtaaaaa cgcagaagaa attgcggggc gagcaacatt aagccaatct 960

ccttatggtg cttgggatag cgaaaagagc acttatttgg caccagttaa atctattagt 1020

gataaagtgc tttctccaga tagatacggt atgaattcag gtaaagattc atttgatgtc 1080

ggctttggcg gtacacgtgg tgaaatcaaa aaatag 1116

<210> 718

<211> 371

<212> PRT

<213> A. pleuropneumoniae SLP 3a

<400> 718

Met Tyr Leu Val Gly Leu Pro Pro Tyr Ser Tyr Gly Trp Gly Gln Ala
1 5 10 15

Cys Phe Tyr Gly Phe Pro Leu Trp Tyr Val Asp Val Gly Ala Gly Asn
20 25 30

Val Ala Arg Ser Leu Gly Tyr Val Phe Tyr Val Thr Ala Val Leu Cys
35 40 45

Thr Thr Tyr Leu Ile Gly Leu Leu Leu Leu Thr Lys Ala Lys Pro Phe
50 55 60

Leu Ser Glu Ser Cys Ile Lys Leu Val Arg Ala Thr Ile Leu Cys Ala
65 70 75 80

Leu Ala Thr Leu Pro Ile Leu Ile Ile Ser Thr Leu Leu Asn Gly Lys
85 90 95

Ile Tyr Gln Gln Ala Val Ile Ser Tyr Phe Cys Ala Val Leu Leu Phe
100 105 110

Ile Ile Ala Leu Arg Asn Val Ile Asn Arg His Ile Ser Asn Ile Asn
115 120 125

Ile Tyr Ser Ala Ile Gln Phe Phe Gln Ser His Lys Ser Asn Val Leu
130 135 140

Ile Phe Thr Tyr Val Tyr Phe Val Ile Phe Ala Phe Met Val Gly Tyr
145 150 155 160

Leu Arg Pro His Phe Lys Thr Arg Phe Asp Met Ile Glu Ile Asn Ala

165 170 175

Gln Met Tyr Tyr Val Leu Ala Lys Tyr Asn Lys Thr Phe Ile Leu Ser
180 185 190
Lys Glu Leu Lys Ile Asp Asn Asp Glu Phe Tyr Leu Tyr Glu Leu Asn
195 200 205
Pro Asn Gln Leu Gly His Ile Gln Ile Val Asp Ala His His Pro Phe
210 215 220
Gly Leu Gln Met Ala Phe Asp Ser His Ser Gln Gly Thr Leu Thr Tyr
225 230 235 240

Asn Val Asp Phe Ala Lys Lys Thr Gly Gln Gly Ser Ile Glu Gly Leu
245 250 255
Glu His Ile Gly Arg Leu Thr Leu Asp Gln Gly Glu Ile Tyr Lys Ser
260 265 270
Ala Ser Ser Gly Gly Met Arg Ala Arg Gly Arg Ile Ser Ala Asp Glu
275 280 285
Trp Lys Asn Val Arg Asp Thr Ser Gly Asp Tyr Gln Leu Gly Phe Tyr
290 295 300

Gly Lys Asn Ala Glu Glu Ile Ala Gly Arg Ala Thr Leu Ser Gln Ser
305 310 315 320
Pro Tyr Gly Ala Trp Asp Ser Glu Lys Ser Thr Tyr Leu Ala Pro Val
325 330 335
Lys Ser Ile Ser Asp Lys Val Leu Ser Pro Asp Arg Tyr Gly Met Asn
340 345 350
Ser Gly Lys Asp Ser Phe Asp Val Gly Phe Gly Gly Thr Arg Gly Glu
355 360 365

Ile Lys Lys
370

<210> 719
<211> 777
<212> DNA
<213> A. segnis SLP 1a

<400> 719

atgaaaaact caattgttaa attcacttta actacactag ccgtgttaac tttggctgct 60

tgtggaagtg gcggtggtga tagctcacca tcatcttctt ctgtgaataa tactcaaaaa 120

caacaagcgg aatctgttaa acctacagta ccgtcacagc cgacgacacc agagaaaaaa 180

aacgacttgg tcatttcagg tcaggatgac aaagttcaag ttaaaaatgt tgtgcttact 240

gattcaaata taaaggaatt aagcattgat gggcgtagaa ttaaactagc ttatcctgga 300

atttatgcag atggttggca aattgtaaat ggtacaaacg tttgctgtgg aaaatatgaa 360

aatgttcgta ttggtgctgt tatgagccaa ggccctggag aatctgatat tatcttctac 420

aatggcattc caacaaaaaa tatgcctcag agcggttctg tgtcctacaa aggagatagc 480

atcatttctg gggctgatat taatgatgaa gattatgtat ctggaaaatc taactttact 540

gtgaactttg atagcaaaaa acttagtggt tctattaccg caaattcaat gtctgcaatt 600

aacgtaaatg ctgatatttc aggcaatagt tttaaaggta cggctaaatc ttcccaattt 660

acttcagaag gtaaagttga aggtaagttt tatggaaata acgcggctga attaggtggt 720

ttagctaaag ggaatgacaa ttcctgggga gctgcttttg ctggtaagaa acagtaa 777

<210> 720

<211> 258

<212> PRT

<213> A. segnis SLP 1a

<400> 720

Met Lys Asn Ser Ile Val Lys Phe Thr Leu Thr Thr Leu Ala Val Leu
1 5 10 15

Thr Leu Ala Ala Cys Gly Ser Gly Gly Gly Asp Ser Ser Pro Ser Ser
20 25 30

Ser Ser Val Asn Asn Thr Gln Lys Gln Gln Ala Glu Ser Val Lys Pro
35 40 45

Thr Val Pro Ser Gln Pro Thr Thr Pro Glu Lys Lys Asn Asp Met Val
50 55 60

Ile Ser Gly Gln Asp Asp Lys Val Gln Val Lys Asn Val Val Leu Thr
65 70 75 80

Asp Ser Asn Ile Lys Glu Leu Ser Ile Asp Gly Arg Arg Ile Lys Leu
85 90 95

Ala Tyr Pro Gly Ile Tyr Ala Asp Gly Trp Gln Ile Val Asn Gly Thr

100 105 110

Asn Val Cys Cys Gly Lys Tyr Glu Asn Val Arg Ile Gly Ala Val Met

115 120 125

Ser Gln Gly Pro Gly Glu Ser Asp Ile Ile Phe Tyr Asn Gly Ile Pro

130 135 140

Thr Lys Asn Met Pro Gln Ser Gly Ser Val Ser Tyr Lys Gly Asp Ser

145 150 155 160

Ile Ile Ser Gly Ala Asp Ile Asn Asp Glu Asp Tyr Val Ser Gly Lys

165 170 175

Ser Asn Phe Thr Val Asn Phe Asp Ser Lys Lys Leu Ser Gly Ser Ile

180 185 190

Thr Ala Asn Ser Met Ser Ala Ile Asn Val Asn Ala Asp Ile Ser Gly

195 200 205

Asn Ser Phe Lys Gly Thr Ala Lys Ser Ser Gln Phe Thr Ser Glu Gly

210 215 220

Lys Val Glu Gly Lys Phe Tyr Gly Asn Asn Ala Ala Glu Leu Gly Gly

225 230 235 240

Leu Ala Lys Gly Asn Asp Asn Ser Trp Gly Ala Ala Phe Ala Gly Lys

245 250 255

Lys Gln

<210> 721

<211> 930

<212> DNA

<213> A. succinogenes SLP 1a

<400> 721

atgagcaaat ttacaaatgt tgcgctggcg cttttaatgt cattggggat cggggcttgt 60

tcttcaagta ccggcgactc gtcatcaacc tccggctccg ttacggcatc cactaccccg 120

acaaatacct atactgcatc gacctcggag gatgattcgg cgtcagacgc tggcggttcg 180

acttcaaaca atgacggttc ggcgtcagac gatggcgact cgacttcgga tgatacggct 240

acgctaagtc aaattattgt aggtacaaat ccaagcgctt cggattccgc atctgcagcc 300

tacaactata tcaacaatga tacggatacg ttgctttccg caattgcttc cgtcggtaca 360

tcgacgctga gcgccagctg ttcaagcagt tccagcggcg cctgttcaag cgccaataaa 420

tctcaggggg aggtaatgat tgccaaaacc caaagctatt caagttatgc ggtaattcgt 480

gaagattata acgctgaaga tgttccggct aactcttatg tcgcggtaaa taccaatccg 540

acatcggcgg cgaatttatc atccgcatta aacgcgactt attcgggaca ggcaacttat 600

agcgtcaaaa atagagcgaa tgcgttaacg cgcgatttta ctatgacggt aacggattcg 660

actgtgagcg gttctgtcta cacaacggca acgaacggaa acacgacgac ttgggtaacg 720

tttaatgacg gaacgatttc ggtcgatacc ggagcgatta catttagcgg caccgcaaca 780

tttaaagaaa gcacttttgg cgtaacggac ggtacttacc aaggatcatt tgccggtgaa 840

aatgcggaag aagtggtggg tacgtttgaa tctaacgaat cgacggattc cggatcggta 900

caaggcgcat ttgcagggac taaagactga 930

<210> 722

<211> 309

<212> PRT

<213> A. succinogenes SLP 1a

<400> 722

Met Ser Lys Phe Thr Asn Val Ala Leu Ala Leu Leu Met Ser Leu Gly
1 5 10 15

Ile Gly Ala Cys Ser Ser Ser Thr Gly Asp Ser Ser Ser Thr Ser Gly
20 25 30

Ser Val Thr Ala Ser Thr Thr Pro Thr Asn Thr Tyr Thr Ala Ser Thr
35 40 45

Ser Glu Asp Asp Ser Ala Ser Asp Ala Gly Gly Ser Thr Ser Asn Asn
50 55 60

Asp Gly Ser Ala Ser Asp Asp Gly Asp Ser Thr Ser Asp Asp Thr Ala
65 70 75 80

Thr Leu Ser Gln Ile Ile Val Gly Thr Asn Pro Ser Ala Ser Asp Ser
85 90 95

Ala Ser Ala Ala Tyr Asn Tyr Ile Asn Asn Asp Thr Asp Thr Leu Leu
100 105 110

Ser Ala Ile Ala Ser Val Gly Thr Ser Thr Leu Ser Ala Ser Cys Ser
115 120 125

Ser Ser Ser Ser Gly Ala Cys Ser Ser Ala Asn Lys Ser Gln Gly Glu
130 135 140

Val Met Ile Ala Lys Thr Gln Ser Tyr Ser Ser Tyr Ala Val Ile Arg
145 150 155 160
Glu Asp Tyr Asn Ala Glu Asp Val Pro Ala Asn Ser Tyr Val Ala Val
165 170 175
Asn Thr Asn Pro Thr Ser Ala Ala Asn Leu Ser Ser Ala Leu Asn Ala
180 185 190
Thr Tyr Ser Gly Gln Ala Thr Tyr Ser Val Lys Asn Arg Ala Asn Ala
195 200 205

Leu Thr Arg Asp Phe Thr Met Thr Val Thr Asp Ser Thr Val Ser Gly
210 215 220
Ser Val Tyr Thr Thr Ala Thr Asn Gly Asn Thr Thr Thr Trp Val Thr
225 230 235 240
Phe Asn Asp Gly Thr Ile Ser Val Asp Thr Gly Ala Ile Thr Phe Ser
245 250 255
Gly Thr Ala Thr Phe Lys Glu Ser Thr Phe Gly Val Thr Asp Gly Thr
260 265 270

Tyr Gln Gly Ser Phe Ala Gly Glu Asn Ala Glu Glu Val Val Gly Thr
275 280 285
Phe Glu Ser Asn Glu Ser Thr Asp Ser Gly Ser Val Gln Gly Ala Phe
290 295 300
Ala Gly Thr Lys Asp
305

<210> 723
<211> 600
<212> DNA
<213> A. succinogenes SLP 2a
<400> 723
atgaaaaaat ttatttttc tacgttactg gttgcttgtt taacggcatg tagtggtggc 60
ggaggtggcg gcggtacggc agaaacaccg gacggcactc ggatcgatct ttctcatagc 120

ccgaaaggtg acatcgtagc caagactacg gatggtgagt tttatggaaa aaatcacgat 180

gattcttttt atggtgtttg gattaatgat accaaaacaa taaaagaagt tcgttatcaa 240

ggtacgccgg caacgaattt accttcgggt tcagcaactt atatcgggac tgcatattgg 300

gtagacggta tcacaggttt gccttccaaa ggcggcagaa ccgtattaaa tgcagatttt 360

tctcaaaaaa ccattgatgg gaaaattgaa tttaatatgt taaatgatgg gcggttacaa 420

gatattacat tgcacaaaac tcaattaaat ggcgctaagt ttgatggtgt cgcgactaca 480

atatcacaaa caggtaccta tgaaggcgga ttgttcggta aagatgcaaa agaagcggca 540

ggtattgcca catttaatga cagttcctat aacacagctt ttggcggtat tcgttattag 600

<210> 724

<211> 199

<212> PRT

<213> A. succinogenes SLP 2a

<400> 724

Met Lys Lys Phe Ile Phe Ser Thr Leu Leu Val Ala Cys Leu Thr Ala
1 5 10 15

Cys Ser Gly Gly Gly Gly Gly Gly Gly Thr Ala Glu Thr Pro Asp Gly
20 25 30

Thr Arg Ile Asp Leu Ser His Ser Pro Lys Gly Asp Ile Val Ala Lys
35 40 45

Thr Thr Asp Gly Glu Phe Tyr Gly Lys Asn His Asp Asp Ser Phe Tyr
50 55 60

Gly Val Trp Ile Asn Asp Thr Lys Thr Ile Lys Glu Val Arg Tyr Gln
65 70 75 80

Gly Thr Pro Ala Thr Asn Leu Pro Ser Gly Ser Ala Thr Tyr Ile Gly
85 90 95

Thr Ala Tyr Trp Val Asp Gly Ile Thr Gly Leu Pro Ser Lys Gly Gly
100 105 110

Arg Thr Val Leu Asn Ala Asp Phe Ser Gln Lys Thr Ile Asp Gly Lys
115 120 125

Ile Glu Phe Asn Met Leu Asn Asp Gly Arg Leu Gln Asp Ile Thr Leu
130 135 140

His Lys Thr Gln Leu Asn Gly Ala Lys Phe Asp Gly Val Ala Thr Thr

145 150 155 160

Ile Ser Gln Thr Gly Thr Tyr Glu Gly Gly Leu Phe Gly Lys Asp Ala

165 170 175

Lys Glu Ala Ala Gly Ile Ala Thr Phe Asn Asp Ser Ser Tyr Asn Thr

180 185 190

Ala Phe Gly Gly Ile Arg Tyr

195

<210> 725

<211> 1245

<212> DNA

<213> A. suis SLP 2a

<400> 725

atgaaaaata ttttaaataa acaagtatta aatacggcgg caacaatttt attgtctatc 60

ggggtaacag cgtgttcatc tgggggaagt gatcagcccg gaattgatca aagcactcgc 120

ttaagccaag tcgcggtaca acatttatta gaagataaat tacaagctca agaacacctt 180

gacgaggtaa aacaagcatt ggatgctctg caattagctt tagttaaagc acaagcggct 240

aattcgacat cagatgtaca acaaacatta aaagatgcta gtagcttatt agaaaaagcg 300

aaattggcag ccgaaaatgc taaagatgaa gcgaaaaatg ctgcttcacg agtatcaagt 360

gcaagtgcac aattatctac cgctgtagat gaagcgaata atgtaatgaa cattgcgaat 420

caagcaaata gcgtgttatt agaggcaact aacaccttta atcaaattca atcagtgctt 480

gctgatttaa ctcaaaaaga ggtggcaaaa gctgaagagc agacgaaaaa aatagcacaa 540

gaaaagcaaa tagcgacaaa taaagcgatt accactgcaa tatcttataa caacctcgat 600

tcgattgtgc atgattatgg taatagcgag gcacgagaag cattattagc aaaattacaa 660

aaacaaggct caaatgcgcc agcctcttgt agtaatgcaa aaacctcaac ttgccataaa 720

gaggtagcaa gaggcagtgt cgtagttaat tacaatcaag cttattcaag ttatgcggtt 780

attcgtgaaa cctataataa tgaaaatcca cagccgagta atgcttttat tgtattagcg 840

aaggagagcg atttaaccac agatcgtgct gcagtcgtaa atgcaactta tacgggtaaa 900

gcgtcttata gtgcaaaaaa tgtgccggcg gtaatgacgc gagatttcac cttaaaagtg 960

gaaaatgaca aagtaagtgg ttcggttttc caaaaaacga ttaattcgaa ggggatagaa 1020

aaagtaacag aaaatgtagc gttaaatgaa ggaaagatca gtgttgataa tggagtagtg 1080

ggctttagtg gctcagcaaa attcggtgcg atcgcaagca atgccgaagg tacttataaa 1140

ggcgtattcg taggtaaaaa tgcagaggaa gtgatcggta cttttgaaac aaatagcaca 1200

gaaaaagctt cttcagcaca aggtgctttt gcaggaaaaa aataa 1245

<210> 726

<211> 414

<212> PRT

<213> A. suis SLP 2a

<400> 726

Met Lys Asn Ile Leu Asn Lys Gln Val Leu Asn Thr Ala Ala Thr Ile
1 5 10 15

Leu Leu Ser Ile Gly Val Thr Ala Cys Ser Ser Gly Gly Ser Asp Gln
20 25 30

Pro Gly Ile Asp Gln Ser Thr Arg Leu Ser Gln Val Ala Val Gln His
35 40 45

Leu Leu Glu Asp Lys Leu Gln Ala Gln Glu His Leu Asp Glu Val Lys
50 55 60

Gln Ala Leu Asp Ala Leu Gln Leu Ala Leu Val Lys Ala Gln Ala Ala
65 70 75 80

Asn Ser Thr Ser Asp Val Gln Gln Thr Leu Lys Asp Ala Ser Ser Leu
85 90 95

Leu Glu Lys Ala Lys Leu Ala Ala Glu Asn Ala Lys Asp Glu Ala Lys
100 105 110

Asn Ala Ala Ser Arg Val Ser Ser Ala Ser Ala Gln Leu Ser Thr Ala
115 120 125

Val Asp Glu Ala Asn Asn Val Met Asn Ile Ala Asn Gln Ala Asn Ser
130 135 140

Val Leu Leu Glu Ala Thr Asn Thr Phe Asn Gln Ile Gln Ser Val Leu
145 150 155 160

Ala Asp Leu Thr Gln Lys Glu Val Ala Lys Ala Glu Glu Gln Thr Lys
165 170 175

Lys Ile Ala Gln Glu Lys Gln Ile Ala Thr Asn Lys Ala Ile Thr Thr
180 185 190

Ala Ile Ser Tyr Asn Asn Leu Asp Ser Ile Val His Asp Tyr Gly Asn

195 200 205

Ser Glu Ala Arg Glu Ala Leu Leu Ala Lys Leu Gln Lys Gln Gly Ser

210 215 220

Asn Ala Pro Ala Ser Cys Ser Asn Ala Lys Thr Ser Thr Cys His Lys

225 230 235 240

Glu Val Ala Arg Gly Ser Val Val Val Asn Tyr Asn Gln Ala Tyr Ser

245 250 255

Ser Tyr Ala Val Ile Arg Glu Thr Tyr Asn Asn Glu Asn Pro Gln Pro

260 265 270

Ser Asn Ala Phe Ile Val Leu Ala Lys Glu Ser Asp Leu Thr Thr Asp

275 280 285

Arg Ala Ala Val Val Asn Ala Thr Tyr Thr Gly Lys Ala Ser Tyr Ser

290 295 300

Ala Lys Asn Val Pro Ala Val Met Thr Arg Asp Phe Thr Leu Lys Val

305 310 315 320

Glu Asn Asp Lys Val Ser Gly Ser Val Phe Gln Lys Thr Ile Asn Ser

325 330 335

Lys Gly Ile Glu Lys Val Thr Glu Asn Val Ala Leu Asn Glu Gly Lys

340 345 350

Ile Ser Val Asp Asn Gly Val Val Gly Phe Ser Gly Ser Ala Lys Phe

355 360 365

Gly Ala Ile Ala Ser Asn Ala Glu Gly Thr Tyr Lys Gly Val Phe Val

370 375 380

Gly Lys Asn Ala Glu Glu Val Ile Gly Thr Phe Glu Thr Asn Ser Thr

385 390 395 400

Glu Lys Ala Ser Ser Ala Gln Gly Ala Phe Ala Gly Lys Lys

405 410

<210> 727

<211> 792

<212> DNA

<213> Acinetobacter calcoaceticus NIPH 13 SLP 1a

<400> 727

atgaaaatct ctcaattgtt cttgggtctt gttgcttgtt caactgcatt tgcttatgca 60

ggtattgatg gtatttcgag taatgaaagt aacatcaaaa tcggtgctgc tgccaatgca 120

agtcatccgg gtggcgtagc agcggtatcg gttcaagctg cgggtgcgcc atataacgct 180

tttacaggtt ttaattcgtt aaaaggtttg gctcaggctt ttgctgctca gggaacgagt 240

aacaccaatg taacggttgg cagcaaaacc tttaatattt cgcatattcc agtgtctgca 300

atgccacctt cacacagtgc attaggtaat tttaattttg gtcaggtggg cacacaggaa 360

gtctattttg gtgaatggtg gaaagcgggt gacacaccgg caagcgcgag ccataccgtt 420

tactacgcgg gtgataacac caataccact gttccaaccg cgggtactgc aacctatacc 480

gttgcaggaa ttaacggctc tgcaagcaat ctgttaagtg gtacgttcac ggcgaactat 540

ggcgcgggca cacttgaagg aacgcttaca ggaacaggta cggctgtttc atctttaagt 600

ctagatggtg tggcatttaa cccgggcact gctgcgtttg caggtttggc aacggctaac 660

ggtacggctg gggtagataa ctctggtgtg gttcaaggtc aattcttcgg tgcaaatgct 720

tcggctttag ctggtattgc ccagtttgat aacgtgtctt acaacactgc ttttggcggt 780

gctaaaaatt aa 792

<210> 728

<211> 263

<212> PRT

<213> Acinetobacter calcoaceticus NIPH 13 SLP 1a

<400> 728

Met Lys Ile Ser Gln Leu Phe Leu Gly Leu Val Ala Cys Ser Thr Ala
1 5 10 15

Phe Ala Tyr Ala Gly Ile Asp Gly Ile Ser Ser Asn Glu Ser Asn Ile
20 25 30

Lys Ile Gly Ala Ala Ala Asn Ala Ser His Pro Gly Gly Val Ala Ala
35 40 45

Val Ser Val Gln Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60

Asn Ser Leu Lys Gly Leu Ala Gln Ala Phe Ala Ala Gln Gly Thr Ser
65 70 75 80

Asn Thr Asn Val Thr Val Gly Ser Lys Thr Phe Asn Ile Ser His Ile
85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn

100 105 110

Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys

115 120 125

Ala Gly Asp Thr Pro Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly

130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ala Gly Thr Ala Thr Tyr Thr

145 150 155 160

Val Ala Gly Ile Asn Gly Ser Ala Ser Asn Leu Leu Ser Gly Thr Phe

165 170 175

Thr Ala Asn Tyr Gly Ala Gly Thr Leu Glu Gly Thr Leu Thr Gly Thr

180 185 190

Gly Thr Ala Val Ser Ser Leu Ser Leu Asp Gly Val Ala Phe Asn Pro

195 200 205

Gly Thr Ala Ala Phe Ala Gly Leu Ala Thr Ala Asn Gly Thr Ala Gly

210 215 220

Val Asp Asn Ser Gly Val Val Gln Gly Gln Phe Phe Gly Ala Asn Ala

225 230 235 240

Ser Ala Leu Ala Gly Ile Ala Gln Phe Asp Asn Val Ser Tyr Asn Thr

245 250 255

Ala Phe Gly Gly Ala Lys Asn

260

<210> 729

<211> 792

<212> DNA

<213> Acinetobacter sp. CIP 64.2 SLP 1a

<400> 729

atgaaaatct ctcaactgtt catcggtctt gttgcatgtt ctgctgtgtt tgcacatgca 60

ggtattgatg gtgcttcaag taatgaaaac aatatcatta ttggtgctgc tgcaaatgcc 120

agccacccag gcggtgtagc agctgtttct gtacaagcgg ctggtgcacc atacaatgca 180

tttacaggtt ttagctcgtt aaaaggtttg gcacaagcgt tctctgcacg tggtgctagc 240

aatactgatg ttactgtcgg tactaaaact tttaatatct cccatattcc tgtttcggca 300

atgccacctt cacatagtgc cttaggtaat ttcaattttg gtcaggtggg cacacaggaa 360

gtctattttg gtgaatggtg gaaagcgggc gatacagcag caaatgcaag tcatactgtt 420

tattacgcag gtgacaatac caatacgaca gtaccgactt ctggtacggc gacttatacc 480

gttgcaggga ttaatggttc agcaaccaat ctgttaagtg gtaatttaac tgctaacttt 540

ggtgcaggca ctttagaagg gtcattaact ggaacaggga ctgctgtttc aagcttaagc 600

ttggacggtg tgacatttaa tccaggtact gcggcattca gtggcggtgc aagtgcaaat 660

ggtacggctg ggctaaataa ttcaggtatt gttcaaggac acttctttgg tgcaaatgcc 720

gcagctttag cgggtattgc cgagtttaat aatgctgctt ataacactgc atttggtggt 780

gcgaaaaact aa 792

<210> 730

<211> 263

<212> PRT

<213> Acinetobacter sp. CIP 64.2 SLP 1a

<400> 730

Met Lys Ile Ser Gln Leu Phe Ile Gly Leu Val Ala Cys Ser Ala Val
1 5 10 15

Phe Ala His Ala Gly Ile Asp Gly Ala Ser Ser Asn Glu Asn Asn Ile
20 25 30

Ile Ile Gly Ala Ala Ala Asn Ala Ser His Pro Gly Gly Val Ala Ala
35 40 45

Val Ser Val Gln Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Ser Ala Arg Gly Ala Ser
65 70 75 80

Asn Thr Asp Val Thr Val Gly Thr Lys Thr Phe Asn Ile Ser His Ile
85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn
100 105 110

Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys
115 120 125

Ala Gly Asp Thr Ala Ala Asn Ala Ser His Thr Val Tyr Tyr Ala Gly

130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ser Gly Thr Ala Thr Tyr Thr
145 150 155 160
Val Ala Gly Ile Asn Gly Ser Ala Thr Asn Leu Leu Ser Gly Asn Leu
165 170 175
Thr Ala Asn Phe Gly Ala Gly Thr Leu Glu Gly Ser Leu Thr Gly Thr
180 185 190
Gly Thr Ala Val Ser Ser Leu Ser Leu Asp Gly Val Thr Phe Asn Pro
195 200 205

Gly Thr Ala Ala Phe Ser Gly Gly Ala Ser Ala Asn Gly Thr Ala Gly
210 215 220
Leu Asn Asn Ser Gly Ile Val Gln Gly His Phe Phe Gly Ala Asn Ala
225 230 235 240
Ala Ala Leu Ala Gly Ile Ala Glu Phe Asn Asn Ala Ala Tyr Asn Thr
245 250 255
Ala Phe Gly Gly Ala Lys Asn
260

<210> 731
<211> 792
<212> DNA
<213> Acinetobacter sp. CIP 70.18 SLP 1a

<400> 731
atgaaaatct ctcaactgtt catcggtctt gttgcatgtt ctgctgtgtt tgcacatgca 60
ggtattgatg gtgcttcaag taatgaaaac aatatcatta ttggtgctgc tgcaaatgca 120
agccatccag gtggtgcagc agccgtttct gtacaagctg ctggttcacc atataatgca 180
tttacaggtt ttagctcgct aaaaggtttg gcacaagcgt tttctgcacg cggtacaagc 240
aataccgatg ttactgtcgg tagcaaaact tttaatatct cgcatattcc tgtttcggca 300
atgccgcctt cacacagtgc cttaggtaat ttcaattttg gtcaggtggg cacacaggaa 360
gtctattttg gtgaatggtg gaaagcaggc gatacagctg cgagcgcaag tcatactgtt 420

tattacgcag gtgacaatac caatacgaca gtaccaactt ctggtacggc gacctacacc 480
gttgcaggga ttaatggttc agcaaccaat ctgttaagcg gtaatttgac tgctaacttt 540

ggtgcaggca ctttacaagg gtcattaact ggaacaggga ctgctgtttc aagcttaagt 600

ttgaacggtg tgacatttag tccaggtact gctgaattca gtggcgcggc aagtgcaaat 660

ggtacagctg gggtaaataa ttcaggtatc gttcaaggac acttctttgg tgcaaatgct 720

gcagctttag cgggtattgc cgagtttaat aatgtttcat ataacactgc atttggtggt 780

gcgaagaact aa 792

<210> 732

<211> 263

<212> PRT

<213> Acinetobacter sp. CIP 70.18 SLP 1a

<400> 732

Met Lys Ile Ser Gln Leu Phe Ile Gly Leu Val Ala Cys Ser Ala Val
1 5 10 15

Phe Ala His Ala Gly Ile Asp Gly Ala Ser Ser Asn Glu Asn Asn Ile
20 25 30

Ile Ile Gly Ala Ala Ala Asn Ala Ser His Pro Gly Gly Ala Ala Ala
35 40 45

Val Ser Val Gln Ala Ala Gly Ser Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Ser Ala Arg Gly Thr Ser
65 70 75 80

Asn Thr Asp Val Thr Val Gly Ser Lys Thr Phe Asn Ile Ser His Ile
85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn
100 105 110

Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys
115 120 125

Ala Gly Asp Thr Ala Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly
130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ser Gly Thr Ala Thr Tyr Thr
145 150 155 160

Val Ala Gly Ile Asn Gly Ser Ala Thr Asn Leu Leu Ser Gly Asn Leu
165 170 175

Thr Ala Asn Phe Gly Ala Gly Thr Leu Gln Gly Ser Leu Thr Gly Thr

180 185 190

Gly Thr Ala Val Ser Ser Leu Ser Leu Asn Gly Val Thr Phe Ser Pro

195 200 205

Gly Thr Ala Glu Phe Ser Gly Ala Ala Ser Ala Asn Gly Thr Ala Gly

210 215 220

Val Asn Asn Ser Gly Ile Val Gln Gly His Phe Phe Gly Ala Asn Ala

225 230 235 240

Ala Ala Leu Ala Gly Ile Ala Glu Phe Asn Asn Val Ser Tyr Asn Thr

245 250 255

Ala Phe Gly Gly Ala Lys Asn

260

<210> 733

<211> 792

<212> DNA

<213> Acinetobacter sp. MN12 SLP 1a

<400> 733

atgaaaatct ctcaactgtt catcggtctt gttgcatgtt ctgctgtgtt tgcacatgca 60

ggtattgatg gtgcttcaag taatgaaaac aatatcatta ttggtgctgc tgcaaatgca 120

agccatctag gtggtgcagc agccgtttct gtacaagctg ctggttcacc atacaatgca 180

tttacaggtt ttagctcgct aaaaggtttg gcacaagcgt tttctgcacg cggtacaagc 240

aataccgatg ttactgtcgg tagcaaaact tttaatatct cccatattcc tgtttcggca 300

atgccgcctt cacacagtgc cttaggtaat ttcaattttg gtcaggtggg cacacaggaa 360

gtctattttg gtgaatggtg gaaagcaggc gatacagcag cgagcgcaag tcatactgtt 420

tattacgcag gtgacaatac caatacgaca gtaccaacct caggtacggc gacctatacc 480

gttgcaggga ttaatggttc agcaaccaat ctgttaagcg gtaatttgac tgctaacttt 540

ggtgcaggca ctttacaagg gtcattaact ggaacaggga ctgctgtttc aagcttaagt 600

ttgaacggtg tgacatttag tccaggtact gctgaattca gtggcgcggc aagtgcaaat 660

ggtacagctg gggtgaataa ttcaggtatt gttcaaggac acttctttgg tgcaaatgct 720

gcagctttag cgggtatcgc cgagtttaat aatgtttcat ataacactgc atttggtggt 780

gcgaagaact aa 792

<210> 734

<211> 263

<212> PRT

<213> Acinetobacter sp. MN12 SLP 1a

<400> 734

Met Lys Ile Ser Gln Leu Phe Ile Gly Leu Val Ala Cys Ser Ala Val
1 5 10 15

Phe Ala His Ala Gly Ile Asp Gly Ala Ser Ser Asn Glu Asn Asn Ile
20 25 30

Ile Ile Gly Ala Ala Ala Asn Ala Ser His Leu Gly Gly Ala Ala Ala
35 40 45

Val Ser Val Gln Ala Ala Gly Ser Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Ser Ala Arg Gly Thr Ser
65 70 75 80

Asn Thr Asp Val Thr Val Gly Ser Lys Thr Phe Asn Ile Ser His Ile
85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn
100 105 110

Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys
115 120 125

Ala Gly Asp Thr Ala Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly
130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ser Gly Thr Ala Thr Tyr Thr
145 150 155 160

Val Ala Gly Ile Asn Gly Ser Ala Thr Asn Leu Leu Ser Gly Asn Leu
165 170 175

Thr Ala Asn Phe Gly Ala Gly Thr Leu Gln Gly Ser Leu Thr Gly Thr
180 185 190

Gly Thr Ala Val Ser Ser Leu Ser Leu Asn Gly Val Thr Phe Ser Pro
195 200 205

Gly Thr Ala Glu Phe Ser Gly Ala Ala Ser Ala Asn Gly Thr Ala Gly

210 215 220

Val Asn Asn Ser Gly Ile Val Gln Gly His Phe Phe Gly Ala Asn Ala

225 230 235 240

Ala Ala Leu Ala Gly Ile Ala Glu Phe Asn Asn Val Ser Tyr Asn Thr

245 250 255

Ala Phe Gly Gly Ala Lys Asn

260

<210> 735

<211> 792

<212> DNA

<213> Acinetobacter sp. NIPH 1859 SLP 1a

<400> 735

atgaaaatct ctcaactgtt catcggtctt gttgcatgtt ctgctgtgtt tgcacatgca 60

ggtattgatg gtgcttcaag taatgaaaac aatatcatta ttggtgctgc tgcaaatgcc 120

agccacccag gcggtgcagc agctgtttct gtacaagcgg ctggtgcacc atacaatgca 180

tttacaggtt ttagctcgtt aaaaggtttg gcacaagcgt tctctgcacg tggtgctagc 240

aatactgatg ttactgtcgg tactaaaact tttaatatct cccatattcc tgtttcggca 300

atgccacctt cacatagtgc cttaggtaat ttcaattttg gtcaggtggg tacacaggaa 360

gtctattttg gtgaatggtg gaaagcgggc gatacagcag caagtgcaag tcatactgtt 420

tattacgcag gtgacaatac caatacgaca gtaccgactt ctggtacggc gacttatacc 480

gttgcaggga ttaatggttc agcaaccaat ctgttaagtg gtaatttaac tgctaacttt 540

ggtgcaggca ctttagaagg gtcattaact ggaacaggga ctgctgtttc aagcttaagc 600

ttggacggtg tgacatttaa tccaggtact gcggcattca gtggcggtgc aagtgcaaat 660

ggtacggctg ggctaaataa ttcaggtatt gttcaaggac acttctttgg tgcaaatgcc 720

gcagctttag cgggtattgc cgagtttaat aatgctgctt ataacactgc atttggtggt 780

gcgaaaaact aa 792

<210> 736

<211> 263

<212> PRT

<213> Acinetobacter sp. NIPH 1859 SLP 1a

<400> 736

Met Lys Ile Ser Gln Leu Phe Ile Gly Leu Val Ala Cys Ser Ala Val
1 5 10 15
Phe Ala His Ala Gly Ile Asp Gly Ala Ser Ser Asn Glu Asn Asn Ile
20 25 30
Ile Ile Gly Ala Ala Ala Asn Ala Ser His Pro Gly Gly Ala Ala Ala
35 40 45
Val Ser Val Gln Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Ser Ala Arg Gly Ala Ser
65 70 75 80
Asn Thr Asp Val Thr Val Gly Thr Lys Thr Phe Asn Ile Ser His Ile
85 90 95
Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn
100 105 110
Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys
115 120 125

Ala Gly Asp Thr Ala Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly
130 135 140
Asp Asn Thr Asn Thr Thr Val Pro Thr Ser Gly Thr Ala Thr Tyr Thr
145 150 155 160
Val Ala Gly Ile Asn Gly Ser Ala Thr Asn Leu Leu Ser Gly Asn Leu
165 170 175
Thr Ala Asn Phe Gly Ala Gly Thr Leu Glu Gly Ser Leu Thr Gly Thr
180 185 190

Gly Thr Ala Val Ser Ser Leu Ser Leu Asp Gly Val Thr Phe Asn Pro
195 200 205
Gly Thr Ala Ala Phe Ser Gly Gly Ala Ser Ala Asn Gly Thr Ala Gly
210 215 220
Leu Asn Asn Ser Gly Ile Val Gln Gly His Phe Phe Gly Ala Asn Ala
225 230 235 240
Ala Ala Leu Ala Gly Ile Ala Glu Phe Asn Asn Ala Ala Tyr Asn Thr

245 250 255

Ala Phe Gly Gly Ala Lys Asn

260

<210> 737

<211> 792

<212> DNA

<213> Acinetobacter sp. NIPH 1867 SLP 1a

<400> 737

atgaaaatct ctcaactgtt catcggtctc gttgcatgtt ctgctgtatt tgctcatgca 60

ggtattgaag gtgcttctag caatgaagca aatatcaaag tcggtgcggc agcaagtacc 120

agtcatccgg gtggtgcagc agcagtttct gtgcaggctg caggtgcgcc atataacgct 180

tttacaggct ttagttcact aaaaggttta gcgcaagcat tttctgcaca aggcacaagt 240

aatactaatg tcactgtagg taccaagaca tttaatatct cccatattcc tgtatctgca 300

atgccgcctt cacacagtgc tttaggtaat tttaattttg gtcaagtcgg cacacaggaa 360

gtttatttcg gtgaatggtg gaaagcaggc gatacacctg caagcgcaag ccatacggtt 420

tattacgcgg gtgacaatac caataccaca gtaccaactg caggtactgc aacatatacc 480

gttgcaggga ttaatggctc agcaactaat ctgctaagtg gtaatttcac agcgaacttt 540

ggtgcaggta ctttagaagg ctcattagct ggaacaggta caaccgtttc aaacgtaaca 600

cttgatggtg tgacgtttaa tccaggttca gctgcattta gtggatttgc aattgcaaat 660

ggtacagctg gcttaaatga ctcaggtatt gttcaggggc atttctttgg tgcaaatgcg 720

gctgctttag cgggtatcgc gaaatttgac aatgtttctt ataacactgc atttggcggt 780

gcgaagaact aa 792

<210> 738

<211> 263

<212> PRT

<213> Acinetobacter sp. NIPH 1867 SLP 1a

<400> 738

Met Lys Ile Ser Gln Leu Phe Ile Gly Leu Val Ala Cys Ser Ala Val

1 5 10 15

Phe Ala His Ala Gly Ile Glu Gly Ala Ser Ser Asn Glu Ala Asn Ile

20 25 30

Lys Val Gly Ala Ala Ala Ser Thr Ser His Pro Gly Gly Ala Ala Ala
35 40 45
Val Ser Val Gln Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60
Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Ser Ala Gln Gly Thr Ser
65 70 75 80
Asn Thr Asn Val Thr Val Gly Thr Lys Thr Phe Asn Ile Ser His Ile
85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn
100 105 110
Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys
115 120 125
Ala Gly Asp Thr Pro Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly
130 135 140
Asp Asn Thr Asn Thr Thr Val Pro Thr Ala Gly Thr Ala Thr Tyr Thr
145 150 155 160

Val Ala Gly Ile Asn Gly Ser Ala Thr Asn Leu Leu Ser Gly Asn Phe
165 170 175
Thr Ala Asn Phe Gly Ala Gly Thr Leu Glu Gly Ser Leu Ala Gly Thr
180 185 190
Gly Thr Thr Val Ser Asn Val Thr Leu Asp Gly Val Thr Phe Asn Pro
195 200 205
Gly Ser Ala Ala Phe Ser Gly Phe Ala Ile Ala Asn Gly Thr Ala Gly
210 215 220

Leu Asn Asp Ser Gly Ile Val Gln Gly His Phe Phe Gly Ala Asn Ala
225 230 235 240
Ala Ala Leu Ala Gly Ile Ala Lys Phe Asp Asn Val Ser Tyr Asn Thr
245 250 255
Ala Phe Gly Gly Ala Lys Asn
260

<210> 739
<211> 792

<212> DNA

<213> Acinetobacter sp. NIPH 809 SLP 1a

<400> 739

atgaaaatct ctcaactgtt tatcggtctt gttgcatgtt ctgctgtgtt tgcacatgca 60

ggtattgatg gtgcttcaag taatgaaaac aatatcatta ttggcgctgc tgcaaatgct 120

agccacccag gtggtgcagc agccgtttct gtacaagcgg ctggtgcacc ctacaatgca 180

tttacaggtt ttagctcgtt aaaaggtttg gcacaagcgt tcactgcacg tggtgcaagc 240

aatactgatg ttactgtcgg tagcaaaact tttaatatct cccatattcc tgtttcggca 300

atgccacctt cacatagtgc cttaggtaat ttcaattttg gtcaggtggg cacacaggaa 360

gtctattttg gtgaatggtg gaaagcgggc gatacagcag caagtgcaag tcatactgtt 420

tattacgcag gtgacaatac caataccaca gtaccgactg ctggtacggc tacctatacc 480

gttgcaggga ttaatggttc agcaaccaat ctgttaagtg gtaatttaac tgctaacttt 540

ggtgcaggca ctttagaagg gtcattaact ggaacaggga ctgctgtttc aagcttaagc 600

ttgaacggtg tgacatttaa tccaggtact gcggcattca gtggcggtgc aagtgcaaat 660

ggtacggctg ggctaaataa ttcaggtatt gttcaaggac atttctttgg tgcaaatgct 720

gcagctttag cgggtattgc cgagtttaat aatgctgctt ataacactgc ctttggtggt 780

gcgaaaaact aa 792

<210> 740

<211> 263

<212> PRT

<213> Acinetobacter sp. NIPH 809 SLP 1a

<400> 740

Met Lys Ile Ser Gln Leu Phe Ile Gly Leu Val Ala Cys Ser Ala Val

1 5 10 15

Phe Ala His Ala Gly Ile Asp Gly Ala Ser Ser Asn Glu Asn Asn Ile

20 25 30

Ile Ile Gly Ala Ala Ala Asn Ala Ser His Pro Gly Gly Ala Ala Ala

35 40 45

Val Ser Val Gln Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe

50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Thr Ala Arg Gly Ala Ser

65 70 75 80

Asn Thr Asp Val Thr Val Gly Ser Lys Thr Phe Asn Ile Ser His Ile

85 90 95

Pro Val Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn

100 105 110

Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys

115 120 125

Ala Gly Asp Thr Ala Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly

130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ala Gly Thr Ala Thr Tyr Thr

145 150 155 160

Val Ala Gly Ile Asn Gly Ser Ala Thr Asn Leu Leu Ser Gly Asn Leu

165 170 175

Thr Ala Asn Phe Gly Ala Gly Thr Leu Glu Gly Ser Leu Thr Gly Thr

180 185 190

Gly Thr Ala Val Ser Ser Leu Ser Leu Asn Gly Val Thr Phe Asn Pro

195 200 205

Gly Thr Ala Ala Phe Ser Gly Gly Ala Ser Ala Asn Gly Thr Ala Gly

210 215 220

Leu Asn Asn Ser Gly Ile Val Gln Gly His Phe Phe Gly Ala Asn Ala

225 230 235 240

Ala Ala Leu Ala Gly Ile Ala Glu Phe Asn Asn Ala Ala Tyr Asn Thr

245 250 255

Ala Phe Gly Gly Ala Lys Asn

260

<210> 741

<211> 792

<212> DNA

<213> Acinetobacter sp. WC-323 SLP 1a

<400> 741

atgaaaatct ctcaactgtt catcgctctg gttgcatgtt ctgcggtatt cagccatgca 60

gcaattgaag gcgcttcaag caacgaagca aatatcaaag tcggtgcggc agcaaatgcc 120

agtcatagcg gtggaacagc tgctgtttca gtagaggcgg caggtgcacc ttataatgca 180

ttcaccggtt ttagttcact caaaggtcta gcgcaagcat ttgctgcaca aggaaccagc 240

aatagcaatg taactgtggg tagcaagagc tttaatatct ctcacattcc tgcctctgca 300

atgccgcctt cacatagcgc tttaggtaat tttaactttg gacaggtcgg cacacaggaa 360

gtttatttcg gtgaatggtg gaaagccggt gatacgcctg ccagcgcaag ccatacggtt 420

tattacgcag gtgacaatac caataccaca gtacctactg caggaacggc aacctatacc 480

gttgcaggga ttaatggctc ggcagccaat ctgttaactg gtaatttcac tgcaaacttc 540

ggtgcaggca cgctcgaagg atcattaacc ggaaccggca ctagcgtttc aaacttaaca 600

ctggatggtg tgacctttaa tccgggttcg gctgcattta gcggttttgc aattgcaaat 660

ggtaccgctg gcttaaatga ctccggagcg gttcagggac atttctttgg cgcaaatgcg 720

gctgctttag cgggtatcgc gaaatttgac aatgtgtctt ataacacggc atttggcggt 780

gcgaaaaact aa 792

<210> 742

<211> 263

<212> PRT

<213> Acinetobacter sp. WC-323 SLP 1a

<400> 742

Met Lys Ile Ser Gln Leu Phe Ile Ala Leu Val Ala Cys Ser Ala Val
1 5 10 15

Phe Ser His Ala Ala Ile Glu Gly Ala Ser Ser Asn Glu Ala Asn Ile
20 25 30

Lys Val Gly Ala Ala Ala Asn Ala Ser His Ser Gly Gly Thr Ala Ala
35 40 45

Val Ser Val Glu Ala Ala Gly Ala Pro Tyr Asn Ala Phe Thr Gly Phe
50 55 60

Ser Ser Leu Lys Gly Leu Ala Gln Ala Phe Ala Ala Gln Gly Thr Ser
65 70 75 80

Asn Ser Asn Val Thr Val Gly Ser Lys Ser Phe Asn Ile Ser His Ile
85 90 95

Pro Ala Ser Ala Met Pro Pro Ser His Ser Ala Leu Gly Asn Phe Asn
100 105 110

Phe Gly Gln Val Gly Thr Gln Glu Val Tyr Phe Gly Glu Trp Trp Lys
115 120 125

Ala Gly Asp Thr Pro Ala Ser Ala Ser His Thr Val Tyr Tyr Ala Gly
130 135 140

Asp Asn Thr Asn Thr Thr Val Pro Thr Ala Gly Thr Ala Thr Tyr Thr
145 150 155 160

Val Ala Gly Ile Asn Gly Ser Ala Ala Asn Leu Leu Thr Gly Asn Phe
165 170 175

Thr Ala Asn Phe Gly Ala Gly Thr Leu Glu Gly Ser Leu Thr Gly Thr
180 185 190

Gly Thr Ser Val Ser Asn Leu Thr Leu Asp Gly Val Thr Phe Asn Pro
195 200 205

Gly Ser Ala Ala Phe Ser Gly Phe Ala Ile Ala Asn Gly Thr Ala Gly
210 215 220

Leu Asn Asp Ser Gly Ala Val Gln Gly His Phe Phe Gly Ala Asn Ala
225 230 235 240

Ala Ala Leu Ala Gly Ile Ala Lys Phe Asp Asn Val Ser Tyr Asn Thr
245 250 255

Ala Phe Gly Gly Ala Lys Asn
260

<210> 743

<211> 792

<212> DNA

<213> Aggregatibacter sp. oral taxon 458 SLP 1a

<400> 743

atgaaaaatt caattgttaa gtttagttta acggtattag ccgcattcac attagccgct 60

tgcggaagca gtggcggtag cagtgataat gccgctgcgg caagccatga tcaaaaaact 120

caggtaacgc catctaaaac cgatctgcca acatcgaatt caactgaggt aaatcaaaat 180

caaacattta caggttcagc ttttgttttc tctgaacaag atgacaaatt tcaagtcaaa 240

aaaaatgtta aatttaacga cgcaaatata aatcaattag aggttgatgg acacaagata 300

acgcttactt accccgaagg taacgggcaa gatttagatg atgcagtagt atgttgtgat 360

aagtatgcca atgtccgtat gggggtatct ttaagtaatg gtccggatga ggacgatatt 420

ctgttctata atggcattcc aaccccaaat atgcctgtaa ccggtttggc gtcgtataaa 480

ggcgatggca ttattttgtt caatgatatt ggcgatgatt ctgatgagga tacggtagaa 540

ggtcaatctt cttttgatgt taattttggt gcgaagacgc taagcggttc tattacagct 600

aacaatgtac caaccattaa tattagtgcg aatatttccg gtaatagctt tgagggtacg 660

gctaaatcga caaaattgac tgatggcgca gttgaaggta agttttatgg caataatgcg 720

gtagaattag gcggcttggc aaaagcaaat gataattcat ggggcgccgg ttttgtcggt 780

aagaaacagt aa 792

<210> 744

<211> 263

<212> PRT

<213> Aggregatibacter sp. oral taxon 458 SLP 1a

<400> 744

Met Lys Asn Ser Ile Val Lys Phe Ser Leu Thr Val Leu Ala Ala Phe
1 5 10 15

Thr Leu Ala Ala Cys Gly Ser Ser Gly Gly Ser Ser Asp Asn Ala Ala
20 25 30

Ala Ala Ser His Asp Gln Lys Thr Gln Val Thr Pro Ser Lys Thr Asp
35 40 45

Leu Pro Thr Ser Asn Ser Thr Glu Val Asn Gln Asn Gln Thr Phe Thr
50 55 60

Gly Ser Ala Phe Val Phe Ser Glu Gln Asp Asp Lys Phe Gln Val Lys
65 70 75 80

Lys Asn Val Lys Phe Asn Asp Ala Asn Ile Asn Gln Leu Glu Val Asp
85 90 95

Gly His Lys Ile Thr Leu Thr Tyr Pro Glu Gly Asn Gly Gln Asp Leu
100 105 110

Asp Asp Ala Val Val Cys Cys Asp Lys Tyr Ala Asn Val Arg Met Gly
115 120 125

Val Ser Leu Ser Asn Gly Pro Asp Glu Asp Asp Ile Leu Phe Tyr Asn
130 135 140

Gly Ile Pro Thr Pro Asn Met Pro Val Thr Gly Leu Ala Ser Tyr Lys

145 150 155 160

Gly Asp Gly Ile Ile Leu Phe Asn Asp Ile Gly Asp Asp Ser Asp Glu

165 170 175

Asp Thr Val Glu Gly Gln Ser Ser Phe Asp Val Asn Phe Gly Ala Lys

180 185 190

Thr Leu Ser Gly Ser Ile Thr Ala Asn Asn Val Pro Thr Ile Asn Ile

195 200 205

Ser Ala Asn Ile Ser Gly Asn Ser Phe Glu Gly Thr Ala Lys Ser Thr

210 215 220

Lys Leu Thr Asp Gly Ala Val Glu Gly Lys Phe Tyr Gly Asn Asn Ala

225 230 235 240

Val Glu Leu Gly Gly Leu Ala Lys Ala Asn Asp Asn Ser Trp Gly Ala

245 250 255

Gly Phe Val Gly Lys Lys Gln

260

<210> 745

<211> 618

<212> DNA

<213> Aggregatibacter sp. oral taxon 458 SLP 2a

<400> 745

atgttaaaac aacttaaata cacgtctatt ttggctttat ctgcattagc tgttgcttgt 60

tccggtggtg atagcggggc gggtacagca gaaacaccgg atgggaacaa atttaactta 120

acaaatagta ctaaagggtt ggttgggagt aaaacaatgg atggtaaact catcggctat 180

aaccaaaatc actcttttta cggtgtgtgg gtgaataatg ataaaactcg ccaacaggtt 240

cgttatcaag gaactgccac accaacagat cgtttgccaa gaggagctgc aacttataca 300

ggacatgccg ttcgtgcgcg cgatagcgtt attgcgcaaa atattaatgg tgttcaagct 360

gatggaacaa tgacattaca tgtgaatttt gatacgaaaa aggtttccgg aaagttgggt 420

attccttggg ctcgcgatat taccttgcat gaaaccgatt taaatggtaa ccaatttgcc 480

ggcaaagcca gcgtgttatt caatgatggc ggtcgttata aaggcggatt gtttggcccg 540

aatgcagagg aagctgccgg tatggccacg tttgataaca atccaagttt aaatacttcc 600

tttggtggtt accgttaa 618

<210> 746

<211> 205

<212> PRT

<213> Aggregatibacter sp. oral taxon 458 SLP 2a

<400> 746

Met Leu Lys Gln Leu Lys Tyr Thr Ser Ile Leu Ala Leu Ser Ala Leu
1 5 10 15

Ala Val Ala Cys Ser Gly Gly Asp Ser Gly Ala Gly Thr Ala Glu Thr
20 25 30

Pro Asp Gly Asn Lys Phe Asn Leu Thr Asn Ser Thr Lys Gly Leu Val
35 40 45

Gly Ser Lys Thr Met Asp Gly Lys Leu Ile Gly Tyr Asn Gln Asn His
50 55 60

Ser Phe Tyr Gly Val Trp Val Asn Asn Asp Lys Thr Arg Gln Gln Val
65 70 75 80

Arg Tyr Gln Gly Thr Ala Thr Pro Thr Asp Arg Leu Pro Arg Gly Ala
85 90 95

Ala Thr Tyr Thr Gly His Ala Val Arg Ala Arg Asp Ser Val Ile Ala
100 105 110

Gln Asn Ile Asn Gly Val Gln Ala Asp Gly Thr Met Thr Leu His Val
115 120 125

Asn Phe Asp Thr Lys Lys Val Ser Gly Lys Leu Gly Ile Pro Trp Ala
130 135 140

Arg Asp Ile Thr Leu His Glu Thr Asp Leu Asn Gly Asn Gln Phe Ala
145 150 155 160

Gly Lys Ala Ser Val Leu Phe Asn Asp Gly Gly Arg Tyr Lys Gly Gly
165 170 175

Leu Phe Gly Pro Asn Ala Glu Glu Ala Ala Gly Met Ala Thr Phe Asp
180 185 190

Asn Asn Pro Ser Leu Asn Thr Ser Phe Gly Gly Tyr Arg
195 200 205

<210> 747

<211> 1545

<212> DNA

<213> Aggregatibacter sp. oral taxon 458 SLP 3a

<400> 747

atgaacttta aaaatacaac cattgcagca gcaattttat tttcccttac tgcctgtgga 60

agcagtagtg gcggctctaa cacggttgat aacaaaccaa cggctaaaaa tgaacaaacc 120

caacaacaag tagcagacgc aaaaaaagcg gaagaaacac gtcaagctga aaaagctcgt 180

aaagccgaag aagctcgtca agctgaagaa gcacgtaaag ctgaagaagc tcgtaaagct 240

gaaggagctc gtcaagctga agaagcacgc aaagctgaag aagcgcgtca agccgaagaa 300

gcacgcaaag ctgaagaagc tcgtaaagct gaagaagctc gtaaagccga agaagcacgt 360

caagccgaag aagcacgtaa agctgaagaa gctcgtcaag ccgaagaagc acgcaaagct 420

gaagaagctc gtaaagctga agaaacgcgt caagccgaag aagcacgcaa agctgaagaa 480

gctcgtaaag ccgaagaagc tcgtcaagcc gaagaagcac gcaaagctga agaagctcgt 540

aaagctgaag aagtacgcaa agctgaagaa gcacgtaaag cagaagaaac tcgtcaagct 600

gaagaagcac gtaaagcaga agaagcacgc aaagctgaag aagctcgtaa agaagctgaa 660

gaagctcgtc aagccgaaga agcacgtaaa gccgaagagg ctcgtattgc acaaaaaact 720

gctgagttaa ttgaacaagc taaagctaaa gggctaaacg atgacgaagc aaaacaattt 780

gcgcaaaata atatcaataa tgaagatgat gtatctaaag caaatttaga taacatgatt 840

aaaataaaag atttgacaaa acttgctatt gctgaaggtc ttaatgaaca tcaagccgct 900

gattttgcta aaaataatgt agatttagat gaagatacag caaaagctaa ccttgaaaca 960

cttatcatca ataatgctaa aggaatttat aatggacaat atcgtaatgg gctaactaca 1020

aaccaatatg gcacatcaag tagttcctca tctggttgta caaatggacg ttgctattca 1080

gtagaagaaa ctattactac cggtaaagca atctataacc aaccatattc aattattgtt 1140

gccaatacaa aatcaggtgt tcgtaattat tctcctatta atgaactatc gaatgtacaa 1200

attactggtc taaaaacaaa attagacgcg ataccaacgg aaggaacagc taattatagt 1260

ggtaaagcat ttgatgccaa aaataatgga gcactagatt acaatgttaa ttttgcaaat 1320

aaaacaggct caggaactat taccggctta ggaaataaca ttacattaga acagggttct 1380

atttcaggct ctggtatttc atctagtgca acccaaggtt acaaatcagg ttcttattct 1440

ttagatttct ttggtaaaaa tgcggaagaa attggcggta aagtcactct tgatggaaaa 1500

gatgcagtcg gcttcggtgg tacacgtggc gaaatccaga aataa 1545

<210> 748

<211> 513

<212> PRT

<213> Aggregatibacter sp. oral taxon 458 SLP 3a

<400> 748

Met Asn Phe Lys Asn Thr Thr Ile Ala Ala Ala Ile Leu Phe Ser Leu
1 5 10 15

Thr Ala Cys Gly Ser Ser Ser Gly Gly Ser Asn Thr Val Asp Asn Lys
20 25 30

Pro Thr Ala Lys Asn Glu Gln Thr Gln Gln Gln Val Ala Asp Ala Lys
35 40 45

Lys Ala Glu Glu Thr Arg Gln Ala Glu Lys Ala Arg Lys Ala Glu Glu
50 55 60

Ala Arg Gln Ala Glu Glu Ala Arg Lys Ala Glu Glu Ala Arg Lys Ala
65 70 75 80

Glu Gly Ala Arg Gln Ala Glu Glu Ala Arg Lys Ala Glu Glu Ala Arg
85 90 95

Gln Ala Glu Glu Ala Arg Lys Ala Glu Glu Ala Arg Lys Ala Glu Glu
100 105 110

Ala Arg Lys Ala Glu Glu Ala Arg Gln Ala Glu Glu Ala Arg Lys Ala
115 120 125

Glu Glu Ala Arg Gln Ala Glu Glu Ala Arg Lys Ala Glu Glu Ala Arg
130 135 140

Lys Ala Glu Glu Thr Arg Gln Ala Glu Glu Ala Arg Lys Ala Glu Glu
145 150 155 160

Ala Arg Lys Ala Glu Glu Ala Arg Gln Ala Glu Glu Ala Arg Lys Ala
165 170 175

Glu Glu Ala Arg Lys Ala Glu Glu Val Arg Lys Ala Glu Glu Ala Arg
180 185 190

Lys Ala Glu Glu Thr Arg Gln Ala Glu Glu Ala Arg Lys Ala Glu Glu
195 200 205

Ala Arg Lys Ala Glu Glu Ala Arg Lys Ala Glu Glu Ala Arg Gln Ala
210 215 220

Glu Glu Ala Arg Lys Ala Glu Glu Ala Arg Ile Ala Gln Lys Thr Ala
225 230 235 240
Glu Leu Ile Glu Gln Ala Lys Ala Lys Gly Leu Asn Asp Asp Glu Ala
245 250 255

Lys Gln Phe Ala Gln Asn Asn Ile Asn Asn Glu Asp Asp Val Ser Lys
260 265 270
Ala Asn Leu Asp Asn Met Ile Lys Ile Lys Asp Leu Thr Lys Leu Ala
275 280 285
Ile Ala Glu Gly Leu Asn Glu His Gln Ala Ala Asp Phe Ala Lys Asn
290 295 300
Asn Val Asp Leu Asp Glu Asp Thr Ala Lys Ala Asn Leu Glu Thr Leu
305 310 315 320

Ile Ile Asn Asn Ala Lys Gly Ile Tyr Asn Gly Gln Tyr Arg Asn Gly
325 330 335
Leu Thr Thr Asn Gln Tyr Gly Thr Ser Ser Ser Ser Ser Ser Gly Cys
340 345 350
Thr Asn Gly Arg Cys Tyr Ser Val Glu Glu Thr Ile Thr Thr Gly Lys
355 360 365
Ala Ile Tyr Asn Gln Pro Tyr Ser Ile Ile Val Ala Asn Thr Lys Ser
370 375 380

Gly Val Arg Asn Tyr Ser Pro Ile Asn Glu Leu Ser Asn Val Gln Ile
385 390 395 400
Thr Gly Leu Lys Thr Lys Leu Asp Ala Ile Pro Thr Glu Gly Thr Ala
405 410 415
Asn Tyr Ser Gly Lys Ala Phe Asp Ala Lys Asn Asn Gly Ala Leu Asp
420 425 430
Tyr Asn Val Asn Phe Ala Asn Lys Thr Gly Ser Gly Thr Ile Thr Gly
435 440 445

Leu Gly Asn Asn Ile Thr Leu Glu Gln Gly Ser Ile Ser Gly Ser Gly
450 455 460
Ile Ser Ser Ser Ala Thr Gln Gly Tyr Lys Ser Gly Ser Tyr Ser Leu

465 470 475 480

Asp Phe Phe Gly Lys Asn Ala Glu Glu Ile Gly Gly Lys Val Thr Leu

485 490 495

Asp Gly Lys Asp Ala Val Gly Phe Gly Gly Thr Arg Gly Glu Ile Gln

500 505 510

Lys

<210> 749

<211> 1719

<212> DNA

<213> B. psittacipulmonis SLP 1a

<400> 749

atgtttcaaa aatacaccat cacttatctc atcactgcaa tcctgttaac tgcttgttcg 60

actagcggcg gaacctttga tcctttagat gtaggtagta gtacaaaatc tggactaccg 120

gatagtgcga acaatgtgaa atacgtcaat cccgtgattg aaaccgaccc agaagcacaa 180

tctatcgatg aaacgggata cagcattaat gtgccaattc ctaaagccct atatgaaaat 240

tatgcaaaga gatacttcaa ccccaataca ttaaaaatca acaaagatca taattattta 300

gatactagcg atcaatacga aacattgaca ttaaagattg taagtctgaa cgaaaacgga 360

accccaatca tttctgagag aaaaattcca ttcaaaatca cagaagacac ttggaattat 420

cttgataata ctataaaaga atcagacgaa aacaatatca acacatacca tgataggacc 480

tacaatcctt atttaaagat ttataaatta aataattcac tagtcggaac cattatattt 540

acgaatttaa aagatagttc acttaatatc aataatgtag ctgaagaaaa caaatccgtt 600

caattattct acaagggtca tataaaacca accgtagaaa atatgccgat ttcgggaacg 660

tttggatata atggaaaatg gttttttgtc actcaagtaa ataatttatc tcaggatact 720

gatgcagaat ggggaaaata ctcctcctca ctcccccttt ctttaaccat cgactttacc 780

cagaaaacag taaaaggaaa tctatcacat tcaggagata acgtaacgat aaattacact 840

attgatgccg tcattaaagg gaattacttt aaaggggttg caaagggaaa atacgaatcc 900

acaggaaact cccttaacgg ctcaagtgaa gccgatgcgg atttgatcgg ttctttcttt 960

ggagacactg cagaagaagc tgctggacgt gtcatcgcta gagatttctc atggggtgcg 1020

gtttttgcca cgaaacgaca aagaaatgat ctcagtgatt tagcggctgc gggtatttta 1080

ggctttgatc acaacggtac cttacaagac tatcaagcca atatcgcaac acaaactctc 1140

gatcgattaa tcgttgacgg agaaatcatt gatttctcac aagaatataa tgaactatgt 1200

tgtgccgaaa caaaatttgt gaaatatggc acattcaagc cagaaaacag taacaacatt 1260
caaggtggtt attttattca aggcacagcc acaaccgata tgcctgaaac ggggaatgcc 1320
agctatcgtg gaaactggta tggttttgtt aaagatagta gcacaggata ctcagcaact 1380
gcacaaaaaa atgaagcgac ttatcaagcg aattggggag ataaaaccct atcgggcaaa 1440
ctatttggca aaaatcaaga tattaacagc gatcaaccaa tcggtatctt atctgccaaa 1500
attcaagata acacgtttca gggcaaggtg acctttaaag attgggcagt cgatgaaaac 1560
aaagacaact tagagaacac tcaaaaaatc agtggtgaag cagaagccaa gggatatttt 1620

tatggtgcta aagccaatga gttaggtggg cattttaaaa atcaagacaa ttcagcagga 1680
ggtgtatttg gcggtaaaca aatcgaagta acccccctaa 1719

<210> 750
<211> 572
<212> PRT
<213> B. psittacipulmonis SLP 1a
<400> 750

Met Phe Gln Lys Tyr Thr Ile Thr Tyr Leu Ile Thr Ala Ile Leu Leu
1 5 10 15
Thr Ala Cys Ser Thr Ser Gly Gly Thr Phe Asp Pro Leu Asp Val Gly
20 25 30
Ser Ser Thr Lys Ser Gly Leu Pro Asp Ser Ala Asn Asn Val Lys Tyr
35 40 45
Val Asn Pro Val Ile Glu Thr Asp Pro Glu Ala Gln Ser Ile Asp Glu
50 55 60
Thr Gly Tyr Ser Ile Asn Val Pro Ile Pro Lys Ala Leu Tyr Glu Asn
65 70 75 80
Tyr Ala Lys Arg Tyr Phe Asn Pro Asn Thr Leu Lys Ile Asn Lys Asp
85 90 95
His Asn Tyr Leu Asp Thr Ser Asp Gln Tyr Glu Thr Leu Thr Leu Lys
100 105 110
Ile Val Ser Leu Asn Glu Asn Gly Thr Pro Ile Ile Ser Glu Arg Lys
115 120 125

Ile Pro Phe Lys Ile Thr Glu Asp Thr Trp Asn Tyr Leu Asp Asn Thr
130 135 140
Ile Lys Glu Ser Asp Glu Asn Asn Ile Asn Thr Tyr His Asp Arg Thr
145 150 155 160
Tyr Asn Pro Tyr Leu Lys Ile Tyr Lys Leu Asn Asn Ser Leu Val Gly

165 170 175
Thr Ile Ile Phe Thr Asn Leu Lys Asp Ser Ser Leu Asn Ile Asn Asn
180 185 190
Val Ala Glu Glu Asn Lys Ser Val Gln Leu Phe Tyr Lys Gly His Ile
195 200 205
Lys Pro Thr Val Glu Asn Met Pro Ile Ser Gly Thr Phe Gly Tyr Asn
210 215 220
Gly Lys Trp Phe Phe Val Thr Gln Val Asn Asn Leu Ser Gln Asp Thr

225 230 235 240
Asp Ala Glu Trp Gly Lys Tyr Ser Ser Ser Leu Pro Leu Ser Leu Thr
245 250 255
Ile Asp Phe Thr Gln Lys Thr Val Lys Gly Asn Leu Ser His Ser Gly
260 265 270
Asp Asn Val Thr Ile Asn Tyr Thr Ile Asp Ala Val Ile Lys Gly Asn
275 280 285
Tyr Phe Lys Gly Val Ala Lys Gly Lys Tyr Glu Ser Thr Gly Asn Ser

290 295 300
Leu Asn Gly Ser Ser Glu Ala Asp Ala Asp Leu Ile Gly Ser Phe Phe
305 310 315 320
Gly Asp Thr Ala Glu Glu Ala Ala Gly Arg Val Ile Ala Arg Asp Phe
325 330 335
Ser Trp Gly Ala Val Phe Ala Thr Lys Arg Gln Arg Asn Asp Leu Ser
340 345 350
Asp Leu Ala Ala Ala Gly Ile Leu Gly Phe Asp His Asn Gly Thr Leu

355 360 365
Gln Asp Tyr Gln Ala Asn Ile Ala Thr Gln Thr Leu Asp Arg Leu Ile

370 375 380

Val Asp Gly Glu Ile Ile Asp Phe Ser Gln Glu Tyr Asn Glu Leu Cys

385 390 395 400

Cys Ala Glu Thr Lys Phe Val Lys Tyr Gly Thr Phe Lys Pro Glu Asn

405 410 415

Ser Asn Asn Ile Gln Gly Gly Tyr Phe Ile Gln Gly Thr Ala Thr Thr

420 425 430

Asp Met Pro Glu Thr Gly Asn Ala Ser Tyr Arg Gly Asn Trp Tyr Gly

435 440 445

Phe Val Lys Asp Ser Ser Thr Gly Tyr Ser Ala Thr Ala Gln Lys Asn

450 455 460

Glu Ala Thr Tyr Gln Ala Asn Trp Gly Asp Lys Thr Leu Ser Gly Lys

465 470 475 480

Leu Phe Gly Lys Asn Gln Asp Ile Asn Ser Asp Gln Pro Ile Gly Ile

485 490 495

Leu Ser Ala Lys Ile Gln Asp Asn Thr Phe Gln Gly Lys Val Thr Phe

500 505 510

Lys Asp Trp Ala Val Asp Glu Asn Lys Asp Asn Leu Glu Asn Thr Gln

515 520 525

Lys Ile Ser Gly Glu Ala Glu Ala Lys Gly Tyr Phe Tyr Gly Ala Lys

530 535 540

Ala Asn Glu Leu Gly Gly His Phe Lys Asn Gln Asp Asn Ser Ala Gly

545 550 555 560

Gly Val Phe Gly Gly Lys Gln Ile Glu Val Thr Pro

565 570

<210> 751

<211> 1338

<212> DNA

<213> B. psittacipulmonis SLP 2a

<400> 751

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acaggtggtt caagtggtga aaattccgag ggatcgcaag ttaacggttc agatcagggg 180

gatagcatcg agtcacagcc ggataacagt ggaacaggtg cttcaggttc tggatcgagt 240

gatggcacaa aacaggatgg tgcagggtca tcaacgggtg ataatggaaa ttcagaaaat 300

gctcaagaag tagataatgg agcggctgtg gcagatggcg atgcttccag cgatagtaag 360

aatagtgatt ttcatcctcc tacagagaaa gaaggcgatg ataatacttt tgatgctacc 420

gatattgaag caggaggaaa taatgagact acagaagagg ttcgtgttgc tgataaggaa 480

gctgaaaaaa acgctgccgc tcctttgcac aaatatgctc cacccaccaa agaggcgatt 540

aaagagtggc taacaacacc tgtcactgag ggtgggttag gcgtagagaa tgcagatgat 600

gtagcgtatt atttagatga gggaaaagta ggacgtgatg cattctttca agctaataag 660

ggaaatgcag agaaacaagg ctttcaaacg gctcaaaaac gttggatacg gtcatcagat 720

agtcaccgta tttattatga tcaggaaaat gctccacttt tgtacaatca aaattactca 780

atgattgaag gtgccttggt tactcatctt gttggggatg ggtctggcct gatagatgat 840

tttatgattc tagaaaaagg tcagtttacg agtcgggatg aattgaagtc tctttcaggt 900

aaggtgactt atacaggtaa agcttttgat aaagatacgc aagttgtagt tgtaagaact 960

gactcaggaa gtgactccta ctccgtttta ggatcaggta catttactta cactattgat 1020

tttgataaaa ataaaggtag cggtaagatt actgatatgt catcatatgg tgatattatc 1080

ttaaaggaag tgaatttggc tcctggtcag aaaaaccttc taactggtga aagctattat 1140

ggtgcgggct atcagacagg taatgatagt agaggtgagg ttactttcgc taatggcgtt 1200

gacgataaga cctataagta tagcattgct ttatatggtt atgatggaga agaagtgtta 1260

ggcaaagttc aagaagtaga agaaggtaag ggcattggca aggatgtcat tggttttggt 1320

ggtaagaagc agcagtaa 1338

<210> 752

<211> 445

<212> PRT

<213> B. psittacipulmonis SLP 2a

<400> 752

Met Arg Ser Leu Gly Val Ile Leu Phe Val Ala Leu Leu Thr Ala Cys

1 5 10 15

Ser Ser Ser Ser Gly Asn Lys Ser Ser Asn Leu Val Val His Pro Asn

20 25 30

Ile Pro Val Thr Glu Ser Pro Ser Thr Gly Gly Ser Ser Gly Glu Asn

35 40 45

Ser Glu Gly Ser Gln Val Asn Gly Ser Asp Gln Gly Asp Ser Ile Glu

50 55 60

Ser Gln Pro Asp Asn Ser Gly Thr Gly Ala Ser Gly Ser Gly Ser Ser

65 70 75 80

Asp Gly Thr Lys Gln Asp Gly Ala Gly Ser Ser Thr Gly Asp Asn Gly

85 90 95

Asn Ser Glu Asn Ala Gln Glu Val Asp Asn Gly Ala Ala Val Ala Asp

100 105 110

Gly Asp Ala Ser Ser Asp Ser Lys Asn Ser Asp Phe His Pro Pro Thr

115 120 125

Glu Lys Glu Gly Asp Asp Asn Thr Phe Asp Ala Thr Asp Ile Glu Ala

130 135 140

Gly Gly Asn Asn Glu Thr Thr Glu Glu Val Arg Val Ala Asp Lys Glu

145 150 155 160

Ala Glu Lys Asn Ala Ala Ala Pro Leu His Lys Tyr Ala Pro Pro Thr

165 170 175

Lys Glu Ala Ile Lys Glu Trp Leu Thr Thr Pro Val Thr Glu Gly Gly

180 185 190

Leu Gly Val Glu Asn Ala Asp Asp Val Ala Tyr Tyr Leu Asp Glu Gly

195 200 205

Lys Val Gly Arg Asp Ala Phe Phe Gln Ala Asn Lys Gly Asn Ala Glu

210 215 220

Lys Gln Gly Phe Gln Thr Ala Gln Lys Arg Trp Ile Arg Ser Ser Asp

225 230 235 240

Ser His Arg Ile Tyr Tyr Asp Gln Glu Asn Ala Pro Leu Leu Tyr Asn

245 250 255

Gln Asn Tyr Ser Met Ile Glu Gly Ala Leu Val Thr His Leu Val Gly

260 265 270

Asp Gly Ser Gly Leu Ile Asp Asp Phe Met Ile Leu Glu Lys Gly Gln

275 280 285

Phe Thr Ser Arg Asp Glu Leu Lys Ser Leu Ser Gly Lys Val Thr Tyr
290 295 300
Thr Gly Lys Ala Phe Asp Lys Asp Thr Gln Val Val Val Val Arg Thr
305 310 315 320
Asp Ser Gly Ser Asp Ser Tyr Ser Val Leu Gly Ser Gly Thr Phe Thr

325 330 335
Tyr Thr Ile Asp Phe Asp Lys Asn Lys Gly Ser Gly Lys Ile Thr Asp
340 345 350
Met Ser Ser Tyr Gly Asp Ile Ile Leu Lys Glu Val Asn Leu Ala Pro
355 360 365
Gly Gln Lys Asn Leu Leu Thr Gly Glu Ser Tyr Tyr Gly Ala Gly Tyr
370 375 380
Gln Thr Gly Asn Asp Ser Arg Gly Glu Val Thr Phe Ala Asn Gly Val

385 390 395 400
Asp Asp Lys Thr Tyr Lys Tyr Ser Ile Ala Leu Tyr Gly Tyr Asp Gly
405 410 415
Glu Glu Val Leu Gly Lys Val Gln Glu Val Glu Glu Gly Lys Gly Ile
420 425 430
Gly Lys Asp Val Ile Gly Phe Gly Gly Lys Lys Gln Gln
435 440 445

<210> 753

<211> 1017

<212> DNA

<213> B. trehalosi SLP 3a

<400

> 753

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tgttctgtga atgctggcag tggtagtcaa ggtgatcctg ttattcgagc aacgagtagt 120
gcaacaaata caaacactaa tgagaattcg gataccgaaa cgagtgaaga taatacatta 180
gtagaagagc gtgcggaaag tacaacggag agttcatcaa cagagggcag ctcgaaagat 240
acgactacag atgagcccag ccatacaact acggaaaatg ttgtagataa tatcgacaat 300
gaagacgatg aatcggaatt aattgcgatt ggtggggttg gcgtaatggg tagtcaggca 360

gagaaatact taacttcttt aagtgcacag gatgaacttt ttgcctcaat caacaaaatg 420

gagaatgttg ctactggcag ttgctcaaat tcagctgctt ctggttcaaa atgtgccgta 480
gcgaatgctc aagaaggtga tattctcgct gtttatacgc taaaagataa cgcagctcaa 540
acactggctg gctatgcggt tattcgtgaa gcttatacta gccgtgaaaa tccaaccaat 600
agctatatca cgttattatc tgtcccaacc acggaaaagt cagccgtggt taatgcgact 660
tatacgggga aagcttcact ttcttataac aatagtgctg ctatcaatac gatggagttt 720
gaaatgacag caagcaatga cacagtaagt ggcaaaattt atacgatagc aaatacaggt 780
aaagaatctg tccgtgttac gctcaacagt ggcgatatta atgtgactaa cggattagtt 840

gggtttaatg gtacaacaac ctttaataaa acagcatatg ctgatttggc tgatgtagaa 900
ggtgtttatc agggttggtt tgttggtgaa aatgcagaag gtgtgatcgg cactattcat 960
actaagaatc agactacttc aggcgtgctt caaggtgcat ttgcagggac aaaataa 1017

<210> 754
<211> 338
<212> PRT
<213> B. trehalosi SLP 3a
<400> 754

Met Lys Arg Gln Phe Val Asn Gly Ala Met Ala Leu Leu Ile Ala Leu
1 5 10 15
Gly Val Ser Ala Cys Ser Val Asn Ala Gly Ser Gly Ser Gln Gly Asp
20 25 30

Pro Val Ile Arg Ala Thr Ser Ser Ala Thr Asn Thr Asn Thr Asn Glu
35 40 45
Asn Ser Asp Thr Glu Thr Ser Glu Asp Asn Thr Leu Val Glu Glu Arg
50 55 60
Ala Glu Ser Thr Thr Glu Ser Ser Ser Thr Glu Gly Ser Ser Lys Asp
65 70 75 80
Thr Thr Thr Asp Glu Pro Ser His Thr Thr Thr Glu Asn Val Val Asp
85 90 95

Asn Ile Asp Asn Glu Asp Asp Glu Ser Glu Leu Ile Ala Ile Gly Gly
100 105 110
Val Gly Val Met Gly Ser Gln Ala Glu Lys Tyr Leu Thr Ser Leu Ser

115 120 125

Ala Gln Asp Glu Leu Phe Ala Ser Ile Asn Lys Met Glu Asn Val Ala

130 135 140

Thr Gly Ser Cys Ser Asn Ser Ala Ala Ser Gly Ser Lys Cys Ala Val

145 150 155 160

Ala Asn Ala Gln Glu Gly Asp Ile Leu Ala Val Tyr Thr Leu Lys Asp

165 170 175

Asn Ala Ala Gln Thr Leu Ala Gly Tyr Ala Val Ile Arg Glu Ala Tyr

180 185 190

Thr Ser Arg Glu Asn Pro Thr Asn Ser Tyr Ile Thr Leu Leu Ser Val

195 200 205

Pro Thr Thr Glu Lys Ser Ala Val Val Asn Ala Thr Tyr Thr Gly Lys

210 215 220

Ala Ser Leu Ser Tyr Asn Asn Ser Ala Ala Ile Asn Thr Met Glu Phe

225 230 235 240

Glu Met Thr Ala Ser Asn Asp Thr Val Ser Gly Lys Ile Tyr Thr Ile

245 250 255

Ala Asn Thr Gly Lys Glu Ser Val Arg Val Thr Leu Asn Ser Gly Asp

260 265 270

Ile Asn Val Thr Asn Gly Leu Val Gly Phe Asn Gly Thr Thr Thr Phe

275 280 285

Asn Lys Thr Ala Tyr Ala Asp Leu Ala Asp Val Glu Gly Val Tyr Gln

290 295 300

Gly Trp Phe Val Gly Glu Asn Ala Glu Gly Val Ile Gly Thr Ile His

305 310 315 320

Thr Lys Asn Gln Thr Thr Ser Gly Val Leu Gln Gly Ala Phe Ala Gly

325 330 335

Thr Lys

<210> 755

<211> 1290

<212> DNA

<213> B. trehalosi SLP 3b

<400> 755

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tgtggctctc gacataaaga gactattgtg aacacgacac cgaatacatc agcggcagag 120

ctatctatcg taaaacagca attggcagat gctcaacgtg cgttagctac ggctgaaacc 180

gcagcagctg aagccaaaga ggctcaaaca accgtagaaa acacattaca agcggtacaa 240

attgaggcag aaacggcaaa atctacagca gcggtggcac aaacccagct gacagccgca 300

cagcaagaga ttgagaattt aaaagcacgg cttgcgagca gttccgattc tacagaagtt 360

gaggcgctta aagcagcact tgcagcggca gagcagaaag ctgctcaagc agaaaccgag 420

cttgtgagtg cgaattccgc actagaaaaa gccaatagtg agcttgctgc aacagaaagt 480

caattagcca actatgttgc aaaagagaaa gttgctggcg ataaaattgc ttcagatttg 540

acagctggtg gttttgcagc agatagcacc tcttatactt acgcatatct gaacgacgaa 600

gtaaaaaaag cagaattagc agaagtgatt gcaaacggca cagcgagttg cggttctgca 660

gcaagccctg tgactggtgc agctgttgcg gggtgtttaa gattatcaaa tactgcagag 720

ggtacgattt tatttacaaa agagaatgaa tattctgctt atgctgttgt gcgtgaagcc 780

tatgatgcag atagtggtgt gaatatgccg aaaaattctt ttatcgctct ggttaaaaca 840

ccaacaactg ataaagctca ggtattggga gcaacttatc gtggtttagc aacttattct 900

caaagtgcag gtttaaatgg ctcttctctt gtgggtgaga acattgctgc tacggcagga 960

aaattgaatg tcgttacttt aaatgtggat caaaatgggc aaattagtgg cgaaatttgg 1020

aataaaacca gtgcgaaaga agagaatcat taccgtacgg ttgaactaaa ggcggcagat 1080

gtcttagtca gcaacagtgg tatcgtgttt gaaggtgagg ccgccattaa tgaaaaaatg 1140

ctcaagacag ggactccgtt agaaggaact tataaaggtg catttgcagg gaatgaaggt 1200

caagaagtag tgggaacatt ccaaacaaac tcgcttgaaa caaattatgt gcaaggtgca 1260

tttagtgcaa ccaaagatag tgcagagtaa 1290

<210> 756

<211> 429

<212> PRT

<213> B. trehalosi SLP 3b

<400> 756

Met Lys Lys Thr Val Thr Asn Thr Ala Ile Ala Leu Leu Leu Ser Leu

1 5 10 15

Gly Val Ala Ala Cys Gly Ser Arg His Lys Glu Thr Ile Val Asn Thr
20 25 30
Thr Pro Asn Thr Ser Ala Ala Glu Leu Ser Ile Val Lys Gln Gln Leu
35 40 45
Ala Asp Ala Gln Arg Ala Leu Ala Thr Ala Glu Thr Ala Ala Ala Glu

50 55 60
Ala Lys Glu Ala Gln Thr Thr Val Glu Asn Thr Leu Gln Ala Val Gln
65 70 75 80
Ile Glu Ala Glu Thr Ala Lys Ser Thr Ala Ala Val Ala Gln Thr Gln
85 90 95
Leu Thr Ala Ala Gln Gln Glu Ile Glu Asn Leu Lys Ala Arg Leu Ala
100 105 110
Ser Ser Ser Asp Ser Thr Glu Val Glu Ala Leu Lys Ala Ala Leu Ala

115 120 125
Ala Ala Glu Gln Lys Ala Ala Gln Ala Glu Thr Glu Leu Val Ser Ala
130 135 140
Asn Ser Ala Leu Glu Lys Ala Asn Ser Glu Leu Ala Ala Thr Glu Ser
145 150 155 160
Gln Leu Ala Asn Tyr Val Ala Lys Glu Lys Val Ala Gly Asp Lys Ile
165 170 175
Ala Ser Asp Leu Thr Ala Gly Gly Phe Ala Ala Asp Ser Thr Ser Tyr

180 185 190
Thr Tyr Ala Tyr Leu Asn Asp Glu Val Lys Lys Ala Glu Leu Ala Glu
195 200 205
Val Ile Ala Asn Gly Thr Ala Ser Cys Gly Ser Ala Ala Ser Pro Val
210 215 220
Thr Gly Ala Ala Val Ala Gly Cys Leu Arg Leu Ser Asn Thr Ala Glu
225 230 235 240
Gly Thr Ile Leu Phe Thr Lys Glu Asn Glu Tyr Ser Ala Tyr Ala Val

245 250 255
Val Arg Glu Ala Tyr Asp Ala Asp Ser Gly Val Asn Met Pro Lys Asn

260 265 270

Ser Phe Ile Ala Leu Val Lys Thr Pro Thr Thr Asp Lys Ala Gln Val

275 280 285

Leu Gly Ala Thr Tyr Arg Gly Leu Ala Thr Tyr Ser Gln Ser Ala Gly

290 295 300

Leu Asn Gly Ser Ser Leu Val Gly Glu Asn Ile Ala Ala Thr Ala Gly

305 310 315 320

Lys Leu Asn Val Val Thr Leu Asn Val Asp Gln Asn Gly Gln Ile Ser

325 330 335

Gly Glu Ile Trp Asn Lys Thr Ser Ala Lys Glu Glu Asn His Tyr Arg

340 345 350

Thr Val Glu Leu Lys Ala Ala Asp Val Leu Val Ser Asn Ser Gly Ile

355 360 365

Val Phe Glu Gly Glu Ala Ala Ile Asn Glu Lys Met Leu Lys Thr Gly

370 375 380

Thr Pro Leu Glu Gly Thr Tyr Lys Gly Ala Phe Ala Gly Asn Glu Gly

385 390 395 400

Gln Glu Val Val Gly Thr Phe Gln Thr Asn Ser Leu Glu Thr Asn Tyr

405 410 415

Val Gln Gly Ala Phe Ser Ala Thr Lys Asp Ser Ala Glu

420 425

<210> 757

<211> 618

<212> DNA

<213> B. trehalosi SLP 4a

<400

> 757

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tgtggttcta gcggtggtgg ttcaggctct gctacaaccc ctgatggtga tacaatcaat 120

ttatcaggta gcccacaagg tacaattaca gcagatacta cctatggcaa cttaacaggg 180

caaaataacc caaattcatt ctatggggta tggcaacaca atagtggctc actctatgaa 240

ttgcgttatc aaggtacaga agcaaccaat attccgactt ctggtaaagc aacttatgtt 300

ggtgatgcta tttggttagg ttcactttct aattcttatc gtcaaggtgg aacaactaca 360

ttaaatgtag attttgggca aaaaaccgta gatggcaaaa ttgcatttag tttgttaaat 420

gatggtcgtt ctcgtgatat tacgcttcac caaaccacac ttaatgggac gaaatttagc 480
ggacaagcca gtgtgttatt aaatagcagt ggtacttacg aaggggcttt attcggaaat 540
ggggcaactg aagcagcagg gctggttaat tttgctaatg atagttctct tgatgttagc 600
tttggcggta aacgttaa 618

<210> 758
<211> 205
<212> PRT
<213> B. trehalosi SLP 4a
<400> 758

Met Gln Arg His Phe Leu Lys Ser Leu Phe Ala Thr Ala Val Ile Val
1 5 10 15

Gly Leu Thr Ala Cys Gly Ser Ser Gly Gly Gly Ser Gly Ser Ala Thr
20 25 30
Thr Pro Asp Gly Asp Thr Ile Asn Leu Ser Gly Ser Pro Gln Gly Thr
35 40 45
Ile Thr Ala Asp Thr Thr Tyr Gly Asn Leu Thr Gly Gln Asn Asn Pro
50 55 60
Asn Ser Phe Tyr Gly Val Trp Gln His Asn Ser Gly Ser Leu Tyr Glu
65 70 75 80

Leu Arg Tyr Gln Gly Thr Glu Ala Thr Asn Ile Pro Thr Ser Gly Lys
85 90 95
Ala Thr Tyr Val Gly Asp Ala Ile Trp Leu Gly Ser Leu Ser Asn Ser
100 105 110
Tyr Arg Gln Gly Gly Thr Thr Thr Leu Asn Val Asp Phe Gly Gln Lys
115 120 125
Thr Val Asp Gly Lys Ile Ala Phe Ser Leu Leu Asn Asp Gly Arg Ser
130 135 140

Arg Asp Ile Thr Leu His Gln Thr Thr Leu Asn Gly Thr Lys Phe Ser
145 150 155 160
Gly Gln Ala Ser Val Leu Leu Asn Ser Ser Gly Thr Tyr Glu Gly Ala

165 170 175

Leu Phe Gly Asn Gly Ala Thr Glu Ala Ala Gly Leu Val Asn Phe Ala

180 185 190

Asn Asp Ser Ser Leu Asp Val Ser Phe Gly Gly Lys Arg

195 200 205

<210> 759

<211> 897

<212> DNA

<213> B. trehalosi SLP 5a

<400> 759

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agtggtggtt cgggcggaag ctcaaacaat gtggaaaagc agaatactaa cccacagacg 120

acacagcaac aaaccgataa agcggctaaa gaaaaggcgg aagcagagcg tttagcagca 180

gaaaaagcag ctaaagagaa agccgaagcg gaacgtttag cggcagagaa agcggctaaa 240

gagaaagcgg aagcagaacg tttagcggag gaaaaatcgg cgaaagagag agcggaagcg 300

gagcgtttag aagctgaaaa gatatcaaaa gccaaaggga tagatattga agagaaagga 360

ttttcaacag ccccttactc atctagtcaa gaaggtaata taaaggtaga acattgggga 420

aatttgtata accaaaaata ttctgttgtc gttgtaacaa caaccactaa aagagggtgg 480

gataatgatg tttatgtaaa ttctgatgta tctactgtag atgttagagg tcttaaaact 540

gacgttctac ctaaggaagg taaagctact tacacagggc aagcgtttga ttatagattc 600

tatcgctctg gtgatttgtc atatgatgta gatttttctc aaagaattgg ttctggaaag 660

attagaaatc cacatggaga tagttatacc ttatcgcagg ggaacattga caatggatca 720

atttcgggga cggcatcaaa acatcaaggt aatccagact acaatagcgg aaactataca 780

ggtgggaatt ataaagttca atttttgga ccaaatgctg aagaaattgg aggagagtta 840

aatattggtg atgaaaaact tggtcttgcc ggcactcgtg gcgatatcca acaataa 897

<210> 760

<211> 298

<212> PRT

<213> B. trehalosi SLP 5a

<400> 760

Met Ser Ile Lys Lys Val Thr Leu Ala Ser Leu Ile Leu Leu Ser Leu

1 5 10 15

Thr Ala Cys Ser Ser Gly Gly Ser Gly Gly Ser Ser Asn Asn Val Glu

20 25 30

Lys Gln Asn Thr Asn Pro Gln Thr Thr Gln Gln Gln Thr Asp Lys Ala

35 40 45

Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala Ala Glu Lys Ala Ala

50 55 60

Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala Ala Glu Lys Ala Ala Lys

65 70 75 80

Glu Lys Ala Glu Ala Glu Arg Leu Ala Glu Glu Lys Ser Ala Lys Glu

85 90 95

Arg Ala Glu Ala Glu Arg Leu Glu Ala Glu Lys Ile Ser Lys Ala Lys

100 105 110

Gly Ile Asp Ile Glu Glu Lys Gly Phe Ser Thr Ala Pro Tyr Ser Ser

115 120 125

Ser Gln Glu Gly Asn Ile Lys Val Glu His Trp Gly Asn Leu Tyr Asn

130 135 140

Gln Lys Tyr Ser Val Val Val Val Thr Thr Thr Thr Lys Arg Gly Trp

145 150 155 160

Asp Asn Asp Val Tyr Val Asn Ser Asp Val Ser Thr Val Asp Val Arg

165 170 175

Gly Leu Lys Thr Asp Val Leu Pro Lys Glu Gly Lys Ala Thr Tyr Thr

180 185 190

Gly Gln Ala Phe Asp Tyr Arg Phe Tyr Arg Ser Gly Asp Leu Ser Tyr

195 200 205

Asp Val Asp Phe Ser Gln Arg Ile Gly Ser Gly Lys Ile Arg Asn Pro

210 215 220

His Gly Asp Ser Tyr Thr Leu Ser Gln Gly Asn Ile Asp Asn Gly Ser

225 230 235 240

Ile Ser Gly Thr Ala Ser Lys His Gln Gly Asn Pro Asp Tyr Asn Ser

245 250 255

Gly Asn Tyr Thr Gly Gly Asn Tyr Lys Val Gln Phe Phe Gly Pro Asn

260 265 270

Ala Glu Glu Ile Gly Gly Glu Leu Asn Ile Gly Asp Glu Lys Leu Gly

275 280 285

Leu Ala Gly Thr Arg Gly Asp Ile Gln Gln

290 295

<210> 761

<211> 1962

<212> DNA

<213> C. kuhniae SLP 1a

<400> 761

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aaggaaaccg tcatgaagtc cacattttcc ggtaaaaatc ttttgttgtg cctgctgttg 120

tctgcgtgcg cgggcggcag tttcgatgtc gaccctgtgg tggtggtcag tccgccgccg 180

ccggacgacc gcgccaattt gctgaaagat gccgacaccc cgcccaaaat ttccgcgccc 240

gaagccgaag gctttatgaa gcccgctttg ggctacagca tgccgattct gcgccgcaac 300

aaatcgcgta ccgatgcggc aggcaaggaa attgccaacg gcaaacaggc ggaagagcat 360

ttgctgctca agccgtccga catccgcgcc ctgcacccca ccgacatcgt tgccgcaccg 420

catcgggacg aattggcaaa acgccagccc gatgcggggg tggacgtgtc cacgcccgcg 480

cagcgcggct atcaatttgt gcatgcgggc tatttggtta gcgacaagtt tgattcttca 540

gttgaatttg ataggcgcaa gggcattgat tacgaaggca gcgaaggcta tgtgttttat 600

cagggacgca accccgcgca agccttgccg agccaaaccg tgcgctatga agggcattgg 660

gatttcgtta ccgatgtcaa acgccaccgc accaatttgt ttcacaacgg tgatgagggc 720

ggtgccgaga ttgttggcgg cggtaggcaa atgggttttg aagatttgta tggcgaaagc 780

accggtgcgg tgggcatggc ggaaatcgat gttgccaaag acaaaaaact cggctttcgc 840

gcccgccagc atttgagtga gtttgaagtg gattttgcca acaaatcttt gaccggcaag 900

ctgaactacc gtccccatca gccgataacc ggcgaccccg acctgcccgt gcgtacccgc 960

tacaccattg atgccaaaat caacggcaac cgctttagcg gcaaggtcaa agcggtggac 1020

agggaaaatc cgcgcaatta cttctttctt gccgattcgg attttctgga aggcggtttt 1080

tacggcgggc gcggtgagga gctggcgggc aaattcttgg caaacgacaa ctccctgttc 1140

ggcgtgtttg ccgccaagca ggacaatcct gccgatgccg aaaaaatcac cgatgcctac 1200

gacatcaaca tcagcagcag cgatgcggtc gcgctgcgcc cgatgtccaa tttcggcagt 1260

gccgacaagc tgctggtgga cggcgaaacc ctgtcgctgc tgcccgacaa caacgaattg 1320

ctgacacggc gggacgtaac cctgccttcg gggcgcgaag tgggcgtaac cgtgtgctgc 1380

ggcaatttgt cgtatctgaa attcggtcat atgcgtaaaa ccaagctggc ggacgacccc 1440

gcgcccgttg ctgccggtgc ggacgatgtt gccaccgaca gtgccgcttt tagcggcgca 1500

ccctacggct cgttcctgtt tgtgcagggc gagcgcaccc gcagtgccga tatgcctgcg 1560

gaagacggtg caacctatcg cggcacgtgg gacggcttca gcatgaaaaa catcgcgtgg 1620

cgcagcctgc ccggttcggg cacggcggaa tttaaagtgg atttcggcac gaaagacgtg 1680

agcggacgtt tgaccgaaac caacggcgtg cgccccgctt tctacatcga tgccaaaatt 1740

cagggcaacg gctttgccgg cacggtacgc acccatgcgg acggcatcaa cctcgacccc 1800

ggccgcgaag gcaacagccc caaactgctg ttccgcgatg ttgccgtgca gggcggtttt 1860

tacgggccaa aagcactgga attgggcggc acgtttttca acgacgaaca caaaacgggc 1920

gcggtattcg gcgccaaacg tcaggtatct ggcgacaaat aa 1962

<210> 762

<211> 645

<212> PRT

<213> C. kuhniae SLP 1a

<400> 762

Met His Phe Phe Phe Gly Leu Pro Val Pro Ala Gly Lys Glu Thr Val
1 5 10 15

Met Lys Ser Thr Phe Ser Gly Lys Asn Leu Leu Leu Cys Leu Leu Leu
20 25 30

Ser Ala Cys Ala Gly Gly Ser Phe Asp Val Asp Pro Val Val Val Val
35 40 45

Ser Pro Pro Pro Pro Asp Asp Arg Ala Asn Leu Leu Lys Asp Ala Asp
50 55 60

Thr Pro Pro Lys Ile Ser Ala Pro Glu Ala Glu Gly Phe Met Lys Pro
65 70 75 80

Ala Leu Gly Tyr Ser Met Pro Ile Leu Arg Arg Asn Lys Ser Arg Thr
85 90 95

Asp Ala Ala Gly Lys Glu Ile Ala Asn Gly Lys Gln Ala Glu Glu His
100 105 110

Leu Leu Leu Lys Pro Ser Asp Ile Arg Ala Leu His Pro Thr Asp Ile

115 120 125

Val Ala Ala Pro His Arg Asp Glu Leu Ala Lys Arg Gln Pro Asp Ala
130 135 140
Gly Val Asp Val Ser Thr Pro Ala Gln Arg Gly Tyr Gln Phe Val His
145 150 155 160
Ala Gly Tyr Leu Val Ser Asp Lys Phe Asp Ser Ser Val Glu Phe Asp
165 170 175
Arg Arg Lys Gly Ile Asp Tyr Glu Gly Ser Glu Gly Tyr Val Phe Tyr
180 185 190

Gln Gly Arg Asn Pro Ala Gln Ala Leu Pro Ser Gln Thr Val Arg Tyr
195 200 205
Glu Gly His Trp Asp Phe Val Thr Asp Val Lys Arg His Arg Thr Asn
210 215 220
Leu Phe His Asn Gly Asp Glu Gly Gly Ala Glu Ile Val Gly Gly Gly
225 230 235 240
Arg Gln Met Gly Phe Glu Asp Leu Tyr Gly Glu Ser Thr Gly Ala Val
245 250 255

Gly Met Ala Glu Ile Asp Val Ala Lys Asp Lys Lys Leu Gly Phe Arg
260 265 270
Ala Arg Gln His Leu Ser Glu Phe Glu Val Asp Phe Ala Asn Lys Ser
275 280 285
Leu Thr Gly Lys Leu Asn Tyr Arg Pro His Gln Pro Ile Thr Gly Asp
290 295 300
Pro Asp Leu Pro Val Arg Thr Arg Tyr Thr Ile Asp Ala Lys Ile Asn
305 310 315 320

Gly Asn Arg Phe Ser Gly Lys Val Lys Ala Val Asp Arg Glu Asn Pro
325 330 335
Arg Asn Tyr Phe Phe Leu Ala Asp Ser Asp Phe Leu Glu Gly Gly Phe
340 345 350
Tyr Gly Gly Arg Gly Glu Glu Leu Ala Gly Lys Phe Leu Ala Asn Asp
355 360 365

Asn Ser Leu Phe Gly Val Phe Ala Ala Lys Gln Asp Asn Pro Ala Asp
370 375 380

Ala Glu Lys Ile Thr Asp Ala Tyr Asp Ile Asn Ile Ser Ser Ser Asp
385 390 395 400
Ala Val Ala Leu Arg Pro Met Ser Asn Phe Gly Ser Ala Asp Lys Leu
405 410 415
Leu Val Asp Gly Glu Thr Leu Ser Leu Leu Pro Asp Asn Asn Glu Leu
420 425 430
Leu Thr Arg Arg Asp Val Thr Leu Pro Ser Gly Arg Glu Val Gly Val
435 440 445

Thr Val Cys Cys Gly Asn Leu Ser Tyr Leu Lys Phe Gly His Met Arg
450 455 460
Lys Thr Lys Leu Ala Asp Asp Pro Ala Pro Val Ala Ala Gly Ala Asp
465 470 475 480
Asp Val Ala Thr Asp Ser Ala Ala Phe Ser Gly Ala Pro Tyr Gly Ser
485 490 495
Phe Leu Phe Val Gln Gly Glu Arg Thr Arg Ser Ala Asp Met Pro Ala
500 505 510

Glu Asp Gly Ala Thr Tyr Arg Gly Thr Trp Asp Gly Phe Ser Met Lys
515 520 525
Asn Ile Ala Trp Arg Ser Leu Pro Gly Ser Gly Thr Ala Glu Phe Lys
530 535 540
Val Asp Phe Gly Thr Lys Asp Val Ser Gly Arg Leu Thr Glu Thr Asn
545 550 555 560
Gly Val Arg Pro Ala Phe Tyr Ile Asp Ala Lys Ile Gln Gly Asn Gly
565 570 575

Phe Ala Gly Thr Val Arg Thr His Ala Asp Gly Ile Asn Leu Asp Pro
580 585 590
Gly Arg Glu Gly Asn Ser Pro Lys Leu Leu Phe Arg Asp Val Ala Val
595 600 605
Gln Gly Gly Phe Tyr Gly Pro Lys Ala Leu Glu Leu Gly Gly Thr Phe

610 615 620

Phe Asn Asp Glu His Lys Thr Gly Ala Val Phe Gly Ala Lys Arg Gln

625 630 635 640

Val Ser Gly Asp Lys

645

<210> 763

<211> 666

<212> DNA

<213> C. kuhniae SLP 2a

<400> 763

atgttcacac gcacaatttt ctgcatcagc ctgtgtgccg ccctgtcggc gcacgccgcg 60

cccattccgc aaaccgccac actgcaatat agcggcagct acggcattcc cgccaccatg 120

acgtttaagc gcacgggcga caactacacc gttgccgcgc aaatcaatgt gccgatgtac 180

aaaatccgtt ttgaaagcgg cggcaaaatt gtcggcaacc aattgaaacc cgcttactac 240

cgcgacgtgc gcaacggcaa aacctacgct tcggcacagt tttccggcaa caaagccagc 300

tacggcaaag cgggcgagcc gccgcaaagc cgcaccgtat cggggaatgt gatggatttg 360

tttaccctgt cgtggcagat ggcgtttgca gacgggcagc ttcccgccaa tttaagcatc 420

accaacggca aaaaactcta tccgctcaat ggtatcagca aggcgggcag caagcagatg 480

aatatcggcg gcgggcagac ggctgtaaac caatttcacg tcaaacgcgg cgatgacacg 540

gtttattacg cttttgtgcc cgcgctgaac aacgttcccg ccgtgattac ctatcaggac 600

ggcggtaaaa aatacaactt gacgctcaaa tccgttacca tcaacggcaa agccgtgaaa 660

ccttga 666

<210> 764

<211> 221

<212> PRT

<213> C. kuhniae SLP 2a

<400> 764

Met Phe Thr Arg Thr Ile Phe Cys Ile Ser Leu Cys Ala Ala Leu Ser

1 5 10 15

Ala His Ala Ala Pro Ile Pro Gln Thr Ala Thr Leu Gln Tyr Ser Gly

20 25 30

Ser Tyr Gly Ile Pro Ala Thr Met Thr Phe Lys Arg Thr Gly Asp Asn

35 40 45

Tyr Thr Val Ala Ala Gln Ile Asn Val Pro Met Tyr Lys Ile Arg Phe
50 55 60

Glu Ser Gly Gly Lys Ile Val Gly Asn Gln Leu Lys Pro Ala Tyr Tyr
65 70 75 80

Arg Asp Val Arg Asn Gly Lys Thr Tyr Ala Ser Ala Gln Phe Ser Gly
85 90 95

Asn Lys Ala Ser Tyr Gly Lys Ala Gly Glu Pro Pro Gln Ser Arg Thr
100 105 110

Val Ser Gly Asn Val Met Asp Leu Phe Thr Leu Ser Trp Gln Met Ala
115 120 125

Phe Ala Asp Gly Gln Leu Pro Ala Asn Leu Ser Ile Thr Asn Gly Lys
130 135 140

Lys Leu Tyr Pro Leu Asn Gly Ile Ser Lys Ala Gly Ser Lys Gln Met
145 150 155 160

Asn Ile Gly Gly Gly Gln Thr Ala Val Asn Gln Phe His Val Lys Arg
165 170 175

Gly Asp Asp Thr Val Tyr Tyr Ala Phe Val Pro Ala Leu Asn Asn Val
180 185 190

Pro Ala Val Ile Thr Tyr Gln Asp Gly Gly Lys Lys Tyr Asn Leu Thr
195 200 205

Leu Lys Ser Val Thr Ile Asn Gly Lys Ala Val Lys Pro
210 215 220

<210> 765

<211> 1014

<212> DNA

<213> C. kuhniae SLP 3a

<400> 765

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aatttgggcg agccggtttc gcccgttccc attcccctgc tcgagcctgt gcgcgacaat 120

ccccccgttg atgccgaagc cgcaccgcgc atgcaaacgc tgcgtacggc aggcaatgtc 180

ggcggcacgg tcgaaaccgt gcgcaccacc cgcaacgtca atggcttgag catcaccgaa 240

cccgagctgg tgtaccgcca tcgggacggc accgtgtacc gcttcaatgc ctttagcgac 300

ccgattgtgc cgtcatacgg cagcccgtct tggcaattca tcaccaaaca gcccggacaa 360

gacagccggc acggcaagct gtttgcgtgc tgtacccgtt cggcgcaatt cggttacgcg 420

cccgccacca agctgcaaca cgtccgcttc ggcgcatggc agaaaaacgg catggcagag 480

ctgtttgtcg gcggcaaaac cgccgatgcg gcactgatgc cgggcggcag ccacgatgcg 540

gtacgcaaca ccaaaggcaa agccacatat gaagtttggg cattgcgcgt gaaagacggc 600

gcattcgtta catcgtccta tacgcccaaa gcactgggct ttaacaacaa aggcgaaccc 660

gtactgtcgc tgtttaccgc caacttcaac accggcaaac tcggcggcac catcatcggc 720

aaccaagatt tcggtgccga cgtggtgctg caagatgtgg acattcacgg caacgccttt 780

tccggcactg cccaatcggg cgggcggcaa ggcttggtgg acggacgctt tttcggcgaa 840

ccgcgcacct acggcgacgg tgagaacaaa cgcatcaccg gccctgccac cgacgaaatc 900

ggcggcaaaa tcgtgtttga cgggcaccgc cacctcgata ccgtattcgg cggcaaacgc 960

accaacgaac aatacaacga cacctccacc gatttgaccc cgctcaatcc gtaa 1014

<210> 766

<211> 339

<212> PRT

<213> C. kuhniae SLP 3a

<400> 766

Met Leu Met Lys Val Ile Cys Ala Ala Val Ala Ala Val Phe Leu Leu

1 5 10 15

Gly Gly Cys Leu Gly Ser Asn Leu Gly Glu Pro Val Ser Pro Val Pro

20 25 30

Ile Pro Leu Leu Glu Pro Val Arg Asp Asn Pro Pro Val Asp Ala Glu

35 40 45

Ala Ala Pro Arg Met Gln Thr Leu Arg Thr Ala Gly Asn Val Gly Gly

50 55 60

Thr Val Glu Thr Val Arg Thr Thr Arg Asn Val Asn Gly Leu Ser Ile

65 70 75 80

Thr Glu Pro Glu Leu Val Tyr Arg His Arg Asp Gly Thr Val Tyr Arg

85 90 95

Phe Asn Ala Phe Ser Asp Pro Ile Val Pro Ser Tyr Gly Ser Pro Ser

100 105 110

Trp Gln Phe Ile Thr Lys Gln Pro Gly Gln Asp Ser Arg His Gly Lys

115 120 125

Leu Phe Ala Cys Cys Thr Arg Ser Ala Gln Phe Gly Tyr Ala Pro Ala

130 135 140

Thr Lys Leu Gln His Val Arg Phe Gly Ala Trp Gln Lys Asn Gly Met

145 150 155 160

Ala Glu Leu Phe Val Gly Gly Lys Thr Ala Asp Ala Ala Leu Met Pro

165 170 175

Gly Gly Ser His Asp Ala Val Arg Asn Thr Lys Gly Lys Ala Thr Tyr

180 185 190

Glu Val Trp Ala Leu Arg Val Lys Asp Gly Ala Phe Val Thr Ser Ser

195 200 205

Tyr Thr Pro Lys Ala Leu Gly Phe Asn Asn Lys Gly Glu Pro Val Leu

210 215 220

Ser Leu Phe Thr Ala Asn Phe Asn Thr Gly Lys Leu Gly Gly Thr Ile

225 230 235 240

Ile Gly Asn Gln Asp Phe Gly Ala Asp Val Val Leu Gln Asp Val Asp

245 250 255

Ile His Gly Asn Ala Phe Ser Gly Thr Ala Gln Ser Gly Gly Arg Gln

260 265 270

Gly Leu Val Asp Gly Arg Phe Phe Gly Glu Pro Arg Thr Tyr Gly Asp

275 280 285

Gly Glu Asn Lys Arg Ile Thr Gly Pro Ala Thr Asp Glu Ile Gly Gly

290 295 300

Lys Ile Val Phe Asp Gly His Arg His Leu Asp Thr Val Phe Gly Gly

305 310 315 320

Lys Arg Thr Asn Glu Gln Tyr Asn Asp Thr Ser Thr Asp Leu Thr Pro

325 330 335

Leu Asn Pro

<210> 767

<211> 2121

<212> DNA

<213> C. steedae SLP 1a

<400> 767

atgaaatccg cctttcgccc gtctgctgtg gctatgtgcc tgttgcttgc tgcctgtgct 60

ggcggcggca gttttgacgt tcagcccgtt actgtggtca atcccgaatt caaagaaccc 120

gttgccaccg aaaaagacga aaccaccccg cctaaagtct tgccgcagga agccgagggc 180

atcatgaaac ccgctttggg ctacagcatg ccgattccgc gccgcaatgt ttcgcgttac 240

gatgccgata aaaaactgct tcccgatggc aaacaagtag aagaatatct gcccttaaac 300

ccccaagacc ttaaagcctt acaccccacc gacattaccg ctgcgcccca tgctgccgat 360

ttggcaaaac gtcaggaagg cgtgcggatt gatgtgtcta atcccgccca acgcggttac 420

gaatttgtgc atgcgggcta tattttcagc gactttcacc gttccaaagg cgaagaatca 480

gcaggtttat tgcgcgaagg tgtagacggc tatatttttt atcagggacg caatcccgcc 540

caagccctgc ctgtaggcaa aaccgtaaac tacacaggac attgggaatt tgttagcgat 600

gccaaacgcg cccgcgatac ttattgtaac aatacgggtt gccatgtgta tggcggcggc 660

ggcgcattgg gcttttggtt gggctacggc gacagcgtgg gtgcgacttc gtttgccgaa 720

accgccaccg ccgaatcgcc cgatttgggc tggcgcggac gcgaacacgt cagcgaattt 780

accgccgatt ttgccaataa aaaattaacg ggcacactca aataccgtcc gtggacacgc 840

aggggcgaat caccagccga attaaaaacc cgctacacca ttgatgccac cattcaaaac 900

aaccgtttta gcggcaaagc cacggcagcg gacaagcaaa atccgaaaaa cctgctgttc 960

aaatccgatt ccgcgctgtt ggaaggcggt ttttacggcg ggaatgccca agaattggcg 1020

ggtaaatttt taacggacga caacaccctg tttggcgtgt ttgccgccaa acagcaaaat 1080

cccgccgaaa ccgaaaaagt gatggatgcc taccaaatta accgcgatgg cgaccacccc 1140

gtgttgcgcc agcccatgcc caatttcggt agtgccgaca aattggtatt ggaaggcaaa 1200

accctgtcgc tgttgcccga agatggtaag ttcctaacca gtcgcgaaat cactttggat 1260

tcggggcgca ccgtgaaagt gaccgtgtgt tgcgccaatt tggattattt gaaattcggc 1320

agcgtcagca aatccaaatt ggcaggcgac gacccgccca aagaagacga tgaggaagag 1380

gaagacgaag aatttgacga gggcgaaggg ttggatgaag gcgagggcag cgataccgcc 1440

gaaaacaaca gctcaaccga taacgccaca tcttctgaca acgataaggg cgataacacc 1500

gccgttgcag gtgataacgg cagtaccgat accgccgcca acgacagcag cggcggcgat 1560

tcggaagagg gcgaagacga aggcgaagag ggcgacacac ccaaactggt ggataatcct 1620

gccgaagaca gcttggcgtt tagcggtgcg ccttatggtt cgttcctgtt tattcagggc 1680

gagcgcaccc gcagtgccga tatgccgcaa aacggtcaag cccgttattt ggggacttgg 1740

gaaggtttta ccaataaaga tttggcatgg cgcaccctgc cgggcaacgg gcgtgccgac 1800

agcaaagccg attttcaagt ggattttggt gccaaaactt taagcggcac tttaaccgaa 1860

cacaacggcg tgcgtcccgc tttcttcatt gatgccgatg tgaaaggcaa cggctttgcg 1920

ggtacggtgc gcacccattc cgatggcgtg gtgttggacc ccggtcgtga aggcggcagc 1980

ccccgcttgc tgtttggcga cattcccgta aaaggcggtt tttatggtcc aaaagcgtct 2040

gaattgggcg ggtcgttttt cagtgacgaa cacaaagcag gtgcggtttt tggcggcaaa 2100

cgtcaaagca cggcgcaata a 2121

<210> 768

<211> 706

<212> PRT

<213> C. steedae SLP 1a

<400> 768

Met Lys Ser Ala Phe Arg Pro Ser Ala Val Ala Met Cys Leu Leu Leu

1 5 10 15

Ala Ala Cys Ala Gly Gly Gly Ser Phe Asp Val Gln Pro Val Thr Val

20 25 30

Val Asn Pro Glu Phe Lys Glu Pro Val Ala Thr Glu Lys Asp Glu Thr

35 40 45

Thr Pro Pro Lys Val Leu Pro Gln Glu Ala Glu Gly Ile Met Lys Pro

50 55 60

Ala Leu Gly Tyr Ser Met Pro Ile Pro Arg Arg Asn Val Ser Arg Tyr

65 70 75 80

Asp Ala Asp Lys Lys Leu Leu Pro Asp Gly Lys Gln Val Glu Glu Tyr

85 90 95

Leu Pro Leu Asn Pro Gln Asp Leu Lys Ala Leu His Pro Thr Asp Ile

100 105 110

Thr Ala Ala Pro His Ala Ala Asp Leu Ala Lys Arg Gln Glu Gly Val

115 120 125

Arg Ile Asp Val Ser Asn Pro Ala Gln Arg Gly Tyr Glu Phe Val His

130 135 140

Ala Gly Tyr Ile Phe Ser Asp Phe His Arg Ser Lys Gly Glu Glu Ser
145 150 155 160
Ala Gly Leu Leu Arg Glu Gly Val Asp Gly Tyr Ile Phe Tyr Gln Gly
165 170 175
Arg Asn Pro Ala Gln Ala Leu Pro Val Gly Lys Thr Val Asn Tyr Thr
180 185 190
Gly His Trp Glu Phe Val Ser Asp Ala Lys Arg Ala Arg Asp Thr Tyr

195 200 205

Cys Asn Asn Thr Gly Cys His Val Tyr Gly Gly Gly Gly Ala Leu Gly
210 215 220
Phe Trp Leu Gly Tyr Gly Asp Ser Val Gly Ala Thr Ser Phe Ala Glu
225 230 235 240
Thr Ala Thr Ala Glu Ser Pro Asp Leu Gly Trp Arg Gly Arg Glu His
245 250 255
Val Ser Glu Phe Thr Ala Asp Phe Ala Asn Lys Lys Leu Thr Gly Thr

260 265 270

Leu Lys Tyr Arg Pro Trp Thr Arg Arg Gly Glu Ser Pro Ala Glu Leu
275 280 285
Lys Thr Arg Tyr Thr Ile Asp Ala Thr Ile Gln Asn Asn Arg Phe Ser
290 295 300
Gly Lys Ala Thr Ala Ala Asp Lys Gln Asn Pro Lys Asn Leu Leu Phe
305 310 315 320
Lys Ser Asp Ser Ala Leu Leu Glu Gly Gly Phe Tyr Gly Gly Asn Ala

325 330 335

Gln Glu Leu Ala Gly Lys Phe Leu Thr Asp Asp Asn Thr Leu Phe Gly
340 345 350
Val Phe Ala Ala Lys Gln Gln Asn Pro Ala Glu Thr Glu Lys Val Met
355 360 365
Asp Ala Tyr Gln Ile Asn Arg Asp Gly Asp His Pro Val Leu Arg Gln

370 375 380

Pro Met Pro Asn Phe Gly Ser Ala Asp Lys Leu Val Leu Glu Gly Lys

385 390 395 400

Thr Leu Ser Leu Leu Pro Glu Asp Gly Lys Phe Leu Thr Ser Arg Glu

405 410 415

Ile Thr Leu Asp Ser Gly Arg Thr Val Lys Val Thr Val Cys Cys Ala

420 425 430

Asn Leu Asp Tyr Leu Lys Phe Gly Ser Val Ser Lys Ser Lys Leu Ala

435 440 445

Gly Asp Asp Pro Pro Lys Glu Asp Asp Glu Glu Glu Glu Asp Glu Glu

450 455 460

Phe Asp Glu Gly Glu Gly Leu Asp Glu Gly Glu Gly Ser Asp Thr Ala

465 470 475 480

Glu Asn Asn Ser Ser Thr Asp Asn Ala Thr Ser Ser Asp Asn Asp Lys

485 490 495

Gly Asp Asn Thr Ala Val Ala Gly Asp Asn Gly Ser Thr Asp Thr Ala

500 505 510

Ala Asn Asp Ser Ser Gly Gly Asp Ser Glu Glu Gly Glu Asp Glu Gly

515 520 525

Glu Glu Gly Asp Thr Pro Lys Leu Val Asp Asn Pro Ala Glu Asp Ser

530 535 540

Leu Ala Phe Ser Gly Ala Pro Tyr Gly Ser Phe Leu Phe Ile Gln Gly

545 550 555 560

Glu Arg Thr Arg Ser Ala Asp Met Pro Gln Asn Gly Gln Ala Arg Tyr

565 570 575

Leu Gly Thr Trp Glu Gly Phe Thr Asn Lys Asp Leu Ala Trp Arg Thr

580 585 590

Leu Pro Gly Asn Gly Arg Ala Asp Ser Lys Ala Asp Phe Gln Val Asp

595 600 605

Phe Gly Ala Lys Thr Leu Ser Gly Thr Leu Thr Glu His Asn Gly Val

610 615 620

Arg Pro Ala Phe Phe Ile Asp Ala Asp Val Lys Gly Asn Gly Phe Ala
625 630 635 640
Gly Thr Val Arg Thr His Ser Asp Gly Val Val Leu Asp Pro Gly Arg

645 650 655
Glu Gly Gly Ser Pro Arg Leu Leu Phe Gly Asp Ile Pro Val Lys Gly
660 665 670
Gly Phe Tyr Gly Pro Lys Ala Ser Glu Leu Gly Gly Ser Phe Phe Ser
675 680 685
Asp Glu His Lys Ala Gly Ala Val Phe Gly Gly Lys Arg Gln Ser Thr
690 695 700
Ala Gln
705

<210> 769
<211> 1002

<212> DNA
<213> C. steedae SLP 4a
<400> 769

atgaaaacca tttgtattgc cgtgagcttg gtctgtgtat tgggcgggtg cgcgggcagc 60
agcatcaccg aaccaaaagg acctgtggat atccccactt taccctctgc caacaataat 120
caatcgttta aacccaatga aaccctgcct gcacggatgc aaaccctcag cactgccgat 180
acacccagcg gacaactgga agcagtggat gtccctgcac gctttaccgg cacgcccgaa 240
cccgaattga tgtaccgcac caaagacggc acgctgtacc gcttcagcga gtttaccaat 300
ccgattgtac ccagttcgtt tagcccgtct tggaaaatgg aaacccgaca tcaggggcaa 360

aataccgaaa aacacggcaa aatgatggtg tgttgcagcg gcggcggcgt gttccgttat 420
gcagcggcaa ccgatttgaa acacgtccgt tttggcgcgt ggggcaacgg cgaattgttt 480
gtgggcggca tggtgtccga ccctgccttg atgccaggcg gaagccacga aaaagtacgc 540
gacattaaag gcaaagccac ttacgaagtg tgggcattgc gcgtgaaaga cggacagttt 600
gtcagttcgt cctacacacc caaatcctat accaattcca aaggcgaacc tgtagtgtcg 660
ctgtttaccg ccaacttcaa tacaggaaaa atgggcggaa caattgttgg caacagcgat 720
tttggcgcag acgtagaatt aaagaatgtg gatattcaag gcaatgcctt ttcgggtacg 780

gcacaatcag caggcaaaat cggacaggtg gacggacgct ttttcggcga accgcgcact 840

tacggttatg gtaaatacgt tgaaattacc ggacctgcca ccgaagaaat tggcggcaaa 900

atcgtgtttg acggcaaccg cagtttggat accgtatttg gcggcaaacg tgttaatgag 960

caatacaaag atgattcatc ggatttgaat ccgcttcagt aa 1002

<210> 770

<211> 333

<212> PRT

<213> C. steedae SLP 4a

<400> 770

Met Lys Thr Ile Cys Ile Ala Val Ser Leu Val Cys Val Leu Gly Gly
1 5 10 15

Cys Ala Gly Ser Ser Ile Thr Glu Pro Lys Gly Pro Val Asp Ile Pro
20 25 30

Thr Leu Pro Ser Ala Asn Asn Asn Gln Ser Phe Lys Pro Asn Glu Thr
35 40 45

Leu Pro Ala Arg Met Gln Thr Leu Ser Thr Ala Asp Thr Pro Ser Gly
50 55 60

Gln Leu Glu Ala Val Asp Val Pro Ala Arg Phe Thr Gly Thr Pro Glu
65 70 75 80

Pro Glu Leu Met Tyr Arg Thr Lys Asp Gly Thr Leu Tyr Arg Phe Ser
85 90 95

Glu Phe Thr Asn Pro Ile Val Pro Ser Ser Phe Ser Pro Ser Trp Lys
100 105 110

Met Glu Thr Arg His Gln Gly Gln Asn Thr Glu Lys His Gly Lys Met
115 120 125

Met Val Cys Cys Ser Gly Gly Gly Val Phe Arg Tyr Ala Ala Ala Thr
130 135 140

Asp Leu Lys His Val Arg Phe Gly Ala Trp Gly Asn Gly Glu Leu Phe
145 150 155 160

Val Gly Gly Met Val Ser Asp Pro Ala Leu Met Pro Gly Gly Ser His
165 170 175

Glu Lys Val Arg Asp Ile Lys Gly Lys Ala Thr Tyr Glu Val Trp Ala
180 185 190

Leu Arg Val Lys Asp Gly Gln Phe Val Ser Ser Ser Tyr Thr Pro Lys
195 200 205

Ser Tyr Thr Asn Ser Lys Gly Glu Pro Val Val Ser Leu Phe Thr Ala
210 215 220
Asn Phe Asn Thr Gly Lys Met Gly Gly Thr Ile Val Gly Asn Ser Asp
225 230 235 240
Phe Gly Ala Asp Val Glu Leu Lys Asn Val Asp Ile Gln Gly Asn Ala
245 250 255
Phe Ser Gly Thr Ala Gln Ser Ala Gly Lys Ile Gly Gln Val Asp Gly
260 265 270

Arg Phe Phe Gly Glu Pro Arg Thr Tyr Gly Tyr Gly Lys Tyr Val Glu
275 280 285
Ile Thr Gly Pro Ala Thr Glu Glu Ile Gly Gly Lys Ile Val Phe Asp
290 295 300
Gly Asn Arg Ser Leu Asp Thr Val Phe Gly Gly Lys Arg Val Asn Glu
305 310 315 320
Gln Tyr Lys Asp Asp Ser Ser Asp Leu Asn Pro Leu Gln
325 330

<210> 771

<211> 3396
<212> DNA
<213> C. valvarum SLP 2a
<400> 771
atgaaactaa gcaacctgac tattgccgtc ctcatcgcac tcggcaccgc cgcctgcggt 60
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ccggataacg gcaagaacca gccgggccgc gatgacaaag ccctggttga cccgaccaat 180
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aacaacaccg ataaagacgg cgaatttacc cgcgaacggg tcacccacgt ctataccccg 660

cgttacgaat accgccagcc ctatgtggat tatccccacg ctaaaaacga ggcggatatt 720

ggcaaagaac acgcggaaaa ccggatcggt ccggaaggca caagcttcac caccgcgcca 780

ccaccgccga tttttaataa cccggaaaaa cgaccggaag acagggttac ttccattaac 840

gatctagaaa aaaaactgaa aggcgatcat ctatgggcaa ctcgcaacgt gaacgacaat 900

tcccgctgga tcaccaatat cggcacccgc actacctatg caagtgggga gatctataac 960

gaccaagacc gttacggtaa tttcccggca tccggttccc ccgatccagc tgccgataat 1020

cactatgatg acagccctac cgacggagac ggtcatttcc cggcaacttc atggcgcaac 1080

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aaccgggtgg actggaacgg tagcagtgca aacgactcca aagatcccaa acgttggggc 1260

gcttacgccg gtaagcaacg gggtgataaa cgtattgatg ccggcggcat caccccgcag 1320

gacgcggagc cagattacag gcgggattat cccaacggtg cttaccccaa acatccaaaa 1380

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gaggaatata ccgccatccg tcaaataaaa ggcattcgcc cgctggtgaa tcccgtcccg 1560

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gaaaatgatg gtgcttctcg cacggttaaa gaagggacgc cactgtctga agaggtaaaa 1740

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aacaatagga cgttaactga cggtacggta tgtgacggcg gggcaacctt atgcacgatc 1860

cgtccaggtg gcgaaggcga agagaagagc tgggtcaagc acctgatcag cgccgaatgg 1920

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acccaggaca gcgcctttga aaactgggca accagtgaag gctggaaccc acgtgcccgt 2160

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<210> 772

<211> 1131

<212> PRT

<213> C. valvarum SLP 2a

<400> 772

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Ala Ala Cys Gly Gly Ser Gly Asp Ala Ala Lys Pro Pro His Val Asp
20 25 30

Pro Gln Pro Lys Pro Ala Pro Gln Pro Asp Asn Gly Lys Asn Gln Pro
35 40 45

Gly Arg Asp Asp Lys Ala Leu Val Asp Pro Thr Asn Thr His Val Val
50 55 60

Asp Asn Arg Asp Leu Ser Lys Glu Ser Thr Val Gly Gly Leu Gln Tyr
65 70 75 80
Ile Arg Arg Asp Gly Ser Gly Tyr Asp Arg Ala Asn Asn Pro Glu Lys
85 90 95
Met Ala Ser Ala Thr Pro Leu Leu Gly Val Ser Leu Asn Arg Gln Asn

100 105 110
Pro Lys Leu Thr Asn Ile Val Leu Ala Arg Arg Asp Leu Asp Tyr His
115 120 125
Asp Gly Arg Pro Val Arg Ala Gln Phe Ala Gly Gly Thr Asp Val Glu
130 135 140
Pro Leu Thr Ala Ala Gly Lys Pro Arg Glu Asp Asp Ser Leu Gln Val
145 150 155 160
Glu Asn Phe Lys Asn Val Asp Val Leu Ala Gly Ala Phe Lys Gln Val

165 170 175
Gly Ser Ala Val Phe Ser Asp Pro Asn Asn Arg Leu Asn Gly Thr Thr
180 185 190
His Asn Ile Asp Thr His Ile Gln Asn Asn Thr Asp Lys Asp Gly Glu
195 200 205
Phe Thr Arg Glu Arg Val Thr His Val Tyr Thr Pro Arg Tyr Glu Tyr
210 215 220
Arg Gln Pro Tyr Val Asp Tyr Pro His Ala Lys Asn Glu Ala Asp Ile

225 230 235 240
Gly Lys Glu His Ala Glu Asn Arg Ile Gly Pro Glu Gly Thr Ser Phe
245 250 255
Thr Thr Ala Pro Pro Pro Pro Ile Phe Asn Asn Pro Glu Lys Arg Pro
260 265 270
Glu Asp Arg Val Thr Ser Ile Asn Asp Leu Glu Lys Lys Leu Lys Gly
275 280 285
Asp His Leu Trp Ala Thr Arg Asn Val Asn Asp Asn Ser Arg Trp Ile

290 295 300
Thr Asn Ile Gly Thr Arg Thr Thr Tyr Ala Ser Gly Glu Ile Tyr Asn

305 310 315 320

Asp Gln Asp Arg Tyr Gly Asn Phe Pro Ala Ser Gly Ser Pro Asp Pro

325 330 335

Ala Ala Asp Asn His Tyr Asp Asp Ser Pro Thr Asp Gly Asp Gly His

340 345 350

Phe Pro Ala Thr Ser Trp Arg Asn Asn Leu Thr Gln Leu Pro Asp Arg

355 360 365

Thr Pro Asn Asn Asp Ile Asn His Trp Ser Tyr Lys Tyr Asn Gly Gly

370 375 380

Asn Ile Ala Asp Asp Thr Gly Asn Ile Asp Asp Thr Ala Arg Lys Tyr

385 390 395 400

Asn Arg Val Asp Trp Asn Gly Ser Ser Ala Asn Asp Ser Lys Asp Pro

405 410 415

Lys Arg Trp Gly Ala Tyr Ala Gly Lys Gln Arg Gly Asp Lys Arg Ile

420 425 430

Asp Ala Gly Gly Ile Thr Pro Gln Asp Ala Glu Pro Asp Tyr Arg Arg

435 440 445

Asp Tyr Pro Asn Gly Ala Tyr Pro Lys His Pro Lys Thr Leu Phe Ala

450 455 460

Tyr Pro Asn Arg Pro Tyr Asp Glu Ala Asn Asn Asn Ala Ile Asp Thr

465 470 475 480

Arg Lys Arg Gly Arg Ala Asp Thr Asn Pro Met Asp His Glu His Ile

485 490 495

Tyr Leu Glu Arg Glu Glu Tyr Thr Ala Ile Arg Gln Ile Lys Gly Ile

500 505 510

Arg Pro Leu Val Asn Pro Val Pro Asn Glu Trp Asp Trp Thr Leu Lys

515 520 525

Gln Val Trp Gly Val Thr Tyr Asn Ile Asp Val Gln Lys Arg Lys Gln

530 535 540

Val Trp Val Gln Asn Gly Pro Asn Pro Gly Asp Gly Tyr Tyr Arg Trp

545 550 555 560

Glu Asn Asp Gly Ala Ser Arg Thr Val Lys Glu Gly Thr Pro Leu Ser
565 570 575
Glu Glu Val Lys Pro Pro Val Glu Asp Asn Glu His Thr Thr Ile Thr
580 585 590
Ala Asn Gly Thr Val Ser Asn Leu Asn Asn Arg Thr Leu Thr Asp Gly
595 600 605
Thr Val Cys Asp Gly Gly Ala Thr Leu Cys Thr Ile Arg Pro Gly Gly

610 615 620
Glu Gly Glu Glu Lys Ser Trp Val Lys His Leu Ile Ser Ala Glu Trp
625 630 635 640
Ile Lys Pro Ile Asn Thr Gly Gly Gly Val Arg Gly Glu Phe Arg Gly
645 650 655
Pro Pro Tyr Ile Gly Trp Lys Glu Asp Asp Arg Val Val Arg Phe Ala
660 665 670
Asp Asn Arg Ile Trp Lys Pro Gly Thr Pro Gly Tyr Lys Pro Glu Tyr

675 680 685
Glu Asn Lys Tyr Gly Ala Asn Leu Ile Trp Trp Ser Thr Gln Asp Ser
690 695 700
Ala Phe Glu Asn Trp Ala Thr Ser Glu Gly Trp Asn Pro Arg Ala Arg
705 710 715 720
Arg Val Asp Ile Asn Thr Glu Asn Cys Pro Gly Gly Asp Lys Cys Gly
725 730 735
Glu Gly Lys Glu Asp Leu Val Trp Gly Lys Asn Thr Lys Pro Arg Gly

740 745 750
Val Asn Ala Arg Asp Arg Asp Val Glu Ile Gln Pro Thr Gly Asp Ile
755 760 765
Thr Asn Gly Leu Ile Arg Ile Gly Gly Tyr Gly Asn His Gly Asp Gly
770 775 780
Gln Pro Asp Thr Met Arg Thr Leu Gly Glu Glu Leu Thr Phe Asp Gly
785 790 795 800
Ala Arg Trp Asn Asp His His Lys Thr Thr Thr Arg Ile Phe Gly His

805 810 815

Tyr His Leu Ala Tyr Ala Asp Gln Asp Asp Arg Ser Val Lys Ala Met

820 825 830

Ser Met Asn Ser Tyr Ser Gly Ala Arg Ser Phe Val Ser Gln Val Glu

835 840 845

Gly Thr Leu Ala Thr Pro Thr Ala Gln Gly Tyr Arg Ala Asp Leu Asp

850 855 860

Ser Lys Pro Thr Gln Tyr Ser Leu Gly Ala Lys Pro Ile Thr Leu Lys

865 870 875 880

Lys Val Gln Tyr Gly Arg Val Thr Thr Asn Leu Asp Leu Thr Ala Ser

885 890 895

Gly Thr Lys Leu Leu Pro Asn Gly Phe Leu Arg Ala Pro Phe Glu Lys

900 905 910

Lys Gly Thr Gly Asp Ser Val Asp Asn Tyr Phe Phe Arg Gly Val Asp

915 920 925

Glu Thr Thr Ile Glu Gln Met Asn Ala Leu Pro Ser Asn Gln Val Ala

930 935 940

Arg Tyr Glu Gly His Ala Leu Met Tyr Gly Ile Asp Asn Ser Phe His

945 950 955 960

Gly Ile Arg Thr Asn Arg Ser Gln Lys Asp Leu Pro Asn Ala Phe Asp

965 970 975

Gly Thr Gly Gly Gln Asn Ala Thr Ala His Thr Leu Gly Leu Gly Asn

980 985 990

Phe Val Glu Ala Glu Val Asn Phe Gly Thr Lys Lys Val Thr Gly Asp

995 1000 1005

Val Tyr Asn Ala Trp Leu Glu Gln Leu Asp Lys Pro Gly Val Tyr

1010 1015 1020

Lys Asp Lys Leu Val Thr Phe Ser Gly Asn Val Ile Gly Asn Thr

1025 1030 1035

Val Ile Gly Thr Ala Asp Arg Thr Tyr Ala Pro Gly Asn Asp Glu

1040 1045 1050

Ala Asp Phe Arg Ala Ala Phe Tyr Gly Ser Gln Ala Asp Glu Met

1055 1060 1065

Gly Gly Ser Phe Asn Ser Val Lys Ala Thr Asn Lys Tyr Gly Ser

1070 1075 1080

Ala Tyr Glu Val Gly Asp Trp Gly Gly Val Phe Gly Ala Thr Lys

1085 1090 1095

Val Gly Thr Asn Thr Phe Gln Gly Asp Asp Gly Gly Gln Thr Tyr

1100 1105 1110

Gly Gly Gly Ser Ala Pro Ala Gln Thr Pro Asn Val Ala Asp Arg

1115 1120 1125

Tyr Ala Pro

1130

<210> 773

<211> 765

<212> DNA

<213> Caulobacter sp. AP07 SLP 2a

<400> 773

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accagcacca tcaacgccgg tccgcacacc tccggcaagc cgggcgtcgc cgtcgccggc 180

atcggccttt ccagctacgt cgacttcgcg ggcctgcagg cctcgatccc gccggtcaac 240

ggcgtgacca ccatcaacag cccctccagc gcccccggta gccacaacgg catgggcgtg 300

ttcaacttcg ccaaggtcag caacgccgac ctctatttcg gcgaatggtc ggacaccgcc 360

aacgtcgctg acggcaccca caccgtctac tatgtcggcg acaacaccgg cacgacggtc 420

ccgaccacgg gttcggccac ctatgcggtg aaggggatca gcggctacgc cgccaacggc 480

cccctgaccg gaaccttcac ggccaacttc ggcgccagca ccctgagcgg aagcatcgcc 540

agcgcctcga ccggctacac ggtcaacatc ggctcggtgg gcatctccgg cgccaacatc 600

gccagcacca ccagcaacgc cacggcgacg cagtccacca ccctggcctc gggtggcagc 660

gtcagcggcc agttcttcgg cgccaacgcc gcggccctgg cgggcctcgt caccttcggc 720

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<210> 774

<211> 254

<212> PRT

<213> Caulobacter sp. AP07 SLP 2a

<400> 774

Met Thr Arg Ser Thr Phe Lys Thr Leu Ile Leu Ala Pro Ile Ala Ala
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Leu Ala Leu Cys Gly Val Ala Gln Ala Ala Ile Val Gly Gln Ser Thr
20 25 30

Asp Thr Thr Gln Leu Arg Val Gly Thr Ser Thr Ile Asn Ala Gly Pro
35 40 45

His Thr Ser Gly Lys Pro Gly Val Ala Val Ala Gly Ile Gly Leu Ser
50 55 60

Ser Tyr Val Asp Phe Ala Gly Leu Gln Ala Ser Ile Pro Pro Val Asn
65 70 75 80

Gly Val Thr Thr Ile Asn Ser Pro Ser Ser Ala Pro Gly Ser His Asn
85 90 95

Gly Met Gly Val Phe Asn Phe Ala Lys Val Ser Asn Ala Asp Leu Tyr
100 105 110

Phe Gly Glu Trp Ser Asp Thr Ala Asn Val Ala Asp Gly Thr His Thr
115 120 125

Val Tyr Tyr Val Gly Asp Asn Thr Gly Thr Thr Val Pro Thr Thr Gly
130 135 140

Ser Ala Thr Tyr Ala Val Lys Gly Ile Ser Gly Tyr Ala Ala Asn Gly
145 150 155 160

Pro Leu Thr Gly Thr Phe Thr Ala Asn Phe Gly Ala Ser Thr Leu Ser
165 170 175

Gly Ser Ile Ala Ser Ala Ser Thr Gly Tyr Thr Val Asn Ile Gly Ser
180 185 190

Val Gly Ile Ser Gly Ala Asn Ile Ala Ser Thr Thr Ser Asn Ala Thr
195 200 205

Ala Thr Gln Ser Thr Thr Leu Ala Ser Gly Gly Ser Val Ser Gly Gln
210 215 220

Phe Phe Gly Ala Asn Ala Ala Ala Leu Ala Gly Leu Val Thr Phe Gly
225 230 235 240

Gly Asn Ser Gln Tyr Asp Thr Ala Phe Gly Gly Thr Lys Asn
245 250

<210> 775

<211> 2595

<212> DNA

<213> D. alkaliphilus SLP 1a

<400> 775

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gccctgcgcg gtacggcggt ggcggtggat gccgccggcg ccgagcgtgc cctggccatc 180

aaggcgccca tccaccggca agataccatc cgcaccgggc cccgggggcg gctgcagctg 240

atgttcaccg acaacaccat catcagcctg ggggttaacg ccgagctgga gattgccgaa 300

tatcagtggg accagcagga aggggagctg aacacccggg tcaaccaggg ggcctttcgg 360

gtaatgggcg gctctgtggc ccgcacctcg ccggaaaaat tcaccaccga cacccccgct 420

gccaccatcg gtatccgtgg ctccatgtac gccggccggg taagcgacgg cgccctggcg 480

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gaagaggaga cggtggagga tgagaccccc gccgaagaac cggccgagga ggagtgggaa 720

gatgccgccc tggatgagcc cgaagaggcc gccgccccgg tggccgccgc cccggctccc 780

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tcctcgttga gttcggtttc catttttggc ctggactacg atgactacgg tgatggcgca 1560

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gaaccgggca cgccgccgga actgttccgc agtaccagcg ccgaatattt tgaattgcag 1860

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<210> 776

<211> 864

<212> PRT

<213> D. alkaliphilus SLP 1a

<400> 776

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Val Cys Leu Leu Ala Val Thr Phe Trp Ser Ala Pro Pro Ala Thr Ala

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35 40 45
Val Asp Ala Ala Gly Ala Glu Arg Ala Leu Ala Ile Lys Ala Pro Ile
50 55 60
His Arg Gln Asp Thr Ile Arg Thr Gly Pro Arg Gly Arg Leu Gln Leu
65 70 75 80

Met Phe Thr Asp Asn Thr Ile Ile Ser Leu Gly Val Asn Ala Glu Leu
85 90 95
Glu Ile Ala Glu Tyr Gln Trp Asp Gln Gln Glu Gly Glu Leu Asn Thr
100 105 110
Arg Val Asn Gln Gly Ala Phe Arg Val Met Gly Gly Ser Val Ala Arg
115 120 125
Thr Ser Pro Glu Lys Phe Thr Thr Asp Thr Pro Ala Ala Thr Ile Gly
130 135 140

Ile Arg Gly Ser Met Tyr Ala Gly Arg Val Ser Asp Gly Ala Leu Ala
145 150 155 160
Val Val Phe Gln Gly Gly Thr Gly Ile Ile Val Ser Asn Pro Ala Gly
165 170 175
Thr Val Glu Ile Thr Thr Pro Gly Met Gly Thr Arg Val Ala Ser Arg
180 185 190
Thr Ala Ala Pro Thr Pro Pro Thr Val Phe Thr Gln Glu Asp Leu Gly
195 200 205

Ala Leu Glu Asp Glu Glu Val Asp Glu Glu Ala Ala Glu Glu Glu Thr
210 215 220
Val Glu Asp Glu Thr Pro Ala Glu Glu Pro Ala Glu Glu Glu Trp Glu
225 230 235 240
Asp Ala Ala Leu Asp Glu Pro Glu Glu Ala Ala Ala Pro Val Ala Ala
245 250 255
Ala Pro Ala Pro Ile Thr Asp Thr Ala Val Asp Gln Ala Thr Glu Thr
260 265 270

Thr Thr Asp Ala Ala Gln Asp Glu Trp Glu Gln Thr Val Val Glu Ala

275 280 285

Asp Pro Glu Pro Thr Asp Pro Asp Pro Thr Asp Pro Glu Pro Ile Asp

290 295 300

Pro Glu Pro Thr Asp Pro Ser Glu Ala Val Tyr Ser Gly Arg Gly Ile

305 310 315 320

Glu Ile Ile Tyr Ser Ser Met Gln Glu Glu Val Ala Val Glu His Leu

325 330 335

Val Leu Thr Asp Lys Pro Ser Glu Leu Thr Glu Ile Glu Ala Gly Leu

340 345 350

Leu Glu Tyr Asn Glu Gln Ser Asp Phe Ser Asp Gly Glu Tyr Ser Ala

355 360 365

Val Trp Ser Tyr Thr Asp Ala Thr Gln Val Glu Glu Trp Glu Glu Gly

370 375 380

Asp Asp Phe Asp Phe Gln Phe Thr Phe Val Met Val Asp Asp Arg Gly

385 390 395 400

Glu Phe Trp Leu Tyr Glu Gln Trp Ser Asp Thr Glu Thr Asp Glu Ser

405 410 415

Trp Thr Tyr Ser Glu Lys Met Phe Phe Tyr Gly Ser Glu Thr Pro Val

420 425 430

Asp Leu Met Pro Thr Ser Gly Gly Ala Ile Tyr His Gly Phe Phe Thr

435 440 445

Gly Ala Ser Asp Asp Val Asp Tyr Gly Trp Glu Glu Phe Phe Gly Asp

450 455 460

Phe Ser Leu Ala Val Asn Trp Glu Thr Gly Lys Val Val Gly Tyr Phe

465 470 475 480

Ile Asp Asp Glu His Tyr Gly Arg Pro Ile Pro Val Tyr Leu Thr Gly

485 490 495

Glu Val Asp Gly Ser Ser Leu Ser Ser Val Ser Ile Phe Gly Leu Asp

500 505 510

Tyr Asp Asp Tyr Gly Asp Gly Ala Leu Tyr Asp Ala Trp Ile Thr Thr

515 520 525

Gly Ser Gly Thr Phe Ala Gln Phe Tyr Gly Thr Tyr Tyr Gln Gly Leu
530 535 540
Gly Leu Val Ala Glu Gly Gln Ser Gly Ser Leu Tyr Tyr Asp Asp Ala
545 550 555 560
Gln Glu Asp Trp Ser Val Val Gly Gly Gly Phe Arg Asp Pro Val Phe
565 570 575
Thr Leu Pro Glu Gln Ala Ala Ser Ser Thr Trp Arg Gly Phe Val Thr
580 585 590

Ala Met Glu Ile Asn Leu Val Glu Glu Pro Gly Thr Pro Pro Glu Leu
595 600 605
Phe Arg Ser Thr Ser Ala Glu Tyr Phe Glu Leu Gln Ile Asp Arg Gln
610 615 620
Ala Gly Met Phe Ser Gly Gln Ile Ile Glu Ala Glu Ser Ala Thr Thr
625 630 635 640
Thr Gly Leu Ser Ile Gly Gly Leu Glu Val Ala Gly Phe Tyr Val Ser
645 650 655

Asp Asn Phe Leu Ala Gly Glu Leu Ser Ser Ala Ser Asp Ser Asp Leu
660 665 670
Gln Gly Ala Leu Gly Gly Ser Gly Glu Tyr Tyr Phe Tyr Asp Phe Glu
675 680 685
Asp Glu Ala Asp Tyr Phe Gln Ile Gly Glu Leu Ala Glu His Val Ser
690 695 700
Trp Gly Tyr Trp Gly Ala Ala Phe Thr Gly Gln Asp Glu Met Pro Tyr
705 710 715 720

Leu Ile Ser Pro Ala Gly Ser Phe Trp Val Ala Gly Glu Leu Thr Pro
725 730 735
Ala Asp Thr Val Leu Gly Met Ile Asp Ala Glu Val Thr Gly Thr Tyr
740 745 750
Glu Gly Gly Ala Glu Gly Ile Leu Ile Phe Glu Gly Thr Met Ala Asp
755 760 765
Leu Tyr Asn Gly Gln Thr Thr Leu Asn Ile Asn Phe Gly Asp Ala Asn

770 775 780

Ile Asn Gly Ser Ile Thr Phe Ser Glu Ile Ala Glu Leu Thr Ile Asp
785 790 795 800
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805 810 815
Val Glu Phe Phe Gly Gly Glu Pro Thr Leu Ala Ser Gly Gly Ile Ser
820 825 830
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835 840 845

Ala Glu Gly Gly Gly Ala Gln Phe Leu Gly Ile Phe Gly Gly Asp Arg
850 855 860

<210> 777
<211> 342
<212> DNA
<213> D. nodosus SLP 1a
<400> 777

atgaaattta aattatgctt tttaataacg ctggcaggtt gcgtgcaaag cgacagcatc 60
agtcattttc aaacgcgttc tacattgcgt tatttaggtg acggttttca aagcgaacaa 120
agcggttatc aatatcaaac gggcgccgcg ccgttgggtt ttcaagcggt ggtgcgcggc 180
gacaatatgg cgctggaaat tgaacaaccc gcctttattg aacgcggaca atatcgccct 240

gatatgtgtt tggaaccgtt tttttatcgc gggcggcaat attatcggca agtttcttgc 300
catcattacg agccgcgaag tggtattcgt attacccgtt aa 342

<210> 778
<211> 113
<212> PRT
<213> D. nodosus SLP 1a
<400> 778

Met Lys Phe Lys Leu Cys Phe Leu Ile Thr Leu Ala Gly Cys Val Gln
1 5 10 15
Ser Asp Ser Ile Ser His Phe Gln Thr Arg Ser Thr Leu Arg Tyr Leu
20 25 30

Gly Asp Gly Phe Gln Ser Glu Gln Ser Gly Tyr Gln Tyr Gln Thr Gly

35 40 45

Ala Ala Pro Leu Gly Phe Gln Ala Val Val Arg Gly Asp Asn Met Ala

50 55 60

Leu Glu Ile Glu Gln Pro Ala Phe Ile Glu Arg Gly Gln Tyr Arg Pro

65 70 75 80

Asp Met Cys Leu Glu Pro Phe Phe Tyr Arg Gly Arg Gln Tyr Tyr Arg

85 90 95

Gln Val Ser Cys His His Tyr Glu Pro Arg Ser Gly Ile Arg Ile Thr

100 105 110

Arg

<210> 779

<211> 879

<212> DNA

<213> D. shibae SLP 1a

<400> 779

atgtcaaaga cccttacacg atctgtcgcg ctgcttgtgc tggcccctgt gctgacggcc 60

tgtggcggcg gcgggggctc cggttccgcg accccgttca cctccttcaa cgacctgccc 120

gagaccggca ccgtagagtt gcaaggccag gcccggaccg cgcgcttcgc ggtggatccg 180

gtcaccggcc aactcagcct ctcgaacctg tcggacaccg aggacagcac gctgcggctg 240

acaaccgcca acggcctgat accgcgcgtg gcgatccggg cccccgactc cgccgtcgcg 300

ttcgatctgg accaggggggc cacagtccag gtggatggcc ccgtcgtctt cttcgaaagc 360

gatgatgggc ggcgcttcgc gctgctgctc gatggcggcc ggggcggtcc gttcgagtac 420

cagaccctcg gagcctggct ggacgggttc ggcgcggagc gcggcacctt gggcgcgggg 480

gcttatggcg cgcggacgcc cagcgcgcgg ttgcccaccg ggcaggtcgc cacctatgtc 540

ggtgagggcg ccgggtttgc gcgacgggcc gatggcgagg gctatctcac cgtctcggcc 600

atcgaggtga cgaccgattt ccggcaggcg gagatcctca gcacgcagac gcaggcgatt 660

tccctcgcaa cctcggacac aattcccgcc ccggagctgg atttcgacgg cagtgggccg 720

gtctcgggtg ggggattcac cgcggcggtg tccgggccgg gctcggcggg ggaggcgcag 780

ggcgtgttcc atggccccaa tgccgaggag gtggccggga cctacagcct gagcgggccg 840

ggcggcgtgg cgcatatcgg cgcgttcggc ggcaactga 879

<210> 780

<211> 292

<212> PRT

<213> D. shibae SLP 1a

<400> 780

Met Ser Lys Thr Leu Thr Arg Ser Val Ala Leu Leu Val Leu Ala Pro
1 5 10 15

Val Leu Thr Ala Cys Gly Gly Gly Gly Gly Ser Gly Ser Ala Thr Pro
20 25 30

Phe Thr Ser Phe Asn Asp Leu Pro Glu Thr Gly Thr Val Glu Leu Gln
35 40 45

Gly Gln Ala Arg Thr Ala Arg Phe Ala Val Asp Pro Val Thr Gly Gln
50 55 60

Leu Ser Leu Ser Asn Leu Ser Asp Thr Glu Asp Ser Thr Leu Arg Leu
65 70 75 80

Thr Thr Ala Asn Gly Leu Ile Pro Arg Val Ala Ile Arg Ala Pro Asp
85 90 95

Ser Ala Val Ala Phe Asp Leu Asp Gln Gly Ala Thr Val Gln Val Asp
100 105 110

Gly Pro Val Val Phe Phe Glu Ser Asp Asp Gly Arg Arg Phe Ala Leu
115 120 125

Leu Leu Asp Gly Gly Arg Gly Gly Pro Phe Glu Tyr Gln Thr Leu Gly
130 135 140

Ala Trp Leu Asp Gly Phe Gly Ala Glu Arg Gly Thr Leu Gly Ala Gly
145 150 155 160

Ala Tyr Gly Ala Arg Thr Pro Ser Ala Arg Leu Pro Thr Gly Gln Val
165 170 175

Ala Thr Tyr Val Gly Glu Gly Ala Gly Phe Ala Arg Arg Ala Asp Gly
180 185 190

Glu Gly Tyr Leu Thr Val Ser Ala Ile Glu Val Thr Thr Asp Phe Arg
195 200 205

Gln Ala Glu Ile Leu Ser Thr Gln Thr Gln Ala Ile Ser Leu Ala Thr
210 215 220

Ser Asp Thr Ile Pro Ala Pro Glu Leu Asp Phe Asp Gly Ser Gly Pro
225 230 235 240
Val Ser Gly Gly Gly Phe Thr Ala Ala Val Ser Gly Pro Gly Ser Ala
245 250 255
Gly Glu Ala Gln Gly Val Phe His Gly Pro Asn Ala Glu Glu Val Ala
260 265 270
Gly Thr Tyr Ser Leu Ser Gly Pro Gly Gly Val Ala His Ile Gly Ala
275 280 285

Phe Gly Gly Asn
290

<210> 781
<211> 849
<212> DNA
<213> E. corrodens SLP 1a
<400> 781
atgcaaaagc atcacattct ttacattgcc atcactgccc ttaccctagg cggctgcggc 60
agcgccggta actcactggc caatgcgatt actgatccgt ttacacccaa agaaggcggt 120
tatcgccaac tgagcaatat cggctcggat gagttcaccc acacaggtct actgcccacc 180
ataggcagta gacaggcatc gactatcagg attacagacg accaattcat cggcacacag 240
aatcatgaaa aagactactc cagccgcgat acaatcccta tcggccacaa acggcagaac 300
gccttcacct ccctgcccta tgtgctgaaa gatagcagtg ggaaccaaat ggaaagcggc 360

gttttggaag tttacaaaca ggcctactcc gccgtggtgg gcgcgcaact gcacaacaga 420
atcgagcccg gccatccggc cacgccaacc cgcgacttct atgttcgctc catccaaggt 480
gaattcacca gcaatctgcc cacccaaggc atcatcacct ataaaggccg ggcaatgaca 540
ggctcggtta ccggctcagc tgaccacagc aatggtttga actatcaaat tgattacggt 600
gcaagaaaag gccacggctc gattaccggc ttaaacggtt tcggcaatat tgatttggca 660
gaagcaccga ttacccaaaa cccgcatggt cataatgtga ttaacggcgc agccaattct 720
gccacacacg gggcgggtaa ttacgagctc ggcatttttg gtccgcaagc caatgaaatt 780

gccggtaagg cacatttcaa caatcagccg aacaaggaag tcggtttcgc cggcggacgg 840

gtaaattaa 849

<210> 782

<211> 282

<212> PRT

<213> E. corrodens SLP 1a

<400> 782

Met Gln Lys His His Ile Leu Tyr Ile Ala Ile Thr Ala Leu Thr Leu
1 5 10 15

Gly Gly Cys Gly Ser Ala Gly Asn Ser Leu Ala Asn Ala Ile Thr Asp
20 25 30

Pro Phe Thr Pro Lys Glu Gly Gly Tyr Arg Gln Leu Ser Asn Ile Gly
35 40 45

Ser Asp Glu Phe Thr His Thr Gly Leu Leu Pro Thr Ile Gly Ser Arg
50 55 60

Gln Ala Ser Thr Ile Arg Ile Thr Asp Asp Gln Phe Ile Gly Thr Gln
65 70 75 80

Asn His Glu Lys Asp Tyr Ser Ser Arg Asp Thr Ile Pro Ile Gly His
85 90 95

Lys Arg Gln Asn Ala Phe Thr Ser Leu Pro Tyr Val Leu Lys Asp Ser
100 105 110

Ser Gly Asn Gln Met Glu Ser Gly Val Leu Glu Val Tyr Lys Gln Ala
115 120 125

Tyr Ser Ala Val Val Gly Ala Gln Leu His Asn Arg Ile Glu Pro Gly
130 135 140

His Pro Ala Thr Pro Thr Arg Asp Phe Tyr Val Arg Ser Ile Gln Gly
145 150 155 160

Glu Phe Thr Ser Asn Leu Pro Thr Gln Gly Ile Ile Thr Tyr Lys Gly
165 170 175

Arg Ala Met Thr Gly Ser Val Thr Gly Ser Ala Asp His Ser Asn Gly
180 185 190

Leu Asn Tyr Gln Ile Asp Tyr Gly Ala Arg Lys Gly His Gly Ser Ile
195 200 205

Thr Gly Leu Asn Gly Phe Gly Asn Ile Asp Leu Ala Glu Ala Pro Ile
210 215 220
Thr Gln Asn Pro His Gly His Asn Val Ile Asn Gly Ala Ala Asn Ser

225 230 235 240
Ala Thr His Gly Ala Gly Asn Tyr Glu Leu Gly Ile Phe Gly Pro Gln
245 250 255
Ala Asn Glu Ile Ala Gly Lys Ala His Phe Asn Asn Gln Pro Asn Lys
260 265 270
Glu Val Gly Phe Ala Gly Gly Arg Val Asn
275 280

<210> 783
<211> 975
<212> DNA
<213> E. corrodens SLP 2a
<400> 783

atgaaacacc tgattttatc tttgtctgtg gctgctgcgt tggcaggatg tgccggcagt 60

ggcggggtaa ccattccaga cggtaccgct cctgtaccgc cgctgactcc ggccgactcc 120
agcaaaatcc ttggcccggc cagcacaggc gaaacgccca ccaccttcca aaccggtaac 180
gggcagctgc gttatgtgtc gtggtatgtg gagtattggg gcacgccgtc gtctgaaaac 240
aaattcatct atcaggcgcc aaacggtaaa agttatgcct ttgatgggtt cactaatccg 300
ccaagattct ccagccgttt tacgcccgat aaaaaccaac ccaccaagat ggagccgcaa 360
acctcaagcg atggtaacaa gctgctggtg tgctgtgaaa acggtgatgc taatttcccc 420
gcaggctacc tgcagtctct gcgttatggc gcatggattg gtgccgacgg gcaaaccgat 480

ctattcgcgg gcggcatatt ggccaacacg gcggacatgc agaagcgcaa tggcgccacc 540
gcacccaccg gcaaagctac ctacgaagtt tgggccttcc gcgtgaaagg cggttcggtt 600
gtggcctctt cctataacac tgataccaac cctgctaaac gggttaattc tttgctaacc 660
gttaatttca acaccggaaa agtgggtggc acgattaaag gcaatgccga ttttggtgcg 720
gacatcgatt tcaacgatgt tactgtaaac ggcaatacct tcagcggcac agcctcttcc 780
ggcggggtga gcggccaagt gaacggtggc ttctacggta agagcggttg gtacgacccg 840
gccggtacgg aaatcggcgg taaggttact ttcaacggca accgcagcct cgacagcgta 900

tttggtggtt cagccaccga tactcgccgc gacccggata ccacggccac agatttaacc 960

cccgttaatc cctaa 975

<210> 784

<211> 324

<212> PRT

<213> E. corrodens SLP 2a

<400> 784

Met Lys His Leu Ile Leu Ser Leu Ser Val Ala Ala Ala Leu Ala Gly
1 5 10 15

Cys Ala Gly Ser Gly Gly Val Thr Ile Pro Asp Gly Thr Ala Pro Val
20 25 30

Pro Pro Leu Thr Pro Ala Asp Ser Ser Lys Ile Leu Gly Pro Ala Ser
35 40 45

Thr Gly Glu Thr Pro Thr Thr Phe Gln Thr Gly Asn Gly Gln Leu Arg
50 55 60

Tyr Val Ser Trp Tyr Val Glu Tyr Trp Gly Thr Pro Ser Ser Glu Asn
65 70 75 80

Lys Phe Ile Tyr Gln Ala Pro Asn Gly Lys Ser Tyr Ala Phe Asp Gly
85 90 95

Phe Thr Asn Pro Pro Arg Phe Ser Ser Arg Phe Thr Pro Asp Lys Asn
100 105 110

Gln Pro Thr Lys Met Glu Pro Gln Thr Ser Ser Asp Gly Asn Lys Leu
115 120 125

Leu Val Cys Cys Glu Asn Gly Asp Ala Asn Phe Pro Ala Gly Tyr Leu
130 135 140

Gln Ser Leu Arg Tyr Gly Ala Trp Ile Gly Ala Asp Gly Gln Thr Asp
145 150 155 160

Leu Phe Ala Gly Gly Ile Leu Ala Asn Thr Ala Asp Met Gln Lys Arg
165 170 175

Asn Gly Ala Thr Ala Pro Thr Gly Lys Ala Thr Tyr Glu Val Trp Ala
180 185 190

Phe Arg Val Lys Gly Gly Ser Val Val Ala Ser Ser Tyr Asn Thr Asp
195 200 205

Thr Asn Pro Ala Lys Arg Val Asn Ser Leu Leu Thr Val Asn Phe Asn

210 215 220

Thr Gly Lys Val Gly Gly Thr Ile Lys Gly Asn Ala Asp Phe Gly Ala

225 230 235 240

Asp Ile Asp Phe Asn Asp Val Thr Val Asn Gly Asn Thr Phe Ser Gly

245 250 255

Thr Ala Ser Ser Gly Gly Val Ser Gly Gln Val Asn Gly Gly Phe Tyr

260 265 270

Gly Lys Ser Gly Trp Tyr Asp Pro Ala Gly Thr Glu Ile Gly Gly Lys

275 280 285

Val Thr Phe Asn Gly Asn Arg Ser Leu Asp Ser Val Phe Gly Gly Ser

290 295 300

Ala Thr Asp Thr Arg Arg Asp Pro Asp Thr Thr Ala Thr Asp Leu Thr

305 310 315 320

Pro Val Asn Pro

<210> 785

<211> 945

<212> DNA

<213> E. hoshinae SLP 1a

<400> 785

atgcaacctc gctatagcgc actcttctta ctcttatctt ctacgctgtt gaccgcctgc 60

ggcggcggtg gcgctggtgg cgatgccgcg tcagcgcagg ccatcgcgcc ggcggcacct 120

gtcccccaac cgctcgcagc gacggctccc gccgcccagc ctctcgcacc cgcgccgacg 180

gcacccggcg ttccacccgc gacgcccgct gccgcccccc cggccgccgc cttcggtgag 240

caaggcacag tataccaggc gcaactgcgg gagatcggcc gccacgacgc catcaatata 300

tacggtttta acgcactcag ccccgacagt gagttcaccg ttaaggtgga aggaaccgat 360

atcgctatcg acgtcacgcc catcacccag caccatgaaa aagatagccg cgtcattaac 420

gatcagaaag tcctgacgct gcgcgatgcc gatggcaacc tggcgggtta ctatggccat 480

gtgcacacct atacccaccg cgagacggcg caggatgaaa gcgagcagga tcaaacaacc 540

accagcctgg tctacgcggt caatgccagc gaaaggcacc gtcctgaaac tcaagcggac 600

tatgtgggca ccctgtttta taaccacttc gatatcccgc gtgaggccgc tatccgcctg 660

cactatcagg acaataagat caccggcgat atcaagggca ccggtctagc ccgcgatatc 720

gactacgtta tccgggacga tggtgacaat accgtgagcg aagagggaac cttcggcgcc 780

agactgcgcc atgtcgacgc gcagcgtaac gcggttaacg gccacctgat cggcggcttc 840

tatggcaaag agggcgaggt cgccgctggc gaggtcaaat ttatcgatga ctatagcgta 900

gagcgcggcg gcgtcttcgg cgcacagcgg gtcaagcgca actga 945

<210> 786

<211> 314

<212> PRT

<213> E. hoshinae SLP 1a

<400> 786

Met Gln Pro Arg Tyr Ser Ala Leu Phe Leu Leu Leu Ser Ser Thr Leu
1 5 10 15

Leu Thr Ala Cys Gly Gly Gly Gly Ala Gly Gly Asp Ala Ala Ser Ala
20 25 30

Gln Ala Ile Ala Pro Ala Ala Pro Val Pro Gln Pro Leu Ala Ala Thr
35 40 45

Ala Pro Ala Ala Gln Pro Leu Ala Pro Ala Pro Thr Ala Pro Gly Val
50 55 60

Pro Pro Ala Thr Pro Pro Ala Ala Pro Pro Ala Ala Ala Phe Gly Glu
65 70 75 80

Gln Gly Thr Val Tyr Gln Ala Gln Leu Arg Glu Ile Gly Arg His Asp
85 90 95

Ala Ile Asn Ile Tyr Gly Phe Asn Ala Leu Ser Pro Asp Ser Glu Phe
100 105 110

Thr Val Lys Val Glu Gly Thr Asp Ile Ala Ile Asp Val Thr Pro Ile
115 120 125

Thr Gln His His Glu Lys Asp Ser Arg Val Ile Asn Asp Gln Lys Val
130 135 140

Leu Thr Leu Arg Asp Ala Asp Gly Asn Leu Ala Gly Tyr Tyr Gly His
145 150 155 160

Val His Thr Tyr Thr His Arg Glu Thr Ala Gln Asp Glu Ser Glu Gln

165 170 175

Asp Gln Thr Thr Thr Ser Leu Val Tyr Ala Val Asn Ala Ser Glu Arg

180 185 190

His Arg Pro Glu Thr Gln Ala Asp Tyr Val Gly Thr Leu Phe Tyr Asn

195 200 205

His Phe Asp Ile Pro Arg Glu Ala Ala Ile Arg Leu His Tyr Gln Asp

210 215 220

Asn Lys Ile Thr Gly Asp Ile Lys Gly Thr Gly Leu Ala Arg Asp Ile

225 230 235 240

Asp Tyr Val Ile Arg Asp Asp Gly Asp Asn Thr Val Ser Glu Glu Gly

245 250 255

Thr Phe Gly Ala Arg Leu Arg His Val Asp Ala Gln Arg Asn Ala Val

260 265 270

Asn Gly His Leu Ile Gly Gly Phe Tyr Gly Lys Glu Gly Glu Val Ala

275 280 285

Ala Gly Glu Val Lys Phe Ile Asp Asp Tyr Ser Val Glu Arg Gly Gly

290 295 300

Val Phe Gly Ala Gln Arg Val Lys Arg Asn

305 310

<210> 787

<211> 942

<212

> DNA

<213> E. piscicida SLP 1a

<400> 787

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ggtggcggtg gcggtggtgg tggcggcggt ggcggtggtg gcgctagcga tgccgcgccg 120

gcacaggcca tcgcaccggc ggcgcccgcc tcccagccgc tcgcggtcgt accggcggcg 180

cccgacgttc cccccgttgc gcccgacgtt gcgcccccctg ccgccgccat cgatgaaccg 240

gaggcacaat accgcgggct ggtgcgggag atcggccacc gtgacaccct cagtatatcc 300

ggttttaaca ctctcaatcc caaccgcgag ttcaccgtta aggtggaggg aaccgatatc 360

gccatcgacg tcgccccccct cataaagcgc catgaaaagg acagccgcgt cattaacggt 420

cagaaagtcc tgacgctgcg cgatgccgat ggcaagctgg cgggttacta tggccatgtg 480

cacacctata cccaccgcga gacggcgcag aatgaagacg atcaggacca aacaaccacc 540

agcctggtat acgcggtcaa cgtcaatgaa gggcgccgtc cagagaccca ggcagactat 600

gtgggcaccc tgttttataa ccacttcgat atcccgcgcg aggccgccat ccgtctgcac 660

tatcaggaca acaagatcac cggcaatatc aagggtagcg gtctggccag cgatatcgac 720

tacgttatcc gggaggatgg tgacaatacc gtcagcgagg agggaacctt cggcgccaga 780

ctgcaccgcg tcggcgcgca gcgtaacgcg gttaacggcc acctggtcgg tgggttctat 840

ggcaaagagg gcgaagtcgc cgccggcgag gtcaaattta tcgataacta tagcgtagag 900

cgcggcggcg tcttcggcgc acagcgggtg cagcacgact ga 942

<210> 788

<211> 313

<212> PRT

<213> E. piscicida SLP 1a

<400> 788

Met Lys Pro Arg Tyr Ser Thr Leu Phe Leu Leu Leu Ser Ser Ala Leu
1 5 10 15

Leu Thr Ala Cys Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30

Gly Gly Ala Ser Asp Ala Ala Pro Ala Gln Ala Ile Ala Pro Ala Ala
35 40 45

Pro Ala Ser Gln Pro Leu Ala Val Val Pro Ala Ala Pro Asp Val Pro
50 55 60

Pro Val Ala Pro Asp Val Ala Pro Pro Ala Ala Ala Ile Asp Glu Pro
65 70 75 80

Glu Ala Gln Tyr Arg Gly Leu Val Arg Glu Ile Gly His Arg Asp Thr
85 90 95

Leu Ser Ile Ser Gly Phe Asn Thr Leu Asn Pro Asn Arg Glu Phe Thr
100 105 110

Val Lys Val Glu Gly Thr Asp Ile Ala Ile Asp Val Ala Pro Leu Ile
115 120 125

Lys Arg His Glu Lys Asp Ser Arg Val Ile Asn Gly Gln Lys Val Leu
130 135 140

Thr Leu Arg Asp Ala Asp Gly Lys Leu Ala Gly Tyr Tyr Gly His Val
145 150 155 160

His Thr Tyr Thr His Arg Glu Thr Ala Gln Asn Glu Asp Asp Gln Asp
165 170 175
Gln Thr Thr Thr Ser Leu Val Tyr Ala Val Asn Val Asn Glu Gly Arg
180 185 190
Arg Pro Glu Thr Gln Ala Asp Tyr Val Gly Thr Leu Phe Tyr Asn His
195 200 205
Phe Asp Ile Pro Arg Glu Ala Ala Ile Arg Leu His Tyr Gln Asp Asn
210 215 220

Lys Ile Thr Gly Asn Ile Lys Gly Ser Gly Leu Ala Ser Asp Ile Asp
225 230 235 240
Tyr Val Ile Arg Glu Asp Gly Asp Asn Thr Val Ser Glu Glu Gly Thr
245 250 255
Phe Gly Ala Arg Leu His Arg Val Gly Ala Gln Arg Asn Ala Val Asn
260 265 270
Gly His Leu Val Gly Gly Phe Tyr Gly Lys Glu Gly Glu Val Ala Ala
275 280 285

Gly Glu Val Lys Phe Ile Asp Asn Tyr Ser Val Glu Arg Gly Gly Val
290 295 300
Phe Gly Ala Gln Arg Val Gln His Asp
305 310

<210> 789
<211> 957
<212> DNA
<213> E. tarda SLP 1a
<400> 789

atgaaaccac gctatagcac actcttctta ctcttatcct ctgcgctgtt gaccgcctgc 60
tgcggcggcg gcggcggcgg tagcgatgcc gcgcaggcgc aggccatcgc gccggtggcc 120
ccggcctccc agtccatcgc gccggtagcc ccgccctccc agcccatcgc gccggtggct 180

cccgcctctc aggccattgc ggcagcgccc gaggtgcccc ccgccgcgct ccctgccgcc 240

gccttcggtg agccaggggc ggtataccgc gcacagctgc gggagatcgg cccccatgac 300

accatcaaga tatacggttt tgacgcactc agccccgaca gcgagttcac cgttaaagtc 360

gaggggaccg atatcgccat cgaggtcacg ccccctcccc agcgccatga aaaggatagc 420

cgcaccatta acgatcagac agtcctgacg ctgcgcgatg ccgatggcaa gctggcgggt 480

tactatggcc atgtgcacac ctatacccac cgcgagacgg cgcaggatga agacgatcag 540

gatcagacaa ccagcagcct ggtctacgcg gtcaacgcca gcgaaaggca ccgccctgaa 600

acccaggcgg actatgaagg cacgctgttt tataaccact tcgatatcca gcgcgaggcc 660

gccatccgcc tgcactatca ggacaacaag atcaccggca atatcaaggg cagcggccta 720

gcccgcgata tcgactacgt tatccgagac gatggcggca acaccgtcag cgaggagggc 780

gccttcggcg ccagactgca ccatgtcaac gcgccgcgca acgcggtgaa cggccacctg 840

atcggcggct tctatggcaa agagggtgaa gtcgccgccg gcgaagtcaa atttatcgat 900

gactacagcg tagagcgcgg cggcgtcttc ggcgcacagc gggtcaagcg cgactga 957

<210> 790

<211> 318

<212> PRT

<213> E. tarda SLP 1a

<400> 790

Met Lys Pro Arg Tyr Ser Thr Leu Phe Leu Leu Leu Ser Ser Ala Leu
1 5 10 15

Leu Thr Ala Cys Cys Gly Gly Gly Gly Gly Gly Ser Asp Ala Ala Gln
20 25 30

Ala Gln Ala Ile Ala Pro Val Ala Pro Ala Ser Gln Ser Ile Ala Pro
35 40 45

Val Ala Pro Pro Ser Gln Pro Ile Ala Pro Val Ala Pro Ala Ser Gln
50 55 60

Ala Ile Ala Ala Ala Pro Glu Val Pro Pro Ala Ala Leu Pro Ala Ala
65 70 75 80

Ala Phe Gly Glu Pro Gly Ala Val Tyr Arg Ala Gln Leu Arg Glu Ile
85 90 95

Gly Pro His Asp Thr Ile Lys Ile Tyr Gly Phe Asp Ala Leu Ser Pro
100 105 110

Asp Ser Glu Phe Thr Val Lys Val Glu Gly Thr Asp Ile Ala Ile Glu

115 120 125

Val Thr Pro Leu Pro Gln Arg His Glu Lys Asp Ser Arg Thr Ile Asn
130 135 140
Asp Gln Thr Val Leu Thr Leu Arg Asp Ala Asp Gly Lys Leu Ala Gly
145 150 155 160
Tyr Tyr Gly His Val His Thr Tyr Thr His Arg Glu Thr Ala Gln Asp
165 170 175
Glu Asp Asp Gln Asp Gln Thr Thr Ser Ser Leu Val Tyr Ala Val Asn
180 185 190

Ala Ser Glu Arg His Arg Pro Glu Thr Gln Ala Asp Tyr Glu Gly Thr
195 200 205
Leu Phe Tyr Asn His Phe Asp Ile Gln Arg Glu Ala Ala Ile Arg Leu
210 215 220
His Tyr Gln Asp Asn Lys Ile Thr Gly Asn Ile Lys Gly Ser Gly Leu
225 230 235 240
Ala Arg Asp Ile Asp Tyr Val Ile Arg Asp Asp Gly Gly Asn Thr Val
245 250 255

Ser Glu Glu Gly Ala Phe Gly Ala Arg Leu His His Val Asn Ala Pro
260 265 270
Arg Asn Ala Val Asn Gly His Leu Ile Gly Gly Phe Tyr Gly Lys Glu
275 280 285
Gly Glu Val Ala Ala Gly Glu Val Lys Phe Ile Asp Asp Tyr Ser Val
290 295 300
Glu Arg Gly Gly Val Phe Gly Ala Gln Arg Val Lys Arg Asp
305 310 315

<210> 791
<211> 786
<212> DNA
<213> F. aurantia SLP 1a
<400> 791
atgaaccaca aactcaatac ccgactcggc ctgctgaccc tggggctgtt gctggccgca 60

ggagcccagg ctcaaagctc gatcagcggc gtgaccagtc gaccgaacga acgagacctc 120

atccgggttg gagaatccac cgtcaatggc ggtccccacc actccggggc ccccggtatc 180

ggcgtgcagt ccactgatgc cagcaagctg gtcgacttcg ccggtctggt ccgttatggc 240

cagactgatg ccgccggcgt caccaccctg gcgctggaaa gccccacccc gccgcccggc 300

gcgccaccca gccatgacag ccttggctcc ttccatttcg ccaaggtcag caatgcggac 360

gtctattatg gcgagtggtc gcaaagcgcc agtgccagcg acggtaccca taccagttat 420

tacgtgggtg accacgccgg taccactgtg cccgccaccg gtaccgccac ttatgcggtg 480

caaggcatca gcgactatgc caaccgtggc gccctggccg gtacctttgc cgccgacttc 540

ggcgcccatc agctgacggg ctcgctgtcc aatggcaact atgccgtgga tatcggcacc 600

gccaggattg atggtgcggc gatcagcggc aatcaaggca gtgccagcgt ggccggtgcc 660

accgtagcca gccagggtgc cgtgtccggc agcttcttcg gtgccaatgc agcagccctg 720

gccggtatcg tggccttcga tcaggcccat cagcatgaca ccgcctttgg cggcagcagg 780

caataa 786

<210> 792

<211> 261

<212> PRT

<213> F. aurantia SLP 1a

<400> 792

Met Asn His Lys Leu Asn Thr Arg Leu Gly Leu Leu Thr Leu Gly Leu
1 5 10 15

Leu Leu Ala Ala Gly Ala Gln Ala Gln Ser Ser Ile Ser Gly Val Thr
20 25 30

Ser Arg Pro Asn Glu Arg Asp Leu Ile Arg Val Gly Glu Ser Thr Val
35 40 45

Asn Gly Gly Pro His His Ser Gly Ala Pro Gly Ile Gly Val Gln Ser
50 55 60

Thr Asp Ala Ser Lys Leu Val Asp Phe Ala Gly Leu Val Arg Tyr Gly
65 70 75 80

Gln Thr Asp Ala Ala Gly Val Thr Thr Leu Ala Leu Glu Ser Pro Thr
85 90 95

Pro Pro Pro Gly Ala Pro Pro Ser His Asp Ser Leu Gly Ser Phe His

100 105 110

Phe Ala Lys Val Ser Asn Ala Asp Val Tyr Tyr Gly Glu Trp Ser Gln
115 120 125
Ser Ala Ser Ala Ser Asp Gly Thr His Thr Ser Tyr Tyr Val Gly Asp
130 135 140
His Ala Gly Thr Thr Val Pro Ala Thr Gly Thr Ala Thr Tyr Ala Val
145 150 155 160
Gln Gly Ile Ser Asp Tyr Ala Asn Arg Gly Ala Leu Ala Gly Thr Phe
165 170 175

Ala Ala Asp Phe Gly Ala His Gln Leu Thr Gly Ser Leu Ser Asn Gly
180 185 190
Asn Tyr Ala Val Asp Ile Gly Thr Ala Arg Ile Asp Gly Ala Ala Ile
195 200 205
Ser Gly Asn Gln Gly Ser Ala Ser Val Ala Gly Ala Thr Val Ala Ser
210 215 220
Gln Gly Ala Val Ser Gly Ser Phe Phe Gly Ala Asn Ala Ala Ala Leu
225 230 235 240

Ala Gly Ile Val Ala Phe Asp Gln Ala His Gln His Asp Thr Ala Phe
245 250 255
Gly Gly Ser Arg Gln
260

<210> 793
<211> 1512
<212> DNA
<213> G. anatis SLP 1a
<400> 793
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gcgtgtagct catcttccag tgattctcct gctaaaccac ttacagaagc acaattacag 120
caacagttag ataatgctaa aacaaaatta gccaaagtaa aacagcaatt atctgtagct 180
caagcagatg ttaatcaaca tcaacaatca ttaactcaaa cctcgcagca attaactcaa 240

actaaacagc aattaactaa agcgcaaagt gatgttaaac agcttgcgga tacagtgaat 300

gctaaaaagg cagaagtgag ccgtttaact caagaaatgg cagaattggt agaggtacag 360

aaattaggaa acagcaatga tattcagcaa aaactttcgc aaacccaaca agcattggtg 420

aaagcgaaca gttctttatc tgaagcccaa aaccaattaa ctaatgccga aaagcagtca 480

gcttccctga agaaaactgt tgctgagtta gagagtaaaa agaaatcgtt atctacgcaa 540

attacccaaa aacaggcaca gttaagccaa ttaaccgcac aagtaaaagc gacagaacaa 600

gcattagata aagaaaaatc tcaacttaaa cagctgactc cagataatcc tattgttgag 660

gcacacgctg aagagaatta tatgggagat agatataaat ggcgtagtat taaatttgac 720

gagatgatga atatagaaca aggatcaata tcacaaaata tagatacaaa aggcgtttat 780

tatacctcag agagaccatc cgttcttgtg cctgatccag taggtacagg tataaaagga 840

gacggtcgta attttgaaga tattgacttt tctcaatatc cagtaaattc gcaacagatt 900

caaagtaaag agcagtttgc acaaacatgt gcctcaagag tcgcttgtaa cccaacggtt 960

aatcgtaaaa ttgcggaagc acgttttgtt aaccaaacct actctactta ttttatacat 1020

actgctatga actataattc tagtgatgat aaatattatc ctagatctcc aaatatgggg 1080

tatatattta aagaattacc gcaggataat aatgtatgga ctagaccatc tggccaagag 1140

attgttactt atcgaggtaa agtgcttggt tctttcaagg aatatcaaaa atacactcca 1200

gcgcaaggtg atataacgtt aaaggctaat tttgcagaca atacggtgtc tggcacagta 1260

actaatcgta atggttataa gaataatcag gatatagtct taataaaaac gccaatatca 1320

gaacaaggaa caggtaggat aggtttttct ggtggaatac agtatggttc atatgatgct 1380

aataggggaa cagatggttc atatgagggt atttttgttg gcccgaaagc tgaagaagta 1440

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tcgtccaaat aa 1512

<210> 794

<211> 503

<212> PRT

<213> G. anatis SLP 1a

<400> 794

Met Lys Gln Lys Thr Phe Phe Gln Leu Ser Thr Ile Thr Leu Ala Cys

1 5 10 15

Ala Ala Leu Met Ala Cys Ser Ser Ser Ser Ser Asp Ser Pro Ala Lys

20 25 30

Pro Leu Thr Glu Ala Gln Leu Gln Gln Gln Leu Asp Asn Ala Lys Thr

35 40 45

Lys Leu Ala Lys Val Lys Gln Gln Leu Ser Val Ala Gln Ala Asp Val
50 55 60
Asn Gln His Gln Gln Ser Leu Thr Gln Thr Ser Gln Gln Leu Thr Gln
65 70 75 80
Thr Lys Gln Gln Leu Thr Lys Ala Gln Ser Asp Val Lys Gln Leu Ala
85 90 95
Asp Thr Val Asn Ala Lys Lys Ala Glu Val Ser Arg Leu Thr Gln Glu
100 105 110

Met Ala Glu Leu Val Glu Val Gln Lys Leu Gly Asn Ser Asn Asp Ile
115 120 125
Gln Gln Lys Leu Ser Gln Thr Gln Gln Ala Leu Val Lys Ala Asn Ser
130 135 140
Ser Leu Ser Glu Ala Gln Asn Gln Leu Thr Asn Ala Glu Lys Gln Ser
145 150 155 160
Ala Ser Leu Lys Lys Thr Val Ala Glu Leu Glu Ser Lys Lys Lys Ser
165 170 175

Leu Ser Thr Gln Ile Thr Gln Lys Gln Ala Gln Leu Ser Gln Leu Thr
180 185 190
Ala Gln Val Lys Ala Thr Glu Gln Ala Leu Asp Lys Glu Lys Ser Gln
195 200 205
Leu Lys Gln Leu Thr Pro Asp Asn Pro Ile Val Glu Ala His Ala Glu
210 215 220
Glu Asn Tyr Met Gly Asp Arg Tyr Lys Trp Arg Ser Ile Lys Phe Asp
225 230 235 240

Glu Met Met Asn Ile Glu Gln Gly Ser Ile Ser Gln Asn Ile Asp Thr
245 250 255
Lys Gly Val Tyr Tyr Thr Ser Glu Arg Pro Ser Val Leu Val Pro Asp
260 265 270
Pro Val Gly Thr Gly Ile Lys Gly Asp Gly Arg Asn Phe Glu Asp Ile
275 280 285

Asp Phe Ser Gln Tyr Pro Val Asn Ser Gln Gln Ile Gln Ser Lys Glu
290 295 300

Gln Phe Ala Gln Thr Cys Ala Ser Arg Val Ala Cys Asn Pro Thr Val
305 310 315 320
Asn Arg Lys Ile Ala Glu Ala Arg Phe Val Asn Gln Thr Tyr Ser Thr
325 330 335
Tyr Phe Ile His Thr Ala Met Asn Tyr Asn Ser Ser Asp Asp Lys Tyr
340 345 350
Tyr Pro Arg Ser Pro Asn Met Gly Tyr Ile Phe Lys Glu Leu Pro Gln
355 360 365

Asp Asn Asn Val Trp Thr Arg Pro Ser Gly Gln Glu Ile Val Thr Tyr
370 375 380
Arg Gly Lys Val Leu Gly Ser Phe Lys Glu Tyr Gln Lys Tyr Thr Pro
385 390 395 400
Ala Gln Gly Asp Ile Thr Leu Lys Ala Asn Phe Ala Asp Asn Thr Val
405 410 415
Ser Gly Thr Val Thr Asn Arg Asn Gly Tyr Lys Asn Asn Gln Asp Ile
420 425 430

Val Leu Ile Lys Thr Pro Ile Ser Glu Gln Gly Thr Gly Arg Ile Gly
435 440 445
Phe Ser Gly Gly Ile Gln Tyr Gly Ser Tyr Asp Ala Asn Arg Gly Thr
450 455 460
Asp Gly Ser Tyr Glu Gly Ile Phe Val Gly Pro Lys Ala Glu Glu Val
465 470 475 480
Val Gly Phe Ile Asp Asp Thr Tyr Arg Arg Gly Ile Asn Gly Gln Gln
485 490 495

Val Phe Gly Ala Ser Ser Lys
500

<210> 795
<211> 1527
<212> DNA

<213> G. anatis SLP 1b

<400> 795

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aatacagtgt ttgctgcaga acaaaatcag gaaaaatcac cttctcctac cctgtctaag 120

caacaactta ttgctgaaat taatcaatta aataaggaga tttcagcgaa agagaagaca 180

gcagtagcat taaataatca aataaaagat ttgcaaagta aaattactaa ggcaaaacag 240

gacttacaat caaaaatgaa ggagcgtgat gctttaacta atagtttaca agctagcagt 300

aaagaaaaag cacagctgga agaacaaatt aaatccttaa ctgctcagtt ggctgattta 360

caaaagaaaa ttgatccaaa agtagtggag ttagtagaac aaaaaaatac agcagaaact 420

cagttaaaaa aagtaaatgc tgatgtgagt agtaaaacaa accaattaaa tcaattaacc 480

gcccaaatta aacaatcgac aacgaaagtt gagcaactca aagcacaaat caaaccatta 540

gaaaaccaaa taagcggttt aaattctcaa gttaaacaac aacaagataa actcactaaa 600

attgcagcag agcgaaaagc agtaacaacg aagattgcag aatatactaa aaatcaagag 660

tgggtgaaaa agtatgaatt agatagcaat ggagtaagat ggcgtgatct ctattttgct 720

cgcagtaatt actcattctc aaaatcaaac tttgctaaat cttctggaaa ttcttttcca 780

cgtcatattg aggtaattac tgatgaatta ggaaatccta aactatctga atttactaat 840

actccaacct tacctctttc tcaatataaa gctaatccta gcaaaattaa tgaagttctg 900

attagttctg aacaaccaga gaataaagga aaagcggttg gaaaagtctt ttttgttaat 960

caaaatttct cttcttatgc tgcttggcag cctatattag acagtaaata tagtggagat 1020

aaaggggaaa gagttcaatc tttaggttat ggtttttctt accctaatta tgttgcccgt 1080

actgattatc aaaaaggcgt tgatattaaa tcgcaagcac aacagcgtta tgaatctgta 1140

aaagctaaaa cgccacagat tacatatcgt ggatatatgc tgaatgttgg tggtaaatct 1200

ggcgatatta cattaactgc cgatttagat aaaaacgtgg tgaatggcac agttacaaat 1260

agaatcgtaa atccagtaca ggatggtcga gatttattat taaaaaatgg tcaaatttct 1320

gtagatagag ataggggaat tatttttagt ggaaaccaag gaagatctgt tattcctgta 1380

ggaaataatc caaacaattc gccatttaaa tatgcttatt ttgagggtac ttttgctggt 1440

aaaaatatgg aagaagtagt aggtacaata cataatttac cgagagagag cgcttcagca 1500

tttggtggta cacaggtaac aaaatag 1527

<210> 796

<211> 508

<212> PRT

<213> G. anatis SLP 1b

<400> 796

Met Arg Lys Ser Ile Lys Phe Ser Leu Leu Ala Leu Cys Ile Ser Asn
1 5 10 15

Val Ile Ala Val Asn Thr Val Phe Ala Ala Glu Gln Asn Gln Glu Lys
20 25 30

Ser Pro Ser Pro Thr Leu Ser Lys Gln Gln Leu Ile Ala Glu Ile Asn
35 40 45

Gln Leu Asn Lys Glu Ile Ser Ala Lys Glu Lys Thr Ala Val Ala Leu
50 55 60

Asn Asn Gln Ile Lys Asp Leu Gln Ser Lys Ile Thr Lys Ala Lys Gln
65 70 75 80

Asp Leu Gln Ser Lys Met Lys Glu Arg Asp Ala Leu Thr Asn Ser Leu
85 90 95

Gln Ala Ser Ser Lys Glu Lys Ala Gln Leu Glu Glu Gln Ile Lys Ser
100 105 110

Leu Thr Ala Gln Leu Ala Asp Leu Gln Lys Lys Ile Asp Pro Lys Val
115 120 125

Val Glu Leu Val Glu Gln Lys Asn Thr Ala Glu Thr Gln Leu Lys Lys
130 135 140

Val Asn Ala Asp Val Ser Ser Lys Thr Asn Gln Leu Asn Gln Leu Thr
145 150 155 160

Ala Gln Ile Lys Gln Ser Thr Thr Lys Val Glu Gln Leu Lys Ala Gln
165 170 175

Ile Lys Pro Leu Glu Asn Gln Ile Ser Gly Leu Asn Ser Gln Val Lys
180 185 190

Gln Gln Gln Asp Lys Leu Thr Lys Ile Ala Ala Glu Arg Lys Ala Val
195 200 205

Thr Thr Lys Ile Ala Glu Tyr Thr Lys Asn Gln Glu Trp Val Lys Lys
210 215 220

Tyr Glu Leu Asp Ser Asn Gly Val Arg Trp Arg Asp Leu Tyr Phe Ala
225 230 235 240

Arg Ser Asn Tyr Ser Phe Ser Lys Ser Asn Phe Ala Lys Ser Ser Gly

245 250 255

Asn Ser Phe Pro Arg His Ile Glu Val Ile Thr Asp Glu Leu Gly Asn

260 265 270

Pro Lys Leu Ser Glu Phe Thr Asn Thr Pro Thr Leu Pro Leu Ser Gln

275 280 285

Tyr Lys Ala Asn Pro Ser Lys Ile Asn Glu Val Leu Ile Ser Ser Glu

290 295 300

Gln Pro Glu Asn Lys Gly Lys Ala Val Gly Lys Val Phe Phe Val Asn

305 310 315 320

Gln Asn Phe Ser Ser Tyr Ala Ala Trp Gln Pro Ile Leu Asp Ser Lys

325 330 335

Tyr Ser Gly Asp Lys Gly Glu Arg Val Gln Ser Leu Gly Tyr Gly Phe

340 345 350

Ser Tyr Pro Asn Tyr Val Ala Arg Thr Asp Tyr Gln Lys Gly Val Asp

355 360 365

Ile Lys Ser Gln Ala Gln Gln Arg Tyr Glu Ser Val Lys Ala Lys Thr

370 375 380

Pro Gln Ile Thr Tyr Arg Gly Tyr Met Leu Asn Val Gly Gly Lys Ser

385 390 395 400

Gly Asp Ile Thr Leu Thr Ala Asp Leu Asp Lys Asn Val Val Asn Gly

405 410 415

Thr Val Thr Asn Arg Ile Val Asn Pro Val Gln Asp Gly Arg Asp Leu

420 425 430

Leu Leu Lys Asn Gly Gln Ile Ser Val Asp Arg Asp Arg Gly Ile Ile

435 440 445

Phe Ser Gly Asn Gln Gly Arg Ser Val Ile Pro Val Gly Asn Asn Pro

450 455 460

Asn Asn Ser Pro Phe Lys Tyr Ala Tyr Phe Glu Gly Thr Phe Ala Gly

465 470 475 480

Lys Asn Met Glu Glu Val Val Gly Thr Ile His Asn Leu Pro Arg Glu

485 490 495

Ser Ala Ser Ala Phe Gly Gly Thr Gln Val Thr Lys

500 505

<210> 797

<211> 1293

<212> DNA

<213> G. anatis SLP 2a

<400> 797

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ccacaaattg tgcaaaatga aaaggcacta caaactcagt tagagaagtt gaaacagcaa 180

cagacaagaa cccaaaaaaa ccttgaagat gagcgtcaaa aattagctaa aaaagagaaa 240

gaattacaag atctcaaatc aaataatcaa atcgatcaag aaaaattatc ttccctacaa 300

aaagatctcg aacaaaacaa agcccgcgtt tccagcctag aaaaaacctt atcagaacaa 360

caaactgaag ccgctcaagc tcgccgtaat ttagaagctc aacttgccgc agccaatagt 420

gctttaaatg aaaaaagcaa agcactggaa gatctgcaaa ataaccagaa tgccgatcaa 480

gcagcactac aaaaagcgca aacagaatta aaagcaagcc aaagtgaagt ggaaaaactc 540

aatcgacaac ttgaggaatt aaaacaatta tatccacaag ctgaatttgc aatgggtagc 600

agggtaagaa ttgactctaa acactatagt aagttatctg aaagcctttc tggactatta 660

cctaatactc aaaagatgac tgatgagcaa gttacacgaa atattttatt tgctcccaaa 720

atagctggaa aattaatgcc acaagggcaa atccagcgtc atcaaatcac tcaaaaagta 780

aatggcaaag acgtggaaat ggattacttt agctatcact ataatgaaga tgatacttat 840

ttagcagaag tatggagcga taactcactt ggttacgtaa gtgttgttgc ctatggaggc 900

aaagccacac ctattgagaa attcgatgca ttcaaacagg ctcaagtagt gaaagagtat 960

gatgtcaaaa tggcaccggg aactggtcgt tattgggata gctacgacac aacatttaca 1020

gcagattttg gcaacgaaaa aatttcaggt attgcgaaaa aaatcgatct caacaatgca 1080

tttactgcta atgaagacat tattttccct gaacagccta ttttcgtaaa agatgatgct 1140

attcgctttg gtggcaacaa acctagtgta aaaataaagt tcaagcatat ggaagataca 1200

atgaaatatg aaggaatatt tatcggcgaa aatgctgaaa aaattgtagg gcgagtaggg 1260

ggaagtagcc tgattggtaa ggaaaaagaa taa 1293

<210> 798

<211> 430

<212> PRT

<213> G. anatis SLP 2a

<400> 798

Met His Leu Pro Ile Lys Ile Ser Ser Leu Ala Leu Phe Val Thr Phe
1 5 10 15

Ser Leu Thr Ala Cys Gly Ser Ser Gly Gly Gly Ser Gly Asn Ser Asn
20 25 30

Lys Asn Glu Thr Val Ala Asn Asn Pro Gln Ile Val Gln Asn Glu Lys
35 40 45

Ala Leu Gln Thr Gln Leu Glu Lys Leu Lys Gln Gln Gln Thr Arg Thr
50 55 60

Gln Lys Asn Leu Glu Asp Glu Arg Gln Lys Leu Ala Lys Lys Glu Lys
65 70 75 80

Glu Leu Gln Asp Leu Lys Ser Asn Asn Gln Ile Asp Gln Glu Lys Leu
85 90 95

Ser Ser Leu Gln Lys Asp Leu Glu Gln Asn Lys Ala Arg Val Ser Ser
100 105 110

Leu Glu Lys Thr Leu Ser Glu Gln Gln Thr Glu Ala Ala Gln Ala Arg
115 120 125

Arg Asn Leu Glu Ala Gln Leu Ala Ala Ala Asn Ser Ala Leu Asn Glu
130 135 140

Lys Ser Lys Ala Leu Glu Asp Leu Gln Asn Asn Gln Asn Ala Asp Gln
145 150 155 160

Ala Ala Leu Gln Lys Ala Gln Thr Glu Leu Lys Ala Ser Gln Ser Glu
165 170 175

Val Glu Lys Leu Asn Arg Gln Leu Glu Glu Leu Lys Gln Leu Tyr Pro
180 185 190

Gln Ala Glu Phe Ala Met Gly Ser Arg Val Arg Ile Asp Ser Lys His
195 200 205

Tyr Ser Lys Leu Ser Glu Ser Leu Ser Gly Leu Leu Pro Asn Thr Gln

210 215 220

Lys Met Thr Asp Glu Gln Val Thr Arg Asn Ile Leu Phe Ala Pro Lys
225 230 235 240
Ile Ala Gly Lys Leu Met Pro Gln Gly Gln Ile Gln Arg His Gln Ile
245 250 255
Thr Gln Lys Val Asn Gly Lys Asp Val Glu Met Asp Tyr Phe Ser Tyr
260 265 270
His Tyr Asn Glu Asp Asp Thr Tyr Leu Ala Glu Val Trp Ser Asp Asn
275 280 285

Ser Leu Gly Tyr Val Ser Val Val Ala Tyr Gly Gly Lys Ala Thr Pro
290 295 300
Ile Glu Lys Phe Asp Ala Phe Lys Gln Ala Gln Val Val Lys Glu Tyr
305 310 315 320
Asp Val Lys Met Ala Pro Gly Thr Gly Arg Tyr Trp Asp Ser Tyr Asp
325 330 335
Thr Thr Phe Thr Ala Asp Phe Gly Asn Glu Lys Ile Ser Gly Ile Ala
340 345 350

Lys Lys Ile Asp Leu Asn Asn Ala Phe Thr Ala Asn Glu Asp Ile Ile
355 360 365
Phe Pro Glu Gln Pro Ile Phe Val Lys Asp Asp Ala Ile Arg Phe Gly
370 375 380
Gly Asn Lys Pro Ser Val Lys Ile Lys Phe Lys His Met Glu Asp Thr
385 390 395 400
Met Lys Tyr Glu Gly Ile Phe Ile Gly Glu Asn Ala Glu Lys Ile Val
405 410 415

Gly Arg Val Gly Gly Ser Ser Leu Ile Gly Lys Glu Lys Glu
420 425 430

<210> 799
<211> 666
<212> DNA
<213> G. anatis SLP 3a

<400> 799

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tctcaaaacc aattgtatat acagcctgta atggctcttt atcctttagg cgaggatagt 120

gaagggatgt tggttggtga tagatatctt tataaacaac aatattctgt tgtttatgct 180

aaaaattggt tagcttcttt gcctgatggc gttttatcaa aaggagggcg tttctctgtt 240

aatggcattg gtaacttatt tgaagatgaa ccgacaattc tcccaagtga aggttcagca 300

acgtatcgag gaaaagcatt taatgcgaac aatatgggag atttaactta tcgtgttgat 360

tttgaacagc gaacgggtca aggggaaatc actaattttt caaataatat aggtcatatt 420

accttacatc aaggctcaat taatgatcag gaaattaaag ctgatgcatc aatggcaggc 480

ggaattacag gaaaatatac gctaggtttt tttgggccaa atggggaaga aattgctggt 540

gatctttata ttgatagctc gttagacaat agtattcctg ctaacggagg cacacgaaaa 600

aaatatgagg caaaaaatag aggcgtagca tttggtttag cagctcaaaa agaatcacaa 660

cagtag 666

<210> 800

<211> 221

<212> PRT

<213> G. anatis SLP 3a

<400> 800

Met Gly Ala Thr Leu Asp Asn Pro Trp Leu Met Glu Lys Pro Ile Asn

1 5 10 15

His Asp Gln Leu Ser Gln Asn Gln Leu Tyr Ile Gln Pro Val Met Ala

20 25 30

Leu Tyr Pro Leu Gly Glu Asp Ser Glu Gly Met Leu Val Gly Asp Arg

35 40 45

Tyr Leu Tyr Lys Gln Gln Tyr Ser Val Val Tyr Ala Lys Asn Trp Leu

50 55 60

Ala Ser Leu Pro Asp Gly Val Leu Ser Lys Gly Gly Arg Phe Ser Val

65 70 75 80

Asn Gly Ile Gly Asn Leu Phe Glu Asp Glu Pro Thr Ile Leu Pro Ser

85 90 95

Glu Gly Ser Ala Thr Tyr Arg Gly Lys Ala Phe Asn Ala Asn Asn Met

100 105 110

Gly Asp Leu Thr Tyr Arg Val Asp Phe Glu Gln Arg Thr Gly Gln Gly

115 120 125

Glu Ile Thr Asn Phe Ser Asn Asn Ile Gly His Ile Thr Leu His Gln

130 135 140

Gly Ser Ile Asn Asp Gln Glu Ile Lys Ala Asp Ala Ser Met Ala Gly

145 150 155 160

Gly Ile Thr Gly Lys Tyr Thr Leu Gly Phe Phe Gly Pro Asn Gly Glu

165 170 175

Glu Ile Ala Gly Asp Leu Tyr Ile Asp Ser Ser Leu Asp Asn Ser Ile

180 185 190

Pro Ala Asn Gly Gly Thr Arg Lys Lys Tyr Glu Ala Lys Asn Arg Gly

195 200 205

Val Ala Phe Gly Leu Ala Ala Gln Lys Glu Ser Gln Gln

210 215 220

<210> 801

<211> 2013

<212> DNA

<213> H. aegyptius SLP 1a

<400> 801

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tccttttttac taagtgcttg tagcggagga gggtcttttg atgtagatga cgtctctaat 180

ccctcctctt ctaaaccacg ttatcaagac gatacttcaa gttcaagaac aaaatctaat 240

ttgaaaaagt tgtccattcc ttctttaggg ggagggatga agttagtggc tcagaatctt 300

cgtagtaagg aagaacctag tctcttaaat gaaaatgact atatatcata tttttcctca 360

ctttctacga ttaaagctga tgttgaaaaa gaaaataaac gccatacaaa tccagttggc 420

tcaatagacg agcctagcgc aacacatcca accgaaaatc gtcatggaca aaaatatgta 480

tattcagggc tttattatat tcaatcgtgg aatttaaacg atcctaaaaa taacaagctt 540

tatttaggtt actatggata tgcgttttat tatggtaatc aaactgcaac aaacttgcca 600

gtaaacggtg tagctgaata caaaggaact tggaacttca tcactgcaac taaaaatggc 660

aagacttatg aattgttgag aaattctggc ggtcaagctt attctcgacg tagtgctact 720

ccagaagata ttgatttaga aaacggtgac gcgggcttaa caagtgaatt tagtgtagat 780

tttggtacga aaaagctcac tggagaactt tattataata aaaggaaaac agagcttaat 840

aaagatgaaa atagaaaaca taaactctat gatatagatg ccgatattta tagtaataga 900

ttcagaggta aagtaaagcc aacaacccca aaagattctg aagaacatcc ctttaccagc 960

gagggaacat tagaaggtgg tttttatggg cctaatgctg aagaactagg gggaaaattt 1020

ttagctggcg ataaccgagt ttttggggta tttagtgcca aagaaacgga agaaacaaaa 1080

aacaaagcgt tatccaaaga aaccttaatt gatggcaagc taattacttt ctctactaaa 1140

aaaaccgatg caaaaaccaa taaaacaacc aatacaacaa ccgatgtaaa aaccgatgaa 1200

aaaaacttta cgacagaaaa tatatcaagt tttggtgaag ctgattacct tttaattgat 1260

aattaccctg ttcctctttt acctgaagaa aaaactgatg acttcgtaac gagtaaacat 1320

cacgatattg gaaataaaag atataaagta gaagcatgtt gcaagaatct aagctatgtg 1380

aaatttggta tgtattatga agacccatta aatggagaaa atggcaaaga aaaacaaaaa 1440

gacaaagaag aaaaagacaa acaaacgaca acatctatca agacttatta tcaattctta 1500

ttaggtcacc gtactcccag ttctgaaatt cctacaatgg gaaacgtgaa atatcatggt 1560

agttggtttg gttatattgg tgatggtaca acatcttatt ccactacagg aaataaacaa 1620

caaaataaca atgctgtcgc cgagtttaat gtaaattttg ccgataaaaa gctaacaggc 1680

gaattaaaac gacacgataa tggaaatacc gtatttaaaa ttactgcaga ccttcaaagt 1740

ggtaagaatg acttcactgg tacagcaacc gcaacaaatt ttgtaataga tggtaacaat 1800

agtcaaacta aaagtacccc aattaatatt acaactgaag taaatggggc attttatgga 1860

ccgaacgcta cagaattagg cggttatttc acctataacg gaaattctac agctaaaaat 1920

tccccagccg taccttcacc acccaattca ccaaatgcaa gagctgcagt tgtctttggt 1980

gctaaaaaac aagtagaaac aaacaacaag tag 2013

<210> 802

<211> 670

<212> PRT

<213> H. aegyptius SLP 1a

<400> 802

Met Asn Leu Lys Asn Ser Asn Leu Thr Leu Leu Gln Lys Lys Asn Asn
1 5 10 15

Asn Ala Asn Tyr Tyr Gln Phe Cys Ile Ser Ile Asn Ser Met Lys Ser
20 25 30

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Val Pro Leu Ile Thr Gly Gly Leu Ser Phe Leu Leu Ser Ala Cys Ser
        35                  40                  45
Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro Ser Ser Ser
    50                  55                  60
Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Ser Arg Thr Lys Ser Asn
65                  70                  75                  80

Leu Lys Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly Met Lys Leu Val
                85                  90                  95
Ala Gln Asn Leu Arg Ser Lys Glu Glu Pro Ser Leu Leu Asn Glu Asn
            100                 105                 110
Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Lys Ala Asp Val
        115                 120                 125
Glu Lys Glu Asn Lys Arg His Thr Asn Pro Val Gly Ser Ile Asp Glu
    130                 135                 140

Pro Ser Ala Thr His Pro Thr Glu Asn Arg His Gly Gln Lys Tyr Val
145                 150                 155                 160
Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Asn Leu Asn Asp Pro Lys
                165                 170                 175
Asn Asn Lys Leu Tyr Leu Gly Tyr Tyr Gly Tyr Ala Phe Tyr Tyr Gly
            180                 185                 190
Asn Gln Thr Ala Thr Asn Leu Pro Val Asn Gly Val Ala Glu Tyr Lys
        195                 200                 205

Gly Thr Trp Asn Phe Ile Thr Ala Thr Lys Asn Gly Lys Thr Tyr Glu
    210                 215                 220
Leu Leu Arg Asn Ser Gly Gly Gln Ala Tyr Ser Arg Arg Ser Ala Thr
225                 230                 235                 240
Pro Glu Asp Ile Asp Leu Glu Asn Gly Asp Ala Gly Leu Thr Ser Glu
                245                 250                 255
Phe Ser Val Asp Phe Gly Thr Lys Lys Leu Thr Gly Glu Leu Tyr Tyr
            260                 265                 270

Asn Lys Arg Lys Thr Glu Leu Asn Lys Asp Glu Asn Arg Lys His Lys
```

275 280 285

Leu Tyr Asp Ile Asp Ala Asp Ile Tyr Ser Asn Arg Phe Arg Gly Lys

290 295 300

Val Lys Pro Thr Thr Pro Lys Asp Ser Glu Glu His Pro Phe Thr Ser

305 310 315 320

Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu

325 330 335

Gly Gly Lys Phe Leu Ala Gly Asp Asn Arg Val Phe Gly Val Phe Ser

340 345 350

Ala Lys Glu Thr Glu Glu Thr Lys Asn Lys Ala Leu Ser Lys Glu Thr

355 360 365

Leu Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys Lys Thr Asp Ala

370 375 380

Lys Thr Asn Lys Thr Thr Asn Thr Thr Thr Asp Val Lys Thr Asp Glu

385 390 395 400

Lys Asn Phe Thr Thr Glu Asn Ile Ser Ser Phe Gly Glu Ala Asp Tyr

405 410 415

Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Leu Pro Glu Glu Lys Thr

420 425 430

Asp Asp Phe Val Thr Ser Lys His His Asp Ile Gly Asn Lys Arg Tyr

435 440 445

Lys Val Glu Ala Cys Cys Lys Asn Leu Ser Tyr Val Lys Phe Gly Met

450 455 460

Tyr Tyr Glu Asp Pro Leu Asn Gly Glu Asn Gly Lys Glu Lys Gln Lys

465 470 475 480

Asp Lys Glu Glu Lys Asp Lys Gln Thr Thr Thr Ser Ile Lys Thr Tyr

485 490 495

Tyr Gln Phe Leu Leu Gly His Arg Thr Pro Ser Ser Glu Ile Pro Thr

500 505 510

Met Gly Asn Val Lys Tyr His Gly Ser Trp Phe Gly Tyr Ile Gly Asp

515 520 525

Gly Thr Thr Ser Tyr Ser Thr Thr Gly Asn Lys Gln Gln Asn Asn Asn
530 535 540

Ala Val Ala Glu Phe Asn Val Asn Phe Ala Asp Lys Lys Leu Thr Gly
545 550 555 560

Glu Leu Lys Arg His Asp Asn Gly Asn Thr Val Phe Lys Ile Thr Ala
565 570 575

Asp Leu Gln Ser Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Thr
580 585 590

Asn Phe Val Ile Asp Gly Asn Asn Ser Gln Thr Lys Ser Thr Pro Ile
595 600 605

Asn Ile Thr Thr Glu Val Asn Gly Ala Phe Tyr Gly Pro Asn Ala Thr
610 615 620

Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Ser Thr Ala Lys Asn
625 630 635 640

Ser Pro Ala Val Pro Ser Pro Pro Asn Ser Pro Asn Ala Arg Ala Ala
645 650 655

Val Val Phe Gly Ala Lys Lys Gln Val Glu Thr Asn Asn Lys
660 665 670

<210> 803

<211> 891

<212> DNA

<213> H. influenzae SLP 1a

<400> 803

atgaaactta atctttcgaa attcagctta actattctta caacggtaat gctggcttcc 60

tgtggaagtg gcggcggtga taatactcaa ttagtaagtc caccaaaacc agctgagcaa 120

tccaaaccgg ctgagcaatc gaaaccagct gatcaatcaa aatcagttga acagtcaatt 180

cttggaatgc ctgaacgctt gccaactaat accggtttag cattttctat aaaaacagaa 240

gatgagggaa atattaatac aattaagaat gaacaggagc tcattgctac taataatttt 300

gctagtatca atgttgatgg caaaaatatc cctattgatt ttaaattaga accaagtcaa 360

ggttggacaa aagaaggtgc gtttatcgaa gagctgaatt tagcaccaca tatttgttgt 420

ggaaaataca cagatgtccg ctttggtgca attgcaagtc attcatttgg gcaagatgat 480

attctttttt ataatggaaa tccttcaaac agtgtgccag aatcaggaga agttacttac 540

aagggtgaaa gtataatggc ggataaaggc aatagcgtat ttggtggtta tagaaaaggc 600

acctctgaat ttaaggttaa ttttggtgac aaaaaattat caggaagttt aaacgttgat 660

agtcctaaat atgatgttga atctggagaa agtaaattta ataaagtcaa agttgacatt 720

aatgccgata tttcaggcaa taaattttac ggcagtgcaa aatcttcctc ttttgtttca 780

gaagctgtat cagagggcaa gttttatggg gatggagcta aagaactagg tggaatggta 840

aaagctaaag ataattcttg ggttggagcc tacggtgcaa aagcacagta a 891

<210> 804

<211> 296

<212> PRT

<213> H. influenzae SLP 1a

<400> 804

Met Lys Leu Asn Leu Ser Lys Phe Ser Leu Thr Ile Leu Thr Thr Val
1 5 10 15

Met Leu Ala Ser Cys Gly Ser Gly Gly Gly Asp Asn Thr Gln Leu Val
20 25 30

Ser Pro Pro Lys Pro Ala Glu Gln Ser Lys Pro Ala Glu Gln Ser Lys
35 40 45

Pro Ala Asp Gln Ser Lys Ser Val Glu Gln Ser Ile Leu Gly Met Pro
50 55 60

Glu Arg Leu Pro Thr Asn Thr Gly Leu Ala Phe Ser Ile Lys Thr Glu
65 70 75 80

Asp Glu Gly Asn Ile Asn Thr Ile Lys Asn Glu Gln Glu Leu Ile Ala
85 90 95

Thr Asn Asn Phe Ala Ser Ile Asn Val Asp Gly Lys Asn Ile Pro Ile
100 105 110

Asp Phe Lys Leu Glu Pro Ser Gln Gly Trp Thr Lys Glu Gly Ala Phe
115 120 125

Ile Glu Glu Leu Asn Leu Ala Pro His Ile Cys Cys Gly Lys Tyr Thr
130 135 140

Asp Val Arg Phe Gly Ala Ile Ala Ser His Ser Phe Gly Gln Asp Asp
145 150 155 160

Ile Leu Phe Tyr Asn Gly Asn Pro Ser Asn Ser Val Pro Glu Ser Gly
165 170 175
Glu Val Thr Tyr Lys Gly Glu Ser Ile Met Ala Asp Lys Gly Asn Ser
180 185 190
Val Phe Gly Gly Tyr Arg Lys Gly Thr Ser Glu Phe Lys Val Asn Phe
195 200 205
Gly Asp Lys Lys Leu Ser Gly Ser Leu Asn Val Asp Ser Pro Lys Tyr
210 215 220

Asp Val Glu Ser Gly Glu Ser Lys Phe Asn Lys Val Lys Val Asp Ile
225 230 235 240
Asn Ala Asp Ile Ser Gly Asn Lys Phe Tyr Gly Ser Ala Lys Ser Ser
245 250 255
Ser Phe Val Ser Glu Ala Val Ser Glu Gly Lys Phe Tyr Gly Asp Gly
260 265 270
Ala Lys Glu Leu Gly Gly Met Val Lys Ala Lys Asp Asn Ser Trp Val
275 280 285

Gly Ala Tyr Gly Ala Lys Ala Gln
290 295

<210> 805
<211> 1686
<212> DNA
<213> H. influenzae SLP 2a (TbpB)
<400> 805

atgatatttt cctcacgttc tacgattgaa gaggatgtta aaaataacaa tcaaaacggg 60
gagcacccta ttgactcaat agtcgatcct agagcaccaa attcaaacga aaatcgtcat 120
ggacaaaaat atgtatattc agggctttat tatattcaat cgtggagtct aagagattta 180
ccaaataaaa agttttattc aggttactat ggatatgcgt attactttgg caatacaact 240
gcctctgcat tacctgtagg tggcgtagca acgtataaag gaacttggag cttcatcacc 300

gcagctgaaa atggcaagaa ttatgaattg ttaagaaatt ctggtggcgg tcaagcttat 360
tctcgacgta gtgctactcc agaagatatt gatttagatc gtaagacggg cttaacaagt 420
gaatttactg tcaattttgg tacaaaaaag ctcactggag gactttatta taatttacgt 480
gaaacagatg ctaataaatc acaaaataga acacataaac tctacgatct agaagctgat 540

gtacatagca accgattcag gggtaaagta aagccaacca aaaaagagtc ttctgaagaa 600

catcccttta ccagcgaggg aacattagaa ggtggttttt acgggcctga gggtcaagaa 660

ttaggaggaa agtttttagc tcacgacaaa aaagtttttg gggtatttag tgccaaagaa 720

cagcaagaaa cgtcagaaaa caaaaaatta cccaaagaaa ccttaattga tggcaagcta 780

actactttta aaacaaccaa tgcaacagcc aatgcaacaa ccgatgcaac aaccagtaca 840

acagccagta caaaaaccga tacaacaacc aatgcaacag ccaatacaga aaactttacg 900

acaaaagata taccaagttt tggtgaagct gattatcttt taattgataa ttaccctgtt 960

cctcttttcc ctgagagtgg tgatttcata agtagtaagc accatactgt aggaaagaaa 1020

acctatcaag tagaagcatg ttgcagtaat ctaagctatg taaaatttgg tatgtattat 1080

gaagccccac ctaaagaaga agaaaaagaa aaagacaaag acaaagacaa agacaaagaa 1140

aaagaaaaac aagcgacaac atctatcaag acttattatc aattcttatt aggtctccgt 1200

actcccagtt ctgaaatacc taaagaagga agtgcaaaat atcatggtaa ttggtttggt 1260

tatattagtg atggcgagac atcttactcc gccagtggtg ataaggaacg cagtaaaaat 1320

gctgtcgccg agtttaatgt aaattttgcc gagaaaacat taacaggcga attaaaacga 1380

cacgatactc aaaatcccgt atttaaaatt aatgcaacct ttcaaagtgg taagaatgac 1440

ttcactggta cagcaaccgc aaaagattta gcaatagatg gtaaaaatac acaaggcaca 1500

tctaaagtca atttcacggc aacagtaaac ggggcatttt atggtccgca cgctacagaa 1560

ttaggcggtt atttcaccta taacggaaac aatcctacag ataaaaattc atcatccaat 1620

tcagaaaagg caagagctgc cgttgtgttt ggagctaaaa aacaacaagt agaaacaacc 1680

aagtaa 1686

<210> 806

<211> 561

<212> PRT

<213> H. influenzae SLP 2a (TbpB)

<400> 806

Met Ile Phe Ser Ser Arg Ser Thr Ile Glu Glu Asp Val Lys Asn Asn

1 5 10 15

Asn Gln Asn Gly Glu His Pro Ile Asp Ser Ile Val Asp Pro Arg Ala

20 25 30

Pro Asn Ser Asn Glu Asn Arg His Gly Gln Lys Tyr Val Tyr Ser Gly

35 40 45

Leu Tyr Tyr Ile Gln Ser Trp Ser Leu Arg Asp Leu Pro Asn Lys Lys
50 55 60
Phe Tyr Ser Gly Tyr Tyr Gly Tyr Ala Tyr Tyr Phe Gly Asn Thr Thr
65 70 75 80
Ala Ser Ala Leu Pro Val Gly Gly Val Ala Thr Tyr Lys Gly Thr Trp

85 90 95
Ser Phe Ile Thr Ala Ala Glu Asn Gly Lys Asn Tyr Glu Leu Leu Arg
100 105 110
Asn Ser Gly Gly Gly Gln Ala Tyr Ser Arg Arg Ser Ala Thr Pro Glu
115 120 125
Asp Ile Asp Leu Asp Arg Lys Thr Gly Leu Thr Ser Glu Phe Thr Val
130 135 140
Asn Phe Gly Thr Lys Lys Leu Thr Gly Gly Leu Tyr Tyr Asn Leu Arg

145 150 155 160
Glu Thr Asp Ala Asn Lys Ser Gln Asn Arg Thr His Lys Leu Tyr Asp
165 170 175
Leu Glu Ala Asp Val His Ser Asn Arg Phe Arg Gly Lys Val Lys Pro
180 185 190
Thr Lys Lys Glu Ser Ser Glu Glu His Pro Phe Thr Ser Glu Gly Thr
195 200 205
Leu Glu Gly Gly Phe Tyr Gly Pro Glu Gly Gln Glu Leu Gly Gly Lys

210 215 220
Phe Leu Ala His Asp Lys Lys Val Phe Gly Val Phe Ser Ala Lys Glu
225 230 235 240
Gln Gln Glu Thr Ser Glu Asn Lys Lys Leu Pro Lys Glu Thr Leu Ile
245 250 255
Asp Gly Lys Leu Thr Thr Phe Lys Thr Thr Asn Ala Thr Ala Asn Ala
260 265 270
Thr Thr Asp Ala Thr Thr Ser Thr Thr Ala Ser Thr Lys Thr Asp Thr

275 280 285
Thr Thr Asn Ala Thr Ala Asn Thr Glu Asn Phe Thr Thr Lys Asp Ile

290 295 300

Pro Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Asn Tyr Pro Val

305 310 315 320

Pro Leu Phe Pro Glu Ser Gly Asp Phe Ile Ser Ser Lys His His Thr

325 330 335

Val Gly Lys Lys Thr Tyr Gln Val Glu Ala Cys Cys Ser Asn Leu Ser

340 345 350

Tyr Val Lys Phe Gly Met Tyr Tyr Glu Ala Pro Pro Lys Glu Glu Glu

355 360 365

Lys Glu Lys Asp Lys Asp Lys Asp Lys Asp Lys Glu Lys Glu Lys Gln

370 375 380

Ala Thr Thr Ser Ile Lys Thr Tyr Tyr Gln Phe Leu Leu Gly Leu Arg

385 390 395 400

Thr Pro Ser Ser Glu Ile Pro Lys Glu Gly Ser Ala Lys Tyr His Gly

405 410 415

Asn Trp Phe Gly Tyr Ile Ser Asp Gly Glu Thr Ser Tyr Ser Ala Ser

420 425 430

Gly Asp Lys Glu Arg Ser Lys Asn Ala Val Ala Glu Phe Asn Val Asn

435 440 445

Phe Ala Glu Lys Thr Leu Thr Gly Glu Leu Lys Arg His Asp Thr Gln

450 455 460

Asn Pro Val Phe Lys Ile Asn Ala Thr Phe Gln Ser Gly Lys Asn Asp

465 470 475 480

Phe Thr Gly Thr Ala Thr Ala Lys Asp Leu Ala Ile Asp Gly Lys Asn

485 490 495

Thr Gln Gly Thr Ser Lys Val Asn Phe Thr Ala Thr Val Asn Gly Ala

500 505 510

Phe Tyr Gly Pro His Ala Thr Glu Leu Gly Gly Tyr Phe Thr Tyr Asn

515 520 525

Gly Asn Asn Pro Thr Asp Lys Asn Ser Ser Ser Asn Ser Glu Lys Ala

530 535 540

Arg Ala Ala Val Val Phe Gly Ala Lys Lys Gln Gln Val Glu Thr Thr

545 550 555 560

Lys

<210> 807

<211> 738

<212> DNA

<213> H. influenzae SLP 3a

<400> 807

atgaaaataa catttactag atcattatta gcaacagccg taatggtggg attaactgct 60

tgtggttcag gtggtggtaa tggtatgaat aacaatacaa ctagtcaagt tacaggaaaa 120

acgggcgcaa tgtatacagt ttcattaact aatgataata aaatagggac ggttacgaaa 180

actccattaa ataattctga tattaattct cttaatttag atagcgcatc aacacaacgt 240

attaatgaag ctatgaataa aatttcagag gaatttaaat caaaaacagg attagatgtt 300

gttactggag ctgcaattgt ttctaatgga gaaaagtttc atattatcta taacggtaat 360

ccaacagaaa caatgccagt acaaggttca atccattata aaggttctgc cgttttaggg 420

ggatggtctg cggatgctcc actctcaatt gaaaaaggaa cctctcaatt tgatgtgaat 480

tttgctgata acaccttaac tggaacatta aatgttccga atttttctct tgtttccata 540

tcagctagcg tgtcaggaaa cagtttttct ggtcgagcaa catcccctga tgctcctgat 600

ggtgctgtcg tagagggaaa attttatgga aaagatgctc ttggtttatc aggaatgtta 660

aaaacaaata catttacaga taattttggt ggagcgggga tctttagtgc tattgatgaa 720

acgaaaataa cacaataa 738

<210> 808

<211> 245

<212> PRT

<213> H. influenzae SLP 3a

<400> 808

Met Lys Ile Thr Phe Thr Arg Ser Leu Leu Ala Thr Ala Val Met Val

1 5 10 15

Gly Leu Thr Ala Cys Gly Ser Gly Gly Gly Asn Gly Met Asn Asn Asn

20 25 30

Thr Thr Ser Gln Val Thr Gly Lys Thr Gly Ala Met Tyr Thr Val Ser

35 40 45

Leu Thr Asn Asp Asn Lys Ile Gly Thr Val Thr Lys Thr Pro Leu Asn

50 55 60

Asn Ser Asp Ile Asn Ser Leu Asn Leu Asp Ser Ala Ser Thr Gln Arg

65 70 75 80

Ile Asn Glu Ala Met Asn Lys Ile Ser Glu Glu Phe Lys Ser Lys Thr

85 90 95

Gly Leu Asp Val Val Thr Gly Ala Ala Ile Val Ser Asn Gly Glu Lys

100 105 110

Phe His Ile Ile Tyr Asn Gly Asn Pro Thr Glu Thr Met Pro Val Gln

115 120 125

Gly Ser Ile His Tyr Lys Gly Ser Ala Val Leu Gly Gly Trp Ser Ala

130 135 140

Asp Ala Pro Leu Ser Ile Glu Lys Gly Thr Ser Gln Phe Asp Val Asn

145 150 155 160

Phe Ala Asp Asn Thr Leu Thr Gly Thr Leu Asn Val Pro Asn Phe Ser

165 170 175

Leu Val Ser Ile Ser Ala Ser Val Ser Gly Asn Ser Phe Ser Gly Arg

180 185 190

Ala Thr Ser Pro Asp Ala Pro Asp Gly Ala Val Val Glu Gly Lys Phe

195 200 205

Tyr Gly Lys Asp Ala Leu Gly Leu Ser Gly Met Leu Lys Thr Asn Thr

210 215 220

Phe Thr Asp Asn Phe Gly Gly Ala Gly Ile Phe Ser Ala Ile Asp Glu

225 230 235 240

Thr Lys Ile Thr Gln

245

<210> 809

<211> 570

<212> DNA

<213> H. parahaemolyticus SLP 2a

<400> 809

atgtttaaaa aatcgtttat tttcgcatta ccattcatag taaccgcttg ctcttccaac 60

aatcaaacag aagaggcatt tccaggtcaa tttgctgatg cagattatgt cctttctgac 120

caagatgcac aaaaatgggt ggcagaaagc gaacaggctc gtcaatgtat ttatccaaat 180

ttgacccgta ttcaacaaaa tcatttttca aaagaagata gctatatcca tgcccaatat 240

gttttcttct acccgcttga aaaagtcatt ggcgagcagt atgtaaatat tttgcaggca 300

gacgaaaaat ccatgggcta tgcacaatat caattcaaaa aatttaaaga taagcccacc 360

gagatccaac ctctaacagc ccagcaatgc gaaacactgc gagcacaagc ccgcgatgat 420

ttagcggtcg ttaaagggca atacaaaagt ggcatggtgg aagaaacgaa aaccgcaagc 480

gacgacaaga aaaacagcga tggcgttgcc accaaccaaa ataaattctt ctttgatatt 540

atcaaatggg gatcggcgtt gttgctctaa 570

<210> 810

<211> 189

<212> PRT

<213> H. parahaemolyticus SLP 2a

<400> 810

Met Phe Lys Lys Ser Phe Ile Phe Ala Leu Pro Phe Ile Val Thr Ala
1 5 10 15

Cys Ser Ser Asn Asn Gln Thr Glu Glu Ala Phe Pro Gly Gln Phe Ala
20 25 30

Asp Ala Asp Tyr Val Leu Ser Asp Gln Asp Ala Gln Lys Trp Val Ala
35 40 45

Glu Ser Glu Gln Ala Arg Gln Cys Ile Tyr Pro Asn Leu Thr Arg Ile
50 55 60

Gln Gln Asn His Phe Ser Lys Glu Asp Ser Tyr Ile His Ala Gln Tyr
65 70 75 80

Val Phe Phe Tyr Pro Leu Glu Lys Val Ile Gly Glu Gln Tyr Val Asn
85 90 95

Ile Leu Gln Ala Asp Glu Lys Ser Met Gly Tyr Ala Gln Tyr Gln Phe
100 105 110

Lys Lys Phe Lys Asp Lys Pro Thr Glu Ile Gln Pro Leu Thr Ala Gln
115 120 125

Gln Cys Glu Thr Leu Arg Ala Gln Ala Arg Asp Asp Leu Ala Val Val
130 135 140

Lys Gly Gln Tyr Lys Ser Gly Met Val Glu Glu Thr Lys Thr Ala Ser
145 150 155 160

Asp Asp Lys Lys Asn Ser Asp Gly Val Ala Thr Asn Gln Asn Lys Phe
165 170 175

Phe Phe Asp Ile Ile Lys Trp Gly Ser Ala Leu Leu Leu
180 185

<210> 811

<211> 876

<212> DNA

<213> H. parahaemolyticus SLP 3a

<400> 811

ttattgttta tataaagttt gagagccgat tatttctata tttttatcag atgaagatac 60

atcatatttg aagtatatat catctccatc atatcgatta gtttcacctc catatgaacc 120

tgataagttt tctgttttta acgtttctgt caggatttta cccgttgcct cactattaaa 180

tgctacgcga ttatcatttt tatagagagc agcctcttta aattcaagtt cagcttgagc 240

ttttttcaca tcatctgatg aataaaaatt aaagactgca gaaccgttga tttttttatt 300

atcaaaatca gcatttaaga taacataact ttttccatcg acttttgaag aaatattgtt 360

accattaatt tttgcactag catctatatt ctgagaaaga taggttgctt tgccttttaa 420

attagagcca taaccagata ttgaagactc ttcaaatttt ggtactgcag gcaatttatc 480

ccaaaccact tcttttggcg tattttcagt tgtaggagtt acaacaggaa ctgtaattgt 540

ttctgaaggt ttagcaggtt caactgtagg tgttgttgct gtttccgaag gtttagcggg 600

ttcaacgttt ggagtcgttg ctgtttccac tggtttagcg ggttcaacgt ttggagtcgt 660

tgctgtttcc gtaggtttag caggttcaac ttttggggtt gttggttgtt ctctttgaac 720

ttcagaaact ttttcgccat taaatacacc atttgatgta ttcgttgatg aattagtggc 780

tccattatta ccgctattac caccacctga accacaagca gttaatccca ccattacggc 840

tgttgctaat aatgatctag taaatgtcat tgtcat 876

<210> 812

<211> 291

<212> PRT

<213> H. parahaemolyticus SLP 3a

<400> 812

Met Thr Met Thr Phe Thr Arg Ser Leu Leu Ala Thr Ala Val Met Val
1 5 10 15
Gly Leu Thr Ala Cys Gly Ser Gly Gly Gly Asn Ser Gly Asn Asn Gly
20 25 30
Ala Thr Asn Ser Ser Thr Asn Thr Ser Asn Gly Val Phe Asn Gly Glu
35 40 45
Lys Val Ser Glu Val Gln Arg Glu Gln Pro Thr Thr Pro Lys Val Glu
50 55 60
Pro Ala Lys Pro Thr Glu Thr Ala Thr Thr Pro Asn Val Glu Pro Ala
65 70 75 80
Lys Pro Val Glu Thr Ala Thr Thr Pro Asn Val Glu Pro Ala Lys Pro
85 90 95
Ser Glu Thr Ala Thr Thr Pro Thr Val Glu Pro Ala Lys Pro Ser Glu
100 105 110
Thr Ile Thr Val Pro Val Val Thr Pro Thr Thr Glu Asn Thr Pro Lys
115 120 125
Glu Val Val Trp Asp Lys Leu Pro Ala Val Pro Lys Phe Glu Glu Ser
130 135 140
Ser Ile Ser Gly Tyr Gly Ser Asn Leu Lys Gly Lys Ala Thr Tyr Leu
145 150 155 160
Ser Gln Asn Ile Asp Ala Ser Ala Lys Ile Asn Gly Asn Asn Ile Ser
165 170 175
Ser Lys Val Asp Gly Lys Ser Tyr Val Ile Leu Asn Ala Asp Phe Asp
180 185 190
Asn Lys Lys Ile Asn Gly Ser Ala Val Phe Asn Phe Tyr Ser Ser Asp
195 200 205
Asp Val Lys Lys Ala Gln Ala Glu Leu Glu Phe Lys Glu Ala Ala Leu
210 215 220
Tyr Lys Asn Asp Asn Arg Val Ala Phe Asn Ser Glu Ala Thr Gly Lys
225 230 235 240

Ile Leu Thr Glu Thr Leu Lys Thr Glu Asn Leu Ser Gly Ser Tyr Gly
245 250 255

Gly Glu Thr Asn Arg Tyr Asp Gly Asp Asp Ile Tyr Phe Lys Tyr Asp
260 265 270

Val Ser Ser Ser Asp Lys Asn Ile Glu Ile Ile Gly Ser Gln Thr Leu
275 280 285

Tyr Lys Gln
290

<210> 813

<211> 948

<212> DNA

<213> H. parainfluenzae SLP 1a

<400> 813

atgtcttctt taaatcatat ttttaaattt ggtacaacag cattagctgc tttagtatta 60

tctgcgtgtg gtagcagcgg cggtggtagt gatgactcaa atgtttcagt tccaaccaat 120

aaaactgagc aaactcagcc aagcactact gtcaataata cgactcagca accaagtact 180

actgccaata atacgactca gcaatcaagt actactacgt ctacaaataa tcagacaaca 240

ccaagccaat ctactccagc tgaaaatgta gctcaaccat caacccctaa tactcaaagt 300

ggtaatacta atcgagcact cacagataaa catgttggtt tcatcatacc taaaaaaggc 360

ggaactattc aaaccgcatc catttctggc aatccaaatc tttatgtgct agatgttgaa 420

ggtaaaagta ttaatataat tcctgccggg atgggggggtg gaaaggttct caaaatcacg 480

gccaacaata ttacccgcat agttaacggt tcattatata aaaatgtacg ttggggatta 540

attacagagg atggcttaaa taattattac ttagtctctt acggtatcaa tcctacaacc 600

aacatgccaa ctagcggtag cgctacctat gtaggacaag gtgtacacgg ttatgcagat 660

agtggttcag ctattgatac gtatcgctta agtaacgcaa aatttaatgt aaattttgct 720

gataaatcat ttgaaggctc tattactcca gatgatggaa aagcatttgg caatatcaac 780

gcggttaaac tttctgcgaa aattgatggt aaccaattta acggtaaaac tgctgaaggt 840

acagaagctg tcggtcgttt ctacggaaat aacgctagtg agttagctgg tagctatgta 900

aatgaaaaag cctcttacct tggggtattc ggcgctcaaa aacaataa 948

<210> 814

<211> 315

<212> PRT

<213> H. parainfluenzae SLP 1a

<400> 814

Met Ser Ser Leu Asn His Ile Phe Lys Phe Gly Thr Thr Ala Leu Ala
1 5 10 15

Ala Leu Val Leu Ser Ala Cys Gly Ser Ser Gly Gly Gly Ser Asp Asp

20 25 30

Ser Asn Val Ser Val Pro Thr Asn Lys Thr Glu Gln Thr Gln Pro Ser
35 40 45

Thr Thr Val Asn Asn Thr Thr Gln Gln Pro Ser Thr Thr Ala Asn Asn
50 55 60

Thr Thr Gln Gln Ser Ser Thr Thr Thr Ser Thr Asn Asn Gln Thr Thr
65 70 75 80

Pro Ser Gln Ser Thr Pro Ala Glu Asn Val Ala Gln Pro Ser Thr Pro

85 90 95

Asn Thr Gln Ser Gly Asn Thr Asn Arg Ala Leu Thr Asp Lys His Val
100 105 110

Gly Phe Ile Ile Pro Lys Lys Gly Gly Thr Ile Gln Thr Ala Ser Ile
115 120 125

Ser Gly Asn Pro Asn Leu Tyr Val Leu Asp Val Glu Gly Lys Ser Ile
130 135 140

Asn Ile Ile Pro Ala Gly Met Gly Gly Gly Lys Val Leu Lys Ile Thr

145 150 155 160

Ala Asn Asn Ile Thr Arg Ile Val Asn Gly Ser Leu Tyr Lys Asn Val
165 170 175

Arg Trp Gly Leu Ile Thr Glu Asp Gly Leu Asn Asn Tyr Tyr Leu Val
180 185 190

Ser Tyr Gly Ile Asn Pro Thr Thr Asn Met Pro Thr Ser Gly Ser Ala
195 200 205

Thr Tyr Val Gly Gln Gly Val His Gly Tyr Ala Asp Ser Gly Ser Ala

210 215 220

Ile Asp Thr Tyr Arg Leu Ser Asn Ala Lys Phe Asn Val Asn Phe Ala

225 230 235 240

Asp Lys Ser Phe Glu Gly Ser Ile Thr Pro Asp Asp Gly Lys Ala Phe

245 250 255

Gly Asn Ile Asn Ala Val Lys Leu Ser Ala Lys Ile Asp Gly Asn Gln

260 265 270

Phe Asn Gly Lys Thr Ala Glu Gly Thr Glu Ala Val Gly Arg Phe Tyr

275 280 285

Gly Asn Asn Ala Ser Glu Leu Ala Gly Ser Tyr Val Asn Glu Lys Ala

290 295 300

Ser Tyr Leu Gly Val Phe Gly Ala Gln Lys Gln

305 310 315

<210> 815

<211> 1548

<212> DNA

<213> H. parainfluenzae SLP 2a

<400> 815

atgaaaaaca acaaacttgt taaatttagt ctaacattaa tctgttcagc tgtattagca 60

gcttgtggtt caagtggcgg tagcgataat tcagccgctc aacaacaagc tcaacaacaa 120

gctcaacaac aagcaaaagc agcagctgag aaagcagcag cagaaaaagc agcagcagaa 180

aaagcagcag cagaaaaagc agcagcagaa aaagcagcag cagaaaaagc agcagcagaa 240

aaagcagctc aaacaacttc tagcgagtct aacccaggtt acttactttc taaaaagaac 300

gcatctgatt tcatcgtaaa taaaaatggt gataaagttg actctactca atctgctcca 360

ttgccaatga ctgttcaaaa tttagagcct cgtctagata ctatcgttgt agcttaccca 420

cacgaaggtg ctgagtctaa agcgattgct tatattgaag atttccaatt tgttggtaat 480

gacaaacaag atggtaaatt tactttaact ggcatttata acgactcaat agatcgtagt 540

actactggtg gcactccacg tccagaaagc cgtactaaaa ctgatacaca aggtacagag 600

tctggtgctg ctttagttta cgaaaaagat cgtattgctt actttgaccg tgcagacaga 660

aatgctgagg gtaaagatac attagctgaa gtttacggtt taagaaccaa ttcctatgaa 720

gatggtaaag aattaaaaga tactgatgca aataacctac cattagtaaa agaaactaat 780

aaattagctg ctcaacaaga tggtcaatta cgttttgttc aatatggtcg tgtaacaact 840

aaattacatg accttactga aaaagatcta aacgtataca aaaaaggtct attggacgat 900

aaaaacagta acgtaacaag taacgttatt ggttttgcta actatggtga agcaggtact 960

gaaaactctt acttctatcg tggtttaaac aatactactg gtgaacaatt agctaaactt 1020
tctggtgagc ttgtatacca cggtcacgca gtagcttatg gcttaaacaa tgactaccgt 1080
ccgggtgaag ctaataaaac tggcgcgcca aatgctatcg gtgtagaaaa agaagttgac 1140
gcactaaaaa gtggttacca tgttttggct aaagttaact tagcagataa aaatgttact 1200
ggttctatct ataacacttg gaataacgac aaaaaaggtg actacaatgt tgatttagtt 1260
aactttaatg gtaagttaga caactacggt aacatcgcag gtacttctgc attagcatac 1320
gaagatgcaa ataaagacgg ttcatttaac gcaactttat ttggttctca agcatctgag 1380

ttaggtggta atgttgcagg tagcaaaaat gctgatacca ctgtaacaca atggggtgcg 1440
gtatttggtg ctaagaaata tgaagaagct gtatcaacac cagaaaaaat tgttaataaa 1500
ccttgggcgg ctcgtgctga cgaaaatact gctggtcaag taaaataa 1548

<210> 816
<211> 515
<212> PRT
<213> H. parainfluenzae SLP 2a
<400> 816

Met Lys Asn Asn Lys Leu Val Lys Phe Ser Leu Thr Leu Ile Cys Ser
1 5 10 15
Ala Val Leu Ala Ala Cys Gly Ser Ser Gly Gly Ser Asp Asn Ser Ala

20 25 30
Ala Gln Gln Gln Ala Gln Gln Gln Ala Gln Gln Gln Ala Lys Ala Ala
35 40 45
Ala Glu Lys Ala Ala Ala Glu Lys Ala Ala Ala Glu Lys Ala Ala Ala
50 55 60
Glu Lys Ala Ala Ala Glu Lys Ala Ala Ala Glu Lys Ala Ala Ala Glu
65 70 75 80
Lys Ala Ala Gln Thr Thr Ser Ser Glu Ser Asn Pro Gly Tyr Leu Leu

85 90 95
Ser Lys Lys Asn Ala Ser Asp Phe Ile Val Asn Lys Asn Gly Asp Lys
100 105 110
Val Asp Ser Thr Gln Ser Ala Pro Leu Pro Met Thr Val Gln Asn Leu

115 120 125

Glu Pro Arg Leu Asp Thr Ile Val Val Ala Tyr Pro His Glu Gly Ala

130 135 140

Glu Ser Lys Ala Ile Ala Tyr Ile Glu Asp Phe Gln Phe Val Gly Asn

145 150 155 160

Asp Lys Gln Asp Gly Lys Phe Thr Leu Thr Gly Ile Tyr Asn Asp Ser

165 170 175

Ile Asp Arg Ser Thr Thr Gly Gly Thr Pro Arg Pro Glu Ser Arg Thr

180 185 190

Lys Thr Asp Thr Gln Gly Thr Glu Ser Gly Ala Ala Leu Val Tyr Glu

195 200 205

Lys Asp Arg Ile Ala Tyr Phe Asp Arg Ala Asp Arg Asn Ala Glu Gly

210 215 220

Lys Asp Thr Leu Ala Glu Val Tyr Gly Leu Arg Thr Asn Ser Tyr Glu

225 230 235 240

Asp Gly Lys Glu Leu Lys Asp Thr Asp Ala Asn Asn Leu Pro Leu Val

245 250 255

Lys Glu Thr Asn Lys Leu Ala Ala Gln Gln Asp Gly Gln Leu Arg Phe

260 265 270

Val Gln Tyr Gly Arg Val Thr Thr Lys Leu His Asp Leu Thr Glu Lys

275 280 285

Asp Leu Asn Val Tyr Lys Lys Gly Leu Leu Asp Asp Lys Asn Ser Asn

290 295 300

Val Thr Ser Asn Val Ile Gly Phe Ala Asn Tyr Gly Glu Ala Gly Thr

305 310 315 320

Glu Asn Ser Tyr Phe Tyr Arg Gly Leu Asn Asn Thr Thr Gly Glu Gln

325 330 335

Leu Ala Lys Leu Ser Gly Glu Leu Val Tyr His Gly His Ala Val Ala

340 345 350

Tyr Gly Leu Asn Asn Asp Tyr Arg Pro Gly Glu Ala Asn Lys Thr Gly

355 360 365

Ala Pro Asn Ala Ile Gly Val Glu Lys Glu Val Asp Ala Leu Lys Ser
370 375 380

Gly Tyr His Val Leu Ala Lys Val Asn Leu Ala Asp Lys Asn Val Thr
385 390 395 400

Gly Ser Ile Tyr Asn Thr Trp Asn Asn Asp Lys Lys Gly Asp Tyr Asn

405 410 415

Val Asp Leu Val Asn Phe Asn Gly Lys Leu Asp Asn Tyr Gly Asn Ile
420 425 430

Ala Gly Thr Ser Ala Leu Ala Tyr Glu Asp Ala Asn Lys Asp Gly Ser
435 440 445

Phe Asn Ala Thr Leu Phe Gly Ser Gln Ala Ser Glu Leu Gly Gly Asn
450 455 460

Val Ala Gly Ser Lys Asn Ala Asp Thr Thr Val Thr Gln Trp Gly Ala

465 470 475 480

Val Phe Gly Ala Lys Lys Tyr Glu Glu Ala Val Ser Thr Pro Glu Lys
485 490 495

Ile Val Asn Lys Pro Trp Ala Ala Arg Ala Asp Glu Asn Thr Ala Gly
500 505 510

Gln Val Lys
515

<210> 817
<211> 694
<212> DNA
<213> H. paraphrohaemolyticus SLP 2a
<400> 817

ggaataccaa gcaggattat taaaagcaca atcaataaaa gaaacaaaaa tagggcaggc 60

acttccttat cacttaggca ataatgaaat cggatatatt gatcgtagca aacaaagcat 120

atctcaagat ggtaaattaa ctaaattttc tggaggaaca tatatttata atcaacccta 180

ctctattgtt attgcaaata ctgaaagtga gaatattcaa aatgatgttg atttaacacc 240

tgaatggtat gcttatgatg tggatgttgc aggtttagca accgaggaga aaaatattcc 300

aacgaatgga aaagccacct atatggggca aggatttttt aatggagcta ccgcaacatt 360

tatatataac gtaaatttta atattaaaaa aggtcaaggt agattaactg aaatgggcgg 420

ctcaggaaaa ttaaccttac aagaagcaga tattaagcgt attaatttaa aaggtaataa 480

tattattggc gtagaaggaa aagcagaatc atcttataat catttagttg atggtcacta 540

tcaattagga ttctttggtc ctaatgcaga agaagtttct ggtttagcaa ctttctctat 600

ggaagaaaag agaaaaacag ctggaacaac aaaaaacgat cataataaat ttgagtttgg 660

tttaggtggc acccgcggtg aaattcaaaa ataa 694

<210> 818

<211> 230

<212> PRT

<213> H. paraphrohaemolyticus SLP 2a

<400> 818

Glu Tyr Gln Ala Gly Leu Leu Lys Ala Gln Ser Ile Lys Glu Thr Lys
1 5 10 15

Ile Gly Gln Ala Leu Pro Tyr His Leu Gly Asn Asn Glu Ile Gly Tyr
20 25 30

Ile Asp Arg Ser Lys Gln Ser Ile Ser Gln Asp Gly Lys Leu Thr Lys
35 40 45

Phe Ser Gly Gly Thr Tyr Ile Tyr Asn Gln Pro Tyr Ser Ile Val Ile
50 55 60

Ala Asn Thr Glu Ser Glu Asn Ile Gln Asn Asp Val Asp Leu Thr Pro
65 70 75 80

Glu Trp Tyr Ala Tyr Asp Val Asp Val Ala Gly Leu Ala Thr Glu Glu
85 90 95

Lys Asn Ile Pro Thr Asn Gly Lys Ala Thr Tyr Met Gly Gln Gly Phe
100 105 110

Phe Asn Gly Ala Thr Ala Thr Phe Ile Tyr Asn Val Asn Phe Asn Ile
115 120 125

Lys Lys Gly Gln Gly Arg Leu Thr Glu Met Gly Gly Ser Gly Lys Leu
130 135 140

Thr Leu Gln Glu Ala Asp Ile Lys Arg Ile Asn Leu Lys Gly Asn Asn
145 150 155 160

Ile Ile Gly Val Glu Gly Lys Ala Glu Ser Ser Tyr Asn His Leu Val

165 170 175

Asp Gly His Tyr Gln Leu Gly Phe Phe Gly Pro Asn Ala Glu Glu Val

180 185 190

Ser Gly Leu Ala Thr Phe Ser Met Glu Glu Lys Arg Lys Thr Ala Gly

195 200 205

Thr Thr Lys Asn Asp His Asn Lys Phe Glu Phe Gly Leu Gly Gly Thr

210 215 220

Arg Gly Glu Ile Gln Lys

225 230

<210> 819

<211> 1401

<212> DNA

<213> H. parasuis SLP 1a

<400> 819

atgaaaaaac acctacccct tacccttttt attcccttag tagcaaacgc agcccctgaa 60

ttggaaatca aatccgccga gccaacatta ccagtacaag cggttatttt ttcagaaaaa 120

tcagcaaata atggggaaat cactttaacc caagagctgc tcagtaagcc cgaacttact 180

cgtcaaatgt taaatcgggc gattgatagc cgacaatttc atttattgcc tgagctggtg 240

cggatttatc aacaaacgcc taatcctgat ttggtgctga ttgattatgc taacggtatt 300

attttggcaa gtcaggggga ctataaaacg gcaatcgatc tctatcgtgg cattattgcg 360

aagcacccta attttcagcc cgtgcgtttt cgtttagcac aaatgttgtt tgaagatcgg 420

caaaacgaag ccgcacttgc acaatttcgt aagctacaag cggacggatt gccgccacaa 480

attgcaaatg gggtggaaca atatattgct gccattcaga aacgttcgga ttggtcattc 540

gactttggtg tgaattattt gcacgaaagc aatgttaata atgcctcaag ctcgccttat 600

gttcgagtgg ggaatgtgcc gtttaagaaa acggaagaat cattaccgca atcagcaaat 660

gggttgagct accatctgaa tttggctaag aattggaatg ttagcggatc ccattatcta 720

cattttgaga accaatttag tggaaaatcc tattgggata atcatcaatt tgacgatcag 780

caaaaccgtt caagtcttgg ctatcaatat caaaatgctc aaagtcgtct tgctttttg 840

ccttattatg aaatgcgttg gtatggtaat catcgctata atcacggcta tggcgttcgg 900

ggagaagtag agcattggct tacatcacaa tggcagcttt ctacggctgg cgaaatgggc 960

aagctcaaac atcggggcga aaatcagctt gcagatagca caacattatt tggttctgct 1020

acgctactct atgcctttga tgcgaaaagt tatctctatg gtggtgtaga tttgttgcga 1080

gatcggacgt tagaacgttc tttagcctca aaacgttata cagggcgaat tggttggggg 1140

caagaatggt ggggcggaat ttccagccgt attcagctca gttatggcaa acgtgaattt 1200

gaccaagctc accgcatttt taatcagata cgcaaagata gagagttagg tttgaatgtt 1260

acactttggc atcgtaacct gcatttttgg ggaattacac cgaaaatcag ctatcaatat 1320

cagcgagtga actcaaattt agtggatctt tattcgtata aacgaaatcg agtttatttg 1380

agttttgaga aaagtttcta g 1401

<210> 820

<211> 385

<212> PRT

<213> H. parasuis SLP 1a

<400> 820

Met Arg Leu Ser Val Lys Thr Ala Ala Met Ala Ile Leu Val Ser Leu
1 5 10 15

Gly Val Thr Ala Cys Ser Ser Gly Gly Gly Gly Gly Gly Ser Ser Ala
20 25 30

Pro Ala Asn Asn Pro Glu Gln Ala Lys Gln Ile Glu Ala Leu Lys Lys
35 40 45

Gln Val Glu Ala Glu Gln Gln Ala Val Lys Asn Ala Glu Ala Ala Thr
50 55 60

Ala Ala Glu Gln Ala Lys Ala Gln Ala Ala Ala Glu Lys Ala Ala Gln
65 70 75 80

Asp Leu Ala Lys Ala Gln Glu Ala Val Arg Asn Ala Glu Ala Ala Thr
85 90 95

Ala Ala Glu Gln Ala Lys Ala Gln Ala Ala Ala Glu Lys Ala Ala Gln
100 105 110

Asp Leu Ala Ala Ala Gln Asn Gln Ile Ser Ala Leu Glu Ala Glu Leu
115 120 125

Ala Pro Val Arg Glu Glu Ala Glu Arg Lys Arg Gln Glu Ala Glu Ala
130 135 140

Glu Glu Lys Lys Trp Glu Phe Leu Lys Asp Gly Asn Ala Trp Arg Tyr

145 150 155 160

Val Glu Lys Ser Ser Tyr Asp Asn Asn Ser Ile Val Tyr Gly Gly Glu

165 170 175

Asp Lys Val Gly Gln Leu Val Leu Gln Asn Gln Ala Lys His Trp Ala

180 185 190

Leu Gln Lys Ala Val Asn Phe Asn Glu Ser Gly Ile Ser Asp Asn Val

195 200 205

Ser Thr Leu Pro Ile Tyr Ala Thr Arg Lys Thr Leu Ser Gly Asp Lys

210 215 220

Glu Val Gln Val Ala Asn Ala His Phe Val Asn Gln Gln Tyr Ser Thr

225 230 235 240

Tyr Ile Asn Trp Ser Tyr Asn Pro Asp Leu Leu Thr Asn Asp Asp Val

245 250 255

His Arg Thr Ala Thr Tyr Ile Ala Leu Pro Thr Thr Thr Asn Ser Asp

260 265 270

Tyr Leu Lys Ser Ala Thr Thr Ala Thr Tyr Ser Gly Lys Ala Ile Lys

275 280 285

Arg Asn Trp Asp Asp Asn Leu Ile Ser Thr Gly Asp Phe Ser Leu Thr

290 295 300

Ala Asn Phe Gln Thr Glu Lys Val Thr Gly Ala Ile Thr Asn Leu Asp

305 310 315 320

Gly Arg Asp Tyr Val Phe Asn Glu Gly Asn Ile Ser Val Ser Pro Lys

325 330 335

Asn Asn Leu Ile Phe Ser Gly Ile Val Asp Met Thr Gly Leu Tyr Gly

340 345 350

Gly Ile Asn Thr Asn Tyr Lys Gly Val Phe Ala Gly Pro Asn Ala Glu

355 360 365

Glu Val Val Gly Thr Ala Gly Asn Arg Val Ser Phe Gly Gly Lys Arg

370 375 380

Gln

385

<210> 821

<211> 1641

<212> DNA

<213> H. parasuis SLP 2a

<400> 821

atgcatttta aacttaatcc ctatgcgtta gcgtttactt cgctgtttat tgtcgcttgt 60

tctggcggaa aaggaagttt tgatttagaa gatgttcagc ctaataagac aacgggcgtg 120

tctaaagaag agtatcagga tgtggaaacc gataagaaag taaaagaaca gttaggggaa 180

ttgatggaac ctgctttggg gtatgttgta aaggttccgg tgagtcaaag tggagcaaga 240

agaacggaaa tctcaaatcc agaagcaatt actgatgaag atcttaataa aataccaaat 300

cacgagacta tcaaaagtgt agctgatcaa aattatggct gggtagtaga taaaacagca 360

gataaaacga tgaagtatgt tcgttctggt tatgcaattg atgtagatca ttatggtact 420

cgtgataaag gttatgtgtt ttataaaggc atcactccct caaaagaatt accgcaggga 480

ccagtcctta cctatcaagg tgaatgggat tttacctcgg atgctaattt agatgccaaa 540

agacctaata gtaaccctga atttaatggg tatggtccag ggcagagaat tgcaacaaca 600

tctgcaaatg ctaaaggtag aacctataca tctgaatttg aagttgattt ttcaacaaaa 660

aaattaaaag gaaaattaaa tagcaaaaca gcaaatgcag aatcattaga gcgttacagt 720

attgaagcag aacttaaagg aaatcgtttt agaggtaaag caatagccaa gaatgatagc 780

gatgcaattt taggtaagtc ttctgattat cttgaaggtg gtttctatgg acctaaggca 840

gaagaacttg caggaaaatt tattacaaac gacaaatctc tttttgccgt tttttcagca 900

aaacacaatg gctctaatgt tgacacagtt cgtattattg atgcctcaaa aattgattta 960

actcatttta attcttcaga acttaccaat tttggcgatg cttccgtttt aattattgat 1020

gggaaaaaaa tggatctggc aggtagcgag tttaaaaata agcacattgt tgaaatcaac 1080

ggtaaaacaa tggtagcagt agcttgctgt agtaatttgg aatatatgaa atttggtcaa 1140

ttatggcagc aaacagaggg cgaaaaagcc aaagataata gtttattcct acaaggcgaa 1200

cgtactgcaa cagataagat gccaaaaggc ggaaactata aatatattgg tacttgggat 1260

gctcaggttt caaaagaaaa taactgggtt gctacagcag atgatgatag aaaggctggc 1320

tatcgcacag aatttgatgt tgatttcggc agcaaaaatt taagcggtaa gttatttgat 1380

aaaaacggtg taaatcctgt gtttaccgta gatgcaaaaa ttaatggtaa tggttttact 1440

ggaaaagcta aaacctcaga tactggcttc gctctagact caggcagttc acgttatgac 1500

aatgtgaaat ttagcgatgt agcagttaat ggtggcttct atggtccaac ggcagcagag 1560

cttggcggac aattcttcca taaatcagac aatggcagtg taggtgctgt ctttggtgca 1620

aaacaacaag taaaaaaata a 1641

<210> 822

<211> 546

<212> PRT

<213> H. parasuis SLP 2a

<400> 822

Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1 5 10 15

Ile Val Ala Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Glu Asp Val
20 25 30

Gln Pro Asn Lys Thr Thr Gly Val Ser Lys Glu Glu Tyr Gln Asp Val
35 40 45

Glu Thr Asp Lys Lys Val Lys Glu Gln Leu Gly Glu Leu Met Glu Pro
50 55 60

Ala Leu Gly Tyr Val Val Lys Val Pro Val Ser Gln Ser Gly Ala Arg
65 70 75 80

Arg Thr Glu Ile Ser Asn Pro Glu Ala Ile Thr Asp Glu Asp Leu Asn
85 90 95

Lys Ile Pro Asn His Glu Thr Ile Lys Ser Val Ala Asp Gln Asn Tyr
100 105 110

Gly Trp Val Val Asp Lys Thr Ala Asp Lys Thr Met Lys Tyr Val Arg
115 120 125

Ser Gly Tyr Ala Ile Asp Val Asp His Tyr Gly Thr Arg Asp Lys Gly
130 135 140

Tyr Val Phe Tyr Lys Gly Ile Thr Pro Ser Lys Glu Leu Pro Gln Gly
145 150 155 160

Pro Val Leu Thr Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asp Ala Asn
165 170 175

Leu Asp Ala Lys Arg Pro Asn Ser Asn Pro Glu Phe Asn Gly Tyr Gly
180 185 190

Pro Gly Gln Arg Ile Ala Thr Thr Ser Ala Asn Ala Lys Gly Arg Thr
195 200 205
Tyr Thr Ser Glu Phe Glu Val Asp Phe Ser Thr Lys Lys Leu Lys Gly
210 215 220
Lys Leu Asn Ser Lys Thr Ala Asn Ala Glu Ser Leu Glu Arg Tyr Ser
225 230 235 240

Ile Glu Ala Glu Leu Lys Gly Asn Arg Phe Arg Gly Lys Ala Ile Ala
245 250 255
Lys Asn Asp Ser Asp Ala Ile Leu Gly Lys Ser Ser Asp Tyr Leu Glu
260 265 270
Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Ala Gly Lys Phe Ile
275 280 285
Thr Asn Asp Lys Ser Leu Phe Ala Val Phe Ser Ala Lys His Asn Gly
290 295 300

Ser Asn Val Asp Thr Val Arg Ile Ile Asp Ala Ser Lys Ile Asp Leu
305 310 315 320
Thr His Phe Asn Ser Ser Glu Leu Thr Asn Phe Gly Asp Ala Ser Val
325 330 335
Leu Ile Ile Asp Gly Lys Lys Met Asp Leu Ala Gly Ser Glu Phe Lys
340 345 350
Asn Lys His Ile Val Glu Ile Asn Gly Lys Thr Met Val Ala Val Ala
355 360 365

Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Gln
370 375 380
Thr Glu Gly Glu Lys Ala Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu
385 390 395 400
Arg Thr Ala Thr Asp Lys Met Pro Lys Gly Gly Asn Tyr Lys Tyr Ile
405 410 415
Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn Trp Val Ala Thr
420 425 430

Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr Glu Phe Asp Val Asp

435 440 445

Phe Gly Ser Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys Asn Gly Val

450 455 460

Asn Pro Val Phe Thr Val Asp Ala Lys Ile Asn Gly Asn Gly Phe Thr

465 470 475 480

Gly Lys Ala Lys Thr Ser Asp Thr Gly Phe Ala Leu Asp Ser Gly Ser

485 490 495

Ser Arg Tyr Asp Asn Val Lys Phe Ser Asp Val Ala Val Asn Gly Gly

500 505 510

Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly Gln Phe Phe His Lys

515 520 525

Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala Lys Gln Gln Val

530 535 540

Lys Lys

545

<210> 823

<211> 771

<212> DNA

<213> H. pittmaniae SLP 1a

<400> 823

atgaaaaaat taatcttaaa atttggaatt acagccctga ccgcatttac gttggttgct 60

tgtagtagcg gtggtggtag cgatagtgca cctgcgccgg cggcaccaca agccaataac 120

aacgcagcac agaatcaacc ccagccaaat ccggctcaaa ataatccggt tcaatcagtg 180

ccagccgtgg cctcttatag tttatctggt gacaaattat cggtgaccgg ttctggtatt 240

aatcgaatta ctgttgaagg gcaagaatta gatctgacct atgatgcgaa tccagccact 300

atttggagca gtaaaagtgg cctatcttgc tgtagtaaat tcactgatgt gcgtgtcggt 360

gctggaagaa ttggggattt agtcaatttt aaagatgtcg tgttctatac cggtaacgaa 420

actcaaacta tgccggaaag cggtgttgta acttataacg gctatggatt gattcataga 480

gtggctgctc caggatacac tacagatgat gctcaaggct atgcaacctt tactgcagat 540

tttaatacta agaagctgac aggttctttt ggtaatgcag atgtggaata tgaaaccgtg 600

agtatcgatg cagcaattag tggcaatggt ttctccggta cagcaaattc tccgcagtta 660

ggtcaaggta aaaccgaagg taaattctat ggtgagaatg ccaaagaatt gggcggtgtt 720

gtattgggtg atgataaaac ttgggctggt gctttcgcag cgcaacaata a 771

<210> 824

<211> 256

<212> PRT

<213> H. pittmaniae SLP 1a

<400> 824

Met Lys Lys Leu Ile Leu Lys Phe Gly Ile Thr Ala Leu Thr Ala Phe

1 5 10 15

Thr Leu Val Ala Cys Ser Ser Gly Gly Gly Ser Asp Ser Ala Pro Ala

20 25 30

Pro Ala Ala Pro Gln Ala Asn Asn Asn Ala Ala Gln Asn Gln Pro Gln

35 40 45

Pro Asn Pro Ala Gln Asn Asn Pro Val Gln Ser Val Pro Ala Val Ala

50 55 60

Ser Tyr Ser Leu Ser Gly Asp Lys Leu Ser Val Thr Gly Ser Gly Ile

65 70 75 80

Asn Arg Ile Thr Val Glu Gly Gln Glu Leu Asp Leu Thr Tyr Asp Ala

85 90 95

Asn Pro Ala Thr Ile Trp Ser Ser Lys Ser Gly Leu Ser Cys Cys Ser

100 105 110

Lys Phe Thr Asp Val Arg Val Gly Ala Gly Arg Ile Gly Asp Leu Val

115 120 125

Asn Phe Lys Asp Val Val Phe Tyr Thr Gly Asn Glu Thr Gln Thr Met

130 135 140

Pro Glu Ser Gly Val Val Thr Tyr Asn Gly Tyr Gly Leu Ile His Arg

145 150 155 160

Val Ala Ala Pro Gly Tyr Thr Thr Asp Asp Ala Gln Gly Tyr Ala Thr

165 170 175

Phe Thr Ala Asp Phe Asn Thr Lys Lys Leu Thr Gly Ser Phe Gly Asn

180 185 190

Ala Asp Val Glu Tyr Glu Thr Val Ser Ile Asp Ala Ala Ile Ser Gly

195 200 205

Asn Gly Phe Ser Gly Thr Ala Asn Ser Pro Gln Leu Gly Gln Gly Lys

210 215 220

Thr Glu Gly Lys Phe Tyr Gly Glu Asn Ala Lys Glu Leu Gly Gly Val

225 230 235 240

Val Leu Gly Asp Asp Lys Thr Trp Ala Gly Ala Phe Ala Ala Gln Gln

245 250 255

<210> 825

<211> 750

<212> DNA

<213> H. pittmaniae SLP 1b

<400> 825

atgaagaaaa atctcctaaa gtttggcttt agtgttcttg ccgcatttac cttagctgct 60

tgtagtagcg gtggtggcaa tgatggtgat cctgtaccgc aagccaataa taatgcagta 120

caaacgcaga ccccgtctaa ccagaaccaa accggtcaag ataatactaa tcaaccatct 180

actgcagctg cagtagctta taccacaagc ggtaaaaaat tatcgacaag cggttcgggg 240

attaatagta ttgtggttaa tggacaaact ttacgtttgg ttcatccgaa cctttatgcc 300

ggtacctggc aaaacttgaa cggccaaaac gtttgttgtg gtaagtttag cgatgtgcgt 360

gtaggtgcgt ctaaggtgaa tggtgaagat gttgtgttct acaccggtaa tgctactcag 420

tctatgccaa ataatggtgt ggcaacctat aaaggctatg ctgctattcg tgatgcatct 480

ggtttgcata cagcctccgc agaaaatacc gcagtattta ccgcagattt tgcagcgaag 540

aaactaacag gttcctttac ggcggatagt aaaacggtaa atgttgatgc ggcaattgat 600

ggtaatggat tctctggcac ggcgaactca gctcaattag gccaaggtaa agcggaaggt 660

aaattctatg gtaacaacgc caaggaatta ggcggtcttg cacagggtaa tgataattct 720

tggagtgcag tctttgcggc acaacaatag 750

<210> 826

<211> 249

<212> PRT

<213> H. pittmaniae SLP 1b

<400> 826

Met Lys Lys Asn Leu Leu Lys Phe Gly Phe Ser Val Leu Ala Ala Phe

1 5 10 15

Thr Leu Ala Ala Cys Ser Ser Gly Gly Gly Asn Asp Gly Asp Pro Val
20 25 30
Pro Gln Ala Asn Asn Asn Ala Val Gln Thr Gln Thr Pro Ser Asn Gln
35 40 45
Asn Gln Thr Gly Gln Asp Asn Thr Asn Gln Pro Ser Thr Ala Ala Ala
50 55 60

Val Ala Tyr Thr Thr Ser Gly Lys Lys Leu Ser Thr Ser Gly Ser Gly
65 70 75 80
Ile Asn Ser Ile Val Val Asn Gly Gln Thr Leu Arg Leu Val His Pro
85 90 95
Asn Leu Tyr Ala Gly Thr Trp Gln Asn Leu Asn Gly Gln Asn Val Cys
100 105 110
Cys Gly Lys Phe Ser Asp Val Arg Val Gly Ala Ser Lys Val Asn Gly
115 120 125

Glu Asp Val Val Phe Tyr Thr Gly Asn Ala Thr Gln Ser Met Pro Asn
130 135 140
Asn Gly Val Ala Thr Tyr Lys Gly Tyr Ala Ala Ile Arg Asp Ala Ser
145 150 155 160
Gly Leu His Thr Ala Ser Ala Glu Asn Thr Ala Val Phe Thr Ala Asp
165 170 175
Phe Ala Ala Lys Lys Leu Thr Gly Ser Phe Thr Ala Asp Ser Lys Thr
180 185 190

Val Asn Val Asp Ala Ala Ile Asp Gly Asn Gly Phe Ser Gly Thr Ala
195 200 205
Asn Ser Ala Gln Leu Gly Gln Gly Lys Ala Glu Gly Lys Phe Tyr Gly
210 215 220
Asn Asn Ala Lys Glu Leu Gly Gly Leu Ala Gln Gly Asn Asp Asn Ser
225 230 235 240
Trp Ser Ala Val Phe Ala Ala Gln Gln
245

<210> 827

<211> 1965

<212> DNA

<213> H. somni SLP 1a, TbpB

<400> 827

atgacctctt tcaaattatt aggcttttcg gtcttgagtg tggctttgct ctctgcctgc 60

tcttccggca aaggtggctt tgatttagac gacgtcgagc ataccccccc ctcctcctcg 120

ggtagttccc gccccactta tcaagatgtt ccgactggac aacggcagca agaaatagta 180

gaagaaatca actcacctgc tctaggttat gcgacagaaa ttccgcgtag gaatatttcg 240

ccaatgccca ccacgggcac aaaagaaagt aatgctcgtg ttgccattac tgcccagcaa 300

gttgcccccc ttagcatgcc ttttaattca ataaaagaag attttatcaa aaggctaata 360

gcagaaaaca ccaagaaaaa tgcacgaggt agagatgtaa aatattttga tgatacagat 420

gacgtgttgt ttgcacatga tggatctaat ttagcgcata aacgtgattt acaatatgtt 480

cgagttgggt atgtgttggg tacccgaaag attgaacttg ttttttccca tgataaaaaa 540

acaagagatc aatttcctgc tggttgggta ggttatgttt tttaccaagg cactagccct 600

gcggttacat tacctacaca aaccgtaaca tacaaaggct attgggattt tgttagtgat 660

gccttcaatg aacgaacttt agctgaagat tttacacagg aaaatagttc tgctactagc 720

aatataccgg gcaatcaaat cggtgcgact tcaatggatg cattggttaa tcgcaaagtt 780

tcaggagaaa aaatcaatat tgctcacagt gctgagttta ctgctgattt tggcagtaaa 840

aaactttcag gtgaattaaa aagtaacggt tatgtttcta gaaaagaaaa tgatcaagat 900

gtaaaaacac gctataaaat taatgctgat atcaaaggca accgttttgt cggttcggca 960

acgtcaacag cgaatggaca caccatcttc ggcaaggatg cggacaaacg tctcgaggga 1020

gggttctttg gtcccaaagc cgaggaactg gcagggaaat tcctgaccaa tgataattcc 1080

ctgtttgttg tctttggtgc aaaacgtgaa agtaaaggcg atgaaaaact agaaacccgc 1140

tttgatgccg ttaaaatcag cacggatagt aataaattag aaaaagaaac gatggatacg 1200

ttcggcaatg ccagctattt agtgttggac ggcagacagt ttcctttggt gccggaaagt 1260

aatgccggta cgacgggcgc tggcaacaca ggcaagaatg atttcatcac caccatagac 1320

ggtaaccaat taagcaaaac aaaccatgat aagcacaaaa actacaaagt taccgtatgc 1380

tgcagtaatt tgcaatatgt gaaattcggc agctatgggg aacaaacaac agcaactacg 1440

cataacggca catcaactag ccaattaaca aacggacacc ttttcctaac cggtgaacgc 1500

acttcgcttg ccgatatgga gaaggaaaaa ggcacagcaa actaccgtgg cacttggcag 1560

gctaattttt caagtaatga cggcagagta agtactgttg aaccaggcga ttctcgcaac 1620

ggcaataatg ctaaaagccg tgctgaattt gatgttgact ttggcggtaa gacagttgca 1680

ggcaagtttt ttgatgccga cggtattcaa ccagccctca caatggatag taccatgatt 1740

acaggtaacg ggttctccgg catggctaaa acccaaattg atggctttca gttagataaa 1800

ggcagtacaa ctggtggtac caaagtaagc ttcaccgatg ctaaagtcga gggcgcattc 1860

tacggtccga acgctgaaga aatcggcggt accatcacat cgaatggcgc aggcgataaa 1920

gtcggcgggg tgttcggcgc gaaacgccaa gaaccatcga aatag 1965

<210> 828

<211> 654

<212> PRT

<213> H. somni SLP 1a, TbpB

<400> 828

Met Thr Ser Phe Lys Leu Leu Gly Phe Ser Val Leu Ser Val Ala Leu

1 5 10 15

Leu Ser Ala Cys Ser Ser Gly Lys Gly Gly Phe Asp Leu Asp Asp Val

20 25 30

Glu His Thr Pro Pro Ser Ser Ser Gly Ser Ser Arg Pro Thr Tyr Gln

35 40 45

Asp Val Pro Thr Gly Gln Arg Gln Gln Glu Ile Val Glu Glu Ile Asn

50 55 60

Ser Pro Ala Leu Gly Tyr Ala Thr Glu Ile Pro Arg Arg Asn Ile Ser

65 70 75 80

Pro Met Pro Thr Thr Gly Thr Lys Glu Ser Asn Ala Arg Val Ala Ile

85 90 95

Thr Ala Gln Gln Val Ala Pro Leu Ser Met Pro Phe Asn Ser Ile Lys

100 105 110

Glu Asp Phe Ile Lys Arg Leu Ile Ala Glu Asn Thr Lys Lys Asn Ala

115 120 125

Arg Gly Arg Asp Val Lys Tyr Phe Asp Asp Thr Asp Asp Val Leu Phe

130 135 140

Ala His Asp Gly Ser Asn Leu Ala His Lys Arg Asp Leu Gln Tyr Val

145 150 155 160

Arg Val Gly Tyr Val Leu Gly Thr Arg Lys Ile Glu Leu Val Phe Ser
165 170 175
His Asp Lys Lys Thr Arg Asp Gln Phe Pro Ala Gly Trp Val Gly Tyr
180 185 190
Val Phe Tyr Gln Gly Thr Ser Pro Ala Val Thr Leu Pro Thr Gln Thr

195 200 205
Val Thr Tyr Lys Gly Tyr Trp Asp Phe Val Ser Asp Ala Phe Asn Glu
210 215 220
Arg Thr Leu Ala Glu Asp Phe Thr Gln Glu Asn Ser Ser Ala Thr Ser
225 230 235 240
Asn Ile Pro Gly Asn Gln Ile Gly Ala Thr Ser Met Asp Ala Leu Val
245 250 255
Asn Arg Lys Val Ser Gly Glu Lys Ile Asn Ile Ala His Ser Ala Glu

260 265 270
Phe Thr Ala Asp Phe Gly Ser Lys Lys Leu Ser Gly Glu Leu Lys Ser
275 280 285
Asn Gly Tyr Val Ser Arg Lys Glu Asn Asp Gln Asp Val Lys Thr Arg
290 295 300
Tyr Lys Ile Asn Ala Asp Ile Lys Gly Asn Arg Phe Val Gly Ser Ala
305 310 315 320
Thr Ser Thr Ala Asn Gly His Thr Ile Phe Gly Lys Asp Ala Asp Lys

325 330 335
Arg Leu Glu Gly Gly Phe Phe Gly Pro Lys Ala Glu Glu Leu Ala Gly
340 345 350
Lys Phe Leu Thr Asn Asp Asn Ser Leu Phe Val Val Phe Gly Ala Lys
355 360 365
Arg Glu Ser Lys Gly Asp Glu Lys Leu Glu Thr Arg Phe Asp Ala Val
370 375 380
Lys Ile Ser Thr Asp Ser Asn Lys Leu Glu Lys Glu Thr Met Asp Thr

385 390 395 400
Phe Gly Asn Ala Ser Tyr Leu Val Leu Asp Gly Arg Gln Phe Pro Leu

405 410 415

Val Pro Glu Ser Asn Ala Gly Thr Thr Gly Ala Gly Asn Thr Gly Lys

420 425 430

Asn Asp Phe Ile Thr Thr Ile Asp Gly Asn Gln Leu Ser Lys Thr Asn

435 440 445

His Asp Lys His Lys Asn Tyr Lys Val Thr Val Cys Cys Ser Asn Leu

450 455 460

Gln Tyr Val Lys Phe Gly Ser Tyr Gly Glu Gln Thr Thr Ala Thr Thr

465 470 475 480

His Asn Gly Thr Ser Thr Ser Gln Leu Thr Asn Gly His Leu Phe Leu

485 490 495

Thr Gly Glu Arg Thr Ser Leu Ala Asp Met Glu Lys Glu Lys Gly Thr

500 505 510

Ala Asn Tyr Arg Gly Thr Trp Gln Ala Asn Phe Ser Ser Asn Asp Gly

515 520 525

Arg Val Ser Thr Val Glu Pro Gly Asp Ser Arg Asn Gly Asn Asn Ala

530 535 540

Lys Ser Arg Ala Glu Phe Asp Val Asp Phe Gly Gly Lys Thr Val Ala

545 550 555 560

Gly Lys Phe Phe Asp Ala Asp Gly Ile Gln Pro Ala Leu Thr Met Asp

565 570 575

Ser Thr Met Ile Thr Gly Asn Gly Phe Ser Gly Met Ala Lys Thr Gln

580 585 590

Ile Asp Gly Phe Gln Leu Asp Lys Gly Ser Thr Thr Gly Gly Thr Lys

595 600 605

Val Ser Phe Thr Asp Ala Lys Val Glu Gly Ala Phe Tyr Gly Pro Asn

610 615 620

Ala Glu Glu Ile Gly Gly Thr Ile Thr Ser Asn Gly Ala Gly Asp Lys

625 630 635 640

Val Gly Gly Val Phe Gly Ala Lys Arg Gln Glu Pro Ser Lys

645 650

<210> 829

<211> 801

<212> DNA

<213> H. somnus SLP 2a

<400> 829

atgaaacttt ctttctcaaa aacattatta tcaatggcaa ttttagttgg tttaacagct 60

tgtggatcag gtggtggatc tggcagtaca gcacctcgta cattgtcaag ctcagatgct 120

ggtgccgcct atatagcaaa aaccaataat catggagaaa ttacatccgt cactcattct 180

ataatcaaaa ataaaaatga catttcattt ggcgagaact acatttctat taatggtgaa 240

aagtttccta tgcctgcaga tgcaattcaa gaagctgagc accaatttta tcaaggctta 300

aacgcaataa aaaatgcaac tgatttagat attgaagaca tttcaggggt aggaatatac 360

attgtgtatg ataaaggtgc cgctttctat cttggaaacc ctacaaaaga catgccaatt 420

tcaggaagtg ctacatacct aggaggtgct atgctttttg aaaataaaga atttttggct 480

cctctaaaag aaggaaagac aaaattaatt gctgattttt caaataagaa acttgatggt 540

tctttggtat tttctgatat atcaccaatc aacatatctg ccaatataga tcaaaataac 600

tttacgggta gagcaagctc aaattcatta tcccctggtc atgttgaagg aaaattctat 660

ggtaaaaatg cagcgagtat atctggaata gtgaaaagtg atgatttaca aggcaataaa 720

ggttggattg ctatattcag tggagcggat aaaaaacact ttactccgca aggattaaga 780

gatttaggta ttcaagaata a 801

<210> 830

<211> 266

<212> PRT

<213> H. somnus SLP 2a

<400> 830

Met Lys Leu Ser Phe Ser Lys Thr Leu Leu Ser Met Ala Ile Leu Val
1 5 10 15

Gly Leu Thr Ala Cys Gly Ser Gly Gly Gly Ser Gly Ser Thr Ala Pro
20 25 30

Arg Thr Leu Ser Ser Ser Asp Ala Gly Ala Ala Tyr Ile Ala Lys Thr
35 40 45

Asn Asn His Gly Glu Ile Thr Ser Val Thr His Ser Ile Ile Lys Asn
50 55 60

Lys Asn Asp Ile Ser Phe Gly Glu Asn Tyr Ile Ser Ile Asn Gly Glu
65 70 75 80
Lys Phe Pro Met Pro Ala Asp Ala Ile Gln Glu Ala Glu His Gln Phe
85 90 95
Tyr Gln Gly Leu Asn Ala Ile Lys Asn Ala Thr Asp Leu Asp Ile Glu

100 105 110
Asp Ile Ser Gly Val Gly Ile Tyr Ile Val Tyr Asp Lys Gly Ala Ala
115 120 125
Phe Tyr Leu Gly Asn Pro Thr Lys Asp Met Pro Ile Ser Gly Ser Ala
130 135 140
Thr Tyr Leu Gly Gly Ala Met Leu Phe Glu Asn Lys Glu Phe Leu Ala
145 150 155 160
Pro Leu Lys Glu Gly Lys Thr Lys Leu Ile Ala Asp Phe Ser Asn Lys

165 170 175
Lys Leu Asp Gly Ser Leu Val Phe Ser Asp Ile Ser Pro Ile Asn Ile
180 185 190
Ser Ala Asn Ile Asp Gln Asn Asn Phe Thr Gly Arg Ala Ser Ser Asn
195 200 205
Ser Leu Ser Pro Gly His Val Glu Gly Lys Phe Tyr Gly Lys Asn Ala
210 215 220
Ala Ser Ile Ser Gly Ile Val Lys Ser Asp Asp Leu Gln Gly Asn Lys

225 230 235 240
Gly Trp Ile Ala Ile Phe Ser Gly Ala Asp Lys Lys His Phe Thr Pro
245 250 255
Gln Gly Leu Arg Asp Leu Gly Ile Gln Glu
260 265

<210> 831
<211> 906
<212> DNA
<213> H. sputorum SLP 1a
<400> 831
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tctgcatgcg gtagcagtgg cagtaattct aatagtgcgc cacctgtaaa taatcaagtt 120

caacaaacgc caccaacgcc taccaagaat cctgaggttc agcctaagcc gcaaactgaa 180
atcagtccaa agactacacc aaataatcaa tcacaaccac ctaaagtcaa tatacctgca 240
aataacgtag ttcaagctaa tccacaaact ggccgtgaaa caggcgcagt attggttgct 300
tcaggtcgtg gtgataaggc ttctatgcat cgggtagaga tgaataatta tacccctaaa 360
atgagttcaa ttaatgttga aggaactgat gttgacattg gtatccgtgg acttacagca 420
aagcattggc tcaatttttt aaaagaaaaa aagaaaagac gttttgatgt atgttgtggt 480
atctattcag atatgcgttt tggttcaaat agtggcttga ttgataagag ccatatttat 540

ttcttctata atggcaaccc aactaacgat atgccgacaa caggtacggc atcttatgtt 600
ggtcatgcga ttacttcagt agatcttaat ccattagacc atagagatct ctatcaaggc 660
gattcgcaat ttaatgtgga ttttgggaat aaaacattaa atggcgcatt agatattcga 720
aattttcatg cagacattaa tgcaacaatt gcgggcaact attttaacgg tacagcaaat 780
tcatcattag tatcgacagg acgcgtagaa ggtaaatttt atggttctca agcaaaagaa 840
ctggctgggt tcgttcaagc aaatgataat agttggggcg cggcatttgg cgcaaagcaa 900
gaataa 906

<210> 832
<211> 301
<212> PRT
<213> H. sputorum SLP 1a
<400> 832

Met Ser Ser Leu Asn Tyr Pro Phe Lys Phe Gly Val Thr Val Leu Ala
1 5 10 15
Ala Leu Val Leu Ser Ala Cys Gly Ser Ser Gly Ser Asn Ser Asn Ser
20 25 30
Ala Pro Pro Val Asn Asn Gln Val Gln Gln Thr Pro Pro Thr Pro Thr
35 40 45
Lys Asn Pro Glu Val Gln Pro Lys Pro Gln Thr Glu Ile Ser Pro Lys
50 55 60
Thr Thr Pro Asn Asn Gln Ser Gln Pro Pro Lys Val Asn Ile Pro Ala
65 70 75 80
Asn Asn Val Val Gln Ala Asn Pro Gln Thr Gly Arg Glu Thr Gly Ala

85 90 95

Val Leu Val Ala Ser Gly Arg Gly Asp Lys Ala Ser Met His Arg Val

100 105 110

Glu Met Asn Asn Tyr Thr Pro Lys Met Ser Ser Ile Asn Val Glu Gly

115 120 125

Thr Asp Val Asp Ile Gly Ile Arg Gly Leu Thr Ala Lys His Trp Leu

130 135 140

Asn Phe Leu Lys Glu Lys Lys Lys Arg Arg Phe Asp Val Cys Cys Gly

145 150 155 160

Ile Tyr Ser Asp Met Arg Phe Gly Ser Asn Ser Gly Leu Ile Asp Lys

165 170 175

Ser His Ile Tyr Phe Phe Tyr Asn Gly Asn Pro Thr Asn Asp Met Pro

180 185 190

Thr Thr Gly Thr Ala Ser Tyr Val Gly His Ala Ile Thr Ser Val Asp

195 200 205

Leu Asn Pro Leu Asp His Arg Asp Leu Tyr Gln Gly Asp Ser Gln Phe

210 215 220

Asn Val Asp Phe Gly Asn Lys Thr Leu Asn Gly Ala Leu Asp Ile Arg

225 230 235 240

Asn Phe His Ala Asp Ile Asn Ala Thr Ile Ala Gly Asn Tyr Phe Asn

245 250 255

Gly Thr Ala Asn Ser Ser Leu Val Ser Thr Gly Arg Val Glu Gly Lys

260 265 270

Phe Tyr Gly Ser Gln Ala Lys Glu Leu Ala Gly Phe Val Gln Ala Asn

275 280 285

Asp Asn Ser Trp Gly Ala Ala Phe Gly Ala Lys Gln Glu

290 295 300

<210> 833

<211> 813

<212> DNA

<213> H. sputorum SLP 1b

<400

> 833

atgtcttctg taaatcacgt attcaaattt ggtgcaactg cattagcagc tttagtttta 60

tctgcatgtg gcagcagtgg tggcggtagt aacaataatg aggctacccc agcgaataat 120

caaacacaac aaaaccaatc taatccatct gctgctaaca attcagcaca gcctaatcag 180

caagcaagta gcggaacagg agctgcactt gtggcttctg atagtaccag tctttctatt 240

cgtcgtgtag aactcaaagg ttataatacc actagcatca atgtagatgg aactaatgta 300

gcaattggtt ttccaggaat ttcagctggt gattggttaa atgctaaagc taatggacgt 360

gatttaaaag tgtgttgtgg tatatattca gatatgcgtt ttggtcttac tgatagctta 420

gatgataatg gcaatgctta tgtattctat aatggcaatc caacccgtaa catgccaacc 480

agcggaagtg catcatattc tggtcaatct atcatttcag ctaatgttcc agcattagat 540

aaagaaggtt tctacaccgg cacttcacaa tttaatgtgg attttggcaa caaaacatta 600

aatggctact tagggatcaa taatattcaa cctgtgaaca ttaatgcctc tatttcgggt 660

aacagcttta atggtacagc tacttcctca tcattaccgt ctgctgggcg cgtagagggt 720

aaattctatg gtgatcaagc gaaacagctt gctggattag cacaagcgaa tgataataat 780

tggggtgccg tattcggtgc acaaaaacaa taa 813

<210> 834

<211> 270

<212> PRT

<213> H. sputorum SLP 1b

<400> 834

Met Ser Ser Val Asn His Val Phe Lys Phe Gly Ala Thr Ala Leu Ala

1 5 10 15

Ala Leu Val Leu Ser Ala Cys Gly Ser Ser Gly Gly Gly Ser Asn Asn

20 25 30

Asn Glu Ala Thr Pro Ala Asn Asn Gln Thr Gln Gln Asn Gln Ser Asn

35 40 45

Pro Ser Ala Ala Asn Asn Ser Ala Gln Pro Asn Gln Gln Ala Ser Ser

50 55 60

Gly Thr Gly Ala Ala Leu Val Ala Ser Asp Ser Thr Ser Leu Ser Ile

65 70 75 80

Arg Arg Val Glu Leu Lys Gly Tyr Asn Thr Thr Ser Ile Asn Val Asp

85 90 95

Gly Thr Asn Val Ala Ile Gly Phe Pro Gly Ile Ser Ala Gly Asp Trp
100 105 110
Leu Asn Ala Lys Ala Asn Gly Arg Asp Leu Lys Val Cys Cys Gly Ile

115 120 125
Tyr Ser Asp Met Arg Phe Gly Leu Thr Asp Ser Leu Asp Asp Asn Gly
130 135 140
Asn Ala Tyr Val Phe Tyr Asn Gly Asn Pro Thr Arg Asn Met Pro Thr
145 150 155 160
Ser Gly Ser Ala Ser Tyr Ser Gly Gln Ser Ile Ile Ser Ala Asn Val
165 170 175
Pro Ala Leu Asp Lys Glu Gly Phe Tyr Thr Gly Thr Ser Gln Phe Asn

180 185 190
Val Asp Phe Gly Asn Lys Thr Leu Asn Gly Tyr Leu Gly Ile Asn Asn
195 200 205
Ile Gln Pro Val Asn Ile Asn Ala Ser Ile Ser Gly Asn Ser Phe Asn
210 215 220
Gly Thr Ala Thr Ser Ser Ser Leu Pro Ser Ala Gly Arg Val Glu Gly
225 230 235 240
Lys Phe Tyr Gly Asp Gln Ala Lys Gln Leu Ala Gly Leu Ala Gln Ala

245 250 255
Asn Asp Asn Asn Trp Gly Ala Val Phe Gly Ala Gln Lys Gln
260 265 270

<210> 835
<211> 609
<212> DNA
<213> H. sputorum SLP 2a
<400> 835

atgaaaaaat tacttctttc tgcaatttta gttggatttt taactgcttg tagtggtggt 60
ggcggtggta gtggtagtgg aaccgcaacg acacctgata atactaaagt ggatttagat 120
aacagtgcta aaggcgatat tggtgcaaaa accacggacg gcgaattata tggtcaaaat 180
agtaacgatt ctttctacgg catttggatc aacgatgcga agacggtgaa agaagtgcgt 240

taccaaggaa cagccgcaac taatttacca agcggcacag cgacttattt aggtgatgct 300

tactgggtaa atggcacaac agggcagcca agtaagggcg gtaaaaccag attaaatgtg 360

gatttcgaca aaaaaacggt agatggaaaa gttgaatttt cattgctttc agatggtcga 420

gcacaagata ttacgttaca ccaaacgcag ttaaacggta caaaatttag cggtcgtgcg 480

agtaccttgt tacaagaagg gacatatcaa ggtggcttat ttggcaatgg cgcaaaagaa 540

gcggctggta ttgcaacctt tgaaggcaat cacagctatg acacctcatt tggcggtatt 600

cgttactaa 609

<210> 836

<211> 202

<212> PRT

<213> H. sputorum SLP 2a

<400> 836

Met Lys Lys Leu Leu Leu Ser Ala Ile Leu Val Gly Phe Leu Thr Ala
1 5 10 15

Cys Ser Gly Gly Gly Gly Gly Ser Gly Ser Gly Thr Ala Thr Thr Pro
20 25 30

Asp Asn Thr Lys Val Asp Leu Asp Asn Ser Ala Lys Gly Asp Ile Gly
35 40 45

Ala Lys Thr Thr Asp Gly Glu Leu Tyr Gly Gln Asn Ser Asn Asp Ser

50 55 60

Phe Tyr Gly Ile Trp Ile Asn Asp Ala Lys Thr Val Lys Glu Val Arg
65 70 75 80

Tyr Gln Gly Thr Ala Ala Thr Asn Leu Pro Ser Gly Thr Ala Thr Tyr
85 90 95

Leu Gly Asp Ala Tyr Trp Val Asn Gly Thr Thr Gly Gln Pro Ser Lys
100 105 110

Gly Gly Lys Thr Arg Leu Asn Val Asp Phe Asp Lys Lys Thr Val Asp

115 120 125

Gly Lys Val Glu Phe Ser Leu Leu Ser Asp Gly Arg Ala Gln Asp Ile

130 135 140

Thr Leu His Gln Thr Gln Leu Asn Gly Thr Lys Phe Ser Gly Arg Ala
145 150 155 160

Ser Thr Leu Leu Gln Glu Gly Thr Tyr Gln Gly Gly Leu Phe Gly Asn

165 170 175

Gly Ala Lys Glu Ala Ala Gly Ile Ala Thr Phe Glu Gly Asn His Ser

180 185 190

Tyr Asp Thr Ser Phe Gly Gly Ile Arg Tyr

195 200

<210> 837

<211> 996

<212> DNA

<213> Haemophilus sp. C1 SLP 1a

<400> 837

atgaaaccaa cctttaaaac aaccgcactt gcgattttag tttcattggg tgcaacggct 60

tgtctttcta attctgataa ttcgccagca aaaccaacac ccgttcaacc gcaaaattca 120

tcagatgcgc cagctattac gcttgcaaca cctgaagact ataattatga ggaagcatct 180

aaaacgtcaa atggaacgaa gtggcgtaca ttagatttaa ataatacagc ttcagataat 240

aatccatcag gctctaatga acgttttgga attaatatcg tcgggtctga ttctttagtg 300

gctggtactt tagatttaaa cgaaatttca gggaataaat taggttctca tgaagggaaa 360

aaaacaataa acaatacaga agtgacatat gatgtagtca atttgccata tgctagctat 420

ggaatggcaa cgactgaggt tgatcccgat ccaaggaatc gtgcaagaga atccaaagag 480

catgtaaaat atgtactata ttttgggggga gcatatttac ctcaatctga tggacctggt 540

ttgggggggga ttggcaatgg taagtttgca tatgaaggaa atgttaaggc aatggtaaaa 600

gatattcagg gtgaggtaat tgcttataat aaaaatgatg gtgtagtaaa gctaactata 660

gattctagta aattcttagc ggggcgatcg aaaatacttg atttctctgg tgaaatgagt 720

agtaagctat tagggcgtac aattcaactt aagactgata aaccagagga ctttataact 780

tatcaagatt ataaggttac tggcgatgca atctataaca ctgatactga tggacggttt 840

aaattagaat tttatggtaa gagcggtttt tctgatatgg caggtacagc cactatttat 900

agcaaccctc gttcaccaaa tggtgattta ggtagtattg atggcaaaaa aattagtagt 960

tatgaagcag tatttggcgg acaaatacaa ccataa 996

<210> 838

<211> 331

<212> PRT

<213> Haemophilus sp. C1 SLP 1a

<400> 838

Met Lys Pro Thr Phe Lys Thr Thr Ala Leu Ala Ile Leu Val Ser Leu
1 5 10 15
Gly Ala Thr Ala Cys Leu Ser Asn Ser Asp Asn Ser Pro Ala Lys Pro
20 25 30
Thr Pro Val Gln Pro Gln Asn Ser Ser Asp Ala Pro Ala Ile Thr Leu
35 40 45
Ala Thr Pro Glu Asp Tyr Asn Tyr Glu Glu Ala Ser Lys Thr Ser Asn
50 55 60

Gly Thr Lys Trp Arg Thr Leu Asp Leu Asn Asn Thr Ala Ser Asp Asn
65 70 75 80
Asn Pro Ser Gly Ser Asn Glu Arg Phe Gly Ile Asn Ile Val Gly Ser
85 90 95
Asp Ser Leu Val Ala Gly Thr Leu Asp Leu Asn Glu Ile Ser Gly Asn
100 105 110
Lys Leu Gly Ser His Glu Gly Lys Lys Thr Ile Asn Asn Thr Glu Val
115 120 125

Thr Tyr Asp Val Val Asn Leu Pro Tyr Ala Ser Tyr Gly Met Ala Thr
130 135 140
Thr Glu Val Asp Pro Asp Pro Arg Asn Arg Ala Arg Glu Ser Lys Glu
145 150 155 160
His Val Lys Tyr Val Leu Tyr Phe Gly Gly Ala Tyr Leu Pro Gln Ser
165 170 175
Asp Gly Pro Gly Leu Gly Gly Ile Gly Asn Gly Lys Phe Ala Tyr Glu
180 185 190

Gly Asn Val Lys Ala Met Val Lys Asp Ile Gln Gly Glu Val Ile Ala
195 200 205
Tyr Asn Lys Asn Asp Gly Val Val Lys Leu Thr Ile Asp Ser Ser Lys
210 215 220
Phe Leu Ala Gly Arg Ser Lys Ile Leu Asp Phe Ser Gly Glu Met Ser

225 230 235 240

Ser Lys Leu Leu Gly Arg Thr Ile Gln Leu Lys Thr Asp Lys Pro Glu

245 250 255

Asp Phe Ile Thr Tyr Gln Asp Tyr Lys Val Thr Gly Asp Ala Ile Tyr

260 265 270

Asn Thr Asp Thr Asp Gly Arg Phe Lys Leu Glu Phe Tyr Gly Lys Ser

275 280 285

Gly Phe Ser Asp Met Ala Gly Thr Ala Thr Ile Tyr Ser Asn Pro Arg

290 295 300

Ser Pro Asn Gly Asp Leu Gly Ser Ile Asp Gly Lys Lys Ile Ser Ser

305 310 315 320

Tyr Glu Ala Val Phe Gly Gly Gln Ile Gln Pro

325 330

<210> 839

<211> 789

<212> DNA

<213> Haemophilus sp. FF7 SLP 1a

<400> 839

atgaaaaaat ccattttaac caccgcactt tgcctatctt gcgcaataac actcagcgcc 60

aatgccgaca ttagctccgg catatccaat aacaatgccg cgttgagcgt aaaaaaccct 120

tctgctaaac acgacggctg gttccattcc gatcccggcg gattaccggg tatcgaagtg 180

caaggcgtaa cctctaaagt caccagtttt caatcgctga ccaaggttgc taataacgtg 240

ctggtgccga aatcactggg tgggcaggat aaaaacggtg ttgtggtatt aaacatgaac 300

aacatgccaa gttgggtgcc gggcttccac ggcaaattag gcaactttgc gtttaaaaaa 360

gtcggcacgc aggaattata ctacggtgaa tggctgggca acggcgccaa cgccaagcag 420

gatcgggtgg tatattatgc cggtaacaac caaacacaaa acatgccgac cggcggaaaa 480

gccgtgtata gcgtgcaggg cattaatcag cacggcaagc tgggggctga aatgctgaaa 540

ggcgaactga ccgccgattt cggcaaaaaa caagttaacg gctcaatgag caaaaccggc 600

ttaacggtga gcatcaatga tgcgaagatt aacggcaata ctttctcagg cgccgcagct 660

gcaaataaaa ccgtagcagg taccacacaa ggtcatttct tcggcaataa tgcggcggca 720

ttagccggtt atgcgaaatt cgccggacat aaccaatacg acaccgcatt cggcggaacg 780

aaaaaataa 789

<210> 840

<211> 262

<212> PRT

<213> Haemophilus sp. FF7 SLP 1a

<400> 840

Met Lys Lys Ser Ile Leu Thr Thr Ala Leu Cys Leu Ser Cys Ala Ile
1 5 10 15

Thr Leu Ser Ala Asn Ala Asp Ile Ser Ser Gly Ile Ser Asn Asn Asn
20 25 30

Ala Ala Leu Ser Val Lys Asn Pro Ser Ala Lys His Asp Gly Trp Phe
35 40 45

His Ser Asp Pro Gly Gly Leu Pro Gly Ile Glu Val Gln Gly Val Thr
50 55 60

Ser Lys Val Thr Ser Phe Gln Ser Leu Thr Lys Val Ala Asn Asn Val
65 70 75 80

Leu Val Pro Lys Ser Leu Gly Gly Gln Asp Lys Asn Gly Val Val Val
85 90 95

Leu Asn Met Asn Asn Met Pro Ser Trp Val Pro Gly Phe His Gly Lys
100 105 110

Leu Gly Asn Phe Ala Phe Lys Lys Val Gly Thr Gln Glu Leu Tyr Tyr
115 120 125

Gly Glu Trp Leu Gly Asn Gly Ala Asn Ala Lys Gln Asp Arg Val Val
130 135 140

Tyr Tyr Ala Gly Asn Asn Gln Thr Gln Asn Met Pro Thr Gly Gly Lys
145 150 155 160

Ala Val Tyr Ser Val Gln Gly Ile Asn Gln His Gly Lys Leu Gly Ala
165 170 175

Glu Met Leu Lys Gly Glu Leu Thr Ala Asp Phe Gly Lys Lys Gln Val
180 185 190

Asn Gly Ser Met Ser Lys Thr Gly Leu Thr Val Ser Ile Asn Asp Ala
195 200 205

Lys Ile Asn Gly Asn Thr Phe Ser Gly Ala Ala Ala Ala Asn Lys Thr

210 215 220

Val Ala Gly Thr Thr Gln Gly His Phe Phe Gly Asn Asn Ala Ala Ala

225 230 235 240

Leu Ala Gly Tyr Ala Lys Phe Ala Gly His Asn Gln Tyr Asp Thr Ala

245 250 255

Phe Gly Gly Thr Lys Lys

260

<210> 841

<211> 1338

<212> DNA

<213> Haemophilus sp. oral taxon 851 SLP 1a

<400> 841

atgaaaccaa cgttaaaaac aaccgcatta gcgatgtgta ttgcactaag tttgactgct 60

tgtaaatcta cttcaaattc tggagatgct cgtccaacac cagttcaacc agcagcaact 120

caaccagcag aagaaaaaca caatgaacca caagcagcac caggtgtaag cactccggtt 180

gctgaccaag gtacttcatc tactggttca caaccacaac caggagcaga ttcaaatgga 240

cacaatgcag atgtatcacc agcgcctggc actgcggaaa gccatactgt agaaactcat 300

cctgagggcg aaacaggcag ccacaccgat acagctcacc aagacgagcc gcattctaac 360

gaaacagtag ttcaaccgaa accacctatt tcaagtgaac cagcacgttc agaagataca 420

catgctgcgg aaaatacagg tgcaaccact ggtaaagaag aaaaaccagc aggcactgca 480

gaaactcagc ctgtttctcc agctccagca gaagaccata ctgaatcacc agcagtgact 540

ccgtcacaac catcaacagg tactgatgca ggtacacaac caagtgcacc agtaaattct 600

ggtagttctt ctgaatcttc tgtacccgca cacagtgaac catctgcacc agcagataac 660

atgcatactg aggcaggcgc atcgccaaca gtaggtgcag gtgagcacca tgatgaaacc 720

aaccatgcaa ctgagcaacc gcaaggcaca ccagctcagc caccggttgc accagaacgt 780

catgatgaag caacccataa cacagaagga aacccatcag tgagtggaac aactgaaact 840

caaccagcgg catcttcata cgatgatctt aaaaagctgt atcgagatgt agtagatggt 900

aaatctagcg atttagttga tgcaatttat aaaggtaaag tatttgcaaa agttaagctt 960

agtaacactg acgaggaaag atacgcacaa acgacgacag atgaagacgg tgatgttaca 1020

cttaatgttc aaaaaaattc ttctgataaa tttaaaatgt cgggaactat caatagtaaa 1080

accgtaggta gcattcagtt gggagaaaaa gagattatag aaaataaagt gaaagatggt 1140

catgtagatt ttggggatga tgctgacggt aagtattctg ctactatttc agaaaatggt 1200

gatatagttg gacgtgtgga gtataattct agacgcgcaa tagaggatgg tttttatcca 1260

agctttgaag gcaaagatgg aacaaaatat ctttttggct atgaagcctt ttttgatgca 1320

accaaacaac ctaaataa 1338

<210> 842

<211> 445

<212> PRT

<213> Haemophilus sp. oral taxon 851 SLP 1a

<400> 842

Met Lys Pro Thr Leu Lys Thr Thr Ala Leu Ala Met Cys Ile Ala Leu
1 5 10 15

Ser Leu Thr Ala Cys Lys Ser Thr Ser Asn Ser Gly Asp Ala Arg Pro
20 25 30

Thr Pro Val Gln Pro Ala Ala Thr Gln Pro Ala Glu Glu Lys His Asn
35 40 45

Glu Pro Gln Ala Ala Pro Gly Val Ser Thr Pro Val Ala Asp Gln Gly
50 55 60

Thr Ser Ser Thr Gly Ser Gln Pro Gln Pro Gly Ala Asp Ser Asn Gly
65 70 75 80

His Asn Ala Asp Val Ser Pro Ala Pro Gly Thr Ala Glu Ser His Thr
85 90 95

Val Glu Thr His Pro Glu Gly Glu Thr Gly Ser His Thr Asp Thr Ala
100 105 110

His Gln Asp Glu Pro His Ser Asn Glu Thr Val Val Gln Pro Lys Pro
115 120 125

Pro Ile Ser Ser Glu Pro Ala Arg Ser Glu Asp Thr His Ala Ala Glu
130 135 140

Asn Thr Gly Ala Thr Thr Gly Lys Glu Glu Lys Pro Ala Gly Thr Ala
145 150 155 160

Glu Thr Gln Pro Val Ser Pro Ala Pro Ala Glu Asp His Thr Glu Ser
165 170 175

Pro Ala Val Thr Pro Ser Gln Pro Ser Thr Gly Thr Asp Ala Gly Thr
180 185 190

Gln Pro Ser Ala Pro Val Asn Ser Gly Ser Ser Ser Glu Ser Ser Val
195 200 205
Pro Ala His Ser Glu Pro Ser Ala Pro Ala Asp Asn Met His Thr Glu
210 215 220
Ala Gly Ala Ser Pro Thr Val Gly Ala Gly Glu His His Asp Glu Thr
225 230 235 240
Asn His Ala Thr Glu Gln Pro Gln Gly Thr Pro Ala Gln Pro Pro Val
245 250 255

Ala Pro Glu Arg His Asp Glu Ala Thr His Asn Thr Glu Gly Asn Pro
260 265 270
Ser Val Ser Gly Thr Thr Glu Thr Gln Pro Ala Ala Ser Ser Tyr Asp
275 280 285
Asp Leu Lys Lys Leu Tyr Arg Asp Val Val Asp Gly Lys Ser Ser Asp
290 295 300
Leu Val Asp Ala Ile Tyr Lys Gly Lys Val Phe Ala Lys Val Lys Leu
305 310 315 320

Ser Asn Thr Asp Glu Glu Arg Tyr Ala Gln Thr Thr Thr Asp Glu Asp
325 330 335
Gly Asp Val Thr Leu Asn Val Gln Lys Asn Ser Ser Asp Lys Phe Lys
340 345 350
Met Ser Gly Thr Ile Asn Ser Lys Thr Val Gly Ser Ile Gln Leu Gly
355 360 365
Glu Lys Glu Ile Ile Glu Asn Lys Val Lys Asp Gly His Val Asp Phe
370 375 380

Gly Asp Asp Ala Asp Gly Lys Tyr Ser Ala Thr Ile Ser Glu Asn Gly
385 390 395 400
Asp Ile Val Gly Arg Val Glu Tyr Asn Ser Arg Arg Ala Ile Glu Asp
405 410 415
Gly Phe Tyr Pro Ser Phe Glu Gly Lys Asp Gly Thr Lys Tyr Leu Phe

420 425 430

Gly Tyr Glu Ala Phe Phe Asp Ala Thr Lys Gln Pro Lys

435 440 445

<210> 843

<211> 822

<212> DNA

<213> K. denitrificans SLP 1a

<400> 843

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agcgcaggcg gctctttggc caatgcgatt accgacccgt tcacaccgaa accgcacggc 120

aaaagcagcc ttaccatcaa ccaagaccct aataacggca ttctgaatgt cggtcacacc 180

gtggcggaca ccgtggaaat taacggtctc ccctacggca acaacagcac gctcgacatc 240

gggcataatt tccaaaaccg cctgtccgat tttacctatg tgttgaaaca aagcgggcgc 300

aatgtggaaa gcgggcagct gggcgtgtac aaacgcgctt attcggccgt ggtcggcgca 360

accgtgcaag atcgctacaa ccccaacacc ggcgcgcacg cttcctctcc caatcccaat 420

ttcactatcc gcagcattca gggcgactta acccccgaat cccgactgcc caccagcgga 480

tctatccgtt accaaggaca cgccttttcc ggcttggacg accgcggccc gaacggccat 540

ctgaacagcc gcctggatta cacagtggac tttggcaacc gcaccggttc aggttcgatt 600

accggtttga gccgcttcgg caatatcgaa ttggcgaccg gccggcttga ccgcagcaga 660

agcgcgctgg agggcaccgc catctcccaa caacgcggac gcggccatta cgaactgaac 720

attttcggcc cgaatgcgga cgaaattgcc ggcaaagcca ccggattcac gggcgaccac 780

gaagtcggtt tttccggcag caaaacgcag cagaatccgt aa 822

<210> 844

<211> 273

<212> PRT

<213> K. denitrificans SLP 1a

<400> 844

Met Lys Lys Tyr His Ala Leu Tyr Ile Ala Val Ala Ala Leu Ala Leu

1 5 10 15

Gly Gly Cys Gly Ser Ala Gly Gly Ser Leu Ala Asn Ala Ile Thr Asp

20 25 30

Pro Phe Thr Pro Lys Pro His Gly Lys Ser Ser Leu Thr Ile Asn Gln

35 40 45

Asp Pro Asn Asn Gly Ile Leu Asn Val Gly His Thr Val Ala Asp Thr
50 55 60
Val Glu Ile Asn Gly Leu Pro Tyr Gly Asn Asn Ser Thr Leu Asp Ile
65 70 75 80
Gly His Asn Phe Gln Asn Arg Leu Ser Asp Phe Thr Tyr Val Leu Lys
85 90 95
Gln Ser Gly Arg Asn Val Glu Ser Gly Gln Leu Gly Val Tyr Lys Arg
100 105 110

Ala Tyr Ser Ala Val Val Gly Ala Thr Val Gln Asp Arg Tyr Asn Pro
115 120 125
Asn Thr Gly Ala His Ala Ser Ser Pro Asn Pro Asn Phe Thr Ile Arg
130 135 140
Ser Ile Gln Gly Asp Leu Thr Pro Glu Ser Arg Leu Pro Thr Ser Gly
145 150 155 160
Ser Ile Arg Tyr Gln Gly His Ala Phe Ser Gly Leu Asp Asp Arg Gly
165 170 175

Pro Asn Gly His Leu Asn Ser Arg Leu Asp Tyr Thr Val Asp Phe Gly
180 185 190
Asn Arg Thr Gly Ser Gly Ser Ile Thr Gly Leu Ser Arg Phe Gly Asn
195 200 205
Ile Glu Leu Ala Thr Gly Arg Leu Asp Arg Ser Arg Ser Ala Leu Glu
210 215 220
Gly Thr Ala Ile Ser Gln Gln Arg Gly Arg Gly His Tyr Glu Leu Asn
225 230 235 240

Ile Phe Gly Pro Asn Ala Asp Glu Ile Ala Gly Lys Ala Thr Gly Phe
245 250 255
Thr Gly Asp His Glu Val Gly Phe Ser Gly Ser Lys Thr Gln Gln Asn
260 265 270
Pro

<210> 845

<211> 2403

<212> DNA

<213> K. denitrificans SLP 3a

<400> 845

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gcttgcggcg gcggtggcgg cggcggacaa ccgagcaccc agtcccgccc gaccgtgccg 120

tccacaccaa gcgccgccaa aactgccgca gataacgcca ttgccgatat cgccgccaaa 180

gcacaagccg tgcaggctgc tttgacgcgc aaccacgata ccgacaatga cggcaaaatc 240

tctgccacag aagccgccgc ggccaaccaa gccatcaaca atgccaaagc cgcattgcag 300

gctgccattg ccaatgcaga aaccaaagcc caagatgccg ccttgtcgcc tgccgaaaaa 360

acgcaggcca ccgccgcatt gaccaccgcg aaaaacagcg caaatgtccg taacgcgcag 420

gctgcttccg ccaacgtgca acccactccg gcacccgcac cgcaaccgcc tgccccacaa 480

caaccgagtg ccgccaaaac tgccgcagat aacgccattg ccgatatcgc caccaaagcc 540

caagccgtgc aggctgcttt gacacgcaac cacgataccg acaatgacgg caaaatctcc 600

gccacagaag ccgccgcggc caaccaagcc atcaacaatg ccaaagccgc attgcaggct 660

gccatcgctg atgcagaaac caaagcccaa gatgccgcct tgtcgccagc cgagaaaaca 720

caggccgccg ctgcattgaa cgccgcgaaa aacagcgcaa atatccgtaa cgcgcaggct 780

gcttctgcca acgtgcagcc cactccggcg cctgcaccgc aaccacagcc gcaaccgccc 840

caaccaagcg cagccacagg cttcggccaa gacaacaacg gccgcatgaa acccaatgcc 900

ggcggcgttt ccggcggcgt gctcagtacc gatgctatgc gccaatccga tgaaagctca 960

tacggcagca ttcaaaaccc cgaaggccgc agcaaaaacg aagtggtgct gaacggcgtg 1020

aaaatcgcca ccgccaccac cggccaaaaa cgctacgaaa ccgaagagtc caataaccaa 1080

accgcaaaat ccatccacag tagcgacatt ctgcccgacg tgcgctatgg cgcggtggtc 1140

gatacttctt ccggcgtgat ggccatccgc caaggcctgt tcgtgcaagg cacggcagca 1200

ggcgcggaca cagtggccgt gaaaaccggc acggtggaat acaacggtac cggcctgcat 1260

ttcggcaaac cgagcagcga cgccactgcc ggcctgccgt tcatgaccgc cgacccgtca 1320

tggggtgtga atgcgcccaa cacggaggat ttgtacacca gcggccgcgc cactaaagtg 1380

aaagccagcg tgaacttcga caataaaacc atcggtatcg acatcagcga tccgggcagc 1440

cgtacccaag gtcgtccgaa tgcgtccgaa ctggccggcg cgcccattca ttttgacggc 1500

gtgattcaag gcaattcgtt caccaatgcg gcaggacaag agaaaacctt tgccggcggc 1560

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aacgaatcga gcggtgtatt cggtgcgcag gcaagcacag gcagcaatac ccccgcccct 1680

gcacccactc cttcacctgc gccaacccca acgccgactc cgccaagcag cggcgcagta 1740

accgaatcga cttattataa actgcctgag cagcagcaac tgaccgatgc gaaactgccg 1800

atggccgaaa ccaaccaagc catcagcaaa ggcatccaaa ctttggtggt ggacggcatt 1860

tctatcgccc tgcccgccgc caaccaaggc ttcgagaaag gcatgaatta ttatgcattc 1920

aacaatgcgg gcaatgtgat tgcgggtgcg gcgcagatta tgtcgggtgg caaagaccaa 1980

ggcctgctgt tcgtgcaggg caacctgacg ccgcaagacc aaatcccgac cggcacggcc 2040

aattacagcg gcaaagtgtt gcacttccgc gagcgcgtgg tgcggcatga aaacggcaat 2100

ttggtgaatg tcgatccggg ctatgtattt actcaaggca gcttcaccgc gaaagccgat 2160

tttgccaacc gcaacctgtc ggtaacgatt aattcgggcg actacaacta tatgcgcacg 2220

aaagtgttca ccgccaacat caacggtaat acgttctccg gcaccggatc cgaccgcagc 2280

attgaaggcg gcttctatgg cgcgaatgca gccgcgattg ccggcaaata ccaatattcg 2340

gacggcagca ccagcaaatg gagcgacagc ggcttcggcg tgttcagcgg caacaagcaa 2400

taa 2403

<210> 846

<211> 800

<212> PRT

<213> K. denitrificans SLP 3a

<400> 846

Met Asn Thr Gly Asn Phe Thr Leu Lys Ala Leu Ala Ile Ala Cys Ser
1 5 10 15

Leu Ala Leu Thr Ala Cys Gly Gly Gly Gly Gly Gly Gly Gln Pro Ser
20 25 30

Thr Gln Ser Arg Pro Thr Val Pro Ser Thr Pro Ser Ala Ala Lys Thr
35 40 45

Ala Ala Asp Asn Ala Ile Ala Asp Ile Ala Ala Lys Ala Gln Ala Val
50 55 60

Gln Ala Ala Leu Thr Arg Asn His Asp Thr Asp Asn Asp Gly Lys Ile
65 70 75 80

Ser Ala Thr Glu Ala Ala Ala Ala Asn Gln Ala Ile Asn Asn Ala Lys

85 90 95

Ala Ala Leu Gln Ala Ala Ile Ala Asn Ala Glu Thr Lys Ala Gln Asp

100 105 110

Ala Ala Leu Ser Pro Ala Glu Lys Thr Gln Ala Thr Ala Ala Leu Thr

115 120 125

Thr Ala Lys Asn Ser Ala Asn Val Arg Asn Ala Gln Ala Ala Ser Ala

130 135 140

Asn Val Gln Pro Thr Pro Ala Pro Ala Pro Gln Pro Pro Ala Pro Gln

145 150 155 160

Gln Pro Ser Ala Ala Lys Thr Ala Ala Asp Asn Ala Ile Ala Asp Ile

165 170 175

Ala Thr Lys Ala Gln Ala Val Gln Ala Ala Leu Thr Arg Asn His Asp

180 185 190

Thr Asp Asn Asp Gly Lys Ile Ser Ala Thr Glu Ala Ala Ala Ala Asn

195 200 205

Gln Ala Ile Asn Asn Ala Lys Ala Ala Leu Gln Ala Ala Ile Ala Asp

210 215 220

Ala Glu Thr Lys Ala Gln Asp Ala Ala Leu Ser Pro Ala Glu Lys Thr

225 230 235 240

Gln Ala Ala Ala Ala Leu Asn Ala Ala Lys Asn Ser Ala Asn Ile Arg

245 250 255

Asn Ala Gln Ala Ala Ser Ala Asn Val Gln Pro Thr Pro Ala Pro Ala

260 265 270

Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Ser Ala Ala Thr Gly Phe

275 280 285

Gly Gln Asp Asn Asn Gly Arg Met Lys Pro Asn Ala Gly Gly Val Ser

290 295 300

Gly Gly Val Leu Ser Thr Asp Ala Met Arg Gln Ser Asp Glu Ser Ser

305 310 315 320

Tyr Gly Ser Ile Gln Asn Pro Glu Gly Arg Ser Lys Asn Glu Val Val

325 330 335

Leu Asn Gly Val Lys Ile Ala Thr Ala Thr Thr Gly Gln Lys Arg Tyr
340 345 350

Glu Thr Glu Glu Ser Asn Asn Gln Thr Ala Lys Ser Ile His Ser Ser
355 360 365

Asp Ile Leu Pro Asp Val Arg Tyr Gly Ala Val Val Asp Thr Ser Ser
370 375 380

Gly Val Met Ala Ile Arg Gln Gly Leu Phe Val Gln Gly Thr Ala Ala
385 390 395 400

Gly Ala Asp Thr Val Ala Val Lys Thr Gly Thr Val Glu Tyr Asn Gly
405 410 415

Thr Gly Leu His Phe Gly Lys Pro Ser Ser Asp Ala Thr Ala Gly Leu
420 425 430

Pro Phe Met Thr Ala Asp Pro Ser Trp Gly Val Asn Ala Pro Asn Thr
435 440 445

Glu Asp Leu Tyr Thr Ser Gly Arg Ala Thr Lys Val Lys Ala Ser Val
450 455 460

Asn Phe Asp Asn Lys Thr Ile Gly Ile Asp Ile Ser Asp Pro Gly Ser
465 470 475 480

Arg Thr Gln Gly Arg Pro Asn Ala Ser Glu Leu Ala Gly Ala Pro Ile
485 490 495

His Phe Asp Gly Val Ile Gln Gly Asn Ser Phe Thr Asn Ala Ala Gly
500 505 510

Gln Glu Lys Thr Phe Ala Gly Gly Phe Tyr Gly Ala Ala Ala Asp Gln
515 520 525

Leu Ala Gly Met Tyr Arg Leu Asn Ala Gln Lys Ala Asn Glu Ser Ser
530 535 540

Gly Val Phe Gly Ala Gln Ala Ser Thr Gly Ser Asn Thr Pro Ala Pro
545 550 555 560

Ala Pro Thr Pro Ser Pro Ala Pro Thr Pro Thr Pro Thr Pro Pro Ser
565 570 575

Ser Gly Ala Val Thr Glu Ser Thr Tyr Tyr Lys Leu Pro Glu Gln Gln

580 585 590

Gln Leu Thr Asp Ala Lys Leu Pro Met Ala Glu Thr Asn Gln Ala Ile
595 600 605
Ser Lys Gly Ile Gln Thr Leu Val Val Asp Gly Ile Ser Ile Ala Leu
610 615 620
Pro Ala Ala Asn Gln Gly Phe Glu Lys Gly Met Asn Tyr Tyr Ala Phe
625 630 635 640
Asn Asn Ala Gly Asn Val Ile Ala Gly Ala Ala Gln Ile Met Ser Gly
645 650 655

Gly Lys Asp Gln Gly Leu Leu Phe Val Gln Gly Asn Leu Thr Pro Gln
660 665 670
Asp Gln Ile Pro Thr Gly Thr Ala Asn Tyr Ser Gly Lys Val Leu His
675 680 685
Phe Arg Glu Arg Val Val Arg His Glu Asn Gly Asn Leu Val Asn Val
690 695 700
Asp Pro Gly Tyr Val Phe Thr Gln Gly Ser Phe Thr Ala Lys Ala Asp
705 710 715 720

Phe Ala Asn Arg Asn Leu Ser Val Thr Ile Asn Ser Gly Asp Tyr Asn
725 730 735
Tyr Met Arg Thr Lys Val Phe Thr Ala Asn Ile Asn Gly Asn Thr Phe
740 745 750
Ser Gly Thr Gly Ser Asp Arg Ser Ile Glu Gly Gly Phe Tyr Gly Ala
755 760 765
Asn Ala Ala Ala Ile Ala Gly Lys Tyr Gln Tyr Ser Asp Gly Ser Thr
770 775 780

Ser Lys Trp Ser Asp Ser Gly Phe Gly Val Phe Ser Gly Asn Lys Gln
785 790 795 800

<210> 847

<211> 960

<212> DNA

<213> K. denitrificans SLP 4a

<400> 847

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ggcagcagcg ccccttccac acaaagcaac acaccccaat ctaccgcatc acccgatgcc 120

gagtcttccg ccgttaaaaa ccgctccagc ttggactacc gccgcaatta tgccggagtg 180

gtcagcagca aaagtgtgat tgccgcacaa accctgttgg gaccgcaggc cggcagcaac 240

acgcgcggtg agaaaaacct cacccttacc cttaacggcc gcagttacgg actggccgac 300

cgcatcaaca ttaccgcgct gccggacggc ctgctcgaac tgccctacaa agccgaatgg 360

acgtctttga aagtcgccta ccccgacagc cgagatgtaa aagtggaaga acaagggaaa 420

atgtatatct accaacgccc ctactccatg gtgttggcca ccctgcccac cgcctaccgt 480

tacgatggtg ctaacgaccc gaacaaccga ctcggtcgcg ctgacaccat gaaggtgcag 540

ctggtgagcg gcctgcccgt gaacgatgcc accatcaccc gtctcagcgg caacacgttc 600

aactacagtg gcgaatcttt tgccaatttc ggttctggtt tggaaaaagg cgcatttaac 660

tacagcatca actttaccga taaaaccggt agcggccgca ttaccggcat ggcttccacc 720

ggcgatatcg aactgcgcca agcccgtatc ggcggcgcac tgccatacaa tccgatgctg 780

tcggctgccg aacgcaccaa aggcatcaac ggtgaagccc attccgaacg catgaatgcc 840

taccgatatt acctttctat tttcggcccc aatgctgaag aagtagccgg ttttgtggaa 900

ggcagccgca gcaatcctgg cggccaatgg aatatcggcg tcagcggaac caaacagtaa 960

<210> 848

<211> 319

<212> PRT

<213> K. denitrificans SLP 4a

<400> 848

Met Lys His Leu Phe Ser Thr Thr Ile Ile Ala Leu Ser Leu Ala Ala

1 5 10 15

Cys Gly Ser Ser Gly Ser Ser Ala Pro Ser Thr Gln Ser Asn Thr Pro

20 25 30

Gln Ser Thr Ala Ser Pro Asp Ala Glu Ser Ser Ala Val Lys Asn Arg

35 40 45

Ser Ser Leu Asp Tyr Arg Arg Asn Tyr Ala Gly Val Val Ser Ser Lys

50 55 60

Ser Val Ile Ala Ala Gln Thr Leu Leu Gly Pro Gln Ala Gly Ser Asn

65 70 75 80

Thr Arg Gly Glu Lys Asn Leu Thr Leu Thr Leu Asn Gly Arg Ser Tyr

85 90 95

Gly Leu Ala Asp Arg Ile Asn Ile Thr Ala Leu Pro Asp Gly Leu Leu

100 105 110

Glu Leu Pro Tyr Lys Ala Glu Trp Thr Ser Leu Lys Val Ala Tyr Pro

115 120 125

Asp Ser Arg Asp Val Lys Val Glu Glu Gln Gly Lys Met Tyr Ile Tyr

130 135 140

Gln Arg Pro Tyr Ser Met Val Leu Ala Thr Leu Pro Thr Ala Tyr Arg

145 150 155 160

Tyr Asp Gly Ala Asn Asp Pro Asn Asn Arg Leu Gly Arg Ala Asp Thr

165 170 175

Met Lys Val Gln Leu Val Ser Gly Leu Pro Val Asn Asp Ala Thr Ile

180 185 190

Thr Arg Leu Ser Gly Asn Thr Phe Asn Tyr Ser Gly Glu Ser Phe Ala

195 200 205

Asn Phe Gly Ser Gly Leu Glu Lys Gly Ala Phe Asn Tyr Ser Ile Asn

210 215 220

Phe Thr Asp Lys Thr Gly Ser Gly Arg Ile Thr Gly Met Ala Ser Thr

225 230 235 240

Gly Asp Ile Glu Leu Arg Gln Ala Arg Ile Gly Gly Ala Leu Pro Tyr

245 250 255

Asn Pro Met Leu Ser Ala Ala Glu Arg Thr Lys Gly Ile Asn Gly Glu

260 265 270

Ala His Ser Glu Arg Met Asn Ala Tyr Arg Tyr Tyr Leu Ser Ile Phe

275 280 285

Gly Pro Asn Ala Glu Glu Val Ala Gly Phe Val Glu Gly Ser Arg Ser

290 295 300

Asn Pro Gly Gly Gln Trp Asn Ile Gly Val Ser Gly Thr Lys Gln

305 310 315

<210> 849

<211> 1023

<212> DNA

<213> K. denitrificans SLP 5a, HpuA

<400> 849

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ggcggcagtg ccatcaacga accgctgacc gccgcaccga ttcccgtttt gagggctgtc 120

gatacgacat cgcccaatat tgtggcagac accagcaccg accgcgaaca gcgcacgttc 180

gccacgcagg gtggctcggt caaaccgttc actatcacca agcccagccc ctatattcct 240

ggcctgatgc tgaccaatca ggaaatcctg tatcaggcac cggacggcaa atattacgat 300

ttcggcacat acaacacgct gattatgccc tcttccagca cttcggcgcg cgtcctgccc 360

aacagccacc ccatgcagcc gttggacagc ggcggcaaaa tgattgcctg ctgcaccaac 420

caaacgtcca ccggcatgaa tgcgctgcgc ttgaaaagca tgcaattcgg cgcatggatg 480

tcgcccagca aaaccgtcag ccttttgcc ggcggcacac ctgcaccgac agacacactg 540

caaggcgtcg ataccgccgg ccgccccacc ggcaaggcaa cgtatgaagt catcggcctg 600

cgcgtgaaaa acgaccgcgc cgtcacttcc agctacgaaa cgcgttattc gccgtacaac 660

accggacaag tcgttaccgg ctcgttctta acggtgaact tcaacaccgg caaactgggc 720

ggtacgattg tcggcaattc ggagttcggc gattcgattg aaatgcgcga tgtgaacgtg 780

aacggcaacc agttcagcgg cactgccagc tccggcgggc ataccggcca agtcagcggc 840

ggattgttcg ccaaagaaga acgcttttac agcggcacgt tggagcatcc ttccggcggc 900

gaaatcggcg gcacggtgaa cttcggcagc aacagcccgc tgaatgcgtc ttttggcggc 960

acgcggcgcg aatataacgc ggcagacacc agcacggata cctcgcattt ggtcagcccg 1020

taa 1023

<210> 850

<211> 340

<212> PRT

<213> K. denitrificans SLP 5a, HpuA

<400> 850

Met Asn Leu Pro Ser Ser Ala Leu Ser Leu Leu Ala Leu Ala Thr Leu

1 5 10 15

Ala Ala Cys Ala Gly Gly Ser Ala Ile Asn Glu Pro Leu Thr Ala Ala

20 25 30

Pro Ile Pro Val Leu Arg Ala Val Asp Thr Thr Ser Pro Asn Ile Val
35 40 45
Ala Asp Thr Ser Thr Asp Arg Glu Gln Arg Thr Phe Ala Thr Gln Gly
50 55 60
Gly Ser Val Lys Pro Phe Thr Ile Thr Lys Pro Ser Pro Tyr Ile Pro
65 70 75 80

Gly Leu Met Leu Thr Asn Gln Glu Ile Leu Tyr Gln Ala Pro Asp Gly
85 90 95
Lys Tyr Tyr Asp Phe Gly Thr Tyr Asn Thr Leu Ile Met Pro Ser Ser
100 105 110
Ser Thr Ser Ala Arg Val Leu Pro Asn Ser His Pro Met Gln Pro Leu
115 120 125
Asp Ser Gly Gly Lys Met Ile Ala Cys Cys Thr Asn Gln Thr Ser Thr
130 135 140

Gly Met Asn Ala Leu Arg Leu Lys Ser Met Gln Phe Gly Ala Trp Met
145 150 155 160
Ser Pro Ser Lys Thr Val Ser Leu Phe Ala Gly Gly Thr Pro Ala Pro
165 170 175
Thr Asp Thr Leu Gln Gly Val Asp Thr Ala Gly Arg Pro Thr Gly Lys
180 185 190
Ala Thr Tyr Glu Val Ile Gly Leu Arg Val Lys Asn Asp Arg Ala Val
195 200 205

Thr Ser Ser Tyr Glu Thr Arg Tyr Ser Pro Tyr Asn Thr Gly Gln Val
210 215 220
Val Thr Gly Ser Phe Leu Thr Val Asn Phe Asn Thr Gly Lys Leu Gly
225 230 235 240
Gly Thr Ile Val Gly Asn Ser Glu Phe Gly Asp Ser Ile Glu Met Arg
245 250 255
Asp Val Asn Val Asn Gly Asn Gln Phe Ser Gly Thr Ala Ser Ser Gly
260 265 270

Gly His Thr Gly Gln Val Ser Gly Gly Leu Phe Ala Lys Glu Glu Arg

275 280 285

Phe Tyr Ser Gly Thr Leu Glu His Pro Ser Gly Gly Glu Ile Gly Gly

290 295 300

Thr Val Asn Phe Gly Ser Asn Ser Pro Leu Asn Ala Ser Phe Gly Gly

305 310 315 320

Thr Arg Arg Glu Tyr Asn Ala Ala Asp Thr Ser Thr Asp Thr Ser His

325 330 335

Leu Val Ser Pro

340

<210> 851

<211> 555

<212> DNA

<213> K. kingae SLP 1a

<400> 851

gtggatggtg tcagcattca gttgccaaac aaaacagaca gaacaacttt aacagaagct 60

gacaattacc gtattttcaa taacctagac aatgtggttt atggtgcagc aactggcaac 120

ggtaaacacg ctttgtttgt acaaggtaat ttaactgccg atatgcctag tggcacagca 180

aaatacagcg gacaagtgtt gcactatcgt ggtcgcgttt tgaatggctc tggtgtattg 240

actggctcta atatcgacta cacttacact tacaacggca cattcaccgc aacggctgat 300

ttttcaagca aaaaactgtc tgctatcatt aacagcggag atagttcgta tatgggaaca 360

aaaaccttca atgcggttat taatggcaac agatttaagt cagatagctc atcgcccgat 420

caaacgatag aaggtggttt ctatggtgct aatgcggcag aaattgcagg taagtaccaa 480

tttattgatg gtaagagtga tacactttct gacagtggct tcggcgtatt cggcggtaaa 540

aaacaaacgc cctaa 555

<210> 852

<211> 184

<212> PRT

<213> K. kingae SLP 1a

<400> 852

Met Asp Gly Val Ser Ile Gln Leu Pro Asn Lys Thr Asp Arg Thr Thr

1 5 10 15

Leu Thr Glu Ala Asp Asn Tyr Arg Ile Phe Asn Asn Leu Asp Asn Val

20 25 30

Val Tyr Gly Ala Ala Thr Gly Asn Gly Lys His Ala Leu Phe Val Gln

35 40 45

Gly Asn Leu Thr Ala Asp Met Pro Ser Gly Thr Ala Lys Tyr Ser Gly

50 55 60

Gln Val Leu His Tyr Arg Gly Arg Val Leu Asn Gly Ser Gly Val Leu

65 70 75 80

Thr Gly Ser Asn Ile Asp Tyr Thr Tyr Thr Tyr Asn Gly Thr Phe Thr

85 90 95

Ala Thr Ala Asp Phe Ser Ser Lys Lys Leu Ser Ala Ile Ile Asn Ser

100 105 110

Gly Asp Ser Ser Tyr Met Gly Thr Lys Thr Phe Asn Ala Val Ile Asn

115 120 125

Gly Asn Arg Phe Lys Ser Asp Ser Ser Ser Pro Asp Gln Thr Ile Glu

130 135 140

Gly Gly Phe Tyr Gly Ala Asn Ala Ala Glu Ile Ala Gly Lys Tyr Gln

145 150 155 160

Phe Ile Asp Gly Lys Ser Asp Thr Leu Ser Asp Ser Gly Phe Gly Val

165 170 175

Phe Gly Gly Lys Lys Gln Thr Pro

180

<210> 853

<211> 1062

<212> DNA

<213> K. kingae SLP 2a

<400> 853

atgaaacaac ctattacttt taaacccttg attttagcaa ctttatgtgc ttcggtttta 60

tcggcttgcg gtggcggtgg aggcggttca aatgtaaata caaatggcac caatactgtt 120

ccaactaaac cagcacaacc taataaacca gtgcagccta ataaaccagt gcagcctaat 180

aaaccagtgc agcctaataa accagtgcag cctaataaac cagtgcagcc taataaacca 240

gtgcagccta ataacccagt gcagccacca ttaaccaagc agcaattgac tgacaaaaaa 300

gccattgcag aaaaatctgg ttttggtgta gtacgaaaca atgtagctaa caccattcaa 360

accgccgaag ttaaaatcgg caatcatgtt tacaaaggca aagctgacga tgccagcaaa 420

acgtattatg ttccgttaaa catcaacgat tttaaacagg gtatgagcga aggcaattta 480

agcagcacat ttaaatatgc agatggctct actgtccaaa ccgatagcac ttataaagtg 540

tataaccagc cgttttcgtt tgtggcaggc atctacgata accatgccaa aattcaaagc 600

ccaacggaaa acaataacga caaataccgc attgtatatg gtggaatttc gcccaaggtt 660

ttgcctgaaa acaacacgtt ccactattca ggtgttgcct acaacaaagg cgaaacaggc 720

aaattgaatt ataatattac ctataccgcc aacaacaacg gcaggggcga aggcgacatc 780

acagggctaa accaagtggg cgatattgag ctgagatgga gcgatattca tactactaat 840

gggcatcagc atcctgattt aaaaacaggc aattcaggaa tattacctag ttttggtatt 900

gcaggactgg ctgtacgcaa gaaaacaggc gacgaaatag ggccctacga attgggtatt 960

tatggcacag atgccagcga aatcgcaggc aggattaaga gcaaacatga tctagataat 1020

gtgatgttta ttggcaaaaa acaatctgcg cctaatccgt aa 1062

<210> 854

<211> 353

<212> PRT

<213> K. kingae SLP 2a

<400> 854

Met Lys Gln Pro Ile Thr Phe Lys Pro Leu Ile Leu Ala Thr Leu Cys

1 5 10 15

Ala Ser Val Leu Ser Ala Cys Gly Gly Gly Gly Gly Gly Ser Asn Val

20 25 30

Asn Thr Asn Gly Thr Asn Thr Val Pro Thr Lys Pro Ala Gln Pro Asn

35 40 45

Lys Pro Val Gln Pro Asn Lys Pro Val Gln Pro Asn Lys Pro Val Gln

50 55 60

Pro Asn Lys Pro Val Gln Pro Asn Lys Pro Val Gln Pro Asn Lys Pro

65 70 75 80

Val Gln Pro Asn Asn Pro Val Gln Pro Pro Leu Thr Lys Gln Gln Leu

85 90 95

Thr Asp Lys Lys Ala Ile Ala Glu Lys Ser Gly Phe Gly Val Val Arg

100 105 110

Asn Asn Val Ala Asn Thr Ile Gln Thr Ala Glu Val Lys Ile Gly Asn
115 120 125
His Val Tyr Lys Gly Lys Ala Asp Asp Ala Ser Lys Thr Tyr Tyr Val
130 135 140
Pro Leu Asn Ile Asn Asp Phe Lys Gln Gly Met Ser Glu Gly Asn Leu
145 150 155 160
Ser Ser Thr Phe Lys Tyr Ala Asp Gly Ser Thr Val Gln Thr Asp Ser

165 170 175
Thr Tyr Lys Val Tyr Asn Gln Pro Phe Ser Phe Val Ala Gly Ile Tyr
180 185 190
Asp Asn His Ala Lys Ile Gln Ser Pro Thr Glu Asn Asn Asn Asp Lys
195 200 205
Tyr Arg Ile Val Tyr Gly Gly Ile Ser Pro Lys Val Leu Pro Glu Asn
210 215 220
Asn Thr Phe His Tyr Ser Gly Val Ala Tyr Asn Lys Gly Glu Thr Gly

225 230 235 240
Lys Leu Asn Tyr Asn Ile Thr Tyr Thr Ala Asn Asn Asn Gly Arg Gly
245 250 255
Glu Gly Asp Ile Thr Gly Leu Asn Gln Val Gly Asp Ile Glu Leu Arg
260 265 270
Trp Ser Asp Ile His Thr Thr Asn Gly His Gln His Pro Asp Leu Lys
275 280 285
Thr Gly Asn Ser Gly Ile Leu Pro Ser Phe Gly Ile Ala Gly Leu Ala

290 295 300
Val Arg Lys Lys Thr Gly Asp Glu Ile Gly Pro Tyr Glu Leu Gly Ile
305 310 315 320
Tyr Gly Thr Asp Ala Ser Glu Ile Ala Gly Arg Ile Lys Ser Lys His
325 330 335
Asp Leu Asp Asn Val Met Phe Ile Gly Lys Lys Gln Ser Ala Pro Asn
340 345 350
Pro

<210> 855

<211> 1011

<212> DNA

<213> K. kingae SLP 3a

<400> 855

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tgcagcggta gtggtggcgg ttctggttta tccgcagcag gaacaggaag caatggtttg 120

aattcgggta gcacttctac tacacctaac aatacaggca acaacggtgg ctctacaact 180

gacaatacag gcacaaatac gaatactact accggatatt ctcctgtact agatgcagca 240

gctattaaag atgcctatac caaaattgct gataagaaca aggcaatagt aaccgatccc 300

actactagcg cagtagaaag tttaacagtt tccattacca aaggtactca aaccgataca 360

catttaactg tgagtgacat taatcttaac aaatatctgc cacataatga actcacagat 420

ttaaccatgc agactaaaca taccttaacg tataacgtaa gccaaccaga ccaaaagcaa 480

taccgttatg aaacaactga aaatgtgcgt gcttataacc aaaactactc gactgtgata 540

ggctttgata caactggtat caaaaccaca atgattggtt acgatacaaa gaaatctgaa 600

gaaaaaactt accctgacaa actaatgaat agctatgctg ttacaggtgt atctattgaa 660

caagctgcac tgccagctac tggttcttat acctatacag gtaaagcatt cactgccaca 720

gataatgacg gtgtgttgaa ctacaccatt aattttgata aaaaatcggg cagcggttct 780

attactggta ttgataaaac tggtacgatt actttgggag aaggtcgaat cggcacttac 840

actcatggca ccaagacaag tactgcgggt attggtgaaa cacaagcaac cactgccaat 900

ggcactgctg gtacttacac attaggtatc tttggtgcta atgcagaaga agtagctggt 960

acagtaaact tcaagggctt agagcacgtt ggtttcggtg gtaaacgcta a 1011

<210> 856

<211> 336

<212> PRT

<213> K. kingae SLP 3a

<400> 856

Met Tyr Thr Asn Lys Ser Lys Thr Leu Leu Ala Leu Leu Ile Ala Thr

1 5 10 15

Ala Leu Ser Ala Cys Ser Gly Ser Gly Gly Gly Ser Gly Leu Ser Ala

20 25 30

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Ala Gly Thr Gly Ser Asn Gly Leu Asn Ser Gly Ser Thr Ser Thr Thr
        35                  40                  45
Pro Asn Asn Thr Gly Asn Asn Gly Gly Ser Thr Thr Asp Asn Thr Gly
    50                  55                  60
Thr Asn Thr Asn Thr Thr Thr Gly Tyr Ser Pro Val Leu Asp Ala Ala
65                  70                  75                  80
Ala Ile Lys Asp Ala Tyr Thr Lys Ile Ala Asp Lys Asn Lys Ala Ile
                85                  90                  95

Val Thr Asp Pro Thr Thr Ser Ala Val Glu Ser Leu Thr Val Ser Ile
            100                 105                 110
Thr Lys Gly Thr Gln Thr Asp Thr His Leu Thr Val Ser Asp Ile Asn
        115                 120                 125
Leu Asn Lys Tyr Leu Pro His Asn Glu Leu Thr Asp Leu Thr Met Gln
    130                 135                 140
Thr Lys His Thr Leu Thr Tyr Asn Val Ser Gln Pro Asp Gln Lys Gln
145                 150                 155                 160

Tyr Arg Tyr Glu Thr Thr Glu Asn Val Arg Ala Tyr Asn Gln Asn Tyr
                165                 170                 175
Ser Thr Val Ile Gly Phe Asp Thr Thr Gly Ile Lys Thr Thr Met Ile
            180                 185                 190
Gly Tyr Asp Thr Lys Lys Ser Glu Glu Lys Thr Tyr Pro Asp Lys Leu
        195                 200                 205
Met Asn Ser Tyr Ala Val Thr Gly Val Ser Ile Glu Gln Ala Ala Leu
    210                 215                 220

Pro Ala Thr Gly Ser Tyr Thr Tyr Thr Gly Lys Ala Phe Thr Ala Thr
225                 230                 235                 240
Asp Asn Asp Gly Val Leu Asn Tyr Thr Ile Asn Phe Asp Lys Lys Ser
                245                 250                 255
Gly Ser Gly Ser Ile Thr Gly Ile Asp Lys Thr Gly Thr Ile Thr Leu
            260                 265                 270
Gly Glu Gly Arg Ile Gly Thr Tyr Thr His Gly Thr Lys Thr Ser Thr
```

275 280 285

Ala Gly Ile Gly Glu Thr Gln Ala Thr Thr Ala Asn Gly Thr Ala Gly
290 295 300
Thr Tyr Thr Leu Gly Ile Phe Gly Ala Asn Ala Glu Glu Val Ala Gly
305 310 315 320
Thr Val Asn Phe Lys Gly Leu Glu His Val Gly Phe Gly Gly Lys Arg
325 330 335

<210> 857
<211> 885
<212> DNA
<213> K. oralis SLP 1a
<400> 857

atgaaaatga aattaaccgt attggcgtgt gctgcattgt ttggtttgac tgcgtgtagc 60

agcggtggta attcaggcgt aagttatggt ggcacgattg gtgggggggc aagtgcaaga 120
cctacgcctc ctgcacccaa cccaaatcca gcacctaatc caaaaccagc acccaacccc 180
gcgcctactc caaatcctaa cccagctcca aatccagcac ctgcccctgc ccctgctcca 240
tcagcaacat tcaatggtgt tgctattcca gcagaaagcc aaaatggtgc taatacaccc 300
gttagcgcag ttggtagcag cacactagac aatgttactg taaacggtat taacatcact 360
ttaaaacaac ctggtattac tgctcgtaca tttaccaata tcagaaaaaa cacagaaacc 420
accattgcta gtggtacata tttgagccat atgcgttttg gtgcatatgc tgatttcaac 480

cacaacaaca atcccgattc aaacccatct tatacgtttg cattgggtag tgtaacgcct 540
gttgccgatg ttcccacatc aggcacagct acttacaatg gtttggcagt aggtagcgta 600
attggtggtg gtgcattcca agaaggtaca tcaacattta atgtggattt tggcgcgaaa 660
aaactagatg gttcagttac tattggcgct ttcaatccta ttcctttaac tgctaatatc 720
aacggcaacc aattctctgg tacatcagca gagggagttc ataccgatgg tcgcttctat 780
ggtccacaag cagctgaaat gggcggagta ttcaatggag aagttcctgc accagttggt 840
ggcggtactt tcaaatggat tggttcattt ggcgcgaaaa aataa 885

<210> 858
<211> 294
<212> PRT
<213> K. oralis SLP 1a

<400> 858

Met Lys Met Lys Leu Thr Val Leu Ala Cys Ala Ala Leu Phe Gly Leu
1 5 10 15
Thr Ala Cys Ser Ser Gly Gly Asn Ser Gly Val Ser Tyr Gly Gly Thr
20 25 30
Ile Gly Gly Gly Ala Ser Ala Arg Pro Thr Pro Pro Ala Pro Asn Pro
35 40 45
Asn Pro Ala Pro Asn Pro Lys Pro Ala Pro Asn Pro Ala Pro Thr Pro

50 55 60
Asn Pro Asn Pro Ala Pro Asn Pro Ala Pro Ala Pro Ala Pro Ala Pro
65 70 75 80
Ser Ala Thr Phe Asn Gly Val Ala Ile Pro Ala Glu Ser Gln Asn Gly
85 90 95
Ala Asn Thr Pro Val Ser Ala Val Gly Ser Ser Thr Leu Asp Asn Val
100 105 110
Thr Val Asn Gly Ile Asn Ile Thr Leu Lys Gln Pro Gly Ile Thr Ala

115 120 125
Arg Thr Phe Thr Asn Ile Arg Lys Asn Thr Glu Thr Thr Ile Ala Ser
130 135 140
Gly Thr Tyr Leu Ser His Met Arg Phe Gly Ala Tyr Ala Asp Phe Asn
145 150 155 160
His Asn Asn Asn Pro Asp Ser Asn Pro Ser Tyr Thr Phe Ala Leu Gly
165 170 175
Ser Val Thr Pro Val Ala Asp Val Pro Thr Ser Gly Thr Ala Thr Tyr

180 185 190
Asn Gly Leu Ala Val Gly Ser Val Ile Gly Gly Gly Ala Phe Gln Glu
195 200 205
Gly Thr Ser Thr Phe Asn Val Asp Phe Gly Ala Lys Lys Leu Asp Gly
210 215 220
Ser Val Thr Ile Gly Ala Phe Asn Pro Ile Pro Leu Thr Ala Asn Ile
225 230 235 240

Asn Gly Asn Gln Phe Ser Gly Thr Ser Ala Glu Gly Val His Thr Asp

245 250 255

Gly Arg Phe Tyr Gly Pro Gln Ala Ala Glu Met Gly Gly Val Phe Asn

260 265 270

Gly Glu Val Pro Ala Pro Val Gly Gly Gly Thr Phe Lys Trp Ile Gly

275 280 285

Ser Phe Gly Ala Lys Lys

290

<210> 859

<211> 900

<212> DNA

<213> K. oralis SLP 2a

<400> 859

atgatgtctt taaaacaact cggttcgctc actttggtcg cactttgctt ggcggcgtgc 60

agcagcggcg ggggaggcag ctcgggcaat ctcaacgctc ccgacacggg caacaataac 120

aacgccaata ataagcatac ggataaaagc gtgtccaaac tgatttcggt tgccgagttg 180

agagacaagg cagagattga tttgcaggat gagtttggtg cttccgccaa actgtcttca 240

tacgcgatta agctgaacgg gaaaacctac acccgtggca acattgattt ggctacgctg 300

ggcaacggct tcaaacgtgt tgatgttacc gaaaccgcat ccgccaaaat caacgggcaa 360

acccacaacg taacccaaaa cagcaaattg catctgtatc agcaacctta ttctgttgtg 420

gcttccatgc aaaccatgga tgggcaggtt ggcaatttgg gcaaaattga aaaaggcgaa 480

tttgaagttt ctttgtttga tggtcagcca actaaaacgc ttcccagcgc aggctcgttt 540

aactacaaag gcgttgcctt taccgaaaaa gaacaaggaa atttgaatta caccatcaac 600

tttgacacta aaaaaggcgc aggttccatt agcggcatca atcaaacagg caacattacg 660

ctgcatgaaa gcgatattgt gaaagttcaa gatggtgtgg catttaaaaa taattccgcc 720

tttacttatg gtgagaaaaa agatgtctat ggtgtgctca atggcgcagc aaccactgaa 780

aaacaaggcg tggcaagtta tgaattgggt atttttggac cgaatgccga tgaagtggcc 840

ggggcggttt tccaagaaca cgatgaaggg acggtcggct ttggcggcaa aaaacaataa 900

<210> 860

<211> 299

<212> PRT

<213> K. oralis SLP 2a

<400> 860

Met Met Ser Leu Lys Gln Leu Gly Ser Leu Thr Leu Val Ala Leu Cys
1 5 10 15

Leu Ala Ala Cys Ser Ser Gly Gly Gly Gly Ser Ser Gly Asn Leu Asn
20 25 30

Ala Pro Asp Thr Gly Asn Asn Asn Asn Ala Asn Asn Lys His Thr Asp
35 40 45

Lys Ser Val Ser Lys Leu Ile Ser Val Ala Glu Leu Arg Asp Lys Ala

50 55 60

Glu Ile Asp Leu Gln Asp Glu Phe Gly Ala Ser Ala Lys Leu Ser Ser
65 70 75 80

Tyr Ala Ile Lys Leu Asn Gly Lys Thr Tyr Thr Arg Gly Asn Ile Asp
85 90 95

Leu Ala Thr Leu Gly Asn Gly Phe Lys Arg Val Asp Val Thr Glu Thr
100 105 110

Ala Ser Ala Lys Ile Asn Gly Gln Thr His Asn Val Thr Gln Asn Ser

115 120 125

Lys Leu His Leu Tyr Gln Gln Pro Tyr Ser Val Val Ala Ser Met Gln
130 135 140

Thr Met Asp Gly Gln Val Gly Asn Leu Gly Lys Ile Glu Lys Gly Glu
145 150 155 160

Phe Glu Val Ser Leu Phe Asp Gly Gln Pro Thr Lys Thr Leu Pro Ser
165 170 175

Ala Gly Ser Phe Asn Tyr Lys Gly Val Ala Phe Thr Glu Lys Glu Gln

180 185 190

Gly Asn Leu Asn Tyr Thr Ile Asn Phe Asp Thr Lys Lys Gly Ala Gly
195 200 205

Ser Ile Ser Gly Ile Asn Gln Thr Gly Asn Ile Thr Leu His Glu Ser
210 215 220

Asp Ile Val Lys Val Gln Asp Gly Val Ala Phe Lys Asn Asn Ser Ala
225 230 235 240

Phe Thr Tyr Gly Glu Lys Lys Asp Val Tyr Gly Val Leu Asn Gly Ala

245 250 255

Ala Thr Thr Glu Lys Gln Gly Val Ala Ser Tyr Glu Leu Gly Ile Phe

260 265 270

Gly Pro Asn Ala Asp Glu Val Ala Gly Ala Val Phe Gln Glu His Asp

275 280 285

Glu Gly Thr Val Gly Phe Gly Gly Lys Lys Gln

290 295

<210> 861

<211> 1023

<212> DNA

<213> Kingella sp. Sch538 SLP 2a

<400> 861

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tctagcggtg ggggttcagc tttgagcgcg acaaacacta cgtcttctaa tttgggtgtg 120

aaaaccaata acaataattc ttctaaaaca gaaacaacaa acgaaaacac gactaatacc 180

acaaaggtaa cgttttcacc tgtgttagat gtggcagcta ttaaaacaag tatgaaagaa 240

gctgccgacg ctgcagcaaa agcagagtta tatagagtac ctaaaactat cgtttcttct 300

gcagaaagtt taactattga tttaattgat accaaaaatc aaaccaaaac ttatttaaca 360

gatagtaata ttgagctgaa agattatcta ccgaagaatg aagtaacaga tgtaacgatg 420

aaaatcaaac atacattaac ttataacggt tatgataaag aagataagga agttcaagat 480

tcttaccgtc gagacctcac tcaaactgta cgtgcttata atcaagatta ctctactgtg 540

attggttatg atacgaccaa cgatgatttt gctacattta atagtagtaa agatactagt 600

gtaaaaaaag ttaataaaac aagctattct gataaattga tggatactta tgatgtggtt 660

ggttcatcta ttaaaacagc tgcattgcca actagtggct cttataccta ttcaggtaaa 720

gcattcacag ccactgacaa agatggtgtg ttgagctata cagtagactt tgataaaaaa 780

tcaggtaaag gttctattac aggtatcgac acaactggca cgattacttt ggaagaaggc 840

aaaatcggtt cttatacaca caaaaccaca acttcttctg gtatcggtga aactcaagca 900

actacagcta agggtattgt aggcacttac accgtaggtt tcttcggtcc aaatgctgaa 960

gaagtggctg gtactgccaa ctttaaaggt ttggaacacg ttggttttgg cggcaaacgc 1020

taa 1023

<210> 862

<211> 340

<212> PRT

<213> Kingella sp. Sch538 SLP 2a

<400> 862

Met Ser Lys Asn Ile Val Leu Leu Ala Met Ala Met Ala Thr Ala Leu
1 5 10 15

Ser Ala Cys Gly Ser Ser Gly Gly Gly Ser Ala Leu Ser Ala Thr Asn
20 25 30

Thr Thr Ser Ser Asn Leu Gly Val Lys Thr Asn Asn Asn Asn Ser Ser
35 40 45

Lys Thr Glu Thr Thr Asn Glu Asn Thr Thr Asn Thr Thr Lys Val Thr
50 55 60

Phe Ser Pro Val Leu Asp Val Ala Ala Ile Lys Thr Ser Met Lys Glu
65 70 75 80

Ala Ala Asp Ala Ala Ala Lys Ala Glu Leu Tyr Arg Val Pro Lys Thr
85 90 95

Ile Val Ser Ser Ala Glu Ser Leu Thr Ile Asp Leu Ile Asp Thr Lys
100 105 110

Asn Gln Thr Lys Thr Tyr Leu Thr Asp Ser Asn Ile Glu Leu Lys Asp
115 120 125

Tyr Leu Pro Lys Asn Glu Val Thr Asp Val Thr Met Lys Ile Lys His
130 135 140

Thr Leu Thr Tyr Asn Gly Tyr Asp Lys Glu Asp Lys Glu Val Gln Asp
145 150 155 160

Ser Tyr Arg Arg Asp Leu Thr Gln Thr Val Arg Ala Tyr Asn Gln Asp
165 170 175

Tyr Ser Thr Val Ile Gly Tyr Asp Thr Thr Asn Asp Asp Phe Ala Thr
180 185 190

Phe Asn Ser Ser Lys Asp Thr Ser Val Lys Lys Val Asn Lys Thr Ser
195 200 205

Tyr Ser Asp Lys Leu Met Asp Thr Tyr Asp Val Val Gly Ser Ser Ile
210 215 220

Lys Thr Ala Ala Leu Pro Thr Ser Gly Ser Tyr Thr Tyr Ser Gly Lys
225 230 235 240

Ala Phe Thr Ala Thr Asp Lys Asp Gly Val Leu Ser Tyr Thr Val Asp
245 250 255

Phe Asp Lys Lys Ser Gly Lys Gly Ser Ile Thr Gly Ile Asp Thr Thr
260 265 270

Gly Thr Ile Thr Leu Glu Glu Gly Lys Ile Gly Ser Tyr Thr His Lys
275 280 285

Thr Thr Thr Ser Ser Gly Ile Gly Glu Thr Gln Ala Thr Thr Ala Lys
290 295 300

Gly Ile Val Gly Thr Tyr Thr Val Gly Phe Phe Gly Pro Asn Ala Glu
305 310 315 320

Glu Val Ala Gly Thr Ala Asn Phe Lys Gly Leu Glu His Val Gly Phe
325 330 335

Gly Gly Lys Arg
340

<210> 863
<211> 768
<212> DNA
<213> L. adecarboxylata SLP 1a
<400> 863

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ggtggcggtg gtggcggcgg cggtggaagt gacagtacgc ccccggtaac cactgcgcct 120
gtgcaaacgg ataacggcaa cacggacacc acaccggaaa cccctgtcac ggcaccggaa 180
acccctgcta cggcaccggt cagcctgacc accggcggta ccatttcggg ttggacctac 240
accacacctg agggccgtga atacgttatg cgcggcaccg ggatctctgc tggtctggtg 300
caaacccagc gactcacccg tgacgaccat tccccggtct cctcaacgtc atggtgctgt 360

ggccgtatga gttacaccac cttcggtacc tggacacagt atgaaaaagg tcagcatgac 420
gtcttctaca ccggggatgc cacgctcgcg gctaacgtgc caacccaggg aacggcgacc 480
tatgtgggtc acggcatgcg tgaaaataat ctgagtgatg ctcgctttga cattgatttc 540

gcggcgaaaa ccatcaacgg cacccttgcc ggaaatgata ccttcggtag cgaagttgcg 600

atgcagggca acattgccaa cggtggtttc accggtaatg cgcaatctgg cggacaggaa 660

gggacgttca ccggacattt caatggtccc acagctgaag agttaggcgg tctggcgcag 720

tttgcagaca cgactaaaaa cgcttccttt ggcgcgacac gtcaataa 768

<210> 864

<211> 255

<212> PRT

<213> L. adecarboxylata SLP 1a

<400> 864

Met Gly Ile Leu Lys Pro Gly Leu Leu Leu Thr Ala Phe Val Leu Thr

1 5 10 15

Ala Cys Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asp Ser

20 25 30

Thr Pro Pro Val Thr Thr Ala Pro Val Gln Thr Asp Asn Gly Asn Thr

35 40 45

Asp Thr Thr Pro Glu Thr Pro Val Thr Ala Pro Glu Thr Pro Ala Thr

50 55 60

Ala Pro Val Ser Leu Thr Thr Gly Gly Thr Ile Ser Gly Trp Thr Tyr

65 70 75 80

Thr Thr Pro Glu Gly Arg Glu Tyr Val Met Arg Gly Thr Gly Ile Ser

85 90 95

Ala Gly Leu Val Gln Thr Gln Arg Leu Thr Arg Asp Asp His Ser Pro

100 105 110

Val Ser Ser Thr Ser Trp Cys Cys Gly Arg Met Ser Tyr Thr Thr Phe

115 120 125

Gly Thr Trp Thr Gln Tyr Glu Lys Gly Gln His Asp Val Phe Tyr Thr

130 135 140

Gly Asp Ala Thr Leu Ala Ala Asn Val Pro Thr Gln Gly Thr Ala Thr

145 150 155 160

Tyr Val Gly His Gly Met Arg Glu Asn Asn Leu Ser Asp Ala Arg Phe

165 170 175

Asp Ile Asp Phe Ala Ala Lys Thr Ile Asn Gly Thr Leu Ala Gly Asn

180 185 190

Asp Thr Phe Gly Ser Glu Val Ala Met Gln Gly Asn Ile Ala Asn Gly

195 200 205

Gly Phe Thr Gly Asn Ala Gln Ser Gly Gly Gln Glu Gly Thr Phe Thr

210 215 220

Gly His Phe Asn Gly Pro Thr Ala Glu Glu Leu Gly Gly Leu Ala Gln

225 230 235 240

Phe Ala Asp Thr Thr Lys Asn Ala Ser Phe Gly Ala Thr Arg Gln

245 250 255

<210> 865

<211> 2841

<212> DNA

<213> M. caprae SLP 1a

<400> 865

atgcctaaga gtaccaaatt tagcctattg cctttggcgg tggctgtgac ttcattgatg 60

ctatcagcct gtggtggtgg cagttttgat aacccaagta ccattgtcat cggtcagtct 120

aggatgattg agaagtctga ccaatcaaag aatgtctcaa ccgataaggc tgatgacaat 180

gccaatgcca atgctgatac taagaataaa gcagacagtc gcctaaccat gccagtgttg 240

ggcagtgttt tggcgattcc aaagcgtaat ctggctcttg ataagaaaaa actgactcgt 300

ctagaagagc atgtgccact tgatgaaaat aacatcaaga ccgctcatgc caacccttg 360

ccagctttaa ccaaagagtt acaagagcgc tataaggatg aaaagataca tcagagcgat 420

gataaatata agtttgtaaa agctggttgg atttttgctg gtttgcgtcc ttatgagacg 480

attacaactg atgaggatac agaccaacct aagcgatata ccaaaggcga tggctatctg 540

tactattatg gtgaaaatcc aaccacaggg cttgccaaag gtgtggcaaa ctatacgggg 600

cattgggatt tcgtgactga tgtcaagcga ataagagagt ctcccaccaa agagaataca 660

ggtcgccaag cgttcggtgg tggtttagcc tataggatgg acagcggctt tggtgatgaa 720

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accatcaagg gcaatcgatt tgtgggttct gccatcgcaa aaaataccga aaccagcttt 960

atgaagccta actttttag taaaaatgcc gatgaccgcc tagaaggtgg gttttatggt 1020

gaaaacgctg aggaattggc aggtaagttt ttaaccaatg ataattctgt ctttgcagtg 1080

tttgctggta agcaggacaa ccctgagaaa gttgagaagc ttgagcaggt atttggtggt 1140

gcttatgtcg agctgaccca agacaaggct gtcaaccctg cacaaaagtc acaagtgtta 1200

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taccaaaaaa atagtcaaga tagagcgacc ttaagaaagc aaattactga aaaggtttta 1620

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<210> 866

<211> 946

<212> PRT

<213> M. caprae SLP 1a

<400> 866

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Thr Ser Leu Met Leu Ser Ala Cys Gly Gly Gly Ser Phe Asp Asn Pro
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Ser Thr Ile Val Ile Gly Gln Ser Arg Met Ile Glu Lys Ser Asp Gln
35 40 45

Ser Lys Asn Val Ser Thr Asp Lys Ala Asp Asp Asn Ala Asn Ala Asn
50 55 60

Ala Asp Thr Lys Asn Lys Ala Asp Ser Arg Leu Thr Met Pro Val Leu
65 70 75 80

Gly Ser Val Leu Ala Ile Pro Lys Arg Asn Leu Ala Leu Asp Lys Lys
85 90 95

Lys Leu Thr Arg Leu Glu Glu His Val Pro Leu Asp Glu Asn Asn Ile
100 105 110

Lys Thr Ala His Ala Asn Pro Leu Pro Ala Leu Thr Lys Glu Leu Gln
115 120 125

Glu Arg Tyr Lys Asp Glu Lys Ile His Gln Ser Asp Asp Lys Tyr Lys
130 135 140

Phe Val Lys Ala Gly Trp Ile Phe Ala Gly Leu Arg Pro Tyr Glu Thr
145 150 155 160

Ile Thr Thr Asp Glu Asp Thr Asp Gln Pro Lys Arg Tyr Thr Lys Gly
165 170 175

Asp Gly Tyr Leu Tyr Tyr Tyr Gly Glu Asn Pro Thr Thr Gly Leu Ala
180 185 190

Lys Gly Val Ala Asn Tyr Thr Gly His Trp Asp Phe Val Thr Asp Val
195 200 205
Lys Arg Ile Arg Glu Ser Pro Thr Lys Glu Asn Thr Gly Arg Gln Ala
210 215 220
Phe Gly Gly Gly Leu Ala Tyr Arg Met Asp Ser Gly Phe Gly Asp Glu
225 230 235 240

Val Gly Ala Thr Ser Phe Ala Glu Gln Val Phe Gly Gln Val Ser Pro
245 250 255
Arg Gln Gly Asn His Arg Ala Val Phe Lys Ala Asp Phe Asp Ala Lys
260 265 270
Lys Leu Thr Gly Thr Leu Ser Thr Lys Gln Lys Ala Ile Ala Ser Ser
275 280 285
Pro Glu Thr Tyr Leu Asp Arg Tyr Asp Ile Asp Ala Thr Ile Lys Gly
290 295 300

Asn Arg Phe Val Gly Ser Ala Ile Ala Lys Asn Thr Glu Thr Ser Phe
305 310 315 320
Met Lys Pro Asn Phe Phe Ser Lys Asn Ala Asp Asp Arg Leu Glu Gly
325 330 335
Gly Phe Tyr Gly Glu Asn Ala Glu Glu Leu Ala Gly Lys Phe Leu Thr
340 345 350
Asn Asp Asn Ser Val Phe Ala Val Phe Ala Gly Lys Gln Asp Asn Pro
355 360 365

Glu Lys Val Glu Lys Leu Glu Gln Val Phe Gly Gly Ala Tyr Val Glu
370 375 380
Leu Thr Gln Asp Lys Ala Val Asn Pro Ala Gln Lys Ser Gln Val Leu
385 390 395 400
Ser Leu Val Asn Phe Gly Asn Val Asp Gln Leu Gln Leu Gly Asp His
405 410 415
Thr Ile Thr Leu Leu Pro Gln Glu Ala Gly Lys Thr Thr Gln Gln Ser
420 425 430

Val Lys Leu Pro Thr Gly Gln Thr Ala Val Ile Thr Ser Phe Gly Ser

435 440 445

Ser Asp Gly Val Leu Arg Leu Gly Ser Val Ser Lys Thr Ala Lys Thr

450 455 460

Ile Glu Thr Thr Ala Lys Ser Lys Pro Ala Glu Asn Val Lys Val Thr

465 470 475 480

Asn Lys Asp Lys Val Gly Glu Pro Ala Lys Pro Thr Ala Glu Gln Leu

485 490 495

Glu Ala Ala Lys Glu Lys Leu Thr Glu Lys Met Asp Glu Leu Lys Ala

500 505 510

Glu Leu Thr Ile Leu Leu Asp Ser Tyr Gln Lys Asn Ser Gln Asp Arg

515 520 525

Ala Thr Leu Arg Lys Gln Ile Thr Glu Lys Val Leu Leu Gly Tyr Asn

530 535 540

Asp Glu Ser Ser Lys Lys Asn Val Ala Glu Val Leu Gln Asp Met Phe

545 550 555 560

Asn Ser Leu Val Asp Ser Asp Glu Glu Glu Arg Glu Trp Ala Ala Asp

565 570 575

Asn Ile Leu Glu Met Leu Val Thr Gly Asp Lys Phe Asn Ser Asp Asn

580 585 590

Leu Glu Asn Leu Lys Glu Phe Leu Val Gln Asn Ser Leu Ala Gln Ser

595 600 605

Val Pro Ser His Thr Gln Asp Gln Ile Ala Lys Ala Lys Ala Asp Leu

610 615 620

Lys Val Lys Leu Glu Thr Glu Lys Gln Glu Leu Lys Asp Leu Leu Asp

625 630 635 640

Ile Phe Ala Ile Glu Asn Gly Asn Phe Asn Phe Gly Asn Asn Glu Glu

645 650 655

Ser Asn Glu Thr Ala Gln Asn Pro Ala Glu Asp Asp Asp Glu Arg Val

660 665 670

Asn Gly Ala Thr Asp Ser Ala Asp Glu Val Ala Ser Ala Asp Val Asp

675 680 685

Asp Leu Glu Glu Leu Lys Ala Glu Val Ile Asp Lys Ile Lys Thr Ala
690 695 700

Tyr Thr Lys Asp Arg Gln Asp Val Ile Gly Lys Gln Ala Val Thr Leu
705 710 715 720

Leu Glu Glu Leu Lys Asn Gly Asn Glu Glu Ala Ser Gly Lys Leu Val
725 730 735

Ala Leu Phe Ala Gln Gly Asp Lys Phe Asn Ser Asp Asn Leu Glu Asn
740 745 750

Leu Thr Ala Tyr Leu Pro Ala Leu Pro Ser Thr Pro Asp Ala Ser Thr
755 760 765

Pro Glu Gln Ser Asp Ala Ile Pro Leu Ile Gly Ile Glu Asp Ser Leu
770 775 780

Thr Gly Leu Tyr Ile Leu Gly Gln Arg Thr Pro Ala Ser Gln Ile Ala
785 790 795 800

Asn Gln Gly Gln Ala Ser Tyr Gln Gly Thr Trp His Gly Arg Ile Gly
805 810 815

His His Trp Gln Ser Gln Ala Gly Tyr Gly Lys Tyr Asp Gly Lys Ala
820 825 830

Asn Phe Glu Val Asp Phe Gly Ala Lys Gln Leu Thr Gly Thr Leu Thr
835 840 845

Glu Lys Ser Gly Ile Glu Pro Ala Phe Asn Leu Lys Ala Thr Ile Asn
850 855 860

Gly Asn Gly Phe Ser Gly Thr Ala Thr Ser Arg Ser Asn Gly Ile Tyr
865 870 875 880

Leu Asp Glu Gly Arg Gln Gln Asn Gln Gln Ile Leu Thr Val Glu Ser
885 890 895

Asn Asn Leu Thr Gly Ala Phe Tyr Gly Glu Asn Ala Lys His Leu Gly
900 905 910

Gly Ser Phe Ser Phe Glu Lys Asn Leu Ser Asp Asp Glu Thr Val Val
915 920 925

Gly Gly Ala Val Phe Tyr Gly Thr Lys Thr Thr Glu Asp Glu Lys Lys

930 935 940

Gln Lys

945

<210> 867

<211> 2124

<212> DNA

<213> M. catarrhalis SLP 1, TbpB

<400> 867

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tcaggtaata ctggcaacac tggtaatgct ggcggtactg ataatacagc caatgcaggt 180

aatacaggcg gtgcaagctc tggtacaggc agtgccaaca caccagaacc aaaatatcaa 240

gatgtgccaa ctgataaaaa tgaaaaaagc atgaaaaaag ctgaagtttc agacatacaa 300

aaacctgcca tgggttatgc aatggaatta aagcttcgta atgctcaccc tgagaatcca 360

aataaagaga ccgaaaaaca catcgcctta gaccaaaaag atttggtggc ggtagagggc 420

gacctaacca atattccttt tgataaaaat cttattgaat accttaaaaa atcacccgag 480

gttgtaagta aattcaatga acaaaaaggc ggtattgaaa ataacacaaa attaacatac 540

aaagattcat tattatcatc agagcaaaaa aaagcaaaag tcaaagaagc gttggacaat 600

gctttaactc aatttgccca agaaaaatac aaggagctaa ttgagaatgc ccatgataaa 660

aaatctgacg cacgcaaccg tgacctaaaa tatgtcaagt ctggttttaa ctatctttct 720

ggatataccg ccaccgacca cgataaaaaa ccaattatcg tggctattat ggtgcgttgt 780

attataaagg cagtgaaacc gccaaagagt taccacaaac aagtgcaaaa tataaaggtt 840

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aaaaaacaag aagtcaaacc atga 2124

<210> 868

<211> 707

<212> PRT

<213> M. catarrhalis SLP 1, TbpB

<400> 868

Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
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Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
20 25 30

Thr Pro Ile Pro Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn Thr Gly
35 40 45

Asn Ala Gly Gly Thr Asp Asn Thr Ala Asn Ala Gly Asn Thr Gly Gly
50 55 60

Ala Ser Ser Gly Thr Gly Ser Ala Asn Thr Pro Glu Pro Lys Tyr Gln
65 70 75 80

Asp Val Pro Thr Asp Lys Asn Glu Lys Ser Met Lys Lys Ala Glu Val
85 90 95

Ser Asp Ile Gln Lys Pro Ala Met Gly Tyr Ala Met Glu Leu Lys Leu

100 105 110

Arg Asn Ala His Pro Glu Asn Pro Asn Lys Glu Thr Glu Lys His Ile

115 120 125

Ala Leu Asp Gln Lys Asp Leu Val Ala Val Glu Gly Asp Leu Thr Asn

130 135 140

Ile Pro Phe Asp Lys Asn Leu Ile Glu Tyr Leu Lys Lys Ser Pro Glu

145 150 155 160

Val Val Ser Lys Phe Asn Glu Gln Lys Gly Gly Ile Glu Asn Asn Thr

165 170 175

Lys Leu Thr Tyr Lys Asp Ser Leu Leu Ser Ser Glu Gln Lys Lys Ala

180 185 190

Lys Val Lys Glu Ala Leu Asp Asn Ala Leu Thr Gln Phe Ala Gln Glu

195 200 205

Lys Tyr Lys Glu Leu Ile Glu Asn Ala His Asp Lys Lys Ser Asp Ala

210 215 220

Arg Asn Arg Asp Leu Lys Tyr Val Lys Ser Gly Phe Asn Tyr Leu Ser

225 230 235 240

Gly Tyr Thr Ala Thr Asp His Asp Lys Lys Pro Ile Ile Val Ala Ile

245 250 255

Met Val Arg Cys Ile Ile Lys Ala Val Lys Pro Pro Lys Ser Tyr His

260 265 270

Lys Gln Val Gln Asn Ile Lys Val Ile Gly Thr Leu Met Thr Asp Ala

275 280 285

Thr Phe Asp Asn Lys Tyr Thr Asp Leu Pro Gly Ile Ala Arg Gln Thr

290 295 300

Gln Trp Arg Ser Leu Val Ser Thr Asp Glu Tyr Ala Thr Leu Leu Thr

305 310 315 320

Asp Lys Asn Asn Lys Pro Ser Asn Tyr Asn Gly Ala Tyr Gly His Ser

325 330 335

Ser Glu Phe Asp Val Asp Phe Ala Asn Lys Lys Val Thr Gly Lys Leu

340 345 350

Ile Ser Asn Gln Leu Ser Gly Thr Ala Val Thr Ala Lys Glu Arg Tyr

355 360 365

Lys Ile Glu Ala Asp Ile His Gly Asn Arg Phe Arg Gly Ser Ala Thr

370 375 380

Ala Ser Asp Lys Ala Glu Asp Ser Lys Ser Lys His Pro Phe Thr Ser

385 390 395 400

Asp Ala Lys Asp Arg Leu Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu

405 410 415

Glu Leu Ala Gly Lys Phe Leu Thr Asp Asp Asn Lys Leu Phe Gly Val

420 425 430

Phe Gly Ala Lys Gln Glu Gly Lys Val Glu Lys Thr Glu Ala Ile Leu

435 440 445

Asp Ala Tyr Ala Leu Gly Thr Phe Asn Asn Thr Asn Lys Ala Thr Thr

450 455 460

Phe Thr Pro Phe Thr Lys Lys Gln Leu Asp Asn Phe Gly Asn Ala Lys

465 470 475 480

Lys Leu Val Leu Gly Ser Thr Val Ile Asp Leu Val Pro Thr Asp Ala

485 490 495

Thr Lys Asp Val Asn Glu Phe Thr Lys Asp Lys Pro Thr Ser Ala Thr

500 505 510

Asn Lys Ala Gly Glu Thr Leu Met Val Asn Asp Glu Val Ser Val Lys

515 520 525

Thr Tyr Gly Lys Asn Phe Glu Tyr Leu Lys Phe Gly Glu Leu Ser Val

530 535 540

Gly Gly Ser His Ser Val Phe Leu Gln Gly Glu Arg Thr Ala Thr Thr

545 550 555 560

Gly Glu Lys Ala Val Pro Thr Thr Gly Thr Ala Lys Tyr Leu Gly Asn

565 570 575

Trp Val Gly Tyr Ile Thr Gly Lys Asp Thr Gly Ala Gly Ser Ser Lys

580 585 590

Gly Phe Thr Asp Ala Lys Asp Val Ala Asp Phe Asp Ile Asp Phe Glu

595 600 605

Lys Lys Ser Val Asn Gly Lys Leu Thr Thr Gln Gly Arg Gln Asp Pro

610 615 620

Val Phe Ser Ile Thr Gly Asn Ile Ser Gly Asn Gly Trp Thr Gly Thr

625 630 635 640

Ala Ser Thr Thr Lys Ala Asn Ala Gly Gly Tyr Lys Ile Asp Ser Ser

645 650 655

Ser Thr Gly Lys Ser Ile Val Ile Glu Asn Ala Asp Val Thr Gly Gly

660 665 670

Phe Tyr Gly Pro Asn Ala Asn Glu Met Gly Gly Ser Phe Thr His Asp

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Thr Asn Asp Ser Lys Ala Ser Val Val Phe Gly Thr Lys Lys Gln Glu

690 695 700

Val Lys Pro

705

<210> 869

<211> 2847

<212> DNA

<213> M. catarrhalis SLP 2a, LbpB

<400> 869

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accaataaca ccaacaatca gggcaacaac acggataaca gtaccagcac aactgaccca 360

aatggcgata acaaccaact gacacaagca caaaaaactg ccgccgccgc agggtttttt 420

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<210> 870

<211> 948

<212> PRT

<213> M. catarrhalis SLP 2a, LbpB

<400> 870

Met Ser Phe Cys Leu Val Val Cys Leu Trp Glu Leu Ile Val Leu Thr
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Leu Val Val Asp Ala Trp Ala Asp Leu Ile Lys Arg Ser Ser Gln His
20 25 30

Thr Lys Arg Asp Ile Thr Met Ser Thr Val Lys Thr Pro His Ile Phe
35 40 45

Tyr Gln Lys Arg Thr Leu Ser Leu Ala Ile Ala Ser Ile Phe Ala Ala
50 55 60

Leu Val Met Thr Gly Cys Arg Ser Asp Asp Ile Ser Val Asn Ala Pro
65 70 75 80

Asn Val Thr Gln Leu Pro Gln Gly Thr Val Ser Pro Ile Pro Asn Thr
85 90 95

Gly His Asp Asn Thr Asn Asn Thr Asn Asn Gln Gly Asn Asn Thr Asp
100 105 110

Asn Ser Thr Ser Thr Thr Asp Pro Asn Gly Asp Asn Asn Gln Leu Thr
115 120 125

Gln Ala Gln Lys Thr Ala Ala Ala Ala Gly Phe Phe Val Met Gly Lys
130 135 140

Ile Arg Asp Thr Ser Pro Lys Asn Asp Pro Asp Tyr Gly Asp Asp Leu
145 150 155 160

Lys Gln Gln Trp Leu Gly Lys Leu Tyr Val Gly Ile Asp Ala His Arg
165 170 175
Pro Asp Gly Ile Gly Lys Gly Lys Asn Leu Arg Gln Pro Ile Thr Ala
180 185 190
Asn Asp Ile Lys Pro Leu Tyr Phe Asn Lys Phe Pro Ala Leu Ser Asp
195 200 205
Leu His Leu Asp Ser Glu Arg His Arg Phe Asp Pro Gln Lys Ile Asn

210 215 220
Thr Ile Lys Val Tyr Gly Tyr Gly Asn Leu Thr Thr Pro Ser Asn Asn
225 230 235 240
Asn Thr His Ile Asn His Gln Gln Ala Asp Asn Ala Lys Ala Lys Lys
245 250 255
Pro Thr Asp Ala Tyr Glu Asn Ile Arg Phe Gly Tyr Leu Glu Leu Gln
260 265 270
Gly Ser Ser Leu Thr Gln Lys Asn Ala Asp Asn Gln Asn Asp Gln Asp

275 280 285
Arg Ile Pro Lys Pro Met Pro Ile Leu Phe Tyr His Gly Glu Asn Ala
290 295 300
Ser Ser Gln Leu Pro Ser Ala Gly Lys Phe Asn Tyr Thr Gly Asn Trp
305 310 315 320
Leu Tyr Leu Ser Asp Val Lys Lys Arg Pro Ala Leu Ser Ala Ser Asp
325 330 335
Asp Arg Val Gly Val Tyr Leu Asn Ala Ser Gly Lys Ala Asn Glu Gly

340 345 350
Asp Val Val Ser Ala Ala His Ile Tyr Leu Asn Gly Phe Gln Tyr Lys
355 360 365
His Thr Pro Ala Thr Tyr Gln Val Asp Phe Asp Thr Asn Ser Leu Thr
370 375 380
Gly Lys Leu Ser Tyr Tyr Asp Asn Pro Asn Lys Lys Thr Ala Gln Gly
385 390 395 400
Glu Tyr Leu Lys Ser Gln Phe Asp Thr Ser Lys Lys Val Asn Glu Thr

405 410 415

Asp Val Tyr Gln Ile Asp Ala Lys Ile Asn Gly Asn Arg Phe Val Gly

420 425 430

Thr Ala Lys Ser Leu Val Asn Glu Asn Thr Lys Thr Ala Pro Phe Ile

435 440 445

Lys Glu Leu Phe Ser Lys Lys Ala Asn Pro Asn Asn Pro Asp Pro Asn

450 455 460

Ser Asp Thr Leu Glu Gly Gly Phe Tyr Gly Lys Ser Gly Asp Glu Leu

465 470 475 480

Ala Gly Lys Phe Leu Ser Asn Asp Asn Ala Thr Tyr Val Val Phe Gly

485 490 495

Gly Lys Arg Asp Lys Thr Ala Glu Pro Val Ala Thr Lys Thr Val Tyr

500 505 510

Phe Ser Ala Gly Phe Glu Lys Pro Ser Thr Ser Phe Val Asp Asn Glu

515 520 525

Thr Ile Gly Arg Ile Ile Asn Ser Lys Gly Leu Asn Asp Asn Ile Glu

530 535 540

Glu Asp Ala Ile Thr Pro Ser Asp Asn Ser Tyr Tyr Glu Tyr Asn Trp

545 550 555 560

Gly Lys Pro Glu Lys Gln Phe Thr Lys Lys Val Ser Ser Ser Thr Gln

565 570 575

Ala Val Pro Ala Tyr Phe Gly Gln His Asp Lys Phe Tyr Phe Asn Gly

580 585 590

Asn Tyr Tyr Asp Leu Ser Ala Ser Ser Val Asp Lys Leu Ala Pro Ala

595 600 605

Asp Ala Val Lys Ala Asn Gln Ser Ile Lys Glu Lys Tyr Pro Asn Ala

610 615 620

Thr Leu Asn Lys Asp Lys Val Thr Thr Ile Val Leu Gln Glu Ala Lys

625 630 635 640

Asp Asn Lys Pro Tyr Thr Ala Ile His Ala Lys Ser Tyr Asp His Ile

645 650 655

Ser Phe Gly Glu Val Leu Tyr Asn Asp Asn Lys Gly Asn Pro Thr Arg

660 665 670

Ser Tyr Phe Val Gln Gly Gly Gln Ala Asp Val Ser Thr Gln Leu Pro

675 680 685

Ser Ala Gly Lys Phe Thr Tyr Asn Gly Leu Trp Ala Gly Tyr Leu Ala

690 695 700

Gln Lys Lys Asp Lys Gly Tyr Ser Asn Lys Glu Glu Thr Ile Lys Ala

705 710 715 720

Lys Gly His Gln Asp Tyr Leu Leu Thr Glu Asp Phe Thr Pro Glu Asp

725 730 735

Asp Asp Asn Asp Leu Ile Ala Ser Asp Asp Ser Gln Asp Asp Asn Thr

740 745 750

His Gly Asp Asp Asp Leu Ile Ala Ser Asp Asp Ser Gln Asp Asp Asn

755 760 765

Thr His Gly Asp Asp Asp Leu Ile Ala Ser Asp Asp Ser Gln Asp Asp

770 775 780

Asp Ala Asp Gly Asp Asp Asp Ser Asp Asp Leu Gly Asp Gly Ala Asp

785 790 795 800

Asp Asp Ala Ala Gly Lys Val Tyr His Ala Gly Asn Ile Arg Pro Glu

805 810 815

Phe Glu Asn Lys Tyr Leu Pro Ile Asn Glu Pro Thr His Glu Lys Thr

820 825 830

Phe Ala Leu Asp Gly Lys Asn Lys Ala Lys Phe Asp Val Asp Phe Asp

835 840 845

Thr Asn Ser Leu Thr Gly Lys Leu Asn Asp Glu Arg Gly Asp Ile Val

850 855 860

Phe Asp Ile Lys Asn Gly Lys Ile Asp Gly Thr Gly Phe Thr Ala Lys

865 870 875 880

Ala Asp Val Pro Asn Tyr Arg Glu Glu Val Gly Asn Asn Gln Gly Gly

885 890 895

Gly Phe Leu Tyr Asn Ile Gln Asp Ile Asp Val Lys Gly Gln Phe Phe

900 905 910

Gly Thr Asn Gly Glu Glu Leu Ala Gly Gln Leu Gln Tyr Asp Lys Gly

915 920 925

Asp Gly Ile Asn Asp Thr Ala Glu Lys Ala Gly Ala Val Phe Gly Ala

930 935 940

Val Lys Asp Lys

945

<210> 871

<211> 792

<212> DNA

<213> M. granulomatis SLP 1a

<400> 871

atgaaaaaat tagcaaaact cagccttaca ttattagcag tcaccgtaat ttcggcatgt 60

ggtagttctg gcggtagtag cgacaattct aattcacaag caactccatc aaaaccgact 120

gtaaccacta cagctccgac gaagcagaca accaccaatc caacaacaaa acctaccaca 180

acgaaaccaa caacatcaac tagctctagc gacaaaatgg gaacagcttt ccgcgttaac 240

gatagtaaag agttcgatat taaaaaagcc tcaacatata aaacagaatt agtagttgac 300

agtaaaacat tacctgtagc ttggaatggc attgtatcgg gtggattcac aaaactaagc 360

aatgcaacaa tcaatggggt aacttataaa gactttaccg ttagtggtgc aagatattct 420

tctgtaaaat ttggtcatat tgatggctac gtatttacac aaggagatgt aacaccaaaa 480

gctagtattc caaccagcgg caacgcaact tatcttgtgg atggtgtttt tgttgcaaac 540

ggtaaaacct caacttccca aggtcatagc ctaaacgttg attttgcgaa taaaacttta 600

aatggtacta tcgcaactga tgtaacagta acaaacgcta aaatcagtgg caatgaattt 660

gaaggtaaag ccgtccataa tggtaaatca gcagaactag aagggcattt ctatggctca 720

aatgctgctg aaattggtgg aacttatagc tcatcgaact tctcaggtgc atttggcggt 780

aaaaaacaat aa 792

<210> 872

<211> 263

<212> PRT

<213> M. granulomatis SLP 1a

<400> 872

Met Lys Lys Leu Ala Lys Leu Ser Leu Thr Leu Leu Ala Val Thr Val

1 5 10 15

Ile Ser Ala Cys Gly Ser Ser Gly Gly Ser Ser Asp Asn Ser Asn Ser
20 25 30
Gln Ala Thr Pro Ser Lys Pro Thr Val Thr Thr Thr Ala Pro Thr Lys
35 40 45
Gln Thr Thr Thr Asn Pro Thr Thr Lys Pro Thr Thr Thr Lys Pro Thr
50 55 60
Thr Ser Thr Ser Ser Ser Asp Lys Met Gly Thr Ala Phe Arg Val Asn
65 70 75 80

Asp Ser Lys Glu Phe Asp Ile Lys Lys Ala Ser Thr Tyr Lys Thr Glu
85 90 95
Leu Val Val Asp Ser Lys Thr Leu Pro Val Ala Trp Asn Gly Ile Val
100 105 110
Ser Gly Gly Phe Thr Lys Leu Ser Asn Ala Thr Ile Asn Gly Val Thr
115 120 125
Tyr Lys Asp Phe Thr Val Ser Gly Ala Arg Tyr Ser Ser Val Lys Phe
130 135 140

Gly His Ile Asp Gly Tyr Val Phe Thr Gln Gly Asp Val Thr Pro Lys
145 150 155 160
Ala Ser Ile Pro Thr Ser Gly Asn Ala Thr Tyr Leu Val Asp Gly Val
165 170 175
Phe Val Ala Asn Gly Lys Thr Ser Thr Ser Gln Gly His Ser Leu Asn
180 185 190
Val Asp Phe Ala Asn Lys Thr Leu Asn Gly Thr Ile Ala Thr Asp Val
195 200 205

Thr Val Thr Asn Ala Lys Ile Ser Gly Asn Glu Phe Glu Gly Lys Ala
210 215 220
Val His Asn Gly Lys Ser Ala Glu Leu Glu Gly His Phe Tyr Gly Ser
225 230 235 240
Asn Ala Ala Glu Ile Gly Gly Thr Tyr Ser Ser Ser Asn Phe Ser Gly
245 250 255

Ala Phe Gly Gly Lys Lys Gln
260

<210> 873

<211> 606

<212> DNA

<213> M. granulomatis SLP 2a

<400> 873

atgaaaaaac tacttctttg ttcagtggcc ggcttatctg ttttattaac tgcttgtggt 60

ggaggtggag gcagtggatc tgctaaaacg cctgatggta ctaaagtgga tttaacaaat 120

agccaaaaag gcgatgttgc tggtaataca gcagcgggtt ctttatatgg aaaaaaccag 180

aatgattcat tttatggcgt atggttaaat gatgctaaaa cagtgagaga attacgttat 240

caaggtacgg aggccacaaa tctaccttca ggttctgcaa cttatgtagg tgaatcttac 300

tggatgagtg gcacaacagg tgaagtatca aaaggtggtg taacaaccct taatgtagat 360

tttgaccaaa aaacggtaga tggaaaaatt gaatattcat tgctaagaga cggtagaact 420

caagacatta ctctacattc aacatcctta aatggtacaa aatttaatgg taatgcaagt 480

acgttattgc aaaatggtac ttatgaaggc gcattatttg gcaaagaggc taaagaagct 540

gcgggattgg tgaagttccc taattcaagc tcttacgata cttcatttgg tggcgttcgt 600

tattaa 606

<210> 874

<211> 201

<212> PRT

<213> M. granulomatis SLP 2a

<400> 874

Met Lys Lys Leu Leu Leu Cys Ser Val Ala Gly Leu Ser Val Leu Leu
1 5 10 15

Thr Ala Cys Gly Gly Gly Gly Gly Ser Gly Ser Ala Lys Thr Pro Asp
20 25 30

Gly Thr Lys Val Asp Leu Thr Asn Ser Gln Lys Gly Asp Val Ala Gly
35 40 45

Asn Thr Ala Ala Gly Ser Leu Tyr Gly Lys Asn Gln Asn Asp Ser Phe
50 55 60

Tyr Gly Val Trp Leu Asn Asp Ala Lys Thr Val Arg Glu Leu Arg Tyr

65 70 75 80

Gln Gly Thr Glu Ala Thr Asn Leu Pro Ser Gly Ser Ala Thr Tyr Val
85 90 95
Gly Glu Ser Tyr Trp Met Ser Gly Thr Thr Gly Glu Val Ser Lys Gly
100 105 110
Gly Val Thr Thr Leu Asn Val Asp Phe Asp Gln Lys Thr Val Asp Gly
115 120 125
Lys Ile Glu Tyr Ser Leu Leu Arg Asp Gly Arg Thr Gln Asp Ile Thr
130 135 140

Leu His Ser Thr Ser Leu Asn Gly Thr Lys Phe Asn Gly Asn Ala Ser
145 150 155 160
Thr Leu Leu Gln Asn Gly Thr Tyr Glu Gly Ala Leu Phe Gly Lys Glu
165 170 175
Ala Lys Glu Ala Ala Gly Leu Val Lys Phe Pro Asn Ser Ser Ser Tyr
180 185 190
Asp Thr Ser Phe Gly Gly Val Arg Tyr
195 200

<210> 875

<211> 921

<212> DNA

<213> M. granulomatis SLP 3a

<400> 875

atgtttatga aaaaaataac attggccagc ttaattttat ttagtctaac ggcatgtagt 60

ggttcgggtg gtggctctaa tgcaaaatca cctaaccaga aaattacaga gcaaaaacaa 120

gggctaaaag ataaggcaga taaagcaaaa actgatgcag aacgtttagc aaaagagaaa 180

gctgaaaagg cgaaagcaga agcagagcgt ttggcgaaag aggctgaaaa agcgaaaaaa 240

gaagcagagc gtttagcaaa agaaaagtct gaaaaagcga aagcagaagc agagcgttta 300

gcaaaagagg ctgaaaaagc aaaagcggaa gaagctaaaa aaattattga tgctaaaggc 360

gttgatgata aaaactatgg actaagaaaa ttagaggact cggttaaacc taacactaat 420

aatggagagg ttagaaccta tggttatctc tataatcagc cttattctgt tgttactgct 480

cggatgacaa ccacagtagg tgcgaattta aatcaacttg agccaacggt tgaagtaaga 540

gggttaaaga cagaacagtt acctactgaa ggtaaagcta tttatcaggg gaagtctttt 600

gattctcatg gtgataaagg agtatatggt ggtagtttaa cttataatgt tgattttgcg 660

ggacgtaaag gttcaggtga aatagttaat atattagggg gatctattaa gttaggcgag 720

ggtatgataa atactaatgg tgcaatttct tctactgtta ctcatactgc agctcaaaat 780

aatgttgttc ataatggaac ctacgaggtt caattctttg gacctaatgc agaagaaatc 840

ggtggtaaag tagagattaa agatggagag agaacagatc gctttggtat tagcggaact 900

cgaggcgaaa ttcaaaaata a 921

<210> 876

<211> 306

<212> PRT

<213> M. granulomatis SLP 3a

<400> 876

Met Phe Met Lys Lys Ile Thr Leu Ala Ser Leu Ile Leu Phe Ser Leu
1 5 10 15

Thr Ala Cys Ser Gly Ser Gly Gly Gly Ser Asn Ala Lys Ser Pro Asn
20 25 30

Gln Lys Ile Thr Glu Gln Lys Gln Gly Leu Lys Asp Lys Ala Asp Lys
35 40 45

Ala Lys Thr Asp Ala Glu Arg Leu Ala Lys Glu Lys Ala Glu Lys Ala
50 55 60

Lys Ala Glu Ala Glu Arg Leu Ala Lys Glu Ala Glu Lys Ala Lys Lys
65 70 75 80

Glu Ala Glu Arg Leu Ala Lys Glu Lys Ser Glu Lys Ala Lys Ala Glu
85 90 95

Ala Glu Arg Leu Ala Lys Glu Ala Glu Lys Ala Lys Ala Glu Glu Ala
100 105 110

Lys Lys Ile Ile Asp Ala Lys Gly Val Asp Asp Lys Asn Tyr Gly Leu
115 120 125

Arg Lys Leu Glu Asp Ser Val Lys Pro Asn Thr Asn Asn Gly Glu Val
130 135 140

Arg Thr Tyr Gly Tyr Leu Tyr Asn Gln Pro Tyr Ser Val Val Thr Ala
145 150 155 160

Arg Met Thr Thr Thr Val Gly Ala Asn Leu Asn Gln Leu Glu Pro Thr

165 170 175

Val Glu Val Arg Gly Leu Lys Thr Glu Gln Leu Pro Thr Glu Gly Lys

180 185 190

Ala Ile Tyr Gln Gly Lys Ser Phe Asp Ser His Gly Asp Lys Gly Val

195 200 205

Tyr Gly Gly Ser Leu Thr Tyr Asn Val Asp Phe Ala Gly Arg Lys Gly

210 215 220

Ser Gly Glu Ile Val Asn Ile Leu Gly Gly Ser Ile Lys Leu Gly Glu

225 230 235 240

Gly Met Ile Asn Thr Asn Gly Ala Ile Ser Ser Thr Val Thr His Thr

245 250 255

Ala Ala Gln Asn Asn Val Val His Asn Gly Thr Tyr Glu Val Gln Phe

260 265 270

Phe Gly Pro Asn Ala Glu Glu Ile Gly Gly Lys Val Glu Ile Lys Asp

275 280 285

Gly Glu Arg Thr Asp Arg Phe Gly Ile Ser Gly Thr Arg Gly Glu Ile

290 295 300

Gln Lys

305

<210> 877

<211> 1458

<212> DNA

<213> M. haemolytica SLP 1a

<400> 877

atgcgttcta cattcaaact tactcttgca gctttagctg tttctattgt tttaagtggc 60

tgtaaatcta gccaaggtcc atctattgtt gcagacagcc ctccacctaa ggaaataaca 120

gctactgatg gcaacgataa agagaaaacc gataacaaag agaaaaagtc tgcgcaacca 180

aataaatccg atcctcaacc ggataaacct gctaacgcaa aagacccagt aaaacctgat 240

gcggagacaa ataaaccaag taaaaaagat aaagaatata caccacctgc tactgaaaaa 300

atcgataact catcagtaca gccggataaa atggtgccta atcctatcga gaataaggaa 360

aacgacagta ataaacctaa ccccaaagaa agcgatagcg ataataatga caaagtcact 420

gaaggcaata aaccaaatgc cccaacagaa acagtaaata aagataaaga agctgagaaa 480

agtaaaaagg agaataaaga ggactcaagc aataatactc ctaacattaa ttttgacggg 540

gcaaagccta tagatacaga tagtaaaggt agcccgtacc gagtaataaa cctaaatccg 600

agaaaaagcg tagtaaatgc aagtgctatg caaaaagtag atttcgactc ttttacggat 660

gaatctgttg aaaattcacc atttgtcagt agcgatactg aaaaagaata caataataca 720

cttgtttttg ggcttggtgc cggagataaa gattcttatt ttaagaactt aaatcaaaaa 780

ggggataaac atttaggtat tcatagtggc gtgtatgaag atgcgaattt agaaggtaat 840

actaaaaaaa ttaactatct ctatgtaaat caaccttatt cgagctatgg tgctttattt 900

acggaccaaa aagacagcca tttattcaac gttcgtctga ccgctggtag agatgatgta 960

aaagaaaatg gagatagtta tgccgaatat ggtgtattca cacaatcagg aaaagaagct 1020

aaatggaatg ataacctgat tggtgatgcc acttacaaag gtcaagctat tgctcgcgtt 1080

attcgtcagg taaatgggga acaagtcgca ggtattcctc aatttgatgg tgatgttaca 1140

ttaaatttac acctttccaa agaatggaat gaaagtaaac taaacggcaa aattgatagc 1200

caaagtgttg gggtaattac acttaaagaa agtgaaatag ctaaccctac cgcactccgc 1260

tcaaatattg gttttggaga agaagtcata gttgagaata aagagaatct tgtgggtgat 1320

tacgctgtcg attttaccgg gcctcagctt gaagaggcgg taggcgttgt tgaattagaa 1380

aacgaagccg agacattctc tgaaaatgaa gtcattaaat acaatgcggt atttggcgta 1440

agcaaagcgg cgaaatag 1458

<210> 878

<211> 485

<212> PRT

<213> M. haemolytica SLP 1a

<400> 878

Met Arg Ser Thr Phe Lys Leu Thr Leu Ala Ala Leu Ala Val Ser Ile
1 5 10 15

Val Leu Ser Gly Cys Lys Ser Ser Gln Gly Pro Ser Ile Val Ala Asp
20 25 30

Ser Pro Pro Pro Lys Glu Ile Thr Ala Thr Asp Gly Asn Asp Lys Glu
35 40 45

Lys Thr Asp Asn Lys Glu Lys Lys Ser Ala Gln Pro Asn Lys Ser Asp

50 55 60

Pro Gln Pro Asp Lys Pro Ala Asn Ala Lys Asp Pro Val Lys Pro Asp
65 70 75 80
Ala Glu Thr Asn Lys Pro Ser Lys Lys Asp Lys Glu Tyr Thr Pro Pro
85 90 95
Ala Thr Glu Lys Ile Asp Asn Ser Ser Val Gln Pro Asp Lys Met Val
100 105 110
Pro Asn Pro Ile Glu Asn Lys Glu Asn Asp Ser Asn Lys Pro Asn Pro
115 120 125

Lys Glu Ser Asp Ser Asp Asn Asn Asp Lys Val Thr Glu Gly Asn Lys
130 135 140
Pro Asn Ala Pro Thr Glu Thr Val Asn Lys Asp Lys Glu Ala Glu Lys
145 150 155 160
Ser Lys Lys Glu Asn Lys Glu Asp Ser Ser Asn Asn Thr Pro Asn Ile
165 170 175
Asn Phe Asp Gly Ala Lys Pro Ile Asp Thr Asp Ser Lys Gly Ser Pro
180 185 190

Tyr Arg Val Ile Asn Leu Asn Pro Arg Lys Ser Val Val Asn Ala Ser
195 200 205
Ala Met Gln Lys Val Asp Phe Asp Ser Phe Thr Asp Glu Ser Val Glu
210 215 220
Asn Ser Pro Phe Val Ser Ser Asp Thr Glu Lys Glu Tyr Asn Asn Thr
225 230 235 240
Leu Val Phe Gly Leu Gly Ala Gly Asp Lys Asp Ser Tyr Phe Lys Asn
245 250 255

Leu Asn Gln Lys Gly Asp Lys His Leu Gly Ile His Ser Gly Val Tyr
260 265 270
Glu Asp Ala Asn Leu Glu Gly Asn Thr Lys Lys Ile Asn Tyr Leu Tyr
275 280 285
Val Asn Gln Pro Tyr Ser Ser Tyr Gly Ala Leu Phe Thr Asp Gln Lys
290 295 300

Asp Ser His Leu Phe Asn Val Arg Leu Thr Ala Gly Arg Asp Asp Val
305 310 315 320

Lys Glu Asn Gly Asp Ser Tyr Ala Glu Tyr Gly Val Phe Thr Gln Ser
325 330 335
Gly Lys Glu Ala Lys Trp Asn Asp Asn Leu Ile Gly Asp Ala Thr Tyr
340 345 350
Lys Gly Gln Ala Ile Ala Arg Val Ile Arg Gln Val Asn Gly Glu Gln
355 360 365
Val Ala Gly Ile Pro Gln Phe Asp Gly Asp Val Thr Leu Asn Leu His
370 375 380

Leu Ser Lys Glu Trp Asn Glu Ser Lys Leu Asn Gly Lys Ile Asp Ser
385 390 395 400
Gln Ser Val Gly Val Ile Thr Leu Lys Glu Ser Glu Ile Ala Asn Pro
405 410 415
Thr Ala Leu Arg Ser Asn Ile Gly Phe Gly Glu Glu Val Ile Val Glu
420 425 430
Asn Lys Glu Asn Leu Val Gly Asp Tyr Ala Val Asp Phe Thr Gly Pro
435 440 445

Gln Leu Glu Glu Ala Val Gly Val Val Glu Leu Glu Asn Glu Ala Glu
450 455 460
Thr Phe Ser Glu Asn Glu Val Ile Lys Tyr Asn Ala Val Phe Gly Val
465 470 475 480
Ser Lys Ala Ala Lys
485

<210> 879
<211> 1176
<212> DNA
<213> M. haemolytica SLP 2a
<400> 879
atgtctatca aaaaagtaac tttagccagt ttgattttat tgggtttaac ggcgtgtagt 60
agtggtggtt cgggcagtag ctcaaacaat gtggcaaaac cgaatactaa accgcaaact 120

actcagcaac aaaccgataa agcggcagca gaaaaagcag caaaagacaa ggcagcgaaa 180

gagaaagcag aagcagaacg tttagcagca gaaaaagcag ctaaagagaa agcggaagca 240

gaacgtttag cggcggaaaa agcagcgaaa gaaaaagccg aagcggaacg tttagcggcg 300

gaaaaagcag cgaaagaaaa agccgaagca gaacgtttag cggcagaaaa agcggcgaaa 360

gagaaagcgg aagcggagcg tttagcggcg gaaaaagcag cgaaagaaaa agccgaagca 420

gaacgtttag cggcggaaaa agcggcgaaa gagaaagcgg aagcggagcg tttagcggcg 480

gaaaaagcag cgaaagaaaa agccgaagca gaacgtttag cggcggaaaa agcggcgaaa 540

gagaaagcgg aagcggagcg tttagcagca gaaaaagaag tagatcctat agctattatt 600

aaagcaaaag gtattgatga tacaaattac ggcttaaaac ttggtaatag taaagaaact 660

attgagggta aagtcacagt cagaacacag agttatttat ataatcagcc atattctgta 720

gtaacagcac aagcagttca aagaaatggc tgggaaaacg gtaattatat tgataaagtt 780

gatggaacag ttacagttaa aggattgaaa acagagaaat taccaacaga gggtactgca 840

acatattcag gaaaagcatt taaccacgat ggagctaaag gttttaatgg tggtgatcta 900

acctataatg ttaatttctc taagcgtacc ggttcaggta gagttgaggg agaatttgga 960

aacttaatcg tattagaaga ggggacgatt aataatactc agatttcttc aacagtacat 1020

ggcaataatc ctttaaacct ttctggaaaa tatacagtcg aatttttcgg taaaaatgca 1080

gaggaaattg ccggtgaaat tcagacaaaa gcaaatctta ctggggaagt gagtaatttt 1140

ggacttgccg gcactcgtgg cgatatccaa aaataa 1176

<210> 880

<211> 391

<212> PRT

<213> M. haemolytica SLP 2a

<400> 880

Met Ser Ile Lys Lys Val Thr Leu Ala Ser Leu Ile Leu Leu Gly Leu
1 5 10 15

Thr Ala Cys Ser Ser Gly Gly Ser Gly Ser Ser Ser Asn Asn Val Ala
20 25 30

Lys Pro Asn Thr Lys Pro Gln Thr Thr Gln Gln Gln Thr Asp Lys Ala
35 40 45

Ala Ala Glu Lys Ala Ala Lys Asp Lys Ala Ala Lys Glu Lys Ala Glu
50 55 60

Ala Glu Arg Leu Ala Ala Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala

65 70 75 80

Glu Arg Leu Ala Ala Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu
85 90 95
Arg Leu Ala Ala Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu Arg
100 105 110
Leu Ala Ala Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu
115 120 125
Ala Ala Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala
130 135 140

Ala Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala Ala
145 150 155 160
Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala Ala Glu
165 170 175
Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala Ala Glu Lys
180 185 190
Glu Val Asp Pro Ile Ala Ile Ile Lys Ala Lys Gly Ile Asp Asp Thr
195 200 205

Asn Tyr Gly Leu Lys Leu Gly Asn Ser Lys Glu Thr Ile Glu Gly Lys
210 215 220
Val Thr Val Arg Thr Gln Ser Tyr Leu Tyr Asn Gln Pro Tyr Ser Val
225 230 235 240
Val Thr Ala Gln Ala Val Gln Arg Asn Gly Trp Glu Asn Gly Asn Tyr
245 250 255
Ile Asp Lys Val Asp Gly Thr Val Thr Val Lys Gly Leu Lys Thr Glu
260 265 270

Lys Leu Pro Thr Glu Gly Thr Ala Thr Tyr Ser Gly Lys Ala Phe Asn
275 280 285
His Asp Gly Ala Lys Gly Phe Asn Gly Gly Asp Leu Thr Tyr Asn Val
290 295 300
Asn Phe Ser Lys Arg Thr Gly Ser Gly Arg Val Glu Gly Glu Phe Gly
305 310 315 320

Asn Leu Ile Val Leu Glu Glu Gly Thr Ile Asn Asn Thr Gln Ile Ser
325 330 335

Ser Thr Val His Gly Asn Asn Pro Leu Asn Leu Ser Gly Lys Tyr Thr
340 345 350
Val Glu Phe Phe Gly Lys Asn Ala Glu Glu Ile Ala Gly Glu Ile Gln
355 360 365
Thr Lys Ala Asn Leu Thr Gly Glu Val Ser Asn Phe Gly Leu Ala Gly
370 375 380
Thr Arg Gly Asp Ile Gln Lys
385 390

<210> 881
<211> 825
<212> DNA
<213> M. haemolytica SLP 3a

<400> 881
atgaagagta tcaaaaaatt aaccctagcc actttgattt tagtgggttt aactgcttgt 60
ggtagcggtg gttcaggtag cagttctaat aatgctaaat cgaaaccaca agttgagtta 120
aaaaaaactg aagaggataa aaaaactgaa gaggataaaa aaactgaaga ggataaaaaa 180
actgaagagg ataaaaaaac tgaagaggat aaaaaggctg aagaagcaaa aaaaattgca 240
gaggcaaaag gaattggcaa taaagaatat aaagatggat taaatgagtt agaagaaaaa 300
aatgaaacag gtaaaaacgg agaagagatt cgaacccatg gttatctcta taacagccat 360
tattccgttg taactgccaa aatgaaacaa actttacagg aaaatggtcg tcaaatggaa 420

cctacggttg aagtgaaagg gcttaaaact gagaatttac cgacagaggg caaagcaaca 480
tataaaggag aagcctttga ttctcacggt aataacagca attcagtagt aggtggagaa 540
ttaatctata atgttgattt ctctagtcgt accggatcag gtctagttaa aaatgtacag 600
ggcggttcta tcgagttagc acaaggcgaa ataaaaaatg atagtattat agcttctgct 660
caccaaaagt ataatgatca ggctgttgga aatggtagtt acaatatcca attctttggt 720
ccaaatgcag aagaaattgg agggaaaatt gagcttaatg gtgagggcga aggctcaatg 780
aagcagatgt taggtattgc aggaacccga gaagaacaaa aataa 825

<210> 882
<211> 274

<212> PRT

<213> M. haemolytica SLP 3a

<400> 882

Met Lys Ser Ile Lys Lys Leu Thr Leu Ala Thr Leu Ile Leu Val Gly
1 5 10 15

Leu Thr Ala Cys Gly Ser Gly Gly Ser Gly Ser Ser Ser Asn Asn Ala
20 25 30

Lys Ser Lys Pro Gln Val Glu Leu Lys Lys Thr Glu Glu Asp Lys Lys
35 40 45

Thr Glu Glu Asp Lys Lys Thr Glu Glu Asp Lys Lys Thr Glu Glu Asp

50 55 60

Lys Lys Thr Glu Glu Asp Lys Lys Ala Glu Glu Ala Lys Lys Ile Ala
65 70 75 80

Glu Ala Lys Gly Ile Gly Asn Lys Glu Tyr Lys Asp Gly Leu Asn Glu
85 90 95

Leu Glu Glu Lys Asn Glu Thr Gly Lys Asn Gly Glu Glu Ile Arg Thr
100 105 110

His Gly Tyr Leu Tyr Asn Ser His Tyr Ser Val Val Thr Ala Lys Met

115 120 125

Lys Gln Thr Leu Gln Glu Asn Gly Arg Gln Met Glu Pro Thr Val Glu
130 135 140

Val Lys Gly Leu Lys Thr Glu Asn Leu Pro Thr Glu Gly Lys Ala Thr
145 150 155 160

Tyr Lys Gly Glu Ala Phe Asp Ser His Gly Asn Asn Ser Asn Ser Val
165 170 175

Val Gly Gly Glu Leu Ile Tyr Asn Val Asp Phe Ser Ser Arg Thr Gly

180 185 190

Ser Gly Leu Val Lys Asn Val Gln Gly Gly Ser Ile Glu Leu Ala Gln
195 200 205

Gly Glu Ile Lys Asn Asp Ser Ile Ile Ala Ser Ala His Gln Lys Tyr
210 215 220

Asn Asp Gln Ala Val Gly Asn Gly Ser Tyr Asn Ile Gln Phe Phe Gly

225 230 235 240

Pro Asn Ala Glu Glu Ile Gly Gly Lys Ile Glu Leu Asn Gly Glu Gly

245 250 255

Glu Gly Ser Met Lys Gln Met Leu Gly Ile Ala Gly Thr Arg Glu Glu

260 265 270

Gln Lys

<210> 883

<211> 2571

<212> DNA

<213> M. macacae SLP 1a

<400> 883

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cccaacatca ccaccttgcc aaaaggcacg gtaccgcctg cagttgccaa tcccaataaa 180

ccggataaca ataacaacgg tggaagcgat aacaataacg gcggaagcgg tggtaacgat 240

aacaacggta gcggtagtga taataaccaa gcacaaaccc cgcaaaaccc acaaacccag 300

cctgccgcgg gctttttttat ggtgggtaaa atccgcgaca ccagtaaaac caataatcca 360

gaacgcaccg atgcatcgca atatcttggc acggataaaa tattacccga tggcacaacc 420

gcaggcacaa atttgcgcca agcactcacc gaaaacgaca ttaaacccat gaattttaac 480

caattcccca cttggcaaca attgcacatt gacagtccaa cgcatgcact caaaggtgat 540

tggcttaaac gcgccaaagt ttatggttat ggcaaacttt cacccttaaa cgaccaaaac 600

aatactcata ttaatcactt acaagacgaa aataaaaaag ccaaaaaatc cgccgataat 660

tatgaacaca ttcgttttgg ttatttagac atcgcaggtt taggcttaaa ccaaaaagca 720

ggtgaaaaaa acctccacaa tggtaaaatg ccgattttat tttatcatgg tgataacgtt 780

agcacacaat tacccagtgc tggcacgttt gaatacaaag gcaattggct gtatttaagt 840

gatgtcaaaa aacgccctgc cctaactggc aaagatgaaa aagttggcac ttattttaac 900

gcttacagca aaaccaacga agctgatgaa attagtgccg cccatattta tctaaacaac 960

atgaagtaca aacacacgcc ggctacttat aaagtggatt ttgataaaaa caccttaaca 1020

ggtaaattat cgtattatga caatcccaat aaacaaaaca gcagtggcaa ttatattgcc 1080

agccaatttg acaccaccaa aaaagttaat gaagtagatg tttatcaaat tgacggtaaa 1140

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gcgccgttta ttaaagaatt gttttctaaa aaagccaatc ccaataatcc cgacccagat 1260

tcaaatgccc tagaaggcgg cttttatggt gaaacgggcg atgaattggc gggtaaattt 1320

ttatccaatg atggctcggc gtatgtggta tttggcggca aacgcaatga taaaaacaaa 1380

aaacccgaaa caaaaccgtt ttatttttagt gcaggctttg aaaaaccgat tattagcaat 1440

atttctaatg aagatattgg caaagtgatt gaaaagaaaa aactaaatga agaaattgat 1500

gcaaagattg acgagggcga aataccaatt agcgatgacc aatatgaatc ttacccttgg 1560

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tattttggac aacacgataa gttttatttt aatggcaatt attacaattt aaaggcaaac 1680

tcaaaagata atttagaagt aaaaaatgcc aataacacac aaactattaa aaataaatac 1740

cctgatgtaa aagttgagca aaaagacaat gtaaccaaaa tcaccttaca agaaaaacaa 1800

ggcgataaac cttataccgc gattaatgcc aaaacttaca atcatattag ctttggcgaa 1860

gtattgtata acgatgacaa aaataaccca acgcgcagtt attttgtgca aggcggcgac 1920

caagagcaaa ccaccacttt accaagtgca ggtaaattta cttataacgg cttgtgggcg 1980

ggatatttga ttcagaaaaa agataaaggt tttagcaata atgaagacat aattaagaaa 2040

aaaggacata aagattatat cttagcccaa gattttaccc cagagtcaga agaagatgaa 2100

gaagaaaatg acgaagagag cacagatact gataaaacct atcttaaagg cgagattaaa 2160

cctgaatacc gtgataaata tctaccaata aacgaaaaaa cccatcaaaa aacgttttca 2220

ttggatggta aaaataaagc cagttttgat gtggattttg ataccaatac tttaaaaggt 2280

gcattaaccg atgaaaatgg tcatagcgtg tttgatatta aagacggtaa aataaatgac 2340

acagggttta ccgccaaagc cgatgttaac aattaccgcg aagaagttgg caataccaat 2400

agcggcggtt ttttatatga cataaaagac attgatgtca atgggcaatt ctttggcact 2460

gatggcgaag aattggcagg acaattgcat tatgataaag gcgacggcgt aaccgaagaa 2520

gtgaaaaaag cgggcgcggt atttggtgcg gttaaaggcg ataaaaaata a 2571

<210> 884

<211> 856

<212> PRT

<213> M. macacae SLP 1a

<400> 884

Met Thr Thr Ser Lys Thr Pro Lys Met Phe Lys Lys Ser His Leu Ala

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20 25 30
Gly Asp Ser Ile Lys Ser Ala Ala Pro Asn Ile Thr Thr Leu Pro Lys
35 40 45
Gly Thr Val Pro Pro Ala Val Ala Asn Pro Asn Lys Pro Asp Asn Asn
50 55 60
Asn Asn Gly Gly Ser Asp Asn Asn Asn Gly Gly Ser Gly Gly Asn Asp

65 70 75 80
Asn Asn Gly Ser Gly Ser Asp Asn Asn Gln Ala Gln Thr Pro Gln Asn
85 90 95
Pro Gln Thr Gln Pro Ala Ala Gly Phe Phe Met Val Gly Lys Ile Arg
100 105 110
Asp Thr Ser Lys Thr Asn Asn Pro Glu Arg Thr Asp Ala Ser Gln Tyr
115 120 125
Leu Gly Thr Asp Lys Ile Leu Pro Asp Gly Thr Thr Ala Gly Thr Asn

130 135 140
Leu Arg Gln Ala Leu Thr Glu Asn Asp Ile Lys Pro Met Asn Phe Asn
145 150 155 160
Gln Phe Pro Thr Trp Gln Gln Leu His Ile Asp Ser Pro Thr His Ala
165 170 175
Leu Lys Gly Asp Trp Leu Lys Arg Ala Lys Val Tyr Gly Tyr Gly Lys
180 185 190
Leu Ser Pro Leu Asn Asp Gln Asn Asn Thr His Ile Asn His Leu Gln

195 200 205
Asp Glu Asn Lys Lys Ala Lys Lys Ser Ala Asp Asn Tyr Glu His Ile
210 215 220
Arg Phe Gly Tyr Leu Asp Ile Ala Gly Leu Gly Leu Asn Gln Lys Ala
225 230 235 240
Gly Glu Lys Asn Leu His Asn Gly Lys Met Pro Ile Leu Phe Tyr His
245 250 255
Gly Asp Asn Val Ser Thr Gln Leu Pro Ser Ala Gly Thr Phe Glu Tyr

260 265 270

Lys Gly Asn Trp Leu Tyr Leu Ser Asp Val Lys Lys Arg Pro Ala Leu

275 280 285

Thr Gly Lys Asp Glu Lys Val Gly Thr Tyr Phe Asn Ala Tyr Ser Lys

290 295 300

Thr Asn Glu Ala Asp Glu Ile Ser Ala Ala His Ile Tyr Leu Asn Asn

305 310 315 320

Met Lys Tyr Lys His Thr Pro Ala Thr Tyr Lys Val Asp Phe Asp Lys

325 330 335

Asn Thr Leu Thr Gly Lys Leu Ser Tyr Tyr Asp Asn Pro Asn Lys Gln

340 345 350

Asn Ser Ser Gly Asn Tyr Ile Ala Ser Gln Phe Asp Thr Thr Lys Lys

355 360 365

Val Asn Glu Val Asp Val Tyr Gln Ile Asp Gly Lys Ile Gln Gly Asn

370 375 380

Arg Phe Thr Gly Thr Ala Lys Ser Leu Ile Thr Glu Asn Ser Lys Thr

385 390 395 400

Ala Pro Phe Ile Lys Glu Leu Phe Ser Lys Lys Ala Asn Pro Asn Asn

405 410 415

Pro Asp Pro Asp Ser Asn Ala Leu Glu Gly Gly Phe Tyr Gly Glu Thr

420 425 430

Gly Asp Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Gly Ser Ala Tyr

435 440 445

Val Val Phe Gly Gly Lys Arg Asn Asp Lys Asn Lys Lys Pro Glu Thr

450 455 460

Lys Pro Phe Tyr Phe Ser Ala Gly Phe Glu Lys Pro Ile Ile Ser Asn

465 470 475 480

Ile Ser Asn Glu Asp Ile Gly Lys Val Ile Glu Lys Lys Lys Leu Asn

485 490 495

Glu Glu Ile Asp Ala Lys Ile Asp Glu Gly Glu Ile Pro Ile Ser Asp

500 505 510

Asp Gln Tyr Glu Ser Tyr Pro Trp Gly Lys Pro Gln Ala Asp Phe Thr

515 520 525

Lys Gln Thr Ser Thr Ser Lys Gln Val Ile Pro Ala Tyr Phe Gly Gln

530 535 540

His Asp Lys Phe Tyr Phe Asn Gly Asn Tyr Tyr Asn Leu Lys Ala Asn

545 550 555 560

Ser Lys Asp Asn Leu Glu Val Lys Asn Ala Asn Asn Thr Gln Thr Ile

565 570 575

Lys Asn Lys Tyr Pro Asp Val Lys Val Glu Gln Lys Asp Asn Val Thr

580 585 590

Lys Ile Thr Leu Gln Glu Lys Gln Gly Asp Lys Pro Tyr Thr Ala Ile

595 600 605

Asn Ala Lys Thr Tyr Asn His Ile Ser Phe Gly Glu Val Leu Tyr Asn

610 615 620

Asp Asp Lys Asn Asn Pro Thr Arg Ser Tyr Phe Val Gln Gly Gly Asp

625 630 635 640

Gln Glu Gln Thr Thr Thr Leu Pro Ser Ala Gly Lys Phe Thr Tyr Asn

645 650 655

Gly Leu Trp Ala Gly Tyr Leu Ile Gln Lys Lys Asp Lys Gly Phe Ser

660 665 670

Asn Asn Glu Asp Ile Ile Lys Lys Lys Gly His Lys Asp Tyr Ile Leu

675 680 685

Ala Gln Asp Phe Thr Pro Glu Ser Glu Glu Asp Glu Glu Glu Asn Asp

690 695 700

Glu Glu Ser Thr Asp Thr Asp Lys Thr Tyr Leu Lys Gly Glu Ile Lys

705 710 715 720

Pro Glu Tyr Arg Asp Lys Tyr Leu Pro Ile Asn Glu Lys Thr His Gln

725 730 735

Lys Thr Phe Ser Leu Asp Gly Lys Asn Lys Ala Ser Phe Asp Val Asp

740 745 750

Phe Asp Thr Asn Thr Leu Lys Gly Ala Leu Thr Asp Glu Asn Gly His

755 760 765

Ser Val Phe Asp Ile Lys Asp Gly Lys Ile Asn Asp Thr Gly Phe Thr

770 775 780

Ala Lys Ala Asp Val Asn Asn Tyr Arg Glu Glu Val Gly Asn Thr Asn

785 790 795 800

Ser Gly Gly Phe Leu Tyr Asp Ile Lys Asp Ile Asp Val Asn Gly Gln

805 810 815

Phe Phe Gly Thr Asp Gly Glu Glu Leu Ala Gly Gln Leu His Tyr Asp

820 825 830

Lys Gly Asp Gly Val Thr Glu Glu Val Lys Lys Ala Gly Ala Val Phe

835 840 845

Gly Ala Val Lys Gly Asp Lys Lys

850 855

<210> 885

<211> 873

<212> DNA

<213> M. mediterranea SLP 1a

<400> 885

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gggggagaac ccagcggtgg tgacggcaac tacacagtcg gcggaaccac cgttcaactc 180

aggaacggat ccgtcacctc ggttgccgat acgacaggtg actacaccga agatgacaat 240

ggtaatcttt ccgtcagctt cacgtccggg ccctatgccg gccagagcgt gtccttcagc 300

gagggcagtg acacagccga tctggacggc cagacggcga cactggaagc gttccttggt 360

tccgacaatg acaacagcac atcgggcgcg ctctacatca ccgttgacgg cgagaatgat 420

gaggggaacg gcaacttcct cgctctttac agcggcgata ccgtatccga tctgccgcag 480

gaaggcaccg gcacttaccg gggcgactat ttcggcagtg cacagaacgg tgaggccggc 540

ggcctggttt cgggctccag cgaaatcgcc gtcgactttc agagcggcgc ggtttcaggc 600

gatttcagcg acctgaccat ctatgacggc gacgatgcaa tcggcgcgat ggacgatgtc 660

ggctttgccg ggacgcttga caagaacagt gcctcctatg ttgccaacag cgtgacgatc 720

gggggcgcag cggccggcga aggttccttg gtccagggtt cgctttatgg cgccggagcc 780

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gtcggcgtgt ttcaggcgga cctggcagac tga 873

<210> 886

<211> 290

<212> PRT

<213> M. mediterranea SLP 1a

<400> 886

Met Asn Lys Ile Phe Leu Ala Ala Leu Ala Gly Thr Ala Met Ile Ala
1 5 10 15

Met Ala Gly Cys Ser Ser Thr Ser Gly Asn Ser Ser Pro Gly Asn Pro
20 25 30

Gly Thr Gly Gly Gly Gly Ser Gln Gly Gly Glu Pro Ser Gly Gly Asp
35 40 45

Gly Asn Tyr Thr Val Gly Gly Thr Thr Val Gln Leu Arg Asn Gly Ser
50 55 60

Val Thr Ser Val Ala Asp Thr Thr Gly Asp Tyr Thr Glu Asp Asp Asn
65 70 75 80

Gly Asn Leu Ser Val Ser Phe Thr Ser Gly Pro Tyr Ala Gly Gln Ser
85 90 95

Val Ser Phe Ser Glu Gly Ser Asp Thr Ala Asp Leu Asp Gly Gln Thr
100 105 110

Ala Thr Leu Glu Ala Phe Leu Gly Ser Asp Asn Asp Asn Ser Thr Ser
115 120 125

Gly Ala Leu Tyr Ile Thr Val Asp Gly Glu Asn Asp Glu Gly Asn Gly
130 135 140

Asn Phe Leu Ala Leu Tyr Ser Gly Asp Thr Val Ser Asp Leu Pro Gln
145 150 155 160

Glu Gly Thr Gly Thr Tyr Arg Gly Asp Tyr Phe Gly Ser Ala Gln Asn
165 170 175

Gly Glu Ala Gly Gly Leu Val Ser Gly Ser Ser Glu Ile Ala Val Asp
180 185 190

Phe Gln Ser Gly Ala Val Ser Gly Asp Phe Ser Asp Leu Thr Ile Tyr

195 200 205

Asp Gly Asp Asp Ala Ile Gly Ala Met Asp Asp Val Gly Phe Ala Gly
210 215 220
Thr Leu Asp Lys Asn Ser Ala Ser Tyr Val Ala Asn Ser Val Thr Ile
225 230 235 240
Gly Gly Ala Ala Ala Gly Glu Gly Ser Leu Val Gln Gly Ser Leu Tyr
245 250 255
Gly Ala Gly Ala Asp Ser Thr Ala Gly Ser Val Ala Ala Phe Asp Asn
260 265 270

Ala Asp Asn Pro Thr Lys Ala Thr Val Gly Val Phe Gln Ala Asp Leu
275 280 285
Ala Asp
290

<210> 887
<211> 795
<212> DNA
<213> M. mediterranea SLP 2a
<400> 887

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acgggccgga tcgacgggtc ggggacggca gaggccggta ttcagatcaa cgacgatgac 180
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gacggcgcgg gcggctatac gaccgacgac gccgaggcct atctgcagct cggttatttc 300
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cttgcgggcg ccatgcaaag cgatctgggc gacattacct tcgatgccac catttccggg 600
gccgagttca actcgaacgc caattcgatc gcgatcggca atgattacgg cgtcatcaac 660

caggggggctt ccggcgtcga gggcgggttc tacggtgccg gcgctgcagg catggcgggg 720
acctatctgc tgaacggtca ggggtcgctg gatggcgcag gcgccgtcgg cgccttcgtc 780

gccgatcgga actga 795

<210> 888

<211> 264

<212> PRT

<213> M. mediterranea SLP 2a

<400> 888

Met Lys Tyr Leu Thr Cys Val Val Leu Gly Ala Ala Ala Leu Ala Ala
1 5 10 15
Gly Cys Gly Asn Asn Gly Asn Asp Gly Ile Ala Thr Asn Ala Leu Gly

20 25 30
Tyr Tyr Gly Asp Val Asn Trp Asp Thr Gly Arg Ile Asp Gly Ser Gly
35 40 45
Thr Ala Glu Ala Gly Ile Gln Ile Asn Asp Asp Asp Ser Val Thr Val
50 55 60
Gln Ile Asn Glu Gly Pro Tyr Ala Gly Glu Thr Thr Thr Phe Tyr Tyr
65 70 75 80
Asp Gly Ala Gly Gly Tyr Thr Thr Asp Asp Ala Glu Ala Tyr Leu Gln

85 90 95
Leu Gly Tyr Phe Asp Asn Pro Asn Val Lys Asp Gly Pro Val Val Ala
100 105 110
Leu Ile Asp Val Asn Asp Asn Asp Glu Glu Leu Thr Leu Met Ala Leu
115 120 125
Arg Ser Ser Asn Asp Met Thr Ala Glu Ser Asp Met Pro Val Thr Gly
130 135 140
Phe Ala Thr Tyr Thr Gly Ser His Leu Gly Gly Ala Thr Ile Pro Gly

145 150 155 160
Gln Tyr Leu Asp Tyr Ile Glu Gly Gly Phe Gln Ala Asn Val Asp Phe
165 170 175
Gly Ala Gly Gln Leu Ala Gly Ala Met Gln Ser Asp Leu Gly Asp Ile
180 185 190
Thr Phe Asp Ala Thr Ile Ser Gly Ala Glu Phe Asn Ser Asn Ala Asn
195 200 205

Ser Ile Ala Ile Gly Asn Asp Tyr Gly Val Ile Asn Gln Gly Ala Ser

210 215 220

Gly Val Glu Gly Gly Phe Tyr Gly Ala Gly Ala Ala Gly Met Ala Gly

225 230 235 240

Thr Tyr Leu Leu Asn Gly Gln Gly Ser Leu Asp Gly Ala Gly Ala Val

245 250 255

Gly Ala Phe Val Ala Asp Arg Asn

260

<210> 889

<211> 780

<212> DNA

<213> M. morganii SLP 1a

<400> 889

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aactatatat ctgtcggcgt aaccgctgca tcagagcgtc aggggcatcc gtcaccgggc 180

ggagaaccgg gaattggtta ttccggcatg cacaacggaa ccaaagtcag ctttgccgga 240

ctgcagggac ccaaccgtgc aacaccaaac gataacggtg tttctgttat cacctcaact 300

ccgcagtcac accgcagtat gggctctttt aattttgcca aaatagccga tgccgatatt 360

tattacggtg aatgggtttc cggtactgat ttcagcgatg attcccatat ggtgtattac 420

gccgggaaag atattaccgc cgccatgcca tccgaaggga cggcacagta cagcattaaa 480

ggactcagcg ggtacagcag cggtgaacag atcagcggta catttagtac ggattttgat 540

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atcagtggtt caacctttga tggaaccgca tctgtcagca ccaccggtac cgataccaca 660

gccgtcagcg gtacgaccaa cgggcatttc tttggtgaca atgcacagca ggttgccggt 720

tatgctgagt tcagcagtga taaagcgaag aatatcgcgt tcggcggaac caagtcttaa 780

<210> 890

<211> 259

<212> PRT

<213> M. morganii SLP 1a

<400> 890

Met Asn Thr Phe Asn Met Lys Thr Pro Leu Ala Thr Leu Val Thr Leu

1 5 10 15

Cys Ala Ala Phe Ser Ala Val Gln Ala Gln Ala Asp Ala Gly Tyr Gly

20 25 30

Ser Ser Ser Ala Glu Gly Leu Ser Asn Tyr Ile Ser Val Gly Val Thr

35 40 45

Ala Ala Ser Glu Arg Gln Gly His Pro Ser Pro Gly Gly Glu Pro Gly

50 55 60

Ile Gly Tyr Ser Gly Met His Asn Gly Thr Lys Val Ser Phe Ala Gly

65 70 75 80

Leu Gln Gly Pro Asn Arg Ala Thr Pro Asn Asp Asn Gly Val Ser Val

85 90 95

Ile Thr Ser Thr Pro Gln Ser His Arg Ser Met Gly Ser Phe Asn Phe

100 105 110

Ala Lys Ile Ala Asp Ala Asp Ile Tyr Tyr Gly Glu Trp Val Ser Gly

115 120 125

Thr Asp Phe Ser Asp Asp Ser His Met Val Tyr Tyr Ala Gly Lys Asp

130 135 140

Ile Thr Ala Ala Met Pro Ser Glu Gly Thr Ala Gln Tyr Ser Ile Lys

145 150 155 160

Gly Leu Ser Gly Tyr Ser Ser Gly Glu Gln Ile Ser Gly Thr Phe Ser

165 170 175

Thr Asp Phe Asp Ala Asn Thr Phe Ser Gly Ser Leu Ser Ser Thr Glu

180 185 190

Leu Ser Tyr Ser Leu Ser Gly Asp Ile Ser Gly Ser Thr Phe Asp Gly

195 200 205

Thr Ala Ser Val Ser Thr Thr Gly Thr Asp Thr Thr Ala Val Ser Gly

210 215 220

Thr Thr Asn Gly His Phe Phe Gly Asp Asn Ala Gln Gln Val Ala Gly

225 230 235 240

Tyr Ala Glu Phe Ser Ser Asp Lys Ala Lys Asn Ile Ala Phe Gly Gly

245 250 255

Thr Lys Ser

<210> 891

<211> 750

<212> DNA

<213> M. morosus SLP 1a

<400> 891

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ggtttttgtt tggtgctggg ctatttgtta tcaggctgcg caacgcaacc cggccctgtt 120

gccaccgaag gcgcgacgac ttcccgtgcc ttaatcttgg cggtttggga ttttgacaat 180

aattccatgg cgggtggcga tgttgactat ctcagtaagg cgctttcgga aatgttgata 240

accgaccttt cgcaggtctc ggatatgcgt ttggtggagc gggtaaactt acgggcggca 300

ttggaagagc agcatcttag cactagccaa ctcgcatccg atgaaacccg gctgaaatta 360

ggcaggatag caggcgccaa cctgctggca ttcggtagtt atatggcgat ggctggtcaa 420

gtcaggattg acgtcagggt ggttgatgca gaaacctcgc tagtaaagtt tagtgaagct 480

acgtcaggtt cgccgcaaga cgcagccaaa cagatgcaga cgatagccgt gcatcttgcc 540

agtaaattgg atgccagtgt tatttctgga aaagaaaacg ccacggacat gatgctttgg 600

aagcgttatg aagaagggat ttctttgatg gacaagcatc tttacgaacc ggcaattaca 660

atatttaaag agatactgca agctaaccct agctttgctg cggcagaaaa gcagatcaaa 720

ttggccttag aattgcaaac aagacaataa 750

<210> 892

<211> 249

<212> PRT

<213> M. morosus SLP 1a

<400> 892

Met Lys Pro Gln Ile Thr Ala Thr Val His Asn Leu Phe Tyr Arg Lys

1 5 10 15

Ile Thr Arg Tyr Gly Phe Cys Leu Val Leu Gly Tyr Leu Leu Ser Gly

20 25 30

Cys Ala Thr Gln Pro Gly Pro Val Ala Thr Glu Gly Ala Thr Thr Ser

35 40 45

Arg Ala Leu Ile Leu Ala Val Trp Asp Phe Asp Asn Asn Ser Met Ala

50 55 60

Gly Gly Asp Val Asp Tyr Leu Ser Lys Ala Leu Ser Glu Met Leu Ile
65 70 75 80

Thr Asp Leu Ser Gln Val Ser Asp Met Arg Leu Val Glu Arg Val Asn
85 90 95

Leu Arg Ala Ala Leu Glu Glu Gln His Leu Ser Thr Ser Gln Leu Ala
100 105 110

Ser Asp Glu Thr Arg Leu Lys Leu Gly Arg Ile Ala Gly Ala Asn Leu

115 120 125

Leu Ala Phe Gly Ser Tyr Met Ala Met Ala Gly Gln Val Arg Ile Asp
130 135 140

Val Arg Val Val Asp Ala Glu Thr Ser Leu Val Lys Phe Ser Glu Ala
145 150 155 160

Thr Ser Gly Ser Pro Gln Asp Ala Ala Lys Gln Met Gln Thr Ile Ala
165 170 175

Val His Leu Ala Ser Lys Leu Asp Ala Ser Val Ile Ser Gly Lys Glu

180 185 190

Asn Ala Thr Asp Met Met Leu Trp Lys Arg Tyr Glu Glu Gly Ile Ser
195 200 205

Leu Met Asp Lys His Leu Tyr Glu Pro Ala Ile Thr Ile Phe Lys Glu
210 215 220

Ile Leu Gln Ala Asn Pro Ser Phe Ala Ala Ala Glu Lys Gln Ile Lys
225 230 235 240

Leu Ala Leu Glu Leu Gln Thr Arg Gln
245

<210> 893

<211> 1017

<212> DNA

<213> M. varigena SLP 1a

<400> 893

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agtggcggct ccggtggcaa ctcaaacaat gcaacaaaac cgaatgctaa accgcaaacc 120

actcaacaac aaaccgataa agccgctgcc gaaaaagcgg ctaaagagaa agcggaagcg 180

gaacgtttag cggcagaaaa agcagcgaaa gagaaagcag aagcggaacg tttagcagcg 240

gaaaaggcag cgaaagagaa agcggaagca gagcgtttag cagccgaaaa agtagcgaaa 300

gagaaagcag aagcagagcg tttagcagcc gaaaaggcag caatagaaaa agcggcgaaa 360

gaggaagcgg aacgtttagc agcagaaaaa gcagcgaaag agaaagcaga agcagagcgt 420

ttagcaattg ttaaagcaaa aggcattgat gatgaaaatt acggtataag atttaatgat 480

tttaacgaaa aaacagaagg aaaaatcaaa gttagaacac aaagctactt atataatcaa 540

ccatattcag ttgttacagc acaagaggtt aaaagaacag gctgggaaaa tggaaaatat 600

attgatatat cagataaaac aattacagtt aaaggattaa aaacagaaaa attaccacct 660

gaaggtaaag caacttatga aggaaaagct tttaattata atggggatta tgacggtgca 720

atcggtggtc atttaacata cgatgttgat tttactaatc gtactggttc gggaaagata 780

gagggaggtt atgctagaag tataacattg gctaaaggaa atttagaaaa aaatagtatt 840

tcatctactg ctagtcttta ttatggaact catcatcatg gtgatggaag ctataaggta 900

gaatttttg gtccaaacgc agaagaaatt agtggctata taaaaatgga aacagatatt 960

aatgggaatc cagatagctt tggtttctca ggcattcgtg gagaagtcca aaaataa 1017

<210> 894

<211> 338

<212> PRT

<213> M. varigena SLP 1a

<400> 894

Met Ser Ile Lys Lys Val Thr Leu Ala Ser Leu Ile Leu Leu Ser Leu
1 5 10 15

Thr Ala Cys Gly Ser Gly Gly Ser Gly Gly Asn Ser Asn Asn Ala Thr
20 25 30

Lys Pro Asn Ala Lys Pro Gln Thr Thr Gln Gln Gln Thr Asp Lys Ala
35 40 45

Ala Ala Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala
50 55 60

Ala Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala Ala

65 70 75 80

Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala Ala Glu
85 90 95
Lys Val Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala Ala Glu Lys
100 105 110
Ala Ala Ile Glu Lys Ala Ala Lys Glu Glu Ala Glu Arg Leu Ala Ala
115 120 125
Glu Lys Ala Ala Lys Glu Lys Ala Glu Ala Glu Arg Leu Ala Ile Val
130 135 140

Lys Ala Lys Gly Ile Asp Asp Glu Asn Tyr Gly Ile Arg Phe Asn Asp
145 150 155 160
Phe Asn Glu Lys Thr Glu Gly Lys Ile Lys Val Arg Thr Gln Ser Tyr
165 170 175
Leu Tyr Asn Gln Pro Tyr Ser Val Val Thr Ala Gln Glu Val Lys Arg
180 185 190
Thr Gly Trp Glu Asn Gly Lys Tyr Ile Asp Ile Ser Asp Lys Thr Ile
195 200 205

Thr Val Lys Gly Leu Lys Thr Glu Lys Leu Pro Pro Glu Gly Lys Ala
210 215 220
Thr Tyr Glu Gly Lys Ala Phe Asn Tyr Asn Gly Asp Tyr Asp Gly Ala
225 230 235 240
Ile Gly Gly His Leu Thr Tyr Asp Val Asp Phe Thr Asn Arg Thr Gly
245 250 255
Ser Gly Lys Ile Glu Gly Gly Tyr Ala Arg Ser Ile Thr Leu Ala Lys
260 265 270

Gly Asn Leu Glu Lys Asn Ser Ile Ser Ser Thr Ala Ser Leu Tyr Tyr
275 280 285
Gly Thr His His His Gly Asp Gly Ser Tyr Lys Val Glu Phe Phe Gly
290 295 300
Pro Asn Ala Glu Glu Ile Ser Gly Tyr Ile Lys Met Glu Thr Asp Ile
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Asn Gly Asn Pro Asp Ser Phe Gly Phe Ser Gly Ile Arg Gly Glu Val
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Gln Lys

<210> 895
<211> 606
<212> DNA
<213> M. varigena SLP 2a
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agtccaaaag atgatgtagc aggtaaaacc gttggaggtg aattctatgg taaaaaccaa 180
aatgactcat tctatggggt ttggatcaat gatgcgaaaa cggtaagaga attacgttat 240
caaggtacag aagctactca acttccgtct ggatcagcaa cttatttcgg tgattcttat 300
tggttaagtg gtgcaactgg cgaggtatct aaaggtggta aaactacgtt gaatgtggat 360

tttgaccgta aaactgtaga tggaaaaatt gaatactcac tgttaaatga tggtagagtt 420
caagatatta ccttgcacga aacatcatta aatggttcaa aattcaatgg cgaggcaagt 480
acgcttttag agaagggcac ttatgaaggg gcgttatttg gtcaaggtgc gaaagaagca 540
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tattaa 606
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<212> PRT
<213> M. varigena SLP 2a
<400> 896
Met Lys Lys Leu Leu Phe Cys Ser Val Ala Thr Leu Ser Val Leu Leu

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20 25 30
Gly Thr Lys Val Asp Leu Thr Asn Ser Pro Lys Asp Asp Val Ala Gly
35 40 45
Lys Thr Val Gly Gly Glu Phe Tyr Gly Lys Asn Gln Asn Asp Ser Phe

50 55 60

Tyr Gly Val Trp Ile Asn Asp Ala Lys Thr Val Arg Glu Leu Arg Tyr

65 70 75 80

Gln Gly Thr Glu Ala Thr Gln Leu Pro Ser Gly Ser Ala Thr Tyr Phe

85 90 95

Gly Asp Ser Tyr Trp Leu Ser Gly Ala Thr Gly Glu Val Ser Lys Gly

100 105 110

Gly Lys Thr Thr Leu Asn Val Asp Phe Asp Arg Lys Thr Val Asp Gly

115 120 125

Lys Ile Glu Tyr Ser Leu Leu Asn Asp Gly Arg Val Gln Asp Ile Thr

130 135 140

Leu His Glu Thr Ser Leu Asn Gly Ser Lys Phe Asn Gly Glu Ala Ser

145 150 155 160

Thr Leu Leu Glu Lys Gly Thr Tyr Glu Gly Ala Leu Phe Gly Gln Gly

165 170 175

Ala Lys Glu Ala Ala Gly Leu Val Lys Phe Pro Lys Ala Pro Ser Tyr

180 185 190

Asp Thr Ser Phe Gly Gly Ile Arg Tyr

195 200

<210> 897

<211> 1203

<212> DNA

<213> M. varigena SLP 3a

<400> 897

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aagcaacagc taaaagataa agctgataca gcaaaagtgg aagcggaacg cttgaagaaa 180

caagctgaaa aagcaaaaga aaaagcagaa agtctggcaa aagaggcaga aaaagcaaaa 240

acagaagcgg aacgtttagc acaagaaaaa gcagaaaaag cgaaggctga agcagagcgt 300

ttggcaaaag aagcagaaaa agcgaaaatg gaagcagaac gtttagcgaa ggaaaaggta 360

gaaaaagcaa aaacagaagc ggaacgttta gcacaagaaa aagcagaaaa ggcgaaagct 420

gaagcagagc gtttggcaaa agaagcagaa aaggcaaaaa tggaagcaga acgtttagcg 480

aaggaagagg cagaaaaagc aaaaacagaa gcggaacgtt tagcacaaga aaaagcagaa 540

aaagcgaaag ctgaagcaga acgtttggcg aaagaagcag aaaaagcgaa ggcggaagca 600

gagcgtttag ctaaggaaaa agcagagaaa gagaagtcag aagagcaaaa aattattgat 660

gccaaaggtg gagttgataa taaacagatt gggttaagtg aaattcctgt tattaaggaa 720

gatggtggta aaaaagagac ttacggtagt ctctataatc agaaatattc tgttgtgaaa 780

gctcaaatag ttaaaacagg agatgattta agcaatgtta attcaattgt tgaagtaaaa 840

ggcttaaata cagaaaaatt accttctgaa ggcaaagcta cttataatgg aaaagccttt 900

gatgctcacg gggatgaagg tatttatgca ggtaacttaa cttatgaagt taatttttct 960

gagcgtacag gttcaggtca aataattaat acattggatg gtactattga cttggataaa 1020

ggtaacatag ataaaggttt gatttcttcc actgcacatc atcgtaaggg agagcatact 1080

caaagcggta gatatgaagt tcaatttttt ggacctaatg cagaagaaat tggtggtaaa 1140

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taa 1203

<210> 898

<211> 400

<212> PRT

<213> M. varigena SLP 3a

<400> 898

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Thr Ala Cys Gly Ser Ser Gly Ser Gly Ser Gly Ser Asn His Lys Ser
20 25 30

Pro Glu Gln Lys Ile Thr Glu Gln Lys Gln Gln Leu Lys Asp Lys Ala
35 40 45

Asp Thr Ala Lys Val Glu Ala Glu Arg Leu Lys Lys Gln Ala Glu Lys
50 55 60

Ala Lys Glu Lys Ala Glu Ser Leu Ala Lys Glu Ala Glu Lys Ala Lys
65 70 75 80

Thr Glu Ala Glu Arg Leu Ala Gln Glu Lys Ala Glu Lys Ala Lys Ala
85 90 95

Glu Ala Glu Arg Leu Ala Lys Glu Ala Glu Lys Ala Lys Met Glu Ala

100 105 110

Glu Arg Leu Ala Lys Glu Lys Val Glu Lys Ala Lys Thr Glu Ala Glu
115 120 125
Arg Leu Ala Gln Glu Lys Ala Glu Lys Ala Lys Ala Glu Ala Glu Arg
130 135 140
Leu Ala Lys Glu Ala Glu Lys Ala Lys Met Glu Ala Glu Arg Leu Ala
145 150 155 160
Lys Glu Glu Ala Glu Lys Ala Lys Thr Glu Ala Glu Arg Leu Ala Gln
165 170 175

Glu Lys Ala Glu Lys Ala Lys Ala Glu Ala Glu Arg Leu Ala Lys Glu
180 185 190
Ala Glu Lys Ala Lys Ala Glu Ala Glu Arg Leu Ala Lys Glu Lys Ala
195 200 205
Glu Lys Glu Lys Ser Glu Glu Gln Lys Ile Ile Asp Ala Lys Gly Gly
210 215 220
Val Asp Asn Lys Gln Ile Gly Leu Ser Glu Ile Pro Val Ile Lys Glu
225 230 235 240

Asp Gly Gly Lys Lys Glu Thr Tyr Gly Ser Leu Tyr Asn Gln Lys Tyr
245 250 255
Ser Val Val Lys Ala Gln Ile Val Lys Thr Gly Asp Asp Leu Ser Asn
260 265 270
Val Asn Ser Ile Val Glu Val Lys Gly Leu Asn Thr Glu Lys Leu Pro
275 280 285
Ser Glu Gly Lys Ala Thr Tyr Asn Gly Lys Ala Phe Asp Ala His Gly
290 295 300

Asp Glu Gly Ile Tyr Ala Gly Asn Leu Thr Tyr Glu Val Asn Phe Ser
305 310 315 320
Glu Arg Thr Gly Ser Gly Gln Ile Ile Asn Thr Leu Asp Gly Thr Ile
325 330 335
Asp Leu Asp Lys Gly Asn Ile Asp Lys Gly Leu Ile Ser Ser Thr Ala
340 345 350

His His Arg Lys Gly Glu His Thr Gln Ser Gly Arg Tyr Glu Val Gln
355 360 365

Phe Phe Gly Pro Asn Ala Glu Glu Ile Gly Gly Lys Val Asp Ile Gln
370 375 380
Asp Asp Gly Arg Thr His Ser Phe Gly Ile Ser Gly Thr Lys Ala Asn
385 390 395 400

<210> 899
<211> 1344
<212> DNA
<213> M. viscosa SLP 1a
<400> 899

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aacagcacgg ataaagacaa acaactctta acctataaat ggtcgttaaa taccaaacct 240
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ggaatagaca aaacccatgc gattggcacc cccgtgttaa ttgccgcaac cgtaaccgac 480
gctgacaatg atgccttaac ttacacttgg tctattgaaa ccaaggctgc taatagcatg 540
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actctagagt cagcaaacgt cgcaccaata gcaaaagcag gggcggatca aaacgcagtt 720
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<210> 900

<211> 447

<212> PRT

<213> M. viscosa SLP 1a

<400> 900

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Leu Ala Ala Cys Lys Ser Gly Gly Val Asn Ser Thr Lys Asp Val Ala
20 25 30

Ala Thr Lys Asn Gln Val Pro Ile Ala Val Pro Gly Gln Asn Gln Asn
35 40 45

Val Ala Phe Gly Ser Leu Val Lys Leu Asp Gly Lys Asn Ser Thr Asp
50 55 60

Lys Asp Lys Gln Leu Leu Thr Tyr Lys Trp Ser Leu Asn Thr Lys Pro
65 70 75 80

Thr Gly Ser Thr Ala Thr Leu Ser Ala Thr Asp Ala Val Ser Pro Glu
85 90 95

Phe Thr Pro Asp Lys Ala Gly Ser Tyr Val Ile Ser Leu Val Val Asn
100 105 110

Asp Gly Lys Ile Asp Ser Lys Ser Val Asp Val Thr Ile Glu Val Ala
115 120 125

Pro Lys Ala Val Asn Ser Leu Pro Met Val Ser Ala Gly Ile Asp Lys
130 135 140

Thr His Ala Ile Gly Thr Pro Val Leu Ile Ala Ala Thr Val Thr Asp
145 150 155 160

Ala Asp Asn Asp Ala Leu Thr Tyr Thr Trp Ser Ile Glu Thr Lys Ala
165 170 175

Ala Asn Ser Met Pro Thr Leu Thr Asn Ser Asp Thr Lys Thr Val Thr

180 185 190

Leu Asn Ala Asn Val Gln Gly Asp Tyr Leu Leu Gln Leu Ser Val Ser
195 200 205

Asp Gly Lys Asn Thr Val Lys Asp Ser Val Lys Val Thr Leu Glu Ser
210 215 220

Ala Asn Val Ala Pro Ile Ala Lys Ala Gly Ala Asp Gln Asn Ala Val
225 230 235 240

Lys Asp Ala Val Val Asn Leu Asp Gly Ser Gly Ser Ser Asp Ala Asn
245 250 255

Asn Asp Val Met Leu Tyr Glu Trp Thr Phe Val Ser Lys Pro Glu His
260 265 270

Ser Val Ala Asp Leu Ser Gly Thr Asn Thr Ile Thr Pro Ser Phe Thr
275 280 285

Ala Asp Leu Ile Gly Asp Tyr Val Leu Ser Leu Thr Val Ser Asp Gly
290 295 300

Ala Leu Thr Ser Ala Pro Ser Asn Ile Lys Val Thr Val Thr Glu Ser
305 310 315 320

Leu Lys Ser Glu Leu Lys Ile Val Phe His Asp Arg Asp Pro Ala Gln
325 330 335

Asn Thr Leu Pro Tyr Val Phe Asn Pro Ile Thr Ile Asp Lys Thr Phe
340 345 350

Ser Asp Pro Lys Pro Ala Thr Tyr Lys Leu Ala Ser Phe Thr Leu Glu
355 360 365

Ala Val Gly Gln Asp Tyr Thr Ile Lys Glu Val Thr Pro Trp Gly Ile
370 375 380

Met Gly Val Val Thr Pro Ile Ile Asn Gly Val Val Glu Gly Gln Val
385 390 395 400

Ile Lys Ala Gly Glu Lys Val Glu Ile Glu Leu Leu Ser Pro Leu Thr
405 410 415

Gly Gly Lys Gln Ala Met Leu Ser Phe Ser Val Ile Ile Lys Glu Asn
420 425 430

Met Gly Asp Asn Tyr Ile Asn Ala Ser Tyr Phe Leu Thr Thr His
435 440 445

<210> 901
<211> 1371
<212> DNA
<213> M. viscosa SLP 1b
<400> 901

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cctattgcta tcgcaggagt aaatcagaat gtaaaagtaa ataccaaggt taaattggac 180
ggcaccagca gtgttgatga agataacgac ctcatcactt atcaatggaa ttttgaatcc 240
aaaccccaaa taagccaagc aacactcatt aatagcaaca acgccttatc agaatttaca 300
gcggatgcta tagggactta tatcattaat ttaattgtta atgatggtaa agcaaacagt 360

cgtccaaatc aggttcgaat cgttgttgcg tcttccggga caaattctcc tccgacactc 420
aatttatcca gcgaccaaaa actaaattta atcaataccg cgcatctaaa cgccaatgcc 480
cgagacgcag acaaggacaa acttttctat ctttggcaga ttatagagca accgacggat 540
agcaacccag tattaaatga tgagggtaca tccatcagat ttaaaacaga cattgcagga 600
gactatgtcg taaaactcac agtgtcagat ggactcgcta tcgcaacaga tacagtaacg 660
ctcagctact attatgctaa cgtccccccct agcgcaaaga caggcaccgc tatctatgca 720
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aacgctataa actacagtga tgccaagctt aaaccctatt tcattggcct atctgaaggt 1200

gaaattgtga ccgtaaaaaa aggtgagcga atgacatttc aactggctac accgtcgacc 1260
aatggtgaaa ctgtacggtt aggttttagt ttttcatgga gcttaaacgg ttacggcgac 1320
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<210> 902

<211> 456

<212> PRT

<213> M. viscosa SLP 1b

<400> 902

Met Asn Asp Lys Phe Lys Trp Leu Thr Cys Val Ala Thr Leu Ser Phe
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Leu Leu Gly Cys Asn Gly Gly Asp Glu Ser Gly Thr Lys Asp Thr Gly
20 25 30

Ser Ser Lys Leu Glu Asn Gln Ser Pro Ile Ala Ile Ala Gly Val Asn
35 40 45

Gln Asn Val Lys Val Asn Thr Lys Val Lys Leu Asp Gly Thr Ser Ser
50 55 60

Val Asp Glu Asp Asn Asp Leu Ile Thr Tyr Gln Trp Asn Phe Glu Ser
65 70 75 80

Lys Pro Gln Ile Ser Gln Ala Thr Leu Ile Asn Ser Asn Asn Ala Leu
85 90 95

Ser Glu Phe Thr Ala Asp Ala Ile Gly Thr Tyr Ile Ile Asn Leu Ile
100 105 110

Val Asn Asp Gly Lys Ala Asn Ser Arg Pro Asn Gln Val Arg Ile Val
115 120 125

Val Ala Ser Ser Gly Thr Asn Ser Pro Pro Thr Leu Asn Leu Ser Ser
130 135 140

Asp Gln Lys Leu Asn Leu Ile Asn Thr Ala His Leu Asn Ala Asn Ala
145 150 155 160

Arg Asp Ala Asp Lys Asp Lys Leu Phe Tyr Leu Trp Gln Ile Ile Glu
165 170 175

Gln Pro Thr Asp Ser Asn Pro Val Leu Asn Asp Glu Gly Thr Ser Ile
180 185 190

Arg Phe Lys Thr Asp Ile Ala Gly Asp Tyr Val Val Lys Leu Thr Val
195 200 205

Ser Asp Gly Leu Ala Ile Ala Thr Asp Thr Val Thr Leu Ser Tyr Tyr

210 215 220

Tyr Ala Asn Val Pro Pro Ser Ala Lys Thr Gly Thr Ala Ile Tyr Ala
225 230 235 240
Thr Glu Gly Met Ile Val Pro Val Asp Ala Ser Met Ser Asn Asp Pro
245 250 255
Asn Gly Asp Pro Ile Thr Tyr Gln Trp Asp Phe Val Ser Lys Pro Pro
260 265 270
Asn Ser Asn Thr Val Ile Val Asp Pro Ser Ala Met Ile Ser Glu Phe
275 280 285

Tyr Ala Asp Ala Pro Gly Thr Tyr Val Val Gly Leu Thr Val Ser Asp
290 295 300
Gly Glu Phe Thr Ser Lys Pro Tyr Lys Pro Phe Tyr Val Lys Val Tyr
305 310 315 320
Gly Leu Gln Ala Pro His Thr Lys Leu Phe Val Gly Asn Asp Ser Lys
325 330 335
Leu Gln Leu Phe Pro Tyr Lys Glu Lys Phe Val Val Asn Lys Thr Thr
340 345 350

Asp Ser Gly Ser Ile Pro Asp Glu Tyr Ile Leu Gly Asn Tyr Thr Ile
355 360 365
Glu Ala Val Gly Lys Asp Val Thr Ile Ser Gly Ile Asn Ala Ile Asn
370 375 380
Tyr Ser Asp Ala Lys Leu Lys Pro Tyr Phe Ile Gly Leu Ser Glu Gly
385 390 395 400
Glu Ile Val Thr Val Lys Lys Gly Glu Arg Met Thr Phe Gln Leu Ala
405 410 415

Thr Pro Ser Thr Asn Gly Glu Thr Val Arg Leu Gly Phe Ser Phe Ser
420 425 430
Trp Ser Leu Asn Gly Tyr Gly Asp Phe Ser Ser Gln Glu Thr Phe Trp
435 440 445
Ala Gly Tyr Gln Phe Thr Ser Arg
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<210> 903

<211> 747

<212> DNA

<213> M. viscosa SLP 1c

<400> 903

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gtttgggttc cgtttttcca ctcaaaaggc aaagccggca ttggcagctc aaaaagtaag 180

accgttgatt tcgatggcct agctggcaac acattctcaa gtgattatcg taacgataac 240

aataacgaaa aaggcgttca cacttcgggc agcaaacatt ttggtaattc tcattacaac 300

tttgcgcaag tagccaatag cgatatttgg ttcggtgagt ggtatgaagg aacccaagat 360

caagacttca ataatcgtac cgtctactac ataggtaacg atgctggcac aacggtcccg 420

actagtggca cagcgacgta caacatcaca ggcattaata aattctctgg cagcaacaag 480

ctgactggtg cctttgatgc tgactttggc gcacaaacac tgtctggcaa catttctaat 540

ggttcactaa aagtgaatgt aacagcgcaa attaatgccg cgacagcagc ctttacgggt 600

aacgcaacgg caacacaaaa tgccgtagct acggcgggta gttctaaagg tcatttcttt 660

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<210> 904

<211> 248

<212> PRT

<213> M. viscosa SLP 1c

<400> 904

Met Lys Pro Val Lys Leu Ser Trp Ile Thr Ala Ala Met Leu Gly Leu
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Ser Ser Leu Ala His Ala Gly Phe Asp Gly Ala Ile Ser Asp Asn Ser
20 25 30

Leu Arg Gln Val Gly Glu Ser Gln Val Trp Val Pro Phe Phe His Ser
35 40 45

Lys Gly Lys Ala Gly Ile Gly Ser Ser Lys Ser Lys Thr Val Asp Phe
50 55 60

Asp Gly Leu Ala Gly Asn Thr Phe Ser Ser Asp Tyr Arg Asn Asp Asn

65 70 75 80

Asn Asn Glu Lys Gly Val His Thr Ser Gly Ser Lys His Phe Gly Asn
85 90 95
Ser His Tyr Asn Phe Ala Gln Val Ala Asn Ser Asp Ile Trp Phe Gly
100 105 110
Glu Trp Tyr Glu Gly Thr Gln Asp Gln Asp Phe Asn Asn Arg Thr Val
115 120 125
Tyr Tyr Ile Gly Asn Asp Ala Gly Thr Thr Val Pro Thr Ser Gly Thr
130 135 140

Ala Thr Tyr Asn Ile Thr Gly Ile Asn Lys Phe Ser Gly Ser Asn Lys
145 150 155 160
Leu Thr Gly Ala Phe Asp Ala Asp Phe Gly Ala Gln Thr Leu Ser Gly
165 170 175
Asn Ile Ser Asn Gly Ser Leu Lys Val Asn Val Thr Ala Gln Ile Asn
180 185 190
Ala Ala Thr Ala Ala Phe Thr Gly Asn Ala Thr Ala Thr Gln Asn Ala
195 200 205

Val Ala Thr Ala Gly Ser Ser Lys Gly His Phe Phe Gly Ala Asn Ala
210 215 220
Ala Ala Leu Ala Gly Phe Ala Lys Phe Asp Thr Asn Ser Gln Leu Asp
225 230 235 240
Thr Ala Phe Gly Gly Glu Lys Gln
245

<210> 905
<211> 768
<212> DNA
<213> Marinomonas sp. MWYL1 SLP 1a
<400> 905
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acagccaccg tcaatggtgg tcctcatacc tctggcggcg caggtattgg cgtgaatgct 180

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ggagtattca acttcgctca agtaggtacc agtgatgtat gggtcggtga gtggtcagcc 360

tatggcacca gcggcgattc aactcgtacc gtttactatg ccggagcaaa tgcagacacc 420

tctgtgccaa cctctggtac ggccacctat acagtcgtgg gtatcaataa ctacgacggc 480

acagcagcaa gcttgctaaa cggtacatta accgctgact ttgctgcggc aacactaaca 540

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gacgctagtg tttctggtag caatgctact gcgactcagt ccggttcatt agtggcctat 660

aatggtgatg tctctgctca gttctacaat ggccaagcag atctagcggg gcttgttgac 720

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<210> 906

<211> 255

<212> PRT

<213> Marinomonas sp. MWYL1 SLP 1a

<400> 906

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Leu Val Phe Ser Gly Met Ala Ser Ala Ala Val Val Gly Glu Ser Ser
20 25 30

Asn Thr Asn Tyr Val Lys Val Gly Thr Ala Thr Val Asn Gly Gly Pro
35 40 45

His Thr Ser Gly Gly Ala Gly Ile Gly Val Asn Ala Thr Gly Ile Asp
50 55 60

Lys Leu Val Asn Phe Gln Gly Leu Thr Ala Tyr Gly Ala Lys Asp Ala
65 70 75 80

Gln Asp Val Tyr Thr Leu Asn Phe Pro Tyr Thr Gly Ser Pro Thr Ser
85 90 95

His Asp Asn Leu Gly Val Phe Asn Phe Ala Gln Val Gly Thr Ser Asp
100 105 110

Val Trp Val Gly Glu Trp Ser Ala Tyr Gly Thr Ser Gly Asp Ser Thr
115 120 125

Arg Thr Val Tyr Tyr Ala Gly Ala Asn Ala Asp Thr Ser Val Pro Thr

130 135 140

Ser Gly Thr Ala Thr Tyr Thr Val Val Gly Ile Asn Asn Tyr Asp Gly
145 150 155 160
Thr Ala Ala Ser Leu Leu Asn Gly Thr Leu Thr Ala Asp Phe Ala Ala
165 170 175
Ala Thr Leu Thr Gly Ser Ile Ala Asn Thr Asn Gly Phe Ala Val Asn
180 185 190
Val Gly Thr Ala Ala Ile Asn Ser Asp Ala Ser Val Ser Gly Ser Asn
195 200 205

Ala Thr Ala Thr Gln Ser Gly Ser Leu Val Ala Tyr Asn Gly Asp Val
210 215 220
Ser Ala Gln Phe Tyr Asn Gly Gln Ala Asp Leu Ala Gly Leu Val Asp
225 230 235 240
Phe Ala Gly Thr Glu Tyr Asp Thr Ala Phe Gly Gly Ser Lys Asp
245 250 255

<210> 907
<211> 801
<212> DNA
<213> Martelella sp. AD-3 SLP 1a
<400> 907
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gacatgccct tggcgggccg cgcgacctat tccggccagc atctcggcgc ggcggcgctt 480

ccgggcgagt atctcgacta tatcgacggc tcgttcaacg ccaatgtgga tttcggcagt 540
ggacaactgg ccggggcgat ggacacccag gtgggcgacg tcaccttcca ggcgacgatt 600
tccggttcgg aattcaactc caatgccaat tcgattgccg tcggcaatga ttatgtaaat 660

gtcgatcagg caaactcgaa cgtgaacggg gccttttacg gcaatcgcgc tgccggcatc 720

gccggaacct acagggtgaa cggcgcgcgg gctgatgccg gggcgggcat gatcggcacc 780

tttgtcggcg aacggaactg a 801

<210> 908

<211> 266

<212> PRT

<213> Martelella sp. AD-3 SLP 1a

<400> 908

Met Thr Ala Leu Met Gly Thr Met Ala Leu Ala Val Leu Ala Gly Cys
1 5 10 15

Ser Gly Gly Gly Gly Gly Gly Gly Pro Leu Ala Pro Asn Ala Leu Gly
20 25 30

Tyr Tyr Gly Asp Val Asp Thr Trp Asn Ala Ala Val Thr Gly Ser Gly
35 40 45

Ser Ala Ser Ala Asn Ile Gln Met Asn Gly Asp Gly Thr Val Gly Val
50 55 60

Glu Ile Thr Gly Gly Pro Asp Thr Gly Glu Thr Ala Leu Phe Tyr Pro
65 70 75 80

Asp Gly Glu Gly Tyr Thr Ala Asn Leu Gly Asp Gly Ala Glu Ala Tyr
85 90 95

Met Arg Leu Gly Tyr Phe Gly Val Asp Gly Ile Lys Asp Gly Pro Val
100 105 110

Val Ala Leu Ile Asp Ala Asp Thr Trp Asp Asp Asn Val Val Ala Met
115 120 125

Ala Phe Arg Ser Thr Asp Gly Val Thr Ala Pro Gly Asp Met Pro Leu
130 135 140

Ala Gly Arg Ala Thr Tyr Ser Gly Gln His Leu Gly Ala Ala Ala Leu
145 150 155 160

Pro Gly Glu Tyr Leu Asp Tyr Ile Asp Gly Ser Phe Asn Ala Asn Val
165 170 175

Asp Phe Gly Ser Gly Gln Leu Ala Gly Ala Met Asp Thr Gln Val Gly

180 185 190

Asp Val Thr Phe Gln Ala Thr Ile Ser Gly Ser Glu Phe Asn Ser Asn
195 200 205

Ala Asn Ser Ile Ala Val Gly Asn Asp Tyr Val Asn Val Asp Gln Ala
210 215 220

Asn Ser Asn Val Asn Gly Ala Phe Tyr Gly Asn Arg Ala Ala Gly Ile
225 230 235 240

Ala Gly Thr Tyr Arg Val Asn Gly Ala Arg Ala Asp Ala Gly Ala Gly
245 250 255

Met Ile Gly Thr Phe Val Gly Glu Arg Asn
260 265

<210> 909

<211> 873

<212> DNA

<213> Martelella sp. AD-3 SLP 2a

<400> 909

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ggaggccaac ccggcggcgg cgacggcagc tacaccgttg gcggaaccac tgttcaactg 180

aggaacggat ccgtcacgac ggttgccgat gcgacgggcg actataccga agatgacaat 240

ggcaacattt cggttagctt cacatccggc acctataacg gccagagcct gtccttcagc 300

gaggttggca gcacctccga gctgaacggc cagacagcga cactggaagc attcctcggt 360

tccgaagatg acaacagctc ttcgggcgcc atgtatatca ccgtggacga tgaaaatgac 420

gaggggaacg gcgacttcat cgctctttac agcggcgaca ccatatccga tctgccgcag 480

gaaggcactg gcacctatcg gggcgactat ttcggcgagg cgcagaatgg cgccgccggc 540

ggcctggtgt ccggctcgag cgcaatcacc gtcgactttc agaacggcgc ggtttcgggt 600

gatttcagcg acctgaccat ctatgacggc gacgcgccga tcggcgccat ggacgatgtt 660

ggcttctcgg gcactatgga caagaacagc gctgcctatg tggctgacag cgtgacgatc 720

ggcggtgatc cggccggcga aggctccagc gtcaagggtt cgctttttgg cggcggcgcg 780

agttcgacgg ccggcagtgt ggctgccttt gacaatgccg acaatccgac caaggcaacc 840

atcggcgtgt tccaggcgaa ccgggcagac tga 873

<210> 910

<211> 290

<212> PRT

<213> Martelella sp. AD-3 SLP 2a

<400> 910

Met Asn Lys Asn Phe Leu Ala Ala Leu Ala Gly Thr Ala Met Ile Ala
1 5 10 15
Val Ala Gly Cys Ser Ser Thr Ser Gly Asn Ser Ser Ser Gly Asp Pro

20 25 30
Gly Asn Gly Gly Gly Gly Ala Pro Gly Gly Gln Pro Gly Gly Gly Asp
35 40 45
Gly Ser Tyr Thr Val Gly Gly Thr Thr Val Gln Leu Arg Asn Gly Ser
50 55 60
Val Thr Thr Val Ala Asp Ala Thr Gly Asp Tyr Thr Glu Asp Asp Asn
65 70 75 80
Gly Asn Ile Ser Val Ser Phe Thr Ser Gly Thr Tyr Asn Gly Gln Ser

85 90 95
Leu Ser Phe Ser Glu Val Gly Ser Thr Ser Glu Leu Asn Gly Gln Thr
100 105 110
Ala Thr Leu Glu Ala Phe Leu Gly Ser Glu Asp Asp Asn Ser Ser Ser
115 120 125
Gly Ala Met Tyr Ile Thr Val Asp Asp Glu Asn Asp Glu Gly Asn Gly
130 135 140
Asp Phe Ile Ala Leu Tyr Ser Gly Asp Thr Ile Ser Asp Leu Pro Gln

145 150 155 160
Glu Gly Thr Gly Thr Tyr Arg Gly Asp Tyr Phe Gly Glu Ala Gln Asn
165 170 175
Gly Ala Ala Gly Gly Leu Val Ser Gly Ser Ser Ala Ile Thr Val Asp
180 185 190
Phe Gln Asn Gly Ala Val Ser Gly Asp Phe Ser Asp Leu Thr Ile Tyr
195 200 205

Asp Gly Asp Ala Pro Ile Gly Ala Met Asp Asp Val Gly Phe Ser Gly

210 215 220

Thr Met Asp Lys Asn Ser Ala Ala Tyr Val Ala Asp Ser Val Thr Ile

225 230 235 240

Gly Gly Asp Pro Ala Gly Glu Gly Ser Ser Val Lys Gly Ser Leu Phe

245 250 255

Gly Gly Gly Ala Ser Ser Thr Ala Gly Ser Val Ala Ala Phe Asp Asn

260 265 270

Ala Asp Asn Pro Thr Lys Ala Thr Ile Gly Val Phe Gln Ala Asn Arg

275 280 285

Ala Asp

290

<210> 911

<211> 861

<212> DNA

<213> N. aromaticivorans SLP 1a

<400> 911

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ccggtctaca cctacaagac gctcgaccag ttgagcggag accagacctt ccagtcgggg 120

ggcatcgccg gccagccggc cagcgatggc cgcctcgtcc agaccacgaa gcctttcggc 180

cagggcatcg agatcaagta tttcgccgcg agcgacacct acaacctcaa cgacggcgcc 240

ggcctcgtcg cggaatttgc cccggccgac gtgcgcgtgg tcgatgaagc ggcgggcgcg 300

gtccagtacc agaaggtcgt cggcagcgat ctcaacgtgc tcacgctcat caatccgcgt 360

ctcaacggcg tgccgctcag ctataccacg atcggctcgt ggctgcacct cagcccctcg 420

gctgcggcaa cgcgcttcta tctgatggtc ggcggcgttc cgacccaggc cggcgacgtc 480

ccgcgcagcg gcagcgccac ctacaccacc gccgtcggcg gtggcggcac cttcaatggc 540

acgaactaca acttctccgc caacagcacc ggcacgttca gcgccaattt cgccaacaac 600

accgtcagca cttcggtcca tctctccggc ctgccgaacg gcacgaccgt cgggacgccg 660

ttcgatgcgg gaacctacaa cggcaccggc aacatctcgt ccaccggccc cggcttcacg 720

ggcacgctga ccggcaccgc agccaacggc gcgttctccg gtgcgttctt cggtccccgg 780

gccaccgagt tcggctatgc cttctacctc gatggcaccg gcacccagat ccagggaacg 840

atggtcggca agaagaactg a 861

<210> 912

<211> 286

<212> PRT

<213> N. aromaticivorans SLP 1a

<400> 912

Met Leu Leu Ala Ser Cys Gly Gly Gly Gly Gly Gly Gly Ser Val Gly
1 5 10 15

Ser Thr Pro Thr Pro Val Tyr Thr Tyr Lys Thr Leu Asp Gln Leu Ser
20 25 30

Gly Asp Gln Thr Phe Gln Ser Gly Gly Ile Ala Gly Gln Pro Ala Ser
35 40 45

Asp Gly Arg Leu Val Gln Thr Thr Lys Pro Phe Gly Gln Gly Ile Glu
50 55 60

Ile Lys Tyr Phe Ala Ala Ser Asp Thr Tyr Asn Leu Asn Asp Gly Ala
65 70 75 80

Gly Leu Val Ala Glu Phe Ala Pro Ala Asp Val Arg Val Val Asp Glu
85 90 95

Ala Ala Gly Ala Val Gln Tyr Gln Lys Val Val Gly Ser Asp Leu Asn
100 105 110

Val Leu Thr Leu Ile Asn Pro Arg Leu Asn Gly Val Pro Leu Ser Tyr
115 120 125

Thr Thr Ile Gly Ser Trp Leu His Leu Ser Pro Ser Ala Ala Ala Thr
130 135 140

Arg Phe Tyr Leu Met Val Gly Gly Val Pro Thr Gln Ala Gly Asp Val
145 150 155 160

Pro Arg Ser Gly Ser Ala Thr Tyr Thr Thr Ala Val Gly Gly Gly Gly
165 170 175

Thr Phe Asn Gly Thr Asn Tyr Asn Phe Ser Ala Asn Ser Thr Gly Thr
180 185 190

Phe Ser Ala Asn Phe Ala Asn Asn Thr Val Ser Thr Ser Val His Leu
195 200 205

Ser Gly Leu Pro Asn Gly Thr Thr Val Gly Thr Pro Phe Asp Ala Gly

210 215 220

Thr Tyr Asn Gly Thr Gly Asn Ile Ser Ser Thr Gly Pro Gly Phe Thr

225 230 235 240

Gly Thr Leu Thr Gly Thr Ala Ala Asn Gly Ala Phe Ser Gly Ala Phe

245 250 255

Phe Gly Pro Arg Ala Thr Glu Phe Gly Tyr Ala Phe Tyr Leu Asp Gly

260 265 270

Thr Gly Thr Gln Ile Gln Gly Thr Met Val Gly Lys Lys Asn

275 280 285

<210> 913

<211> 1945

<212> DNA

<213> N. cinerea SLP 2a

<400> 913

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acgtaaagcc gaagaagccc gcaagctgaa gaagctcgta aagccgaaga ggcacgtaaa 120

gccgaagagg cacgtaaagc cgaagaagca cgtaaagctg aggaagcgcg taaagctgaa 180

gaggcacgta aagccgaaga aacgtaaggc tgaggaagca cgtaaagctg aagaagctcg 240

taaagctgaa gaagcacgta aagccgaaga agcacgtaaa gccgaagagg cacgtaaagc 300

tgaagaagcg cgtattgctg cgcgtaaggc tgatttggtg aaaaaagcca ccgaagcggg 360

tttgaaccaa aaacaggccg cagcttttgc cgagtccaat gtggatacgg ccgattccga 420

aattcagacg gccttggatg ctgcgtttaa agcggcagtt gccgaagcca aaggcggcgt 480

gtatgcaaaa ggctttgacg agcagaaaaa tcaggtttcg caatcgtcgg aatatcggga 540

agtgctgaca ccggcaggca aaacaacgac atggcagacg acaaccgttt catccgtgca 600

gaaagcctac aaccaggatt attccgtcgt agtcggcaac ggtacggtta cggaaacaaa 660

cgacggctac aacggcacgc agaccgacac gacgtttgcc gtcagcaaag tggcgggtta 720

cgccacgcct gacaaagccg tgccgaccac aggctctgcc gaatatcagg gcaaagcatt 780

ctcgaaagag ggcaaaggcg atttgaacta caccgtcaat ttcgacaaac gtaccggctc 840

gggcaggatt accgatattg ccgaaacagg ccgcattgat ttggccgaag gcaagcttgg 900

caaagtcagc gtcggagata aaaccgtaac cggtatcagc gcggcggctt ccgccgaaaa 960

cggctcgaaa ggcacatacc gcctcggcct gttcggcaaa gcggcagaag aaatcgcagg 1020

atcggccaag ctgccggaaa gcgaaatcgg cttcggcggc aaacgcgggg actttatcag 1080

ccgcgaagaa accgaacgcc tggaaaaacg caaagccgag ttgaacaaaa acgcaaccga 1140

aggcgggctg actgccgctc aggccaaaga ctatgccgaa aaacacctga aacaggacga 1200

tgtggcggcg caggcagcgt taaaagaact ggtgaccaaa aaagcctatc aggacggctt 1260

ggcggcggcc aaagaagaaa aagcgaagct ggatatttat ccggcggtgg atgtaaacag 1320

ctatgcggtg gatgctaaac aaacgcattt cgttaatcaa aattttacca acgtcaatga 1380

cgatggcgaa gtaaccagat ttaaaggatc aagtcagatt taccagcagc cgttttccgt 1440

cgtactcagc caacgtgttg aggaagacat ccgcaacaat caaaatttgt ctcctgagta 1500

cagtagaatc agcagttata ttgcaggttt tgccacccct gagaatgccc tgccgaccat 1560

cggaacagcc gtttacaagg gtttggcttt aaaaacaccg tacgagggag tttttactta 1620

taaagtcaat ttcgacaaac gtactggctc gggttcgatt gcgggggttg aatatgcaaa 1680

aatgatttcc cttgccgaag gaaatatcgg taaagtgaat atgcagggca aagagataat 1740

tgggatcaat ggcactgcgg atgtaacttc aaaatcagta ttatatgaat taaccaacgg 1800

ttcgtacacc ttgggtttct tcggttcggc tgcacaagaa gtggcaggta ctgtccgatt 1860

tgattctgac ctcaaaagtg gtctcaccaa ggacggaaaa tttgaaatcg gctttggcgg 1920

ccagcgtggc gaaatcaaaa aataa 1945

<210> 914

<211> 647

<212> PRT

<213> N. cinerea SLP 2a

<400> 914

Glu Ala Arg Lys Ala Glu Glu Ala Arg Lys Ala Glu Glu Ala Arg Lys

1 5 10 15

Ala Glu Glu Ala Arg Lys Ala Glu Glu Ala Arg Lys Leu Lys Lys Leu

20 25 30

Val Lys Pro Lys Arg His Val Lys Pro Lys Arg His Val Lys Pro Lys

35 40 45

Lys His Val Lys Leu Arg Lys Arg Val Lys Leu Lys Arg His Val Lys

50 55 60

Pro Lys Lys Arg Lys Ala Glu Glu Ala Arg Lys Ala Glu Glu Ala Arg

65 70 75 80

Lys Ala Glu Glu Ala Arg Lys Ala Glu Glu Ala Arg Lys Ala Glu Glu

85 90 95

Ala Arg Lys Ala Glu Glu Ala Arg Ile Ala Ala Arg Lys Ala Asp Leu

100 105 110

Val Lys Lys Ala Thr Glu Ala Gly Leu Asn Gln Lys Gln Ala Ala Ala

115 120 125

Phe Ala Glu Ser Asn Val Asp Thr Ala Asp Ser Glu Ile Gln Thr Ala

130 135 140

Leu Asp Ala Ala Phe Lys Ala Ala Val Ala Glu Ala Lys Gly Gly Val

145 150 155 160

Tyr Ala Lys Gly Phe Asp Glu Gln Lys Asn Gln Val Ser Gln Ser Ser

165 170 175

Glu Tyr Arg Glu Val Leu Thr Pro Ala Gly Lys Thr Thr Thr Trp Gln

180 185 190

Thr Thr Thr Val Ser Ser Val Gln Lys Ala Tyr Asn Gln Asp Tyr Ser

195 200 205

Val Val Val Gly Asn Gly Thr Val Thr Glu Thr Asn Asp Gly Tyr Asn

210 215 220

Gly Thr Gln Thr Asp Thr Thr Phe Ala Val Ser Lys Val Ala Gly Tyr

225 230 235 240

Ala Thr Pro Asp Lys Ala Val Pro Thr Thr Gly Ser Ala Glu Tyr Gln

245 250 255

Gly Lys Ala Phe Ser Lys Glu Gly Lys Gly Asp Leu Asn Tyr Thr Val

260 265 270

Asn Phe Asp Lys Arg Thr Gly Ser Gly Arg Ile Thr Asp Ile Ala Glu

275 280 285

Thr Gly Arg Ile Asp Leu Ala Glu Gly Lys Leu Gly Lys Val Ser Val

290 295 300

Gly Asp Lys Thr Val Thr Gly Ile Ser Ala Ala Ala Ser Ala Glu Asn

305 310 315 320

Gly Ser Lys Gly Thr Tyr Arg Leu Gly Leu Phe Gly Lys Ala Ala Glu
325 330 335
Glu Ile Ala Gly Ser Ala Lys Leu Pro Glu Ser Glu Ile Gly Phe Gly
340 345 350
Gly Lys Arg Gly Asp Phe Ile Ser Arg Glu Glu Thr Glu Arg Leu Glu
355 360 365
Lys Arg Lys Ala Glu Leu Asn Lys Asn Ala Thr Glu Gly Gly Leu Thr

370 375 380
Ala Ala Gln Ala Lys Asp Tyr Ala Glu Lys His Leu Lys Gln Asp Asp
385 390 395 400
Val Ala Ala Gln Ala Ala Leu Lys Glu Leu Val Thr Lys Lys Ala Tyr
405 410 415
Gln Asp Gly Leu Ala Ala Ala Lys Glu Glu Lys Ala Lys Leu Asp Ile
420 425 430
Tyr Pro Ala Val Asp Val Asn Ser Tyr Ala Val Asp Ala Lys Gln Thr

435 440 445
His Phe Val Asn Gln Asn Phe Thr Asn Val Asn Asp Asp Gly Glu Val
450 455 460
Thr Arg Phe Lys Gly Ser Ser Gln Ile Tyr Gln Gln Pro Phe Ser Val
465 470 475 480
Val Leu Ser Gln Arg Val Glu Glu Asp Ile Arg Asn Asn Gln Asn Leu
485 490 495
Ser Pro Glu Tyr Ser Arg Ile Ser Ser Tyr Ile Ala Gly Phe Ala Thr

500 505 510
Pro Glu Asn Ala Leu Pro Thr Ile Gly Thr Ala Val Tyr Lys Gly Leu
515 520 525
Ala Leu Lys Thr Pro Tyr Glu Gly Val Phe Thr Tyr Lys Val Asn Phe
530 535 540
Asp Lys Arg Thr Gly Ser Gly Ser Ile Ala Gly Val Glu Tyr Ala Lys
545 550 555 560
Met Ile Ser Leu Ala Glu Gly Asn Ile Gly Lys Val Asn Met Gln Gly

565 570 575

Lys Glu Ile Ile Gly Ile Asn Gly Thr Ala Asp Val Thr Ser Lys Ser

580 585 590

Val Leu Tyr Glu Leu Thr Asn Gly Ser Tyr Thr Leu Gly Phe Phe Gly

595 600 605

Ser Ala Ala Gln Glu Val Ala Gly Thr Val Arg Phe Asp Ser Asp Leu

610 615 620

Lys Ser Gly Leu Thr Lys Asp Gly Lys Phe Glu Ile Gly Phe Gly Gly

625 630 635 640

Gln Arg Gly Glu Ile Lys Lys

645

<210> 915

<211> 963

<212> DNA

<213> N. cinerea SLP 3a

<400> 915

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gcagcagaac ccggtatcaa agattacggc ggttcttccg aacttaagaa tgtagagcct 120

ggccaatcgg gtgtcatccc cttcggtgcg ggcaaggccg gtttgcgctt tgtaaacggc 180

ggcaattggt cggcctccat caacctgcaa aacggtccgg tacagcatat ccgcaacaaa 240

tataacgacg gcaaaaatcc gattaacggt actgatccgt atgccaacgt tgatggcaca 300

cgtaattcgc aatatctgat gttgcgcgat gtcgccccgg taatcggctg gttctacaat 360

ccgaaattag gtcaggtgtg gtatgaaaac cgccacaaca acaccgaagt gtacagcgta 420

cgccaaataa ccgaaccgaa actcttcttt gcacccaagt tcagcggcct ggtaatcgcc 480

aaagtgccgg gtatgagtga aggcaacaac gtgttcttcg gcgaatgggc accacgtgcc 540

ggcaacccgc cgaaaaacag caccgacctg aatatggcgg acggcaaacg caccgtttgg 600

tatgtgggcg acaatccgac ccaaaatatg ccggtactgt ccgaagccac ttataacgtg 660

ctgggtgtga ataagcatac cccgggtcag aacgacttct ataccggcgt gctgaccgcc 720

aactatggcg cgggtaaaaa caccttggaa ggcagcttgt cccgccctgg cgatagcgtg 780

aaatttgacg gtaccaatat tcggagcaac ggtacgtttg acaacggtaa ggctgacgaa 840

cgcattaccg gtcgcttcta cggcagcggc gcggaggctc tggccggtat tgtggatcgg 900

gatggccaag ccggagtaga tagggatatt gccttcggtg gtaagaaaat cccgccgcaa 960

taa 963

<210> 916

<211> 320

<212> PRT

<213> N. cinerea SLP 3a

<400> 916

Met Ser Ile Phe Lys Lys Thr Leu Leu Ala Ala Val Leu Cys Gly Val
1 5 10 15

Phe Gly Val Ala Ala Ala Glu Pro Gly Ile Lys Asp Tyr Gly Gly Ser
20 25 30

Ser Glu Leu Lys Asn Val Glu Pro Gly Gln Ser Gly Val Ile Pro Phe
35 40 45

Gly Ala Gly Lys Ala Gly Leu Arg Phe Val Asn Gly Gly Asn Trp Ser
50 55 60

Ala Ser Ile Asn Leu Gln Asn Gly Pro Val Gln His Ile Arg Asn Lys
65 70 75 80

Tyr Asn Asp Gly Lys Asn Pro Ile Asn Gly Thr Asp Pro Tyr Ala Asn
85 90 95

Val Asp Gly Thr Arg Asn Ser Gln Tyr Leu Met Leu Arg Asp Val Ala
100 105 110

Pro Val Ile Gly Trp Phe Tyr Asn Pro Lys Leu Gly Gln Val Trp Tyr
115 120 125

Glu Asn Arg His Asn Asn Thr Glu Val Tyr Ser Val Arg Gln Ile Thr
130 135 140

Glu Pro Lys Leu Phe Phe Ala Pro Lys Phe Ser Gly Leu Val Ile Ala
145 150 155 160

Lys Val Pro Gly Met Ser Glu Gly Asn Asn Val Phe Phe Gly Glu Trp
165 170 175

Ala Pro Arg Ala Gly Asn Pro Pro Lys Asn Ser Thr Asp Leu Asn Met
180 185 190

Ala Asp Gly Lys Arg Thr Val Trp Tyr Val Gly Asp Asn Pro Thr Gln

195 200 205

Asn Met Pro Val Leu Ser Glu Ala Thr Tyr Asn Val Leu Gly Val Asn

210 215 220

Lys His Thr Pro Gly Gln Asn Asp Phe Tyr Thr Gly Val Leu Thr Ala

225 230 235 240

Asn Tyr Gly Ala Gly Lys Asn Thr Leu Glu Gly Ser Leu Ser Arg Pro

245 250 255

Gly Asp Ser Val Lys Phe Asp Gly Thr Asn Ile Arg Ser Asn Gly Thr

260 265 270

Phe Asp Asn Gly Lys Ala Asp Glu Arg Ile Thr Gly Arg Phe Tyr Gly

275 280 285

Ser Gly Ala Glu Ala Leu Ala Gly Ile Val Asp Arg Asp Gly Gln Ala

290 295 300

Gly Val Asp Arg Asp Ile Ala Phe Gly Gly Lys Lys Ile Pro Pro Gln

305 310 315 320

<210> 917

<211> 993

<212> DNA

<213> N. cinerea SLP 4a

<400> 917

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ggaggaggtg catccgagcc gaaagttccc gtttccatac caacggcgca gcccatcgct 120

aatatcaagt tgagcgatga aagcagtgca ataaaaacca tcaacaccct ttccggaaaa 180

ggcggcagct tgcatgaagc agaactcgaa gtgaaaacat catggggcag ctataccgat 240

aaacaatatg tctaccaaac cccttccggc aactattaca acatcagctc atattccgac 300

ccaattgtcc cttcctactc aagcccatcc tatgtagtcc gtacccgcca cgaaggtcag 360

cctttatccg aaggcggcaa gctgtttgtc tgctgcagca gttccggaca atttactgat 420

gccccagcaa ccaaacagga ccacctcaaa ttcggcgcat ggataaatgc agacggcacg 480

gcagacctgt ttgtcggtgg caaacccgtc ggaacggcaa aaccgtctta ttacactccg 540

tctgacagta ctgtggcaaa aggcaagact acatacgaag tttgggcagt acgcgtacgc 600

aacggcaatt tcgttacctc tacctacgag cccaaaaacc cctataagtc gtctgaaaag 660

accgctccca agctttcact gctgacagcc aatttcaaca ccaacaaact cggcggcacg 720

attttaggta atgcggatta cggtccggac gttgtgatga aagatgtagg catcaacggc 780

gttgatttct caggcactgc cgaatcagac ggtaaaaacg gcaaagtcga aggaaaattc 840

ttcggtcaat ttgacggcga taaaacagaa gtcaacatag gcggcaaagt aaccttcgat 900

gccgataaat cgttggatac cgtattcggc ggcgtgaaga atgatgacga ccgcaatacg 960

acggatacaa gtttgacacc tgtcagcaag taa 993

<210> 918

<211> 330

<212> PRT

<213> N. cinerea SLP 4a

<400> 918

Met Lys Ile Asn Ile Ser Ala Ile Ser Ala Ala Thr Ser Leu Ile Leu
1 5 10 15

Thr Ala Cys Ala Gly Gly Gly Ala Ser Glu Pro Lys Val Pro Val Ser
20 25 30

Ile Pro Thr Ala Gln Pro Ile Ala Asn Ile Lys Leu Ser Asp Glu Ser
35 40 45

Ser Ala Ile Lys Thr Ile Asn Thr Leu Ser Gly Lys Gly Gly Ser Leu
50 55 60

His Glu Ala Glu Leu Glu Val Lys Thr Ser Trp Gly Ser Tyr Thr Asp
65 70 75 80

Lys Gln Tyr Val Tyr Gln Thr Pro Ser Gly Asn Tyr Tyr Asn Ile Ser
85 90 95

Ser Tyr Ser Asp Pro Ile Val Pro Ser Tyr Ser Ser Pro Ser Tyr Val
100 105 110

Val Arg Thr Arg His Glu Gly Gln Pro Leu Ser Glu Gly Gly Lys Leu
115 120 125

Phe Val Cys Cys Ser Ser Ser Gly Gln Phe Thr Asp Ala Pro Ala Thr
130 135 140

Lys Gln Asp His Leu Lys Phe Gly Ala Trp Ile Asn Ala Asp Gly Thr
145 150 155 160

Ala Asp Leu Phe Val Gly Gly Lys Pro Val Gly Thr Ala Lys Pro Ser

165 170 175

Tyr Tyr Thr Pro Ser Asp Ser Thr Val Ala Lys Gly Lys Thr Thr Tyr

180 185 190

Glu Val Trp Ala Val Arg Val Arg Asn Gly Asn Phe Val Thr Ser Thr

195 200 205

Tyr Glu Pro Lys Asn Pro Tyr Lys Ser Ser Glu Lys Thr Ala Pro Lys

210 215 220

Leu Ser Leu Leu Thr Ala Asn Phe Asn Thr Asn Lys Leu Gly Gly Thr

225 230 235 240

Ile Leu Gly Asn Ala Asp Tyr Gly Pro Asp Val Val Met Lys Asp Val

245 250 255

Gly Ile Asn Gly Val Asp Phe Ser Gly Thr Ala Glu Ser Asp Gly Lys

260 265 270

Asn Gly Lys Val Glu Gly Lys Phe Phe Gly Gln Phe Asp Gly Asp Lys

275 280 285

Thr Glu Val Asn Ile Gly Gly Lys Val Thr Phe Asp Ala Asp Lys Ser

290 295 300

Leu Asp Thr Val Phe Gly Gly Val Lys Asn Asp Asp Asp Arg Asn Thr

305 310 315 320

Thr Asp Thr Ser Leu Thr Pro Val Ser Lys

325 330

<210> 919

<211> 1740

<212

> DNA

<213> N. flavescens SLP 2a

<400> 919

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tctgcctgtg cttcaggcgg tggtaagtcg cccgatgttc atcccacaga gacattaaat 120

aaagttactc cttcacccac tgataaaggc agccattctg aaattgtcga tggcaaggat 180

caggatgctg ccacgcctgc acaacctgta gacaaacagg atacaggtac acatgctggt 240

tctgattcag gtacacaggg agatacaccc aagaataaca atccgcaagc cggacagggt 300

gaaactgcta gaagtgttac ggatggcaag gatcagggtg ccgccacgcc tgcacaacct 360

gtagataagc aggatacagg tgagcaaggt agttctgatg caggcgtgtc agtgttgaag 420

ccaaataatt cgaccccgat tgttcctaca acttctgaga aattagacca ggcaattaaa 480

gcaattgaaa atactgataa agagattgcc gataaagaaa aacaagcaga agaaaaagag 540

gcaatcattt catctttgga caactcaggg tctcctccgg ctgatcttat caaaggggct 600

cgagaatata ccaatagtaa gagagatctg caaaacacac atgaggcaaa ggtagcaaaa 660

gagaagcagc aaatcaaaca gcttgaagat gcagttaaat tgctagagct gaggaaggct 720

gaagtccaat cttctgcaga tcaagccgat ttggaaagta aaaaagctga attagagaaa 780

caaataagcg agcagaaagt aaagcttgca tcatcggagc aaaaattaga agaagttaaa 840

acggatgtcc aacgacttga aaaatttacg gaatatttag gaaattcatc attaaaagag 900

gttaaacccg aattgagcca acgggtatgg gaaagtaaac taagggaatt taaaaatctc 960

ggatcatatg aaaaaaaatt tgaaactgcc gcattgttta aagcatactt gattagtgaa 1020

aatcaagata aacaagatac cgcattcact gaggaaaaag tccgggatat ggatgtgtat 1080

atcaatggag aaaaatacga aggtaaagac ggtgatgaat atgctgttaa accgcttggc 1140

ttgcagtcgc agactgtaga aatttatggg caagataaag atcaaaatta tcattcagaa 1200

aaatcttggg tttatgagca gccgtattct gttgtggcag gatattttac ccaaacgata 1260

caaaacggta agaaggatga ggatggagca gacaaacttg acattggatt gagtgatata 1320

caaggcttgg caacagaaga agcacaatta ccgaaggtag gcgctttcga ttatgaaggc 1380

aaggcattcg gcggttcttc ggctaagcct gatagcaagt tggaagaaca tcaaggtgaa 1440

ttcaagtacc gtatcgactt tgacaaacgt aaaggttcgg gctcaattga aggtttgtct 1500

gaatatggcc gtattgattt aaaagaagct gatattgtaa aaggtaataa tttgaagtat 1560

gtcaacaaac cttattacgg gatagacaat ggcgaagcag cttcggaacg tggcgggctt 1620

aaatattatt ccttaggtat tttcgggccg gaggccaatg aggtgacggg tgtagtcggt 1680

acgtccggag accaagataa acttgccagg gatgtcggct tcggcggtca aaaaaagtag 1740

<210> 920

<211> 579

<212> PRT

<213> N. flavescens SLP 2a

<400> 920

Met His Leu Pro Phe Lys Phe Arg Pro Gly Leu Ala Ala Ile Ala Cys

1 5 10 15

Ile Phe Ala Leu Ser Ala Cys Ala Ser Gly Gly Gly Lys Ser Pro Asp
20 25 30
Val His Pro Thr Glu Thr Leu Asn Lys Val Thr Pro Ser Pro Thr Asp

35 40 45
Lys Gly Ser His Ser Glu Ile Val Asp Gly Lys Asp Gln Asp Ala Ala
50 55 60
Thr Pro Ala Gln Pro Val Asp Lys Gln Asp Thr Gly Thr His Ala Gly
65 70 75 80
Ser Asp Ser Gly Thr Gln Gly Asp Thr Pro Lys Asn Asn Asn Pro Gln
85 90 95
Ala Gly Gln Gly Glu Thr Ala Arg Ser Val Thr Asp Gly Lys Asp Gln

100 105 110
Gly Ala Ala Thr Pro Ala Gln Pro Val Asp Lys Gln Asp Thr Gly Glu
115 120 125
Gln Gly Ser Ser Asp Ala Gly Val Ser Val Leu Lys Pro Asn Asn Ser
130 135 140
Thr Pro Ile Val Pro Thr Thr Ser Glu Lys Leu Asp Gln Ala Ile Lys
145 150 155 160
Ala Ile Glu Asn Thr Asp Lys Glu Ile Ala Asp Lys Glu Lys Gln Ala

165 170 175
Glu Glu Lys Glu Ala Ile Ile Ser Ser Leu Asp Asn Ser Gly Ser Pro
180 185 190
Pro Ala Asp Leu Ile Lys Gly Ala Arg Glu Tyr Thr Asn Ser Lys Arg
195 200 205
Asp Leu Gln Asn Thr His Glu Ala Lys Val Ala Lys Glu Lys Gln Gln
210 215 220
Ile Lys Gln Leu Glu Asp Ala Val Lys Leu Leu Glu Leu Arg Lys Ala

225 230 235 240
Glu Val Gln Ser Ser Ala Asp Gln Ala Asp Leu Glu Ser Lys Lys Ala
245 250 255
Glu Leu Glu Lys Gln Ile Ser Glu Gln Lys Val Lys Leu Ala Ser Ser

260 265 270

Glu Gln Lys Leu Glu Glu Val Lys Thr Asp Val Gln Arg Leu Glu Lys

275 280 285

Phe Thr Glu Tyr Leu Gly Asn Ser Ser Leu Lys Glu Val Lys Pro Glu

290 295 300

Leu Ser Gln Arg Val Trp Glu Ser Lys Leu Arg Glu Phe Lys Asn Leu

305 310 315 320

Gly Ser Tyr Glu Lys Lys Phe Glu Thr Ala Ala Leu Phe Lys Ala Tyr

325 330 335

Leu Ile Ser Glu Asn Gln Asp Lys Gln Asp Thr Ala Phe Thr Glu Glu

340 345 350

Lys Val Arg Asp Met Asp Val Tyr Ile Asn Gly Glu Lys Tyr Glu Gly

355 360 365

Lys Asp Gly Asp Glu Tyr Ala Val Lys Pro Leu Gly Leu Gln Ser Gln

370 375 380

Thr Val Glu Ile Tyr Gly Gln Asp Lys Asp Gln Asn Tyr His Ser Glu

385 390 395 400

Lys Ser Trp Val Tyr Glu Gln Pro Tyr Ser Val Val Ala Gly Tyr Phe

405 410 415

Thr Gln Thr Ile Gln Asn Gly Lys Lys Asp Glu Asp Gly Ala Asp Lys

420 425 430

Leu Asp Ile Gly Leu Ser Asp Ile Gln Gly Leu Ala Thr Glu Glu Ala

435 440 445

Gln Leu Pro Lys Val Gly Ala Phe Asp Tyr Glu Gly Lys Ala Phe Gly

450 455 460

Gly Ser Ser Ala Lys Pro Asp Ser Lys Leu Glu Glu His Gln Gly Glu

465 470 475 480

Phe Lys Tyr Arg Ile Asp Phe Asp Lys Arg Lys Gly Ser Gly Ser Ile

485 490 495

Glu Gly Leu Ser Glu Tyr Gly Arg Ile Asp Leu Lys Glu Ala Asp Ile

500 505 510

Val Lys Gly Asn Asn Leu Lys Tyr Val Asn Lys Pro Tyr Tyr Gly Ile
515 520 525

Asp Asn Gly Glu Ala Ala Ser Glu Arg Gly Gly Leu Lys Tyr Tyr Ser
530 535 540

Leu Gly Ile Phe Gly Pro Glu Ala Asn Glu Val Thr Gly Val Val Gly

545 550 555 560

Thr Ser Gly Asp Gln Asp Lys Leu Ala Arg Asp Val Gly Phe Gly Gly
565 570 575

Gln Lys Lys

<210> 921

<211> 996

<212> DNA

<213> N. flavescens SLP 3a

<400> 921

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ggtggaggtg catctgaacc caaagtcccc gttgctattc cgacagctca acctatcgcc 120

aatgttaagc tgagcgatga aaacagtgcg gtacagacca tcaataccct ttccggaaaa 180

ggcggcagcc tgcgtgaagc ggaagtcgaa gtgacaacat catggggcta cagctatccc 240

gagaagcaat atgtctatca aacccccttca ggcaactatt acaacatcag ctcatattcc 300

gatccgattg tccccgactc tttcagcccg tcttatgccc tgcgtacccg ccacgaaggc 360

cagcctttat ctgaaggcgg caagctgttt gtctgttgca gtagttctgg gcagttcacc 420

tatgccccgg caaccaaaca ggaccacctc aaattcggcg catggataaa tgcagacggc 480

acagcatacc tgtttgtcgg cggcaaaccc gtcggaacgg cgaaaccgtc ttattacact 540

ccgtcagaca gtaaagaggc aaaaggcaag accacatacg aagtttgggc ggttcgcgtc 600

cgcaacggca atatcgttac ctctacctac gagcccaaaa aatcctctgt gttgtctgaa 660

aaaactgctc ccaagctttc actgctgaca gccaatttca acacccacaa actcggcggc 720

acgatcttgg gtaatgcgga ttacggtccg gatgttgtga tgaaagatgt tggcatcagc 780

ggcgttaatt tctcgggcac tgccacctcc aatggcaaaa ccggcacagt tgaaggaaaa 840

ttcttcggtc agtttaacgc tgatcaatct gaagtcagca taggcggcaa agtaaccttc 900

gatgccgata aatcgttgga taccgtattc ggcggcgtga aaaattcatc aaaccgcgat 960

acgcaagata caagcttgga acctgtcagc cagtaa 996

<210> 922

<211> 331

<212> PRT

<213> N. flavescens SLP 3a

<400> 922

Met Lys Ile Asn Val Phe Ile Val Pro Ile Ala Thr Ala Phe Ile Leu
1 5 10 15

Thr Ala Cys Ala Gly Gly Gly Ala Ser Glu Pro Lys Val Pro Val Ala
20 25 30

Ile Pro Thr Ala Gln Pro Ile Ala Asn Val Lys Leu Ser Asp Glu Asn
35 40 45

Ser Ala Val Gln Thr Ile Asn Thr Leu Ser Gly Lys Gly Gly Ser Leu
50 55 60

Arg Glu Ala Glu Val Glu Val Thr Thr Ser Trp Gly Tyr Ser Tyr Pro
65 70 75 80

Glu Lys Gln Tyr Val Tyr Gln Thr Pro Ser Gly Asn Tyr Tyr Asn Ile
85 90 95

Ser Ser Tyr Ser Asp Pro Ile Val Pro Asp Ser Phe Ser Pro Ser Tyr
100 105 110

Ala Leu Arg Thr Arg His Glu Gly Gln Pro Leu Ser Glu Gly Gly Lys
115 120 125

Leu Phe Val Cys Cys Ser Ser Ser Gly Gln Phe Thr Tyr Ala Pro Ala
130 135 140

Thr Lys Gln Asp His Leu Lys Phe Gly Ala Trp Ile Asn Ala Asp Gly
145 150 155 160

Thr Ala Tyr Leu Phe Val Gly Gly Lys Pro Val Gly Thr Ala Lys Pro
165 170 175

Ser Tyr Tyr Thr Pro Ser Asp Ser Lys Glu Ala Lys Gly Lys Thr Thr
180 185 190

Tyr Glu Val Trp Ala Val Arg Val Arg Asn Gly Asn Ile Val Thr Ser

195 200 205

Thr Tyr Glu Pro Lys Lys Ser Ser Val Leu Ser Glu Lys Thr Ala Pro

210 215 220

Lys Leu Ser Leu Leu Thr Ala Asn Phe Asn Thr His Lys Leu Gly Gly

225 230 235 240

Thr Ile Leu Gly Asn Ala Asp Tyr Gly Pro Asp Val Val Met Lys Asp

245 250 255

Val Gly Ile Ser Gly Val Asn Phe Ser Gly Thr Ala Thr Ser Asn Gly

260 265 270

Lys Thr Gly Thr Val Glu Gly Lys Phe Phe Gly Gln Phe Asn Ala Asp

275 280 285

Gln Ser Glu Val Ser Ile Gly Gly Lys Val Thr Phe Asp Ala Asp Lys

290 295 300

Ser Leu Asp Thr Val Phe Gly Gly Val Lys Asn Ser Ser Asn Arg Asp

305 310 315 320

Thr Gln Asp Thr Ser Leu Glu Pro Val Ser Gln

325 330

<210> 923

<211> 1361

<212> DNA

<213> N. gonorrhoeae SLP 2a, HpuA

<400> 923

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ttgataatca aaactattat taatacatca tcaagattga gtatgcgatg aaatacaaag 120

ccctgccctt actgccgctt gccgccgccc ttgccgcctg tgccgggggg ggggtagccg 180

aaccgcacgt ccccgtgtcc atccccaccg ccacgccgct gcccgccggc gaggtaacgt 240

tatcaagcga taacggcaat atcgaaaaca tcaacaccgc cggcgccgga agcgcatccg 300

acgcgccgag ccgcagcaga cgctcgctcg atgccgcccc gcaaaacaca tccggcattt 360

ccattcggca gcgggaagta gaaaaagact atttcggcta taaatcaaaa gaaacatcat 420

tcatcttcaa aacacccggc ggcgcgcaat acgcctttc atcctacgcc gaccccataa 480

ccgtcagcta ctcctccccc gatttcaaaa ttcccgaccg ccacgcaggg cagcggctcg 540

ccgacggcag ccgcatcttt atctgctgca gcgactccgg ggctacttcg tatgcggaaa 600

ttaccaaaca agattatatg aaattcgggg cgtggatagg tcctaacggc gaaatcgacc 660

tcttcgccgg cggcttcccc gtcggcaaaa cgccgcctcc tgcgttctcc tacggcagca 720

gcacgcccga aaccgcattg tcaaagggta aaatcactta tcaggtttgg ggcatccgcg 780

tcagaaacgg gcaatttgtt acttcctctt atacgccgcc gaaaagcggt tcttattatg 840

ggacacttgc caataccccc gtcctttcct ttatcaccgc caatttcaac agcaacacac 900

tggcaggcaa aatcctcggc aacagcgatt acgggccgga tgtggatatt caaaacgcaa 960

cgattaccgg tccgaccttt tccggcgatg ccacgtccgg cgggaaaagc ggcaaattgg 1020

aaggcaagtt ttttggcaag ttcgccagca cccgcagcag cgaagtcagc ataggcggca 1080

aaatcacctt tgacggcgac cgctccctcg ataccgtatt cggcggtgtg agttatgaaa 1140

aaaaacttga tgacaccagt caagatacca accaccttac taaacaataa accacctcat 1200

ccctgcaaag gtttcttatg cccattccct tcaaacccgt attggctgcc gccgccatcg 1260

cccaagcgtt tcccgccttt gcggcagacc ccgcgccgca gtccgcccaa acgctgaacg 1320

aaatcaccgt taccggcacg cacaaaaccc aaaaactcgg c 1361

<210> 924

<211> 360

<212> PRT

<213> N. gonorrhoeae SLP 2a, HpuA

<400> 924

Met Lys Tyr Lys Ala Leu Pro Leu Leu Pro Leu Ala Ala Ala Leu Ala

1 5 10 15

Ala Cys Ala Gly Gly Gly Val Ala Glu Pro His Val Pro Val Ser Ile

20 25 30

Pro Thr Ala Thr Pro Leu Pro Ala Gly Glu Val Thr Leu Ser Ser Asp

35 40 45

Asn Gly Asn Ile Glu Asn Ile Asn Thr Ala Gly Ala Gly Ser Ala Ser

50 55 60

Asp Ala Pro Ser Arg Ser Arg Arg Ser Leu Asp Ala Ala Pro Gln Asn

65 70 75 80

Thr Ser Gly Ile Ser Ile Arg Gln Arg Glu Val Glu Lys Asp Tyr Phe

85 90 95

Gly Tyr Lys Ser Lys Glu Thr Ser Phe Ile Phe Lys Thr Pro Gly Gly

100 105 110

Ala Gln Tyr Ala Leu Ser Ser Tyr Ala Asp Pro Ile Thr Val Ser Tyr

115 120 125

Ser Ser Pro Asp Phe Lys Ile Pro Asp Arg His Ala Gly Gln Arg Leu

130 135 140

Ala Asp Gly Ser Arg Ile Phe Ile Cys Cys Ser Asp Ser Gly Ala Thr

145 150 155 160

Ser Tyr Ala Glu Ile Thr Lys Gln Asp Tyr Met Lys Phe Gly Ala Trp

165 170 175

Ile Gly Pro Asn Gly Glu Ile Asp Leu Phe Ala Gly Gly Phe Pro Val

180 185 190

Gly Lys Thr Pro Pro Pro Ala Phe Ser Tyr Gly Ser Ser Thr Pro Glu

195 200 205

Thr Ala Leu Ser Lys Gly Lys Ile Thr Tyr Gln Val Trp Gly Ile Arg

210 215 220

Val Arg Asn Gly Gln Phe Val Thr Ser Ser Tyr Thr Pro Pro Lys Ser

225 230 235 240

Gly Ser Tyr Tyr Gly Thr Leu Ala Asn Thr Pro Val Leu Ser Phe Ile

245 250 255

Thr Ala Asn Phe Asn Ser Asn Thr Leu Ala Gly Lys Ile Leu Gly Asn

260 265 270

Ser Asp Tyr Gly Pro Asp Val Asp Ile Gln Asn Ala Thr Ile Thr Gly

275 280 285

Pro Thr Phe Ser Gly Asp Ala Thr Ser Gly Gly Lys Ser Gly Lys Leu

290 295 300

Glu Gly Lys Phe Phe Gly Lys Phe Ala Ser Thr Arg Ser Ser Glu Val

305 310 315 320

Ser Ile Gly Gly Lys Ile Thr Phe Asp Gly Asp Arg Ser Leu Asp Thr

325 330 335

Val Phe Gly Gly Val Ser Tyr Glu Lys Lys Leu Asp Asp Thr Ser Gln

340 345 350

Asp Thr Asn His Leu Thr Lys Gln

355 360

<210> 925

<211> 1089

<212> DNA

<213> N. indicus SLP 1a

<400> 925

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tcatccgcca ccaccggctc tggcggttcg ggcggttccc ttgggggcgg tggttccggc 120

ggcagcggtg gatccggtgg cggatcgggc ggcggttcga gcggtggctc gggtgggggt 180

ggggccggca gcggcatcca gcttttcggt ctgaagtcga cctataacaa gaagctgcag 240

acctccacgg gcgtcggccc tgacatctat gaaggcagcg aggtctacgt atccgacgat 300

acggcgagca cgggcgcaca gactataacg ggttccctcg aactcgatgg tggcaagctg 360

gtcgacaagg ttgacgccac ttccacctcg agcgcgggca cggtagtggc tgaaaacggc 420

acggtgctgc cgcgcgccaa cggcacgttg cgtggcgatt tcgtgacttc gcaaacgagc 480

gatccggcga cggcgcttga ccaaatgcgc gtcacctcgc tcgatttcga tggcgacaat 540

gacgacgatt tcttcgtggt cgagcagcat ctcggatacg gatatttcag cggtaccgaa 600

accatcacca ccatgtatgg cggcaagatt gctcctgcct cggcactcgc aggcaagcag 660

acagcggtct atcagcgcac tcgcagcgag ggcggcgccg agttccagta caagactggt 720

cccggcttct cccaggaggg ggccaccttc accggcgatg ccacggtgaa cgcgaacttc 780

gacaccggca aggtcgatgt gctcatcgac aacacccagc gccagcacgg caccaaggga 840

ccgtcgcagg tgggtgtcga actcgccggc gcatcgatca acggcagcca tttctccggc 900

ggcacggtgc ggatgttcga cgaatccaac ggtgccacaa tctccaacct ttcgccgggc 960

agttccgatt attcgggtgc cttcttcggc gacaacgccg agcatgtcgg tggtgtgttc 1020

cagggcaacg gaaccatcaa cggcaatacc cccggcatgg tgaagggatg gttcgccgca 1080

agcgaatga 1089

<210> 926

<211> 362

<212> PRT

<213> N. indicus SLP 1a

<400> 926

Met Lys Lys Ile Ser Ser Thr Leu Ala Leu Leu Leu Val Ser Ala Ser

1 5 10 15

Leu Ala Ala Cys Ser Ser Ala Thr Thr Gly Ser Gly Gly Ser Gly Gly

20 25 30

Ser Leu Gly Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly

35 40 45

Ser Gly Gly Gly Ser Ser Gly Gly Ser Gly Gly Gly Gly Ala Gly Ser

50 55 60

Gly Ile Gln Leu Phe Gly Leu Lys Ser Thr Tyr Asn Lys Lys Leu Gln

65 70 75 80

Thr Ser Thr Gly Val Gly Pro Asp Ile Tyr Glu Gly Ser Glu Val Tyr

85 90 95

Val Ser Asp Asp Thr Ala Ser Thr Gly Ala Gln Thr Ile Thr Gly Ser

100 105 110

Leu Glu Leu Asp Gly Gly Lys Leu Val Asp Lys Val Asp Ala Thr Ser

115 120 125

Thr Ser Ser Ala Gly Thr Val Val Ala Glu Asn Gly Thr Val Leu Pro

130 135 140

Arg Ala Asn Gly Thr Leu Arg Gly Asp Phe Val Thr Ser Gln Thr Ser

145 150 155 160

Asp Pro Ala Thr Ala Leu Asp Gln Met Arg Val Thr Ser Leu Asp Phe

165 170 175

Asp Gly Asp Asn Asp Asp Asp Phe Phe Val Val Glu Gln His Leu Gly

180 185 190

Tyr Gly Tyr Phe Ser Gly Thr Glu Thr Ile Thr Thr Met Tyr Gly Gly

195 200 205

Lys Ile Ala Pro Ala Ser Ala Leu Ala Gly Lys Gln Thr Ala Val Tyr

210 215 220

Gln Arg Thr Arg Ser Glu Gly Gly Ala Glu Phe Gln Tyr Lys Thr Gly

225 230 235 240

Pro Gly Phe Ser Gln Glu Gly Ala Thr Phe Thr Gly Asp Ala Thr Val

245 250 255

Asn Ala Asn Phe Asp Thr Gly Lys Val Asp Val Leu Ile Asp Asn Thr
260 265 270

Gln Arg Gln His Gly Thr Lys Gly Pro Ser Gln Val Gly Val Glu Leu
275 280 285

Ala Gly Ala Ser Ile Asn Gly Ser His Phe Ser Gly Gly Thr Val Arg

290 295 300

Met Phe Asp Glu Ser Asn Gly Ala Thr Ile Ser Asn Leu Ser Pro Gly
305 310 315 320

Ser Ser Asp Tyr Ser Gly Ala Phe Phe Gly Asp Asn Ala Glu His Val
325 330 335

Gly Gly Val Phe Gln Gly Asn Gly Thr Ile Asn Gly Asn Thr Pro Gly
340 345 350

Met Val Lys Gly Trp Phe Ala Ala Ser Glu
355 360

<210> 927

<211> 1023

<212> DNA

<213> N. lactamica SLP 2a

<400> 927

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ggggggggtag ccgaaccgca cgtccccgtg tccatcccca ccgccacgcc gctgcccaaa 120

ggcgaggtaa cgttatcaag cgataacggc aaaatcgaaa acatcaacac caccagcacc 180

ggaagcacat ccggcatttc cattcaagag cgggcggtta caaaaaacta tttcggtgtt 240

gaatcacaag aaaaatcatt catcttcaaa acacccggcg gcgcgcaata cacccctttca 300

tcctacgccg accccataac cgtcagctac tcctcccccg atttcaaaat tcccgaccgc 360

cacgcagggc agcggcttgc cgacggcagc cgcatcttta tctgttgcag cgaatccggg 420

gctacttcgt atgcggaaat caccaaacaa gattatatga aattcggggc gtggataggt 480

cccaacggcg aaatcgacct cttcgccggc ggcttccccg tcggcaaaac gccgaaaccg 540

gcatactcct ggagcgacga cacgcccgaa accgccggca agggcaaaat cacttatcag 600

gtttggggca tccgcgtcag aaatgggcaa tttgttactt cctcttatac gccgccaaaa 660

agcggttatt ggggtccacc taccaacacc cccgtccttt cctttatcac cgccaatttc 720

aacagcaaca aactggcagg caaaatcctc ggcaacagcg attacgggcc ggatgtggaa 780

attaaagaag caacgattaa cggtctgacc ttttccggca ctgccacatc cggtgggcaa 840

accggcaact tggacggcaa gttttttggc aagttcgaca gtagttacag cagcgacacc 900

agtataggcg gcaaaatcac ctttgatggc gaccgctccc tcgataccgt attcggcggt 960

gtgagttata aaaaagaact tgaaaacaac actgatacaa gtaccaccca tctcacaaaa 1020

taa 1023

<210> 928

<211> 340

<212> PRT

<213> N. lactamica SLP 2a

<400> 928

Met Lys Tyr Lys Ala Leu Ser Leu Leu Pro Leu Ala Ala Ala Leu Ala

1 5 10 15

Ala Cys Ala Gly Gly Gly Val Ala Glu Pro His Val Pro Val Ser Ile

20 25 30

Pro Thr Ala Thr Pro Leu Pro Lys Gly Glu Val Thr Leu Ser Ser Asp

35 40 45

Asn Gly Lys Ile Glu Asn Ile Asn Thr Thr Ser Thr Gly Ser Thr Ser

50 55 60

Gly Ile Ser Ile Gln Glu Arg Ala Val Thr Lys Asn Tyr Phe Gly Val

65 70 75 80

Glu Ser Gln Glu Lys Ser Phe Ile Phe Lys Thr Pro Gly Gly Ala Gln

85 90 95

Tyr Thr Leu Ser Ser Tyr Ala Asp Pro Ile Thr Val Ser Tyr Ser Ser

100 105 110

Pro Asp Phe Lys Ile Pro Asp Arg His Ala Gly Gln Arg Leu Ala Asp

115 120 125

Gly Ser Arg Ile Phe Ile Cys Cys Ser Glu Ser Gly Ala Thr Ser Tyr

130 135 140

Ala Glu Ile Thr Lys Gln Asp Tyr Met Lys Phe Gly Ala Trp Ile Gly

145 150 155 160

Pro Asn Gly Glu Ile Asp Leu Phe Ala Gly Gly Phe Pro Val Gly Lys
165 170 175
Thr Pro Lys Pro Ala Tyr Ser Trp Ser Asp Asp Thr Pro Glu Thr Ala
180 185 190
Gly Lys Gly Lys Ile Thr Tyr Gln Val Trp Gly Ile Arg Val Arg Asn

195 200 205
Gly Gln Phe Val Thr Ser Ser Tyr Thr Pro Pro Lys Ser Gly Tyr Trp
210 215 220
Gly Pro Pro Thr Asn Thr Pro Val Leu Ser Phe Ile Thr Ala Asn Phe
225 230 235 240
Asn Ser Asn Lys Leu Ala Gly Lys Ile Leu Gly Asn Ser Asp Tyr Gly
245 250 255
Pro Asp Val Glu Ile Lys Glu Ala Thr Ile Asn Gly Leu Thr Phe Ser

260 265 270
Gly Thr Ala Thr Ser Gly Gly Gln Thr Gly Asn Leu Asp Gly Lys Phe
275 280 285
Phe Gly Lys Phe Asp Ser Ser Tyr Ser Ser Asp Thr Ser Ile Gly Gly
290 295 300
Lys Ile Thr Phe Asp Gly Asp Arg Ser Leu Asp Thr Val Phe Gly Gly
305 310 315 320
Val Ser Tyr Lys Lys Glu Leu Glu Asn Asn Thr Asp Thr Ser Thr Thr

325 330 335
His Leu Thr Lys
340

<210> 929
<211> 1860
<212> DNA
<213> N. lactamica SLP 3a
<400> 929

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ctaacagcgt gcgcgggtgg cggttccggt tcatctatgt cggctcaacc aagcgtttca 120
gaatcaccga aagacaacgc aggcacgggt agcaactccg gtcagccaag cgtttcagaa 180

ccgccgaaag acaacgcagg cacgggtagc aactccggtc agccaagcgt ttcagaaccg 240

ccgaaagaca acgcaggcac gggtagcaac tccggtcagc caagcgtttc agaatcaccg 300

aaagacaacg caggcacggg tagcaactcc ggtcagccaa gcgtttcaga accgccgaaa 360

gacaacgcag gcacgggtag caactccggt cagccaagcg tttcagaatc accgaaagac 420

aacgcaggca cgggtagcaa ctccggtcag ccaagcgttt cagaatcacc gaaagacaac 480

gcaggcacgg gtagcgactc cggtcagcca agcgtttcag agccatcgaa agacaacgca 540

ggcacgggta gcgactccgg tcaaccaagc gtttcagagc catcgaaaga caacgcaggc 600

acgggtagcg actccggtca accaagcgtt tcagagccat cgaaagacaa cgcaggcacg 660

ggtagcgact ccggtcaacc aagcgtttca gagccatcga aagacaacgc aggcacgggt 720

agcgactccg gtcaaccaag cgtttcagag ccatcgaaag acaacgcagg cacgggtagc 780

gactccggtc aaccaagcgt ttcagagcca tcgaaagaca acgcaggcac gggtagcgac 840

tccggtcaac caagcgtttc agagccatcg aaagacaacg caggcacggg tagcaactcc 900

ggtcagccaa gcgtttcaga acaactgaaa gacaatgcaa atgttgatac gaaagatgaa 960

aaagttattg aatatctgga gaaatcatca ttaaaagatg taccaaaaga attgcaagcc 1020

aaagtattag aggttaaagg tgatgaatat acaggagcgc gaaaacaata tgcaggtaag 1080

ctcggtaagg gtgaatccgt caaagcaatg ctatttctag acggcgaaga gccgtttagt 1140

aaggaacaac ttcagaagat ggatgtgtat gttaatggta aaaaatacga aggtagtaag 1200

gggggtgagc tagatgttct ccccaaaggt ttgagtgagc aaaagattga gttttacggt 1260

gcggataaag aacagaatta tgcgctatta aaaacttggg tttatgagca accgtattct 1320

gtggttagag gctattttgg ttacactcga aaagacggta atcctacaga agagaataga 1380

caaaatcctg aagagattcc atttgacttg tctctgggcg acattagagg cgtggcaaca 1440

gatgaagaca aattacccaa ggctgggagc tttcaatatg aagggcgggc atttggcggt 1500

aatggggttt tatccaaaga atcgttagat aaccataatg gcgtatttag atacacaatt 1560

gattttgatc ttagaaaagg ctctggctca attgaaggaa tggaacaata tggcaagatc 1620

aaattagaag aagctgctat tgagagaatc ccttatggag agaacggctc cagcttgggg 1680

ttgaaagacc gggtttctta tttcggcgtg aacgaagggg tggctacgtc agagaaggat 1740

aatgagatta aaaagtatca tttgggtatt ttcggcgaag cggctaatga agtagcaggt 1800

gctgtaagcc aagagcataa atatcaagct gttatcggtt tcggcggcga gaagaaatag 1860

<210> 930

<211> 619

<212> PRT

<213> N. lactamica SLP 3a

<400> 930

Met Lys Val Ser Gln Ser Val Met Asn Lys Leu Val Ile Ala Ala Ile

1 5 10 15

Ala Ser Met Gly Leu Thr Ala Cys Ala Gly Gly Gly Ser Gly Ser Ser

20 25 30

Met Ser Ala Gln Pro Ser Val Ser Glu Ser Pro Lys Asp Asn Ala Gly

35 40 45

Thr Gly Ser Asn Ser Gly Gln Pro Ser Val Ser Glu Pro Pro Lys Asp

50 55 60

Asn Ala Gly Thr Gly Ser Asn Ser Gly Gln Pro Ser Val Ser Glu Pro

65 70 75 80

Pro Lys Asp Asn Ala Gly Thr Gly Ser Asn Ser Gly Gln Pro Ser Val

85 90 95

Ser Glu Ser Pro Lys Asp Asn Ala Gly Thr Gly Ser Asn Ser Gly Gln

100 105 110

Pro Ser Val Ser Glu Pro Pro Lys Asp Asn Ala Gly Thr Gly Ser Asn

115 120 125

Ser Gly Gln Pro Ser Val Ser Glu Ser Pro Lys Asp Asn Ala Gly Thr

130 135 140

Gly Ser Asn Ser Gly Gln Pro Ser Val Ser Glu Ser Pro Lys Asp Asn

145 150 155 160

Ala Gly Thr Gly Ser Asp Ser Gly Gln Pro Ser Val Ser Glu Pro Ser

165 170 175

Lys Asp Asn Ala Gly Thr Gly Ser Asp Ser Gly Gln Pro Ser Val Ser

180 185 190

Glu Pro Ser Lys Asp Asn Ala Gly Thr Gly Ser Asp Ser Gly Gln Pro

195 200 205

Ser Val Ser Glu Pro Ser Lys Asp Asn Ala Gly Thr Gly Ser Asp Ser

210 215 220

Gly Gln Pro Ser Val Ser Glu Pro Ser Lys Asp Asn Ala Gly Thr Gly

225 230 235 240

Ser Asp Ser Gly Gln Pro Ser Val Ser Glu Pro Ser Lys Asp Asn Ala

245 250 255

Gly Thr Gly Ser Asp Ser Gly Gln Pro Ser Val Ser Glu Pro Ser Lys

260 265 270

Asp Asn Ala Gly Thr Gly Ser Asp Ser Gly Gln Pro Ser Val Ser Glu

275 280 285

Pro Ser Lys Asp Asn Ala Gly Thr Gly Ser Asn Ser Gly Gln Pro Ser

290 295 300

Val Ser Glu Gln Leu Lys Asp Asn Ala Asn Val Asp Thr Lys Asp Glu

305 310 315 320

Lys Val Ile Glu Tyr Leu Glu Lys Ser Ser Leu Lys Asp Val Pro Lys

325 330 335

Glu Leu Gln Ala Lys Val Leu Glu Val Lys Gly Asp Glu Tyr Thr Gly

340 345 350

Ala Arg Lys Gln Tyr Ala Gly Lys Leu Gly Lys Gly Glu Ser Val Lys

355 360 365

Ala Met Leu Phe Leu Asp Gly Glu Glu Pro Phe Ser Lys Glu Gln Leu

370 375 380

Gln Lys Met Asp Val Tyr Val Asn Gly Lys Lys Tyr Glu Gly Ser Lys

385 390 395 400

Gly Gly Glu Leu Asp Val Leu Pro Lys Gly Leu Ser Glu Gln Lys Ile

405 410 415

Glu Phe Tyr Gly Ala Asp Lys Glu Gln Asn Tyr Ala Leu Leu Lys Thr

420 425 430

Trp Val Tyr Glu Gln Pro Tyr Ser Val Val Arg Gly Tyr Phe Gly Tyr

435 440 445

Thr Arg Lys Asp Gly Asn Pro Thr Glu Glu Asn Arg Gln Asn Pro Glu

450 455 460

Glu Ile Pro Phe Asp Leu Ser Leu Gly Asp Ile Arg Gly Val Ala Thr

465 470 475 480

Asp Glu Asp Lys Leu Pro Lys Ala Gly Ser Phe Gln Tyr Glu Gly Arg

485 490 495

Ala Phe Gly Gly Asn Gly Val Leu Ser Lys Glu Ser Leu Asp Asn His

500 505 510

Asn Gly Val Phe Arg Tyr Thr Ile Asp Phe Asp Leu Arg Lys Gly Ser

515 520 525

Gly Ser Ile Glu Gly Met Glu Gln Tyr Gly Lys Ile Lys Leu Glu Glu

530 535 540

Ala Ala Ile Glu Arg Ile Pro Tyr Gly Glu Asn Gly Ser Ser Leu Gly

545 550 555 560

Leu Lys Asp Arg Val Ser Tyr Phe Gly Val Asn Glu Gly Val Ala Thr

565 570 575

Ser Glu Lys Asp Asn Glu Ile Lys Lys Tyr His Leu Gly Ile Phe Gly

580 585 590

Glu Ala Ala Asn Glu Val Ala Gly Ala Val Ser Gln Glu His Lys Tyr

595 600 605

Gln Ala Val Ile Gly Phe Gly Gly Glu Lys Lys

610 615

<210> 931

<211> 1026

<212> DNA

<213> N. meningitidis SLP 2a, HpuA

<400> 931

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gggggggtag ccgaaccgca cgtccccgtg tccatcccca ccgccacccc gctgcccacc 120

ggcgaggtaa agttatcaga cgacaatagc aaaatcgaaa acatcaacac cgccgacacc 180

ggaagcacat ccggcatttc cattcagcag cggaaatatg aagtagaaag ttacggcatc 240

aaaagagaag aaaaagcatt catcttccaa acacccggcg gcgcgcaata cgcccttca 300

tcctacgccg accccataac cgtcagctac tcctcccccg atttcaaaat tcccgaccgc 360

cacgcagggc agcggcttgc cgacggcagc cgcatcttta tctgttgcag cgaatccggg 420

gctacttcgt atgcggaaat caccaaacaa gattatatga aattcggggc gtggataggt 480

cccaacggcg aaatcgacct cttcgccggc ggcttccccg tcggcaaaac gccgaagcct 540

aaatactctt ggggcaacac cgaacccgaa accaaaggca agggcaaaat cacttatcag 600

gtttggggca tccgcgtcag aaacaggcaa tttgttactt cctcttatac gccgccgaaa 660

agcggttctt attatgggac acttgccaac acccccgtcc tttcctttat cactgccaat 720

ttcaacagca acaaactggc aggcgaaatc cgcggcaaca gcgattacgg accgagtgtg 780

aaaattgaaa acgcaacgat taacagttta tccttttccg gcactgccac gtccggcggg 840

aaaaccggca atttggaagg caagtttttt ggaaaattca acggctaccg ggacactgaa 900

accagcatag gcggcaaaat caccttttgac ggcgaccgct ccctcgatac cgtattcggc 960

ggtgtgagtt ataaaaaaga acttgaaaac aacactgata caagtaccac ccatctcaca 1020

aaataa 1026

<210> 932

<211> 341

<212> PRT

<213> N. meningitidis SLP 2a, HpuA

<400> 932

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1 5 10 15

Ala Cys Ala Gly Gly Gly Val Ala Glu Pro His Val Pro Val Ser Ile
20 25 30

Pro Thr Ala Thr Pro Leu Pro Thr Gly Glu Val Lys Leu Ser Asp Asp
35 40 45

Asn Ser Lys Ile Glu Asn Ile Asn Thr Ala Asp Thr Gly Ser Thr Ser
50 55 60

Gly Ile Ser Ile Gln Gln Arg Lys Tyr Glu Val Glu Ser Tyr Gly Ile
65 70 75 80

Lys Arg Glu Glu Lys Ala Phe Ile Phe Gln Thr Pro Gly Gly Ala Gln
85 90 95

Tyr Ala Leu Ser Ser Tyr Ala Asp Pro Ile Thr Val Ser Tyr Ser Ser
100 105 110

Pro Asp Phe Lys Ile Pro Asp Arg His Ala Gly Gln Arg Leu Ala Asp
115 120 125

Gly Ser Arg Ile Phe Ile Cys Cys Ser Glu Ser Gly Ala Thr Ser Tyr
130 135 140
Ala Glu Ile Thr Lys Gln Asp Tyr Met Lys Phe Gly Ala Trp Ile Gly
145 150 155 160
Pro Asn Gly Glu Ile Asp Leu Phe Ala Gly Gly Phe Pro Val Gly Lys

165 170 175
Thr Pro Lys Pro Lys Tyr Ser Trp Gly Asn Thr Glu Pro Glu Thr Lys
180 185 190
Gly Lys Gly Lys Ile Thr Tyr Gln Val Trp Gly Ile Arg Val Arg Asn
195 200 205
Arg Gln Phe Val Thr Ser Ser Tyr Thr Pro Pro Lys Ser Gly Ser Tyr
210 215 220
Tyr Gly Thr Leu Ala Asn Thr Pro Val Leu Ser Phe Ile Thr Ala Asn

225 230 235 240
Phe Asn Ser Asn Lys Leu Ala Gly Glu Ile Arg Gly Asn Ser Asp Tyr
245 250 255
Gly Pro Ser Val Lys Ile Glu Asn Ala Thr Ile Asn Ser Leu Ser Phe
260 265 270
Ser Gly Thr Ala Thr Ser Gly Gly Lys Thr Gly Asn Leu Glu Gly Lys
275 280 285
Phe Phe Gly Lys Phe Asn Gly Tyr Arg Asp Thr Glu Thr Ser Ile Gly

290 295 300
Gly Lys Ile Thr Phe Asp Gly Asp Arg Ser Leu Asp Thr Val Phe Gly
305 310 315 320
Gly Val Ser Tyr Lys Lys Glu Leu Glu Asn Asn Thr Asp Thr Ser Thr
325 330 335
Thr His Leu Thr Lys
340

<210> 933
<211> 870
<212> DNA
<213> N. mucosa SLP 3a

<400> 933

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caaaataatc ccgccagtaa tggcaatact gttgcaaaca acgggaataa ccctaccaat 120

agcggtaaca ctgctatcaa taatccgctg ccacgtgttg atttttcggt ttcatacggc 180

gggttgaaaa ccaatgcaat caaggatatt caaaaattag ctaaagattt gggagcacca 240

ggggcaaccg ttaaatcata caatgtaaca ctgggcaatc aatccagcag cggcagcgat 300

cttaagttat ccgaataccc gctcaaaaaa ttagcactca atcaagacta ccgagaaacc 360

gccattgcgc gtgccgaagg taacgattac accgttaccc gaagcggtaa agcccatatc 420

taccgtcaaa actattcttt gattgcaggt atcaatccga ctaatacaac agttagagga 480

tcaggagtca atgaatcaga aaaacttgac gatacttata tcctgattaa aggccaaact 540

acccaaaccc tgccgactgc gggcaaattt gactactcag gtattgcaag cgatggcgca 600

agcaaaggca aattagctta ttctgttgac ttcgacaaca gaaaaggcag cggtaaaatt 660

accggtgtcg gcagcgacat caatctgaat gaagcgtcta tccgggaagg cagctacacc 720

aacgaaatcg ataacaccga aattaaggga tacggtattc aaggctcttc caaccgtggc 780

aattatgctc tcggcttctt cggtccgaat gcggaagaaa tcgtcggtac ggtcaatgac 840

ggtgaaatcg gttttgccgg ctcccgctaa 870

<210> 934

<211> 289

<212> PRT

<213> N. mucosa SLP 3a

<400> 934

Met Thr Asn Pro Ser Asn Gly Ser Gln Thr Asn Asn Gly Asn Ala Ala
1 5 10 15

Ala Ala Asn Asn Gln Asn Asn Pro Ala Ser Asn Gly Asn Thr Val Ala
20 25 30

Asn Asn Gly Asn Asn Pro Thr Asn Ser Gly Asn Thr Ala Ile Asn Asn
35 40 45

Pro Leu Pro Arg Val Asp Phe Ser Val Ser Tyr Gly Gly Leu Lys Thr

50 55 60

Asn Ala Ile Lys Asp Ile Gln Lys Leu Ala Lys Asp Leu Gly Ala Pro
65 70 75 80

Gly Ala Thr Val Lys Ser Tyr Asn Val Thr Leu Gly Asn Gln Ser Ser
85 90 95
Ser Gly Ser Asp Leu Lys Leu Ser Glu Tyr Pro Leu Lys Lys Leu Ala
100 105 110
Leu Asn Gln Asp Tyr Arg Glu Thr Ala Ile Ala Arg Ala Glu Gly Asn

115 120 125
Asp Tyr Thr Val Thr Arg Ser Gly Lys Ala His Ile Tyr Arg Gln Asn
130 135 140
Tyr Ser Leu Ile Ala Gly Ile Asn Pro Thr Asn Thr Thr Val Arg Gly
145 150 155 160
Ser Gly Val Asn Glu Ser Glu Lys Leu Asp Asp Thr Tyr Ile Leu Ile
165 170 175
Lys Gly Gln Thr Thr Gln Thr Leu Pro Thr Ala Gly Lys Phe Asp Tyr

180 185 190
Ser Gly Ile Ala Ser Asp Gly Ala Ser Lys Gly Lys Leu Ala Tyr Ser
195 200 205
Val Asp Phe Asp Asn Arg Lys Gly Ser Gly Lys Ile Thr Gly Val Gly
210 215 220
Ser Asp Ile Asn Leu Asn Glu Ala Ser Ile Arg Glu Gly Ser Tyr Thr
225 230 235 240
Asn Glu Ile Asp Asn Thr Glu Ile Lys Gly Tyr Gly Ile Gln Gly Ser

245 250 255
Ser Asn Arg Gly Asn Tyr Ala Leu Gly Phe Phe Gly Pro Asn Ala Glu
260 265 270
Glu Ile Val Gly Thr Val Asn Asp Gly Glu Ile Gly Phe Ala Gly Ser
275 280 285
Arg

<210> 935
<211> 996
<212> DNA
<213> N. mucosa SLP 4a

<400> 935

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aatgtcaagc tgagtgatga gagcaatgca ataaagacca tcaacaccct ttccggtaaa 180

ggcggcagcc tgcatgaagc ggagctcgaa gttaaaacat catggggcag ctataccgat 240

aaacaatata tctatcaaac cccatccggc aactattaca acatcagctc atattccgac 300

ccgattatcc cctcctactc cagcccgtct tatgccctgc gtactcgcca cgaaggccag 360

cctttgtctg aaggtggaaa actatttgtc tgttgcagca attccggaca attcagctat 420

gcccctgcaa ccaaacatga tcaccttaaa tttggcgcat ggataagttc agacggtacg 480

gcagacctgt ttgtcggcgg caaacctgtc ggatcggcaa aaccgtcatg gagtacaccg 540

tcagacagta ctgtggcaaa aggtaagact acatacgaag tttgggcagt acgcgtccgc 600

aacggcaata tcgttacctc aacctacgat ccgggtaaat cctctgggtc gtctgaaaaa 660

aacacgccca aactttcact gctgacagcc aatttcaaca ccaacaaact cggcggcaca 720

atcttgggta atgcggatta cggtccggat gttgtgatga aagatgttgg catcaacggc 780

gttgatttct cgggcactgc cgaatccgac ggcaaaaacg gcaaagtcga agggaaattc 840

ttcggtcagt tcaatggcgg ttataaaaca gaagtcagca taggcggcaa agtaactttt 900

gatgccgata aatcgttgga taccgtattc ggcggcgtag aaaatttatc agaccgcaat 960

acgacagata caagcttgac acctgtcagc cagtaa 996

<210> 936

<211> 331

<212> PRT

<213> N. mucosa SLP 4a

<400> 936

Met Lys Ile Lys Val Pro Ala Ile Ser Ala Ala Ala Thr Leu Ile Leu
1 5 10 15

Thr Ala Cys Ala Gly Gly Gly Ala Ser Glu Pro Lys Val Pro Val Ala
20 25 30

Ile Pro Thr Ala Gln Pro Ile Ala Asn Val Lys Leu Ser Asp Glu Ser
35 40 45

Asn Ala Ile Lys Thr Ile Asn Thr Leu Ser Gly Lys Gly Gly Ser Leu
50 55 60

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His Glu Ala Glu Leu Glu Val Lys Thr Ser Trp Gly Ser Tyr Thr Asp
65                  70                  75                  80
Lys Gln Tyr Ile Tyr Gln Thr Pro Ser Gly Asn Tyr Tyr Asn Ile Ser
                85                  90                  95
Ser Tyr Ser Asp Pro Ile Ile Pro Ser Tyr Ser Ser Pro Ser Tyr Ala
            100                 105                 110

Leu Arg Thr Arg His Glu Gly Gln Pro Leu Ser Glu Gly Gly Lys Leu
        115                 120                 125
Phe Val Cys Cys Ser Asn Ser Gly Gln Phe Ser Tyr Ala Pro Ala Thr
    130                 135                 140
Lys His Asp His Leu Lys Phe Gly Ala Trp Ile Ser Ser Asp Gly Thr
145                 150                 155                 160
Ala Asp Leu Phe Val Gly Gly Lys Pro Val Gly Ser Ala Lys Pro Ser
                165                 170                 175

Trp Ser Thr Pro Ser Asp Ser Thr Val Ala Lys Gly Lys Thr Thr Tyr
            180                 185                 190
Glu Val Trp Ala Val Arg Val Arg Asn Gly Asn Ile Val Thr Ser Thr
        195                 200                 205
Tyr Asp Pro Gly Lys Ser Ser Gly Ser Ser Glu Lys Asn Thr Pro Lys
    210                 215                 220
Leu Ser Leu Leu Thr Ala Asn Phe Asn Thr Asn Lys Leu Gly Gly Thr
225                 230                 235                 240

Ile Leu Gly Asn Ala Asp Tyr Gly Pro Asp Val Val Met Lys Asp Val
                245                 250                 255
Gly Ile Asn Gly Val Asp Phe Ser Gly Thr Ala Glu Ser Asp Gly Lys
            260                 265                 270
Asn Gly Lys Val Glu Gly Lys Phe Phe Gly Gln Phe Asn Gly Gly Tyr
        275                 280                 285
Lys Thr Glu Val Ser Ile Gly Gly Lys Val Thr Phe Asp Ala Asp Lys
    290                 295                 300

Ser Leu Asp Thr Val Phe Gly Gly Val Glu Asn Leu Ser Asp Arg Asn
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305 310 315 320

Thr Thr Asp Thr Ser Leu Thr Pro Val Ser Gln

325 330

<210> 937

<211> 3393

<212> DNA

<213> N. nitratireducens SLP 1a

<400> 937

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gcgttttgtg gtaacgcata tggtggtagt ggtgttgagg ctgggatcaa tgttgcatta 120

aacggcatta aaggctatca acagtatggc gatgaagaaa aattaaaatc agccatttcg 180

ggagtcgctt ctatcgcaag ttcgattgaa cttagcgcca actttgtcac tgtttcagcc 240

gagaaaatta agacattgac tgagagtttg gcgggtggta cccagcttaa tctttttgaa 300

catactcgcc atggagctac gttagagttg gctgataaag tggggcgtta tgcgaatgcc 360

ttgtctgttg cgactagtgc tgctagcgct agtgttgata ttcacgactt tgcaaagtca 420

gaaaagactc ttgttgattc aatgactcta ttcaaaaatc tatctgtcac agctacttca 480

catgtgccgc tgttaggtac tggggttgtg attgtggata tgtcaacgga tgctttggtt 540

gctcaaatta attctttatt cgatgccgga agagaggcga gcgtatcgga agcgaattac 600

tatcgaacct tgcatgaact tgcttatgca aaaattgatg ccgcaatcat ccaaagtatt 660

agcaatggaa tagatgttga taatgataag atagtcgaaa ttcaaaaaat ggttggcaat 720

gaaatagcaa atattctaga tggcattaaa cctaaaaata gatttttcga tggtgatgtt 780

gctgttaata actataatag gttgagggag ttgagtgata gattaataag agctgagttc 840

tccgatggtt ttttaaatgg aagggttaag cgattcacgg caacgatcaa tgaaataaga 900

atcgccgaga aagaatttgt tgctgccatg aacagtttga tgtcagatat tgacttaatt 960

gccgagttgg atcaaccatt gcagtcctta agaaattccc tgcatgaaag agaaaaactg 1020

cactcaattg atcatagtaa attcagtgaa aaagccatca gtgacgccat cagcaacaag 1080

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ggcgaaactg caacgtccgc ctaccagctg ctacagccga ttaccaacaa cgatgcccag 1380

attacgacgg caatcaatca gtggtatgca tctggtggtg gagattggga agaggccaat 1440

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gtaaactgga cgtctggaaa ggtgtatggc tttgaaagta acgcctccct ggctggcggc 2340
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tacgtattca agacccgtcg cctgacgaca gccgaaaaca gcagcattcc ccgctacatc 2460
cgcgatgcca tgcgcgaaac cacttcgctt cagttctacg gcagcgccta tcccaacggg 2520
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cactggattg caggcacctt gacgccaaca acttccatgc cggtaacagg ctccgcgacc 3060
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agcaccaacc tgaccgcgaa cttcggtacc ggcaatattt ctggacaact gaatgttcaa 3180

tatgccaata cgggagccgc atatgccacc tccaatctga gcggcgtgac gatcagcgga 3240

aaccagttcg gcggaagctt gagcggatcg aataacgctg gggcaattca gggtggattc 3300

tttgggcctg ctgctcagga ggttgggggt aactgggcga tagagaagac ttcaggttcg 3360

aaagctgcgg gggtgttttc tggcaagaga taa 3393

<210> 938

<211> 1130

<212> PRT

<213> N. nitratireducens SLP 1a

<400> 938

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Met Leu Gly Ile Ala Phe Cys Gly Asn Ala Tyr Gly Gly Ser Gly Val

20 25 30

Glu Ala Gly Ile Asn Val Ala Leu Asn Gly Ile Lys Gly Tyr Gln Gln

35 40 45

Tyr Gly Asp Glu Glu Lys Leu Lys Ser Ala Ile Ser Gly Val Ala Ser

50 55 60

Ile Ala Ser Ser Ile Glu Leu Ser Ala Asn Phe Val Thr Val Ser Ala

65 70 75 80

Glu Lys Ile Lys Thr Leu Thr Glu Ser Leu Ala Gly Gly Thr Gln Leu

85 90 95

Asn Leu Phe Glu His Thr Arg His Gly Ala Thr Leu Glu Leu Ala Asp

100 105 110

Lys Val Gly Arg Tyr Ala Asn Ala Leu Ser Val Ala Thr Ser Ala Ala

115 120 125

Ser Ala Ser Val Asp Ile His Asp Phe Ala Lys Ser Glu Lys Thr Leu

130 135 140

Val Asp Ser Met Thr Leu Phe Lys Asn Leu Ser Val Thr Ala Thr Ser

145 150 155 160

His Val Pro Leu Leu Gly Thr Gly Val Val Ile Val Asp Met Ser Thr

165 170 175

```
Asp Ala Leu Val Ala Gln Ile Asn Ser Leu Phe Asp Ala Gly Arg Glu
            180                 185                 190
Ala Ser Val Ser Glu Ala Asn Tyr Tyr Arg Thr Leu His Glu Leu Ala

        195                 200                 205
Tyr Ala Lys Ile Asp Ala Ala Ile Ile Gln Ser Ile Ser Asn Gly Ile
    210                 215                 220
Asp Val Asp Asn Asp Lys Ile Val Glu Ile Gln Lys Met Val Gly Asn
225                 230                 235                 240
Glu Ile Ala Asn Ile Leu Asp Gly Ile Lys Pro Lys Asn Arg Phe Phe
                245                 250                 255
Asp Gly Asp Val Ala Val Asn Asn Tyr Asn Arg Leu Arg Glu Leu Ser

            260                 265                 270
Asp Arg Leu Ile Arg Ala Glu Phe Ser Asp Gly Phe Leu Asn Gly Arg
        275                 280                 285
Val Lys Arg Phe Thr Ala Thr Ile Asn Glu Ile Arg Ile Ala Glu Lys
    290                 295                 300
Glu Phe Val Ala Ala Met Asn Ser Leu Met Ser Asp Ile Asp Leu Ile
305                 310                 315                 320
Ala Glu Leu Asp Gln Pro Leu Gln Ser Leu Arg Asn Ser Leu His Glu

                325                 330                 335
Arg Glu Lys Leu His Ser Ile Asp His Ser Lys Phe Ser Glu Lys Ala
            340                 345                 350
Ile Ser Asp Ala Ile Ser Asn Lys Thr Val Asp Val Thr Arg Thr Ile
        355                 360                 365
Glu Thr Thr Arg Lys Leu Glu Leu Asp Arg Gln Leu Ala Arg Phe Asp
    370                 375                 380
Val Asp Ile Phe Phe Leu Ala Asp Asn Thr Gly Ser Met Gly Gly Leu

385                 390                 395                 400
Val Gly Ser Ala Lys Thr Asn Ala Gln Ala Ile Leu Asp Ala Leu Arg
                405                 410                 415
Thr Asp Ala Arg Phe Ser Lys Val Asn Ala Gln Phe Gly Val Gly Met
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420 425 430

Phe Leu Gly Asp Pro Ser Glu Trp Gly Glu Thr Ala Thr Ser Ala Tyr

435 440 445

Gln Leu Leu Gln Pro Ile Thr Asn Asn Asp Ala Gln Ile Thr Thr Ala

450 455 460

Ile Asn Gln Trp Tyr Ala Ser Gly Gly Gly Asp Trp Glu Glu Ala Asn

465 470 475 480

Phe Tyr Ala Ile His Gln Val Ile Thr Gln Gly Ala Ala Val Pro Arg

485 490 495

Asp Ala Thr Leu Lys Ser Asn Gln Val Thr Gly Trp Arg Pro Gly Ala

500 505 510

Ala Lys Val Ile Val Val Phe Gly Asp Ala Pro Ser Trp Gln Asn Ser

515 520 525

Val Asn Glu Lys Glu Leu Lys Asp Leu Val Arg Thr Thr Gly Ala Arg

530 535 540

Ile Val Phe Ile Asp Thr Ser Gln Ile Asn Val Gly Gln Gln Ser Asn

545 550 555 560

Val Phe Ala Ala Ser Ser Gly Arg Gln Met Gln Asp Ala Ala Leu Glu

565 570 575

Ile Ala Asp Ala Ser Gly Gly Ser Tyr Met His Leu Ser Asp Val Ser

580 585 590

Lys Ile Lys Glu Ala Val Leu Asp Ser Val Tyr Asp Ala Ile Ala Asp

595 600 605

Asn Asn Trp Gly Gly Gly Met Leu Ala Arg Ile Asp Ala Gly Thr Thr

610 615 620

Trp Arg Ser Arg Thr Pro Ser Ser Val Thr Ala Glu Ser Thr Asp Gly

625 630 635 640

Gly Lys Thr Leu Val Phe Thr Leu Arg Tyr Pro Asn Gln Pro Asn Ala

645 650 655

Thr Phe Ser Val Asp Thr Ser Val Ala Gly Lys Val Tyr Gly His Glu

660 665 670

Tyr Tyr Gln Gly Ala Ile Thr Gly Ala Thr Asn Ile Phe Ser Lys Asn
675 680 685
Met Asn Thr Asp Ser Val Phe His Ile Asn Ala Ala Gln Asp Phe Phe
690 695 700
Arg Phe Val Leu Arg Gly Glu Ser Gly Val Val Glu Gly Tyr Phe Gly

705 710 715 720
Glu Arg Leu Ser Ala Thr Thr Lys Leu Pro Thr Ser Gly Val Ser Thr
725 730 735
Tyr Asp Leu Arg His Arg Val Ile Ser Pro Tyr Asp Asn Asn Ala Tyr
740 745 750
Ala Ala Gly Gly Met Lys Leu Phe Val Asn Trp Thr Ser Gly Lys Val
755 760 765
Tyr Gly Phe Glu Ser Asn Ala Ser Leu Ala Gly Gly Thr Gly Thr Ala

770 775 780
Leu Phe Ile Gly Asp Ile Asp Arg Ser Gly Leu Glu Ile Asp Gly Gln
785 790 795 800
Tyr Val Phe Lys Thr Arg Arg Leu Thr Thr Ala Glu Asn Ser Ser Ile
805 810 815
Pro Arg Tyr Ile Arg Asp Ala Met Arg Glu Thr Thr Ser Leu Gln Phe
820 825 830
Tyr Gly Ser Ala Tyr Pro Asn Gly Leu Gly Gly Thr Phe Gly Ser Thr

835 840 845
Phe Tyr Asn Glu Ala Gly Ser Pro Thr Leu Ser Ser Met Leu Met Ser
850 855 860
Gly Tyr Val Asn Glu Lys Thr Val Thr Lys Pro Tyr Ser Pro Ala Asn
865 870 875 880
Asn Glu Val Trp Ser Gly Tyr Ala Val Gly Leu Val Ala Asn Arg Ser
885 890 895
Thr Gly Ala Val Ala Val Ala Tyr Asn Thr Asn Pro Asn Asp Val Gln

900 905 910
Met Thr Leu Arg Pro Val Ser Ala Thr Ala Lys Ala Asp Ile Thr Val

915 920 925

Arg Asp Gly Gly Thr Ala Tyr Asn Phe Gly Ser Asp Trp Ser Asp Thr

930 935 940

Ser Val Tyr Ile Asn Lys Asp Ala Phe Ala Ala Ile Lys Glu Ile Asn

945 950 955 960

Gly Val Pro Ser Tyr Ala Ala Thr Thr Met Thr Glu Asp Asp Gly Tyr

965 970 975

Asn Tyr Leu Ser Trp Gly Val Trp Ser Thr Glu Leu Val Ala Thr Pro

980 985 990

Asn Thr Ser Val Met Asp Gly Ser His Trp Ile Ala Gly Thr Leu Thr

995 1000 1005

Pro Thr Thr Ser Met Pro Val Thr Gly Ser Ala Thr Tyr Thr Gly

1010 1015 1020

Gln Ile Arg Gly Thr Ala His Glu Gly Gly Ala Leu His Ala Leu

1025 1030 1035

Asn Gly Ser Thr Asn Leu Thr Ala Asn Phe Gly Thr Gly Asn Ile

1040 1045 1050

Ser Gly Gln Leu Asn Val Gln Tyr Ala Asn Thr Gly Ala Ala Tyr

1055 1060 1065

Ala Thr Ser Asn Leu Ser Gly Val Thr Ile Ser Gly Asn Gln Phe

1070 1075 1080

Gly Gly Ser Leu Ser Gly Ser Asn Asn Ala Gly Ala Ile Gln Gly

1085 1090 1095

Gly Phe Phe Gly Pro Ala Ala Gln Glu Val Gly Gly Asn Trp Ala

1100 1105 1110

Ile Glu Lys Thr Ser Gly Ser Lys Ala Ala Gly Val Phe Ser Gly

1115 1120 1125

Lys Arg

1130

<210> 939

<211> 1632

<212> DNA

<213> N. nitrogenifigens SLP 1a

<400> 939

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accaccgccg gttcgtcgac cgcgaaaccg ctgacaatca gctatgatgc gacgtcgaac 180

agctacacga tcacgacgca gggacgcagc cagactttcg cgcctgccga catggccagc 240

gccgccaacg gcattgccgt ctacagcaag acgagcggca cgacgaccga ccggctgacc 300

atgctggccg ccaatgtcac cggctacaac agcgcggcgc cgcaatattc gggccttgcc 360

tattggcagc gctacagcgt cagcggcacc ggcgaggcaa cgaccttcga cattttcacc 420

tacggcctcg acacccctgc ctcggccgta ccgcgcaccg gacaggccgc ctatgcgacc 480

acggtcgtgg gtctggtcac gctgcccggc accgaggcgc gcatgttcca ggggaccggg 540

cgactggacg tcgatttcct cgacgggatc ctctcgacca gcgcgacgac caccgaaacc 600

ggccttgcct cgggcgcggt catcggcggc acgggttcgc tcaccggaac gggaaccctg 660

tcctcgtcag ccaatgcctt taccggcacg gtccattaca gcggcagcgg caacagttcg 720

agcggcacgc tctcgggccg cttctatggg ccgagcgcgc aggaactggg cgcagccttt 780

tcctccagcg gcagtgacgg cagcgcggca agcggcgcga tctggggcat cgccagtccc 840

ggaacaaccc cgatcaatct ttccgtcgca aatcccgcga ccgatcagac ttatgcggca 900

gcagccgctg aactcgactc aacgccctcg accggcagct cgaccagcct tggcacgaac 960

ccgcttgccg tcacaactgc aggcgacgtc acgatcggcg ggggcagttc gtacctcgcg 1020

cagaccacgc tggccaacag cgacagggtc gccgcgaccg acaccaattt cacctcgttc 1080

cagaaaaccg tgaacggcgc caccgtggca ctcgacatgt accgccccgg gaacagcgaa 1140

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gggacctcga tctacaccta tttcgtctat gggctgacga ccgacgccgc cacactcgcg 1260

gcccgcaccg gcaccgccca ttatgccggc gtcgcctatg gcaccgcatt cgacagcggc 1320

acgggaaccg gcaacgccgt caagggtgcc tcggctttcg acatcgactt caacatcggc 1380

ggatacgccg ggaccatcgc gctcaagagc agcagcaccg actacggcac gttcaacgca 1440

tcgggaacgc tgtcctcggg aatgcccgcg caaggcagcc tgaccggaac caagggcgga 1500

accgggcaga tcacaccctc gttctatggt cctgcggcac aggaattcgg cggcccgttc 1560

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aaggccaatt ga 1632

<210> 940

<211> 543

<212> PRT

<213> N. nitrogenifigens SLP 1a

<400> 940

Met Ala Ser Ala Asn Thr Thr Pro Ala Ser Asn Ser Ser Leu Ala Lys
1 5 10 15

Leu Val Ala Ser Gln Ser Phe Ala Asn Asp Gly Ala Ser Gln Thr Ala
20 25 30

Ala Phe Asp Leu Val Thr Gly Asn Thr Thr Ala Gly Ser Ser Thr Ala
35 40 45

Lys Pro Leu Thr Ile Ser Tyr Asp Ala Thr Ser Asn Ser Tyr Thr Ile
50 55 60

Thr Thr Gln Gly Arg Ser Gln Thr Phe Ala Pro Ala Asp Met Ala Ser
65 70 75 80

Ala Ala Asn Gly Ile Ala Val Tyr Ser Lys Thr Ser Gly Thr Thr Thr
85 90 95

Asp Arg Leu Thr Met Leu Ala Ala Asn Val Thr Gly Tyr Asn Ser Ala
100 105 110

Ala Pro Gln Tyr Ser Gly Leu Ala Tyr Trp Gln Arg Tyr Ser Val Ser
115 120 125

Gly Thr Gly Glu Ala Thr Thr Phe Asp Ile Phe Thr Tyr Gly Leu Asp
130 135 140

Thr Pro Ala Ser Ala Val Pro Arg Thr Gly Gln Ala Ala Tyr Ala Thr
145 150 155 160

Thr Val Val Gly Leu Val Thr Leu Pro Gly Thr Glu Ala Arg Met Phe
165 170 175

Gln Gly Thr Gly Arg Leu Asp Val Asp Phe Leu Asp Gly Ile Leu Ser
180 185 190

Thr Ser Ala Thr Thr Thr Glu Thr Gly Leu Ala Ser Gly Ala Val Ile
195 200 205

Gly Gly Thr Gly Ser Leu Thr Gly Thr Gly Thr Leu Ser Ser Ser Ala

210 215 220

Asn Ala Phe Thr Gly Thr Val His Tyr Ser Gly Ser Gly Asn Ser Ser

225 230 235 240

Ser Gly Thr Leu Ser Gly Arg Phe Tyr Gly Pro Ser Ala Gln Glu Leu

245 250 255

Gly Ala Ala Phe Ser Ser Ser Gly Ser Asp Gly Ser Ala Ala Ser Gly

260 265 270

Ala Ile Trp Gly Ile Ala Ser Pro Gly Thr Thr Pro Ile Asn Leu Ser

275 280 285

Val Ala Asn Pro Ala Thr Asp Gln Thr Tyr Ala Ala Ala Ala Ala Glu

290 295 300

Leu Asp Ser Thr Pro Ser Thr Gly Ser Ser Thr Ser Leu Gly Thr Asn

305 310 315 320

Pro Leu Ala Val Thr Thr Ala Gly Asp Val Thr Ile Gly Gly Gly Ser

325 330 335

Ser Tyr Leu Ala Gln Thr Thr Leu Ala Asn Ser Asp Arg Val Ala Ala

340 345 350

Thr Asp Thr Asn Phe Thr Ser Phe Gln Lys Thr Val Asn Gly Ala Thr

355 360 365

Val Ala Leu Asp Met Tyr Arg Pro Gly Asn Ser Glu Leu Ala Leu Thr

370 375 380

Tyr Met Ser Phe Gly Arg Trp Arg Glu Thr Pro Asp Ala Ala Ala Gln

385 390 395 400

Gly Thr Ser Ile Tyr Thr Tyr Phe Val Tyr Gly Leu Thr Thr Asp Ala

405 410 415

Ala Thr Leu Ala Ala Arg Thr Gly Thr Ala His Tyr Ala Gly Val Ala

420 425 430

Tyr Gly Thr Ala Phe Asp Ser Gly Thr Gly Thr Gly Asn Ala Val Lys

435 440 445

Gly Ala Ser Ala Phe Asp Ile Asp Phe Asn Ile Gly Gly Tyr Ala Gly

450 455 460

Thr Ile Ala Leu Lys Ser Ser Ser Thr Asp Tyr Gly Thr Phe Asn Ala
465 470 475 480
Ser Gly Thr Leu Ser Ser Gly Met Pro Ala Gln Gly Ser Leu Thr Gly
485 490 495
Thr Lys Gly Gly Thr Gly Gln Ile Thr Pro Ser Phe Tyr Gly Pro Ala
500 505 510

Ala Gln Glu Phe Gly Gly Pro Phe Arg Ile Ser Ile Ser Gly Ser Gly
515 520 525
Ser Ala Thr Thr Thr Ile Val Gly Ala Thr Val Thr Lys Ala Asn
530 535 540

<210> 941
<211> 1140
<212> DNA
<213> N. pentaromativorans SLP 1a
<400> 941

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gatgcgttct tcggcgaatg cacaacctgt ccgccgattc agccggacga tgaggatccc 180

aaccaggaag cccagatcgg agcggtctcc gaacccggcc tcggaacgaa ccccatcgta 240
ccgacttcgt tcgacgaact catcgctggc tcagatagtg acaccgacca gacgataaag 300
ctccgtctcg tccaatcctc gcgcgcgctt tcaatcggcg atgtctcggt ttcctcgtcc 360
gatcctgcga ccgacgatgg cggggcgcac ttcacaatca cgatacccgc cgatcccgat 420
agcgagacga taaccacgtt cacgctgggc aacaatgcct tgggggtcaa ggacgtcgcc 480
tttaccgaag acgattacga atcccctgtc cggaatgtga ccctgtcaga cggcagaaag 540
ctctcggtcg ccatgtttac cgaagacagg aatacgcagg aagcaggcag tgaactcgac 600

tggaccgtgt acggcagttg gggcatccgt tccgcgacga acatcccgca aagaggcgca 660
acgttcgtaa cggggatcga aacgtcggac agcgcaatcc cgacgagcgg cacagcgacc 720
ttcaacggct tcgtggaagg ttctgtcacg gtgcccagcg gaactgccat cgacaccgct 780
tccatccggg gcgatgcgac gatcacggcc aattttgcga acggtacgat atcgggcgcg 840
gcgtccgata ttactgccat tcccatcggc accctgccca tgaccggacc ggttacaccg 900
ggttccccac aagcgtggaa cagcttgagt ttccagggaa ccatgacaag cggcctgaac 960

ggtttttccg gggccacggc cgtcacctcc gctccggaag gcgcctattc gctgctcgac 1020

agcgcaaccg gctattttgc cggcatgttc tacggcccgg gcgcggaaga actgggtgct 1080

gtctggaacc tctacgatgg cattggtgca gccaccggcg tccttatcgg aaagcaatga 1140

<210> 942

<211> 379

<212> PRT

<213> N. pentaromativorans SLP 1a

<400> 942

Met Thr Leu Ile Ser Glu Arg Gln His Gln Arg Gly Gly Thr Gly Lys
1 5 10 15

Phe Ile Leu Leu Gly Ser Val Ala Ala Met Thr Leu Gly Leu Ser Ala
20 25 30

Cys Val Gly Val Arg Ile Pro Glu Asp Ala Phe Phe Gly Glu Cys Thr
35 40 45

Thr Cys Pro Pro Ile Gln Pro Asp Asp Glu Asp Pro Asn Gln Glu Ala
50 55 60

Gln Ile Gly Ala Val Ser Glu Pro Gly Leu Gly Thr Asn Pro Ile Val
65 70 75 80

Pro Thr Ser Phe Asp Glu Leu Ile Ala Gly Ser Asp Ser Asp Thr Asp
85 90 95

Gln Thr Ile Lys Leu Arg Leu Val Gln Ser Ser Arg Ala Leu Ser Ile
100 105 110

Gly Asp Val Ser Val Ser Ser Ser Asp Pro Ala Thr Asp Asp Gly Gly
115 120 125

Ala His Phe Thr Ile Thr Ile Pro Ala Asp Pro Asp Ser Glu Thr Ile
130 135 140

Thr Thr Phe Thr Leu Gly Asn Asn Ala Leu Gly Val Lys Asp Val Ala
145 150 155 160

Phe Thr Glu Asp Asp Tyr Glu Ser Pro Val Arg Asn Val Thr Leu Ser
165 170 175

Asp Gly Arg Lys Leu Ser Val Ala Met Phe Thr Glu Asp Arg Asn Thr

180 185 190

Gln Glu Ala Gly Ser Glu Leu Asp Trp Thr Val Tyr Gly Ser Trp Gly

195 200 205

Ile Arg Ser Ala Thr Asn Ile Pro Gln Arg Gly Ala Thr Phe Val Thr

210 215 220

Gly Ile Glu Thr Ser Asp Ser Ala Ile Pro Thr Ser Gly Thr Ala Thr

225 230 235 240

Phe Asn Gly Phe Val Glu Gly Ser Val Thr Val Pro Ser Gly Thr Ala

245 250 255

Ile Asp Thr Ala Ser Ile Arg Gly Asp Ala Thr Ile Thr Ala Asn Phe

260 265 270

Ala Asn Gly Thr Ile Ser Gly Ala Ala Ser Asp Ile Thr Ala Ile Pro

275 280 285

Ile Gly Thr Leu Pro Met Thr Gly Pro Val Thr Pro Gly Ser Pro Gln

290 295 300

Ala Trp Asn Ser Leu Ser Phe Gln Gly Thr Met Thr Ser Gly Leu Asn

305 310 315 320

Gly Phe Ser Gly Ala Thr Ala Val Thr Ser Ala Pro Glu Gly Ala Tyr

325 330 335

Ser Leu Leu Asp Ser Ala Thr Gly Tyr Phe Ala Gly Met Phe Tyr Gly

340 345 350

Pro Gly Ala Glu Glu Leu Gly Ala Val Trp Asn Leu Tyr Asp Gly Ile

355 360 365

Gly Ala Ala Thr Gly Val Leu Ile Gly Lys Gln

370 375

<210> 943

<211> 1062

<212> DNA

<213> N. pentaromativorans SLP 2a

<400> 943

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gtccttggca ttcttggact ggccctcgct ggctgcggcg gtgacggcgg cgtcaacagc 120

gccaatacca caccgggtcc gatagctaca cccgctccgc ctcccacacc atcatttacc 180

gggaccccgg tcggattcgt cgaaatttct gggaaatatc aggttgatgg aactgagacc 240

ttgaaagctg atggtccata cgatctgtcc gaaaatatcc tggcaatcga ggtcgaggag 300

gcaaccaaca cctatactgt cactgttgaa ggaaactata ttaccgaggt ctttgacccg 360

gaggcgaatg tcggccctgc acaaccaacc gacgaacccg gcaattttct ctattatcgc 420

aaggaggccg gtaccggagt gaagagcctg gaagtgctga gacaagatcc gggtaacgac 480

cggttgcaac ttcaatatct gagttacggc ctttggacgg ctgttgaccc tcacgcccct 540

gaagagcccc gcaatgtctc ggcatattca ttcgtgtttg gccaatcgac cgagaaggcg 600

aacctgcctg ccacgggaac ggcgatctat aacggtattg tcgacggtta ttacggaact 660

taccggttgc tcggaagtac cggcacgctc accgcggatt tcggggaatg gaccgtatct 720

accgaacttt cgctgcgcac agagggtctg cgtatcgcaa acgatcccgc gcttgcgaca 780

ggagccggtt tcgagatcgg tactctaagc ggcaccggcg atatgggctg tccgatcagc 840

tgcggcgtcg acgactatgg cgccgatgac aacgcctatt ggggatcgct ctccggaaca 900

ctggaaggca attcggtttc cggctcgttc gacggattgt tctttggtcc aggcgcggaa 960

gaaacgggat tcagcttcga ggttaacacc tatccctatg acccggcatc agggtcttca 1020

cctgggccga gcgccgccgg cgtcttcgta ggcaagcaat ag 1062

<210> 944

<211> 379

<212> PRT

<213> N. pentaromativorans SLP 2a

<400> 944

Met Thr Leu Ile Ser Glu Arg Gln His Gln Arg Gly Gly Thr Gly Lys
1 5 10 15

Phe Ile Leu Leu Gly Ser Val Ala Ala Met Thr Leu Gly Leu Ser Ala
20 25 30

Cys Val Gly Val Arg Ile Pro Glu Asp Ala Phe Phe Gly Glu Cys Thr
35 40 45

Thr Cys Pro Pro Ile Gln Pro Asp Asp Glu Asp Pro Asn Gln Glu Ala
50 55 60

Gln Ile Gly Ala Val Ser Glu Pro Gly Leu Gly Thr Asn Pro Ile Val
65 70 75 80

Pro Thr Ser Phe Asp Glu Leu Ile Ala Gly Ser Asp Ser Asp Thr Asp
85 90 95
Gln Thr Ile Lys Leu Arg Leu Val Gln Ser Ser Arg Ala Leu Ser Ile
100 105 110
Gly Asp Val Ser Val Ser Ser Ser Asp Pro Ala Thr Asp Asp Gly Gly

115 120 125
Ala His Phe Thr Ile Thr Ile Pro Ala Asp Pro Asp Ser Glu Thr Ile
130 135 140
Thr Thr Phe Thr Leu Gly Asn Asn Ala Leu Gly Val Lys Asp Val Ala
145 150 155 160
Phe Thr Glu Asp Asp Tyr Glu Ser Pro Val Arg Asn Val Thr Leu Ser
165 170 175
Asp Gly Arg Lys Leu Ser Val Ala Met Phe Thr Glu Asp Arg Asn Thr

180 185 190
Gln Glu Ala Gly Ser Glu Leu Asp Trp Thr Val Tyr Gly Ser Trp Gly
195 200 205
Ile Arg Ser Ala Thr Asn Ile Pro Gln Arg Gly Ala Thr Phe Val Thr
210 215 220
Gly Ile Glu Thr Ser Asp Ser Ala Ile Pro Thr Ser Gly Thr Ala Thr
225 230 235 240
Phe Asn Gly Phe Val Glu Gly Ser Val Thr Val Pro Ser Gly Thr Ala

245 250 255
Ile Asp Thr Ala Ser Ile Arg Gly Asp Ala Thr Ile Thr Ala Asn Phe
260 265 270
Ala Asn Gly Thr Ile Ser Gly Ala Ala Ser Asp Ile Thr Ala Ile Pro
275 280 285
Ile Gly Thr Leu Pro Met Thr Gly Pro Val Thr Pro Gly Ser Pro Gln
290 295 300
Ala Trp Asn Ser Leu Ser Phe Gln Gly Thr Met Thr Ser Gly Leu Asn

305 310 315 320
Gly Phe Ser Gly Ala Thr Ala Val Thr Ser Ala Pro Glu Gly Ala Tyr

325 330 335

Ser Leu Leu Asp Ser Ala Thr Gly Tyr Phe Ala Gly Met Phe Tyr Gly

340 345 350

Pro Gly Ala Glu Glu Leu Gly Ala Val Trp Asn Leu Tyr Asp Gly Ile

355 360 365

Gly Ala Ala Thr Gly Val Leu Ile Gly Lys Gln

370 375

<210> 945

<211> 1269

<212> DNA

<213> N. pentaromativorans SLP 2b

<400> 945

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tcgccagttt cacatcgtag catcagacag caattgcacg catgcggatt gctgctggct 180

tcgtcccttg tgctcgcagg ttgcggaggc gggggcggct tggccagcgt tagctccgca 240

cccggtccga ttgcgccctc gtcaggggag gtcacggccg atccgcaggc ggctaaggaa 300

ttgatcgtcg gcgatgccct tgctcctacg cccgcactga ccagtggagg ctacgacacg 360

atcgctctgg taatcgaaga agacaccccc ccttcgtttc tcgcacctgg ctcgcttacg 420

gttgcggtcg acagcacgac gaacacctac tcgttcactt tcgatcctgt cgccgtgccc 480

gagctatccg ccaagtcgtt tgatgatcca gatgggcaga tcgacttcca ggtcgacgac 540

gaagcctacg gccatgaata cgtagcgacg tttagtgagg acggcgtact cgtcagtgtc 600

gaaggcgaag gacgaagcgc ctccctgtac agccatattt tcgacgaagc gatgttcacc 660

acatctgtcg gccaaagcta tgtttcgctg ggccaatgga gctggcccca taccgtcact 720

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ggcaacccag gccctttcaa tctcgacata gcgatgactg ctgactttgg agcgcaatca 960

attgcggccg cagtagaata cgatatcctt tccgatgacg tcgaagctta tcactacgat 1020

ctttcgggac acgcaccaat ctccgaactc ggcgatttcg atattgcgct gagcggatca 1080

cggcttgctg gttcattttc tgaagggatg ttcgcgtctg ggtccgagct tgcgacagct 1140

tcgccggacg gccagttggt cggagccttc ttcggtccca acgccgatca gattggcgga 1200

acgatggcga ttccgggatc tcgcgactac aacatgattg gcgtggcctt cgtcgcgaca 1260

cagccttga 1269

<210> 946

<211> 353

<212> PRT

<213> N. pentaromativorans SLP 2b

<400> 946

Met Met Glu Asp Phe Leu Pro Arg Ala Ser Asp Ile Arg Arg Cys Leu
1 5 10 15

Arg Val Gly Ser Val Leu Gly Ile Leu Gly Leu Ala Leu Ala Gly Cys
20 25 30

Gly Gly Asp Gly Gly Val Asn Ser Ala Asn Thr Thr Pro Gly Pro Ile
35 40 45

Ala Thr Pro Ala Pro Pro Pro Thr Pro Ser Phe Thr Gly Thr Pro Val
50 55 60

Gly Phe Val Glu Ile Ser Gly Lys Tyr Gln Val Asp Gly Thr Glu Thr
65 70 75 80

Leu Lys Ala Asp Gly Pro Tyr Asp Leu Ser Glu Asn Ile Leu Ala Ile
85 90 95

Glu Val Glu Glu Ala Thr Asn Thr Tyr Thr Val Thr Val Glu Gly Asn
100 105 110

Tyr Ile Thr Glu Val Phe Asp Pro Glu Ala Asn Val Gly Pro Ala Gln
115 120 125

Pro Thr Asp Glu Pro Gly Asn Phe Leu Tyr Tyr Arg Lys Glu Ala Gly
130 135 140

Thr Gly Val Lys Ser Leu Glu Val Leu Arg Gln Asp Pro Gly Asn Asp
145 150 155 160

Arg Leu Gln Leu Gln Tyr Leu Ser Tyr Gly Leu Trp Thr Ala Val Asp
165 170 175

Pro His Ala Pro Glu Glu Pro Arg Asn Val Ser Ala Tyr Ser Phe Val

180 185 190

Phe Gly Gln Ser Thr Glu Lys Ala Asn Leu Pro Ala Thr Gly Thr Ala

195 200 205

Ile Tyr Asn Gly Ile Val Asp Gly Tyr Tyr Gly Thr Tyr Arg Leu Leu

210 215 220

Gly Ser Thr Gly Thr Leu Thr Ala Asp Phe Gly Glu Trp Thr Val Ser

225 230 235 240

Thr Glu Leu Ser Leu Arg Thr Glu Gly Leu Arg Ile Ala Asn Asp Pro

245 250 255

Ala Leu Ala Thr Gly Ala Gly Phe Glu Ile Gly Thr Leu Ser Gly Thr

260 265 270

Gly Asp Met Gly Cys Pro Ile Ser Cys Gly Val Asp Asp Tyr Gly Ala

275 280 285

Asp Asp Asn Ala Tyr Trp Gly Ser Leu Ser Gly Thr Leu Glu Gly Asn

290 295 300

Ser Val Ser Gly Ser Phe Asp Gly Leu Phe Phe Gly Pro Gly Ala Glu

305 310 315 320

Glu Thr Gly Phe Ser Phe Glu Val Asn Thr Tyr Pro Tyr Asp Pro Ala

325 330 335

Ser Gly Ser Ser Pro Gly Pro Ser Ala Ala Gly Val Phe Val Gly Lys

340 345 350

Gln

<210> 947

<211> 1014

<212> DNA

<213> N. polysaccharea SLP 2a

<400> 947

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ggggggggtag ccgaaccgca cgtccccgtg tccatcccca ccgccacgcc gctgaccgcc 120

ggcgaggtaa cgttatcaag cgataacggc aacattgaaa acatcaacac cgccggcacc 180

ggaagcacat ccggcatttc cattcagcag cgggaagtag aaaaagaacc tttccccgac 240

tacaaaatca aagaaacatc attcatcttc aaaacacccg gtggcgcgca atacgccctt 300

tcaacctacg ccgaccccat aataccccc agcaacgaaa cccccgattt caaaatgccc 360

gaccgccacg ccggccagcg gcttgccgac ggcagccgca tctttatctg ttgcagcgaa 420

tccggggcta acgatttcgc agaaatcacc aagcaggatt atatgaaatt cggggcgtgg 480

ataggcccca acggcaaaat cgacctcttc gccggcggct tccccgtcgg caaaacgccg 540

gagtctgtcg gcagcaccac acccgaaacc aaaggcaaaa tcacttatca ggtttggggc 600

atccgcgtca gaaacgggca atttgttacc tcctcttata cgccgcccaa aggcagcatt 660

tattacggtt atgaaaacac ccccgtcctt tcctttatta ccgccaattt caacagcaac 720

agactggcag gcgaaatccg cggcaacagc gattacggac cggatgtgga aattaaagac 780

gcaatgattg acggtctgaa cttttccggc actgccacct ccggcggcaa aaccggcaac 840

ttggaaggca agttttttgg caaattcaac ggctaccgcg acagcgaaac cagcataggc 900

ggcaaaatca cttttcaaga cgaccgctcc ctcgataccg tattcggcgg cgtgagttat 960

gaaaaaaaac ctaatgaaac cactgatatg agtaccgacc atctcaaaaa ataa 1014

<210> 948

<211> 337

<212> PRT

<213> N. polysaccharea SLP 2a

<400> 948

Met Lys Tyr Lys Ala Leu Ser Leu Leu Pro Leu Ala Ala Ala Leu Ala

1 5 10 15

Ala Cys Ala Gly Gly Gly Val Ala Glu Pro His Val Pro Val Ser Ile

20 25 30

Pro Thr Ala Thr Pro Leu Thr Ala Gly Glu Val Thr Leu Ser Ser Asp

35 40 45

Asn Gly Asn Ile Glu Asn Ile Asn Thr Ala Gly Thr Gly Ser Thr Ser

50 55 60

Gly Ile Ser Ile Gln Gln Arg Glu Val Glu Lys Glu Pro Phe Pro Asp

65 70 75 80

Tyr Lys Ile Lys Glu Thr Ser Phe Ile Phe Lys Thr Pro Gly Gly Ala

85 90 95

Gln Tyr Ala Leu Ser Thr Tyr Ala Asp Pro Ile Ile Pro Pro Ser Asn

100 105 110

Glu Thr Pro Asp Phe Lys Met Pro Asp Arg His Ala Gly Gln Arg Leu

115 120 125

Ala Asp Gly Ser Arg Ile Phe Ile Cys Cys Ser Glu Ser Gly Ala Asn

130 135 140

Asp Phe Ala Glu Ile Thr Lys Gln Asp Tyr Met Lys Phe Gly Ala Trp

145 150 155 160

Ile Gly Pro Asn Gly Lys Ile Asp Leu Phe Ala Gly Gly Phe Pro Val

165 170 175

Gly Lys Thr Pro Glu Ser Val Gly Ser Thr Thr Pro Glu Thr Lys Gly

180 185 190

Lys Ile Thr Tyr Gln Val Trp Gly Ile Arg Val Arg Asn Gly Gln Phe

195 200 205

Val Thr Ser Ser Tyr Thr Pro Pro Lys Gly Ser Ile Tyr Tyr Gly Tyr

210 215 220

Glu Asn Thr Pro Val Leu Ser Phe Ile Thr Ala Asn Phe Asn Ser Asn

225 230 235 240

Arg Leu Ala Gly Glu Ile Arg Gly Asn Ser Asp Tyr Gly Pro Asp Val

245 250 255

Glu Ile Lys Asp Ala Met Ile Asp Gly Leu Asn Phe Ser Gly Thr Ala

260 265 270

Thr Ser Gly Gly Lys Thr Gly Asn Leu Glu Gly Lys Phe Phe Gly Lys

275 280 285

Phe Asn Gly Tyr Arg Asp Ser Glu Thr Ser Ile Gly Gly Lys Ile Thr

290 295 300

Phe Gln Asp Asp Arg Ser Leu Asp Thr Val Phe Gly Gly Val Ser Tyr

305 310 315 320

Glu Lys Lys Pro Asn Glu Thr Thr Asp Met Ser Thr Asp His Leu Lys

325 330 335

Lys

<210> 949

<211> 858

<212> DNA

<213> N. polysaccharea SLP 3a

<400> 949

atgatgactt tgaacaaagt tttctcattg agcatgattg ccttgggttt ggcggcgtgc 60

agcagcaacg gtactgccaa caacggcaac aactctttag tttccggtcc tggcgtggca 120

acacaaggcg cggttgtcag ttctttttac ggcgtaaaag atgatgtaag gaaagctgtc 180

gacagttggg cagtcaataa gggattcaaa cctacagagg ttgagttggc atcagttacc 240

cagcaggttg gcagcgtctc ctccaagggc agcaatatca atttgtttga tgtcgtaccg 300

gcacaaaaca aggttcaaaa agtggatact gtaaccacag cacgtgttaa agccggcggg 360

gacaattacg agctgatttc aaaaggtcag gcacatatct accgtcaaaa ttattcttta 420

attgccggtc tttccgaact ggaaagaatc gaaaaagacc cgtccggtat caagagaaac 480

ttggatgtcg atgatgacgt tgatttggtt gtgaaaggtt ctgctaccaa aatcctgcca 540

gctgcgggca aatttagcta ctcaggtatt gcaaccgatg gcgaaaaaca aggtgctttg 600

tcttatgtag ttgatttcga gaaaaaaaac ggcaaaggcg aaattaccgg aatcggcaaa 660

accgacatca ctctgagtga agcgcctatc aaagaattca gccataccaa cgaattcgat 720

aacacagtaa ttaagggaca cggcatcgaa ggttctaatt acaaactcgg cttcttcggt 780

cctaacgctg aagaaatcgt cggtgcggtt actcagggta caaatagcat cggctttgcc 840

ggctcccgtc cgcattaa 858

<210> 950

<211> 285

<212> PRT

<213> N. polysaccharea SLP 3a

<400> 950

Met Met Thr Leu Asn Lys Val Phe Ser Leu Ser Met Ile Ala Leu Gly
1 5 10 15

Leu Ala Ala Cys Ser Ser Asn Gly Thr Ala Asn Asn Gly Asn Asn Ser
20 25 30

Leu Val Ser Gly Pro Gly Val Ala Thr Gln Gly Ala Val Val Ser Ser
35 40 45

Phe Tyr Gly Val Lys Asp Asp Val Arg Lys Ala Val Asp Ser Trp Ala

50 55 60

Val Asn Lys Gly Phe Lys Pro Thr Glu Val Glu Leu Ala Ser Val Thr
65 70 75 80

Gln Gln Val Gly Ser Val Ser Ser Lys Gly Ser Asn Ile Asn Leu Phe
85 90 95

Asp Val Val Pro Ala Gln Asn Lys Val Gln Lys Val Asp Thr Val Thr
100 105 110

Thr Ala Arg Val Lys Ala Gly Gly Asp Asn Tyr Glu Leu Ile Ser Lys
115 120 125

Gly Gln Ala His Ile Tyr Arg Gln Asn Tyr Ser Leu Ile Ala Gly Leu
130 135 140

Ser Glu Leu Glu Arg Ile Glu Lys Asp Pro Ser Gly Ile Lys Arg Asn
145 150 155 160

Leu Asp Val Asp Asp Asp Val Asp Leu Val Val Lys Gly Ser Ala Thr
165 170 175

Lys Ile Leu Pro Ala Ala Gly Lys Phe Ser Tyr Ser Gly Ile Ala Thr
180 185 190

Asp Gly Glu Lys Gln Gly Ala Leu Ser Tyr Val Val Asp Phe Glu Lys
195 200 205

Lys Asn Gly Lys Gly Glu Ile Thr Gly Ile Gly Lys Thr Asp Ile Thr
210 215 220

Leu Ser Glu Ala Pro Ile Lys Glu Phe Ser His Thr Asn Glu Phe Asp
225 230 235 240

Asn Thr Val Ile Lys Gly His Gly Ile Glu Gly Ser Asn Tyr Lys Leu
245 250 255

Gly Phe Phe Gly Pro Asn Ala Glu Glu Ile Val Gly Ala Val Thr Gln
260 265 270

Gly Thr Asn Ser Ile Gly Phe Ala Gly Ser Arg Pro His
275 280 285

<210> 951

<211> 798

<212> DNA

<213> N. rosorum SLP 1a

<400> 951

atgaaaaaat ccattttagc caccgcactt tgcctgtcct gcaccgtcgc gctcagcgcc 60

aacgccgcaa ttacctcagg cacctccaac aacaaagcgg cgctcagcgt aaaaaatgcc 120

tcagctaaac acaacggttg gttccattcc gatcccggcg gattaccggg tatcgaagta 180

caaggcgtca cctctaaagt caccagcttt aaatcgctga ccggtgtcgc caacaatgct 240

atggtgccga aatccttggg cggtcaggat aaaaacggtg ttgtggtgtt aaacatgaac 300

aacatgccaa gctgggtgcc gggctttcat ggcaagttag gcaactttgc gtttaaaaaa 360

gtcggcacgc aggaattgta ctacggcgaa tggctgggca acggcgccaa tgccaagcag 420

gatcgggttg tgtattatgc cggcaataat aaaaccgaca acatgccgac cggcggaaaa 480

gccgtatata gcgtacaggg cattaataat cacggcaaac tggatgcgga aatgctgaaa 540

ggcgagctga ccgccgactt cggcaaaaaa caagttaacg gttcaatgag taaaaccggc 600

ctaacggtga atatcaataa cgcccaaatt aatccggctg atgcaagttt ctccggtgat 660

aaagccgcca gtgcaaatgg tgtggtcggt agtgtcaagg gtaatttctt cggcaataat 720

gccgcggcgt tagccggcta tgcgaaattc gcaggccata atcaatatga caccgcattc 780

ggcggaagta aaaaataa 798

<210> 952

<211> 265

<212> PRT

<213> N. rosorum SLP 1a

<400> 952

Met Lys Lys Ser Ile Leu Ala Thr Ala Leu Cys Leu Ser Cys Thr Val
1 5 10 15

Ala Leu Ser Ala Asn Ala Ala Ile Thr Ser Gly Thr Ser Asn Asn Lys
20 25 30

Ala Ala Leu Ser Val Lys Asn Ala Ser Ala Lys His Asn Gly Trp Phe
35 40 45

His Ser Asp Pro Gly Gly Leu Pro Gly Ile Glu Val Gln Gly Val Thr
50 55 60

Ser Lys Val Thr Ser Phe Lys Ser Leu Thr Gly Val Ala Asn Asn Ala
65 70 75 80

Met Val Pro Lys Ser Leu Gly Gly Gln Asp Lys Asn Gly Val Val Val
85 90 95
Leu Asn Met Asn Asn Met Pro Ser Trp Val Pro Gly Phe His Gly Lys
100 105 110
Leu Gly Asn Phe Ala Phe Lys Lys Val Gly Thr Gln Glu Leu Tyr Tyr
115 120 125

Gly Glu Trp Leu Gly Asn Gly Ala Asn Ala Lys Gln Asp Arg Val Val
130 135 140
Tyr Tyr Ala Gly Asn Asn Lys Thr Asp Asn Met Pro Thr Gly Gly Lys
145 150 155 160
Ala Val Tyr Ser Val Gln Gly Ile Asn Asn His Gly Lys Leu Asp Ala
165 170 175
Glu Met Leu Lys Gly Glu Leu Thr Ala Asp Phe Gly Lys Lys Gln Val
180 185 190

Asn Gly Ser Met Ser Lys Thr Gly Leu Thr Val Asn Ile Asn Asn Ala
195 200 205
Gln Ile Asn Pro Ala Asp Ala Ser Phe Ser Gly Asp Lys Ala Ala Ser
210 215 220
Ala Asn Gly Val Val Gly Ser Val Lys Gly Asn Phe Phe Gly Asn Asn
225 230 235 240
Ala Ala Ala Leu Ala Gly Tyr Ala Lys Phe Ala Gly His Asn Gln Tyr
245 250 255

Asp Thr Ala Phe Gly Gly Ser Lys Lys
260 265

<210> 953

<211> 1083

<212> DNA

<213> N. rosorum SLP 2a

<400> 953

aaagcgaagg cggaagcggc tcaaaaagca gcggaagaaa aagcaaaagc ggaagcggct 60

caaaaagcgg cggaagagaa agcgaaggcg gaagcggctc agaaagcggc agaagaaaaa 120

gcgaaggcgg aagctgaacg cctagcagca gaaaaagccg aagctgagcg tatcgccgca 180

caggttgcga aattagaaaa actggcattg gcggcgggac taacaaagga agaagcggct 240

caatttgcta ataattatgt gaatgcttcc gaacaagatg ccgaagcgga attaagtcgt 300

ttagcttatg ataaagccat tgagaaggaa gaaaaagcca gaaaatcttt gtataaagaa 360

gcgattgccg ccggcctgac ggaagaaaat gccaatgaat atgcacagaa taatgtgcat 420

accgatgaag caaccaaaaa acaggtatta gaacaacttg ttattgatca gcataaaggc 480

attaaaagtg caagctataa agatggttat aattatgtcg gttattcaga acaagcagat 540

aataccacca cttgttccga aaacaattgc tcaacttggg atggtaaaac ctctacgagt 600

gaacgacttt acaatcaaaa atattctgta gtgcaatatg tttcgacgaa caaagccgga 660

ttattaaata accaatacat taatgaagat actaccaccg ttgaggcaaa agggcttaaa 720

actgctgcgt cagcaatgcc taacgaagga aaagcggaat attcgggtcg cgtcattcac 780

ccgtatggcg gcgagctggg atatttaacc tataatgtgg attttaatga acgaaaaggc 840

agtggctacg ttcaaggcct tccgaactat aatactaata aggttcactt gaatgaaggg 900

actattgata aatcggccat ttcatccact gtaacggcag gtgttgatga acgtggtgag 960

tacactgttg aatttttgg ccctaaagcg gaagaaatcg gtggaaaaat ggttattcat 1020

aacccgattc ttggtgagca tcatttcggc ttagccggta agcgcggtga aattacaaaa 1080

taa 1083

<210> 954

<211> 360

<212> PRT

<213> N. rosorum SLP 2a

<400> 954

Lys Ala Lys Ala Glu Ala Ala Gln Lys Ala Ala Glu Glu Lys Ala Lys

1 5 10 15

Ala Glu Ala Ala Gln Lys Ala Ala Glu Glu Lys Ala Lys Ala Glu Ala

20 25 30

Ala Gln Lys Ala Ala Glu Glu Lys Ala Lys Ala Glu Ala Glu Arg Leu

35 40 45

Ala Ala Glu Lys Ala Glu Ala Glu Arg Ile Ala Ala Gln Val Ala Lys

50 55 60

Leu Glu Lys Leu Ala Leu Ala Ala Gly Leu Thr Lys Glu Glu Ala Ala

65 70 75 80

Gln Phe Ala Asn Asn Tyr Val Asn Ala Ser Glu Gln Asp Ala Glu Ala
85 90 95
Glu Leu Ser Arg Leu Ala Tyr Asp Lys Ala Ile Glu Lys Glu Glu Lys
100 105 110
Ala Arg Lys Ser Leu Tyr Lys Glu Ala Ile Ala Ala Gly Leu Thr Glu

115 120 125
Glu Asn Ala Asn Glu Tyr Ala Gln Asn Asn Val His Thr Asp Glu Ala
130 135 140
Thr Lys Lys Gln Val Leu Glu Gln Leu Val Ile Asp Gln His Lys Gly
145 150 155 160
Ile Lys Ser Ala Ser Tyr Lys Asp Gly Tyr Asn Tyr Val Gly Tyr Ser
165 170 175
Glu Gln Ala Asp Asn Thr Thr Thr Cys Ser Glu Asn Asn Cys Ser Thr

180 185 190
Trp Asp Gly Lys Thr Ser Thr Ser Glu Arg Leu Tyr Asn Gln Lys Tyr
195 200 205
Ser Val Val Gln Tyr Val Ser Thr Asn Lys Ala Gly Leu Leu Asn Asn
210 215 220
Gln Tyr Ile Asn Glu Asp Thr Thr Thr Val Glu Ala Lys Gly Leu Lys
225 230 235 240
Thr Ala Ala Ser Ala Met Pro Asn Glu Gly Lys Ala Glu Tyr Ser Gly

245 250 255
Arg Val Ile His Pro Tyr Gly Gly Glu Leu Gly Tyr Leu Thr Tyr Asn
260 265 270
Val Asp Phe Asn Glu Arg Lys Gly Ser Gly Tyr Val Gln Gly Leu Pro
275 280 285
Asn Tyr Asn Thr Asn Lys Val His Leu Asn Glu Gly Thr Ile Asp Lys
290 295 300
Ser Ala Ile Ser Ser Thr Val Thr Ala Gly Val Asp Glu Arg Gly Glu

305 310 315 320
Tyr Thr Val Glu Phe Phe Gly Pro Lys Ala Glu Glu Ile Gly Gly Lys

325 330 335

Met Val Ile His Asn Pro Ile Leu Gly Glu His His Phe Gly Leu Ala

340 345 350

Gly Lys Arg Gly Glu Ile Thr Lys

355 360

<210> 955

<211> 1011

<212> DNA

<213> N. shayeganii SLP 1a

<400> 955

atgaaattga ttctaaaaac cgtatcggcc gcatctttgg cggctgtatt gggtgcttgt 60

gcaggaggcg gtgcggtgca tatacccgat tcaacagcga ctatgccaac ggtttcccct 120

ttgaatgttt ctgatgtgca gcctctgcaa ggtagttata cgggtcataa tttcaatgcg 180

gctcagccgg tgtcgtcaca tagcaatccg gctgttggaa cacttaaagc agtgagcttg 240

ccaaaagagg ttctgcttaa cgtttataat gatcgcaaga acgtattcat ttatgaaacg 300

gcagacggta aacaatatgc tttgttagga accggaaatc cttttgtgcc cacggcagcg 360

acgagtgttt ctgttgctcc gccaagagtg aaaatgtcgg aaaccgcagc aggggataaa 420

tttattgtgt gttgtgatca gttttataat agtaggttta taccagcccg agtcggtgat 480

cacgacgacg gggggtgcg ctatggcgtt tggatttcag cttcaggtag ggttgatatg 540

ttttacgggg gcacgcctgc tgttccggct caaatgttag gggcttctgg taatggcggg 600

gtgcctaggg gaaaagcaac ttatgaagtg gccgccttcc gggtgcgtga tgggcaagcg 660

gtgatgtcta cccatgatgt tgcaaatacg gcgaaccgat cattgttaac tgtcaatttt 720

aacagtagga aaatgggcgg taccatttta ggtaatgcgg aatttggcga caatattgta 780

tttggtgatg tgtctgtcga cggcgccagc ttttctggtt cggtaacttc ggctggggtg 840

agcggacaag tagaaggaag tttttatgga cgtaaccata ctaccgggag ctatatcggg 900

gggagagccg tttttaacgg cagaaatgac ttagacagtg tttttggggg aagtattcgt 960

agacaaggtc aagcttccta tgtaggggat gatgtcaatc atttggacta a 1011

<210> 956

<211> 336

<212> PRT

<213> N. shayeganii SLP 1a

<400> 956

Met Lys Leu Ile Leu Lys Thr Val Ser Ala Ala Ser Leu Ala Ala Val
1 5 10 15
Leu Gly Ala Cys Ala Gly Gly Gly Ala Val His Ile Pro Asp Ser Thr
20 25 30
Ala Thr Met Pro Thr Val Ser Pro Leu Asn Val Ser Asp Val Gln Pro

35 40 45
Leu Gln Gly Ser Tyr Thr Gly His Asn Phe Asn Ala Ala Gln Pro Val
50 55 60
Ser Ser His Ser Asn Pro Ala Val Gly Thr Leu Lys Ala Val Ser Leu
65 70 75 80
Pro Lys Glu Val Leu Leu Asn Val Tyr Asn Asp Arg Lys Asn Val Phe
85 90 95
Ile Tyr Glu Thr Ala Asp Gly Lys Gln Tyr Ala Leu Leu Gly Thr Gly

100 105 110
Asn Pro Phe Val Pro Thr Ala Ala Thr Ser Val Ser Val Ala Pro Pro
115 120 125
Arg Val Lys Met Ser Glu Thr Ala Ala Gly Asp Lys Phe Ile Val Cys
130 135 140
Cys Asp Gln Phe Tyr Asn Ser Arg Phe Ile Pro Ala Arg Val Gly Asp
145 150 155 160
His Asp Asp Gly Gly Val Arg Tyr Gly Val Trp Ile Ser Ala Ser Gly

165 170 175
Arg Val Asp Met Phe Tyr Gly Gly Thr Pro Ala Val Pro Ala Gln Met
180 185 190
Leu Gly Ala Ser Gly Asn Gly Gly Val Pro Arg Gly Lys Ala Thr Tyr
195 200 205
Glu Val Ala Ala Phe Arg Val Arg Asp Gly Gln Ala Val Met Ser Thr
210 215 220
His Asp Val Ala Asn Thr Ala Asn Arg Ser Leu Leu Thr Val Asn Phe

225 230 235 240
Asn Ser Arg Lys Met Gly Gly Thr Ile Leu Gly Asn Ala Glu Phe Gly

245 250 255

Asp Asn Ile Val Phe Gly Asp Val Ser Val Asp Gly Ala Ser Phe Ser

260 265 270

Gly Ser Val Thr Ser Ala Gly Val Ser Gly Gln Val Glu Gly Ser Phe

275 280 285

Tyr Gly Arg Asn His Thr Thr Gly Ser Tyr Ile Gly Gly Arg Ala Val

290 295 300

Phe Asn Gly Arg Asn Asp Leu Asp Ser Val Phe Gly Gly Ser Ile Arg

305 310 315 320

Arg Gln Gly Gln Ala Ser Tyr Val Gly Asp Asp Val Asn His Leu Asp

325 330 335

<210> 957

<211> 1950

<212> DNA

<213> N. sicca SLP 2a

<400> 957

atgcacactc aaaataaatc acctattact cattttgttc taagcggtat ttgcgttgca 60

attttagcag cctgcggcag ttcaaatgga ggtggagatt cacccaaaaa tctatctgta 120

gccccaaaaa acaacgtcaa taaagatgac gcaaaaaaag acaataccaa caaaaacaac 180

tctagtaagg ataattctga caaaggtact accaataaaa acaattccaa caaggttaac 240

actgacaaag gaaatgccga caaaaataat gccaataaag ataataaaac taacactaac 300

aaagaaacat tattattaaa taaaggcatt caggataaac tgaccacact aaaactaagt 360

gatgtaataa aaactgaaca attcaatcaa actgaagtga ataccggttt cattgcaaat 420

aacttaagtg cgaccccatt attagagaca gctaaaggtc cacatgatca ccctacctct 480

cacctttaa catccgctta tagaaaagat aaaaccaaac ttttgcgccc tcaaacagtt 540

atattagggg gtgtagcaac gcgttacttt accaactata cagatggtta tgttgcgaag 600

agagccggtt atgacgagat tgatacgcca ttaagtgcaa aaaatctgat tggtgtagat 660

aaacgcaata aaaatggcat cttagttaaa aatggcagga gcgttaacat cttagatcaa 720

actgccagca aactggaatt agatagtgta ggcggtagcc gttatacaaa atggtttaat 780

aattttgcta ctaatgccga taatgaaact gaattggata aaggccgccg tgtattaaca 840

gatgtgaaat acaaattaga tgcaaataat aatcctgtat ggactgtaac taccgaaccc 900

agcagcggtt atcaatatgc acattcttta aatcgttatt ttaacaataa tccagacgat 960

gaattatatg ttaaccaaaa cggtgaatat gcatatcgtt ttacattaaa aaaatcaact 1020

acatttgaag tcagtgcaga atcagcaaaa acccatccgg aacgtgcaga ggcgctcaaa 1080

gcattagggt ggtctgctgg caagcaatat cacttcgcac caggtagcta ctttatggtt 1140

acacaaaaag atggcagcct aaaaattgta gccgataacg gacaaatgac gcaggtatcc 1200

ttatattcag tccatgtcgg tattgatgac aataaagcat tgggtgcatt ccaaaataaa 1260

cgtgtaattg ccgaaatgtt cagtgcatta aactatggca agacaaatga aattcgtgcg 1320

atttatacct atgacgttgg acaagccaat ggcttcaacc aacaatatct ctcattaaac 1380

gcatggcgct ataaaaatgg cgatggcact tatggactca ataatccttt taacatcggc 1440

attttcgacc gagttgctac tgaaaatggt atagttgcca atgtctatga catgaagact 1500

aaaaaaggtt tatctgccaa atatacaggc gttgcctatt ctagccgaga tggtaaacaa 1560

gacggtgtga tgaatatgac tgcacagttc catgaaccag atatggctta caacaatact 1620

gtttcaagca ataacgttac cttcaatggc gcgattacca accgtcgcct agatgacaaa 1680

cgtaatgtat attttgccag cggtaatgta aaaacagaga gtggaatgcc ttctgcaagc 1740

gcggggcaaa aagtttctct agtgggtaga agccaagttg ctcaaaatgt tactgtctgg 1800

atggaaggaa aaaaaccagg tgaaaataaa gtaatttatg gtcaaggtaa cgtacgtttt 1860

gccggtccaa atgctgaaga agtcggtggt ttgttaaaaa tcactaccag ccatggcgaa 1920

aacaatatcg gtttcattgg caaacgctaa 1950

<210> 958

<211> 649

<212> PRT

<213> N. sicca SLP 2a

<400> 958

Met His Thr Gln Asn Lys Ser Pro Ile Thr His Phe Val Leu Ser Gly
1 5 10 15

Ile Cys Val Ala Ile Leu Ala Ala Cys Gly Ser Ser Asn Gly Gly Gly
20 25 30

Asp Ser Pro Lys Asn Leu Ser Val Ala Pro Lys Asn Asn Val Asn Lys
35 40 45

Asp Asp Ala Lys Lys Asp Asn Thr Asn Lys Asn Asn Ser Ser Lys Asp
50 55 60

Asn Ser Asp Lys Gly Thr Thr Asn Lys Asn Asn Ser Asn Lys Val Asn
65 70 75 80
Thr Asp Lys Gly Asn Ala Asp Lys Asn Asn Ala Asn Lys Asp Asn Lys
85 90 95

Thr Asn Thr Asn Lys Glu Thr Leu Leu Leu Asn Lys Gly Ile Gln Asp
100 105 110
Lys Leu Thr Thr Leu Lys Leu Ser Asp Val Ile Lys Thr Glu Gln Phe
115 120 125
Asn Gln Thr Glu Val Asn Thr Gly Phe Ile Ala Asn Asn Leu Ser Ala
130 135 140
Thr Pro Leu Leu Glu Thr Ala Lys Gly Pro His Asp His Pro Thr Ser
145 150 155 160

His Leu Leu Thr Ser Ala Tyr Arg Lys Asp Lys Thr Lys Leu Leu Arg
165 170 175
Pro Gln Thr Val Ile Leu Gly Gly Val Ala Thr Arg Tyr Phe Thr Asn
180 185 190
Tyr Thr Asp Gly Tyr Val Ala Lys Arg Ala Gly Tyr Asp Glu Ile Asp
195 200 205
Thr Pro Leu Ser Ala Lys Asn Leu Ile Gly Val Asp Lys Arg Asn Lys
210 215 220

Asn Gly Ile Leu Val Lys Asn Gly Arg Ser Val Asn Ile Leu Asp Gln
225 230 235 240
Thr Ala Ser Lys Leu Glu Leu Asp Ser Val Gly Gly Ser Arg Tyr Thr
245 250 255
Lys Trp Phe Asn Asn Phe Ala Thr Asn Ala Asp Asn Glu Thr Glu Leu
260 265 270
Asp Lys Gly Arg Arg Val Leu Thr Asp Val Lys Tyr Lys Leu Asp Ala
275 280 285

Asn Asn Asn Pro Val Trp Thr Val Thr Thr Glu Pro Ser Ser Gly Tyr
290 295 300
Gln Tyr Ala His Ser Leu Asn Arg Tyr Phe Asn Asn Asn Pro Asp Asp

305 310 315 320

Glu Leu Tyr Val Asn Gln Asn Gly Glu Tyr Ala Tyr Arg Phe Thr Leu

325 330 335

Lys Lys Ser Thr Thr Phe Glu Val Ser Ala Glu Ser Ala Lys Thr His

340 345 350

Pro Glu Arg Ala Glu Ala Leu Lys Ala Leu Gly Trp Ser Ala Gly Lys

355 360 365

Gln Tyr His Phe Ala Pro Gly Ser Tyr Phe Met Val Thr Gln Lys Asp

370 375 380

Gly Ser Leu Lys Ile Val Ala Asp Asn Gly Gln Met Thr Gln Val Ser

385 390 395 400

Leu Tyr Ser Val His Val Gly Ile Asp Asp Asn Lys Ala Leu Gly Ala

405 410 415

Phe Gln Asn Lys Arg Val Ile Ala Glu Met Phe Ser Ala Leu Asn Tyr

420 425 430

Gly Lys Thr Asn Glu Ile Arg Ala Ile Tyr Thr Tyr Asp Val Gly Gln

435 440 445

Ala Asn Gly Phe Asn Gln Gln Tyr Leu Ser Leu Asn Ala Trp Arg Tyr

450 455 460

Lys Asn Gly Asp Gly Thr Tyr Gly Leu Asn Asn Pro Phe Asn Ile Gly

465 470 475 480

Ile Phe Asp Arg Val Ala Thr Glu Asn Gly Ile Val Ala Asn Val Tyr

485 490 495

Asp Met Lys Thr Lys Lys Gly Leu Ser Ala Lys Tyr Thr Gly Val Ala

500 505 510

Tyr Ser Ser Arg Asp Gly Lys Gln Asp Gly Val Met Asn Met Thr Ala

515 520 525

Gln Phe His Glu Pro Asp Met Ala Tyr Asn Asn Thr Val Ser Ser Asn

530 535 540

Asn Val Thr Phe Asn Gly Ala Ile Thr Asn Arg Arg Leu Asp Asp Lys

545 550 555 560

Arg Asn Val Tyr Phe Ala Ser Gly Asn Val Lys Thr Glu Ser Gly Met
565 570 575

Pro Ser Ala Ser Ala Gly Gln Lys Val Ser Leu Val Gly Arg Ser Gln
580 585 590

Val Ala Gln Asn Val Thr Val Trp Met Glu Gly Lys Lys Pro Gly Glu
595 600 605

Asn Lys Val Ile Tyr Gly Gln Gly Asn Val Arg Phe Ala Gly Pro Asn
610 615 620

Ala Glu Glu Val Gly Gly Leu Leu Lys Ile Thr Thr Ser His Gly Glu
625 630 635 640

Asn Asn Ile Gly Phe Ile Gly Lys Arg
645

<210> 959

<211> 1197

<212> DNA

<213> N. wadsworthii SLP 1a

<400> 959

ttgacggcgc cgaaaacggc gttacggttt ggagaggata taacggtagc aaaagccgca 60

cttaatatcg gcccgatgct gatcagcagc atcagggtgg aaaaaggcgc ttcgctgacc 120

tgcgggtttg aaagctcggt aggcggcatt gcgattaaaa cactggaagc cgacgatatt 180

gtaaagcccg accgcaaatt cggtgccgat atccgggtgg aagcggccaa taatatggcg 240

ggtgaacgtg ttcccgacct caatctggtg ggcacacagc tgcgcgtcag ctatcaagat 300

ttggccaacc attttcacaa gttgcctaaa aaagcaggcg gcgatgccaa aacattcggg 360

catgatcaag ctgcgcgggt tgccgtggcg gccaaaaccg atcgcacgga gctggtggcc 420

gcttatgcct accgctatca cggcaaccat tatccaggta agggcggcaa gcaccgttat 480

gagcagattt atcatgcagg gggagtgatc attcccggta ttgcttcaca aaatattcag 540

gagaatatgt ttgaagagcg tagcgaagta ttgaacactt ctttgaacaa ccgctatttt 600

ttgctgaaag gtacgttcaa acttaccgac aaacagtcta tccagcttgg ctaccgtcgc 660

ttggacagcc gatacggtga aattatgccc tcaaggattt atggtataga aacaagagac 720

ggcccccctac tgccgcaatg gcctttaagc aaaatcaaaa tggataccta cacgctggat 780

taccgctgga agccagaaaa ccgctggctt gatttggaaa gcggcatttg gttgaacaaa 840

gccgatatga tgctgcaaaa cagcggtggc atggtttacg atttgggcaa ctataaaaat 900

tcgcgaaacc atagcttgag tagcctgcag agaaccaccg ttcttcacgg ctcgctgaat 960

aagaacacca ataaccgttt gggcgtttac ctgaccaata aaatgaagct gcacgacact 1020

ttaaacttaa ccttgggcgg cagctatcaa tatgaaaagc tcggcacgcc ggacgatact 1080

tggaggaagt tggcggagca agatgtatct tgggtagcac gcctaggcaa ggtaaacggg 1140

atgaatataa actttatttc aatttcaatt ggcggccgac agaccggatt tcggtaa 1197

<210> 960

<211> 398

<212> PRT

<213> N. wadsworthii SLP 1a

<400> 960

Met Thr Ala Pro Lys Thr Ala Leu Arg Phe Gly Glu Asp Ile Thr Val
1 5 10 15

Ala Lys Ala Ala Leu Asn Ile Gly Pro Met Leu Ile Ser Ser Ile Arg
20 25 30

Val Glu Lys Gly Ala Ser Leu Thr Cys Gly Phe Glu Ser Ser Val Gly
35 40 45

Gly Ile Ala Ile Lys Thr Leu Glu Ala Asp Asp Ile Val Lys Pro Asp
50 55 60

Arg Lys Phe Gly Ala Asp Ile Arg Val Glu Ala Ala Asn Asn Met Ala
65 70 75 80

Gly Glu Arg Val Pro Asp Leu Asn Leu Val Gly Thr Gln Leu Arg Val
85 90 95

Ser Tyr Gln Asp Leu Ala Asn His Phe His Lys Leu Pro Lys Lys Ala
100 105 110

Gly Gly Asp Ala Lys Thr Phe Gly His Asp Gln Ala Ala Arg Val Ala
115 120 125

Val Ala Ala Lys Thr Asp Arg Thr Glu Leu Val Ala Ala Tyr Ala Tyr
130 135 140

Arg Tyr His Gly Asn His Tyr Pro Gly Lys Gly Gly Lys His Arg Tyr
145 150 155 160

Glu Gln Ile Tyr His Ala Gly Gly Val Ile Ile Pro Gly Ile Ala Ser

165 170 175

Gln Asn Ile Gln Glu Asn Met Phe Glu Glu Arg Ser Glu Val Leu Asn

180 185 190

Thr Ser Leu Asn Asn Arg Tyr Phe Leu Leu Lys Gly Thr Phe Lys Leu

195 200 205

Thr Asp Lys Gln Ser Ile Gln Leu Gly Tyr Arg Arg Leu Asp Ser Arg

210 215 220

Tyr Gly Glu Ile Met Pro Ser Arg Ile Tyr Gly Ile Glu Thr Arg Asp

225 230 235 240

Gly Pro Leu Leu Pro Gln Trp Pro Leu Ser Lys Ile Lys Met Asp Thr

245 250 255

Tyr Thr Leu Asp Tyr Arg Trp Lys Pro Glu Asn Arg Trp Leu Asp Leu

260 265 270

Glu Ser Gly Ile Trp Leu Asn Lys Ala Asp Met Met Leu Gln Asn Ser

275 280 285

Gly Gly Met Val Tyr Asp Leu Gly Asn Tyr Lys Asn Ser Arg Asn His

290 295 300

Ser Leu Ser Ser Leu Gln Arg Thr Thr Val Leu His Gly Ser Leu Asn

305 310 315 320

Lys Asn Thr Asn Asn Arg Leu Gly Val Tyr Leu Thr Asn Lys Met Lys

325 330 335

Leu His Asp Thr Leu Asn Leu Thr Leu Gly Gly Ser Tyr Gln Tyr Glu

340 345 350

Lys Leu Gly Thr Pro Asp Asp Thr Trp Arg Lys Leu Ala Glu Gln Asp

355 360 365

Val Ser Trp Val Ala Arg Leu Gly Lys Val Asn Gly Met Asn Ile Asn

370 375 380

Phe Ile Ser Ile Ser Ile Gly Gly Arg Gln Thr Gly Phe Arg

385 390 395

<210> 961

<211> 2067

<212> DNA

<213> N. weaveri SLP 1a

<400> 961

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gcaacaggtg gcggtacggg tggttcgcag tctggaaatg gaagtagtag cggcagtggc 240

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ggcagcaaca ccgaagatag cggaagcggt gatgtgactg ttgaacaagc tgatccggca 360

tcagttgatt tcagtgcgac atttaaagcc gatacagacg gtttgatgca atcaggtgta 420

agaaatggtg catcggttac ctatgaagat aaatcaggta aggttctgtc ttcaggcact 480

tcagctttgg cagatcaata tgatacagaa ccgcataagc tggagattga cagtaaagcg 540

gttcataaat ttgataagta ttctttttct acttctgatg atgaaaaaaa taaagatatt 600

cagattgtga aaaatttcca agtagaagaa ggtacgggca aaggtctttt tggcactgtg 660

ggtgaggacc atgttcgtta cggtgtttat caagatcaag gcaagagtac gttgtttgta 720

catggtgagc ctaaaggttc ttatggtaat atgcctaaag aaggcaagtt cacttttaaa 780

ggcggtgcgg tttatggaaa atcaggtaat tacgtgccgg cgctgtcaca tgtaaacgta 840

gattttgggg atactaaaaa tgtgaatatc cgcattacgc cgagcaacaa tcatgctgct 900

tttgattttt caggaaaaat taacggcaat acctttagcg gcgcagatgg aggagtaaaa 960

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gcggcatatg aagaattcaa tgctcaggtt gccccgcctg cggttcctga agagcctaaa 1140

ccgcctgtat ctgaacctga agagcctaaa ccacagccgc cggttgttgt tcctacgccg 1200

ccttcaagtg aacctgttcc gcctgtttct gtttcaggtg catttgaaga agcaatgaaa 1260

aacggctttg ttcaagatga taagtctaga cctggttaca tgaaatcagg tatcacaagc 1320

tattacgatc ccagtacata tgttaccaat ggtgttattt taactgtagg taaagaaggc 1380

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aatggacata ttattcctct attggctagc ggtcaggatt tgttaaacgg tattagcatg 1500

agagcgttta atgctaaaga tttgaagcga gatggcggag tatatgacga aactaaagac 1560

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cgctttggcg tttatcaatt agaaggaacc aaccatctat ttgtacaagg tcagccaagc 1680

cgttatatgc ctcctgcaag cgataaagat tatgcttatg agggatatgc cgtgcatgtt 1740

gatagtaaca atgcttattc gcgtgttaac ggcgtaaaag ccaaagtcaa ttttggtaag 1800

aagactgttg atgtgactct gaagccggct ggtaatgtgt taggcacaaa tcgtccatat 1860

gatagtgcgt tgtcattttc agccaccatt accggtaata cattcagtag caatagcggt 1920

ggtgtaagca ccaaaggcgg attctttggt ggtctcggtc aggatatggg tggtgtatac 1980

aatgttggaa caacctataa gaatcctgaa taccacaaca gcaagggcgt attcggtaca 2040

acacaagttg atccaagaaa aagataa 2067

<210> 962

<211> 688

<212> PRT

<213> N. weaveri SLP 1a

<400> 962

Met Leu Lys Phe Leu Phe Leu Ile Lys Asn Lys Leu Lys Val Leu Arg
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Arg Trp Leu Ile Met Asp Lys Phe Lys Leu Ser Met Ile Val Val Ala
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Cys Ser Leu Ala Leu Ser Ala Cys Ser Ser Gly Gly Ser Ala Pro Ala
35 40 45

Asn Pro Leu Ala Gln Asp Thr Pro Gly Lys Gly Ala Ala Thr Gly Gly
50 55 60

Gly Thr Gly Gly Ser Gln Ser Gly Asn Gly Ser Ser Ser Gly Ser Gly
65 70 75 80

Ser Ser Thr Glu Gly Ser Gly Ser Asn Thr Glu Gly Ser Gly Ser Asn
85 90 95

Thr Glu Gly Ser Gly Ser Asn Thr Glu Asp Ser Gly Ser Gly Asp Val
100 105 110

Thr Val Glu Gln Ala Asp Pro Ala Ser Val Asp Phe Ser Ala Thr Phe
115 120 125

Lys Ala Asp Thr Asp Gly Leu Met Gln Ser Gly Val Arg Asn Gly Ala
130 135 140

Ser Val Thr Tyr Glu Asp Lys Ser Gly Lys Val Leu Ser Ser Gly Thr
145 150 155 160

Ser Ala Leu Ala Asp Gln Tyr Asp Thr Glu Pro His Lys Leu Glu Ile
165 170 175

Asp Ser Lys Ala Val His Lys Phe Asp Lys Tyr Ser Phe Ser Thr Ser
180 185 190
Asp Asp Glu Lys Asn Lys Asp Ile Gln Ile Val Lys Asn Phe Gln Val
195 200 205
Glu Glu Gly Thr Gly Lys Gly Leu Phe Gly Thr Val Gly Glu Asp His
210 215 220
Val Arg Tyr Gly Val Tyr Gln Asp Gln Gly Lys Ser Thr Leu Phe Val
225 230 235 240

His Gly Glu Pro Lys Gly Ser Tyr Gly Asn Met Pro Lys Glu Gly Lys
245 250 255
Phe Thr Phe Lys Gly Gly Ala Val Tyr Gly Lys Ser Gly Asn Tyr Val
260 265 270
Pro Ala Leu Ser His Val Asn Val Asp Phe Gly Asp Thr Lys Asn Val
275 280 285
Asn Ile Arg Ile Thr Pro Ser Asn Asn His Ala Ala Phe Asp Phe Ser
290 295 300

Gly Lys Ile Asn Gly Asn Thr Phe Ser Gly Ala Asp Gly Gly Val Lys
305 310 315 320
His Arg Gly Gly Phe Phe Arg Ala Gly Trp Arg Asp Glu Ala Gly Tyr
325 330 335
Ala Gly Gly Val Phe Gln Arg Thr Glu Gly Glu Phe Ala Gly Tyr His
340 345 350
Gly Ser Tyr Ala Ser Lys Lys Gln Ala Ala Tyr Glu Glu Phe Asn Ala
355 360 365

Gln Val Ala Pro Pro Ala Val Pro Glu Glu Pro Lys Pro Pro Val Ser
370 375 380
Glu Pro Glu Glu Pro Lys Pro Gln Pro Pro Val Val Val Pro Thr Pro
385 390 395 400
Pro Ser Ser Glu Pro Val Pro Pro Val Ser Val Ser Gly Ala Phe Glu

405 410 415

Glu Ala Met Lys Asn Gly Phe Val Gln Asp Asp Lys Ser Arg Pro Gly

420 425 430

Tyr Met Lys Ser Gly Ile Thr Ser Tyr Tyr Asp Pro Ser Thr Tyr Val

435 440 445

Thr Asn Gly Val Ile Leu Thr Val Gly Lys Glu Gly Lys Phe Ser Ala

450 455 460

Val Arg Pro Glu Gly Lys Glu Ala Asp Ser Phe Arg Glu Leu Lys Leu

465 470 475 480

Asn Gly His Ile Ile Pro Leu Leu Ala Ser Gly Gln Asp Leu Leu Asn

485 490 495

Gly Ile Ser Met Arg Ala Phe Asn Ala Lys Asp Leu Lys Arg Asp Gly

500 505 510

Gly Val Tyr Asp Glu Thr Lys Asp Gly Lys Gly Leu Val Gly Ser Thr

515 520 525

Thr Asp Ser Phe His Ser Glu Gly Phe Lys Ala Met Arg Phe Gly Val

530 535 540

Tyr Gln Leu Glu Gly Thr Asn His Leu Phe Val Gln Gly Gln Pro Ser

545 550 555 560

Arg Tyr Met Pro Pro Ala Ser Asp Lys Asp Tyr Ala Tyr Glu Gly Tyr

565 570 575

Ala Val His Val Asp Ser Asn Asn Ala Tyr Ser Arg Val Asn Gly Val

580 585 590

Lys Ala Lys Val Asn Phe Gly Lys Lys Thr Val Asp Val Thr Leu Lys

595 600 605

Pro Ala Gly Asn Val Leu Gly Thr Asn Arg Pro Tyr Asp Ser Ala Leu

610 615 620

Ser Phe Ser Ala Thr Ile Thr Gly Asn Thr Phe Ser Ser Asn Ser Gly

625 630 635 640

Gly Val Ser Thr Lys Gly Gly Phe Phe Gly Gly Leu Gly Gln Asp Met

645 650 655

Gly Gly Val Tyr Asn Val Gly Thr Thr Tyr Lys Asn Pro Glu Tyr His
660 665 670

Asn Ser Lys Gly Val Phe Gly Thr Thr Gln Val Asp Pro Arg Lys Arg
675 680 685

<210> 963

<211> 2013

<212> DNA

<213> N. weaveri SLP 2a

<400> 963

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caggctgcct taaaacaacc tgccgcaggt tttgtgatga aaggcttgcg ccgcaacaga 180

gccaagcacg atcaaaacgg caatccgttg ttggacgcat cgggcaatcc taccgaagcg 240

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cacacaggca aacagcaaga aggcaaatac caatatatcc gcttcggcca cgttactgcc 420

gattatcccg aagtaattga agaaacggtt agggataaag agggcgattt aaaatggtat 480

acgcaaagag aaggctggaa cgttcacacc ttttatcacg gcacctctgc cgcagccgcc 540

cttcccgttg acaacaacgt aaactatcgg ggtgagtggt atttcatgag cgacgtaaaa 600

aaaggcaaag gaaaagaacc cggaagcaac cctcacctcg gcaacggttt taacagcctg 660

aaaggtaacg gcgatattgc cagtgcaacc ggccaagcaa atgagactac cgacaaaaaa 720

tatacgtctg actttaccgt taatttcgcc gataaaagca tgacaggcgg gcttcattac 780

gaatcacgca tcgaatccaa aaggaagctg tacgacattg aagcacagct caacggcaac 840

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accgttccca aacgggttga tgtggagtac gaagaggaag aagaaatcaa cgaaaccgac 1140

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gaagtccgcc aacacctcac cgaaaccgag cgcaaacctt tagccaattt cggctatgcc 1260

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agctatctgc gcttcggcca attcgtgtta caggaaaaag cagggcaaga ccccgtgcac 1500

gccctctatc ttcaaggcga aagaaccccc gtatccgatc tgccgcaatc aggaaaagcc 1560

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accgacagcc gcagagtatt caatatcgaa gccaatatca acggcagcgg ctttacaggc 1800

cgaggctata ccgacggcag cttccccttc gacccgggta atctcactaa aggctattcc 1860

gcctatgttc ccgatgccaa agtggagggc ggtttctacg gccccggcgc acgcgaactg 1920

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ggtgcggtat tcggcgcaac caaacaagaa taa 2013

<210> 964

<211> 670

<212> PRT

<213> N. weaveri SLP 2a

<400> 964

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Pro Glu Pro Pro Pro Leu Pro Glu Pro Pro Lys Val Glu Lys Val Pro

20 25 30

Glu Pro Arg Gln Asn Pro Glu Glu Gln Ala Ala Leu Lys Gln Pro Ala

35 40 45

Ala Gly Phe Val Met Lys Gly Leu Arg Arg Asn Arg Ala Lys His Asp

50 55 60

Gln Asn Gly Asn Pro Leu Leu Asp Ala Ser Gly Asn Pro Thr Glu Ala

65 70 75 80

Glu Ile Tyr Ile Pro Leu Asn Pro Asn Asp Val Glu Ala Val Asn Asp

85 90 95

Ala Asp Leu Thr Ile Pro Lys Leu Lys Glu Met Gln Asn Asp Pro Ala

100 105 110

Asn Arg Gly Ala His His Val Tyr His Thr Gly Lys Gln Gln Glu Gly

115 120 125

Lys Tyr Gln Tyr Ile Arg Phe Gly His Val Thr Ala Asp Tyr Pro Glu

130 135 140

Val Ile Glu Glu Thr Val Arg Asp Lys Glu Gly Asp Leu Lys Trp Tyr

145 150 155 160

Thr Gln Arg Glu Gly Trp Asn Val His Thr Phe Tyr His Gly Thr Ser

165 170 175

Ala Ala Ala Ala Leu Pro Val Asp Asn Asn Val Asn Tyr Arg Gly Glu

180 185 190

Trp Tyr Phe Met Ser Asp Val Lys Lys Gly Lys Gly Lys Glu Pro Gly

195 200 205

Ser Asn Pro His Leu Gly Asn Gly Phe Asn Ser Leu Lys Gly Asn Gly

210 215 220

Asp Ile Ala Ser Ala Thr Gly Gln Ala Asn Glu Thr Thr Asp Lys Lys

225 230 235 240

Tyr Thr Ser Asp Phe Thr Val Asn Phe Ala Asp Lys Ser Met Thr Gly

245 250 255

Gly Leu His Tyr Glu Ser Arg Ile Glu Ser Lys Arg Lys Leu Tyr Asp

260 265 270

Ile Glu Ala Gln Leu Asn Gly Asn Arg Phe Thr Gly Lys Ala Leu Ser

275 280 285

Lys Val Asn Asp Asp Ser Ser Thr Leu Asp Lys Ala Phe Phe Ala Ala

290 295 300

Asp Ser Asn Leu Leu Glu Gly Gly Phe Tyr Gly Pro Glu Ala Gln Glu

305 310 315 320

Leu Ala Gly Lys Phe Leu Ala Asn Asp Asn Ser Leu Phe Val Val Phe

325 330 335

Gly Ala Lys Arg Asp Ser Asp Asn Pro Asn Gln Pro Lys Lys Thr Asn

340 345 350

Ala Leu Leu Asp Ala Phe Tyr Ile Thr Val Pro Lys Arg Val Asp Val

355 360 365

Glu Tyr Glu Glu Glu Glu Glu Ile Asn Glu Thr Asp Thr Ala Ala Asn

370 375 380

Asp Ala Leu Thr Glu Glu Asp Phe Thr Glu Glu Glu Glu Lys Glu Pro

385 390 395 400

Glu Val Arg Gln His Leu Thr Glu Thr Glu Arg Lys Pro Leu Ala Asn

405 410 415

Phe Gly Tyr Ala Met Lys Leu Arg Phe Gly Asn Lys Val Phe Asp Leu

420 425 430

Glu Lys Ala Glu Leu Asp Glu Met Leu Lys Asn Ala Asn Ala Glu Ile

435 440 445

Gly Ser Asp Thr Thr Gly Lys Thr His Ser Ile Thr Leu Pro Glu Asn

450 455 460

Gly Glu Gly Lys Pro Arg Glu Phe Val Gln Val Cys Cys Ser Asn Leu

465 470 475 480

Ser Tyr Leu Arg Phe Gly Gln Phe Val Leu Gln Glu Lys Ala Gly Gln

485 490 495

Asp Pro Val His Ala Leu Tyr Leu Gln Gly Glu Arg Thr Pro Val Ser

500 505 510

Asp Leu Pro Gln Ser Gly Lys Ala Thr Tyr Leu Gly Ser Trp Thr Gly

515 520 525

Phe Ile Lys Val Gln Pro Pro Gln Arg His Ala Phe Gly Asn Pro Asp

530 535 540

Tyr Gly His Asn Ala Thr Met Lys Asn Ile Ser Ser Ser Ser Arg Ser

545 550 555 560

Gly Val Ser Ser Phe Asp Val Asp Phe Asp Asn Lys Lys Leu Asn Gly

565 570 575

Ala Leu Ile Gly Thr Asp Ser Arg Arg Val Phe Asn Ile Glu Ala Asn

580 585 590

Ile Asn Gly Ser Gly Phe Thr Gly Arg Gly Tyr Thr Asp Gly Ser Phe

595 600 605

Pro Phe Asp Pro Gly Asn Leu Thr Lys Gly Tyr Ser Ala Tyr Val Pro
610 615 620

Asp Ala Lys Val Glu Gly Gly Phe Tyr Gly Pro Gly Ala Arg Glu Leu

625 630 635 640

Gly Gly Thr Leu Ile Tyr Asn Ser Pro Asp Lys Asp Gln Asp Ser Thr
645 650 655

Asp Ile Arg Ala Gly Ala Val Phe Gly Ala Thr Lys Gln Glu
660 665 670

<210> 965

<211> 729

<212> DNA

<213> N. weaveri SLP 3a

<400> 965

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ggcaaagccg cttctgaaga agtaggcgaa aaagtattga aaaacgcggc taaaaaatcg 180

cacgttcact acaaatacct gaaccactac aatgttgccg ccgatgcgaa caacgtgaaa 240

accatccacg cctacaacca aaaacgcggc aactacatgg gcaacttcgc attcagcacc 300

atcaagagcg gcggttccga agtttactac ggcgaatgga acggtaccga gtatgttaaa 360

ggcaaaaacc gcgccgtata ctactccggc gacaaacgtg ctgtaaacat gccgatggcc 420

ggtaatgcaa cttacaacgt acaaggtatc aaccactaca acggcaacaa cgccatgacc 480

ggccaactgc acgccgactt cggcaaacgc accttaaccg gctctatgca aaatgccgct 540

gtgaaaatgg acgtatactc aaacatcaac ccatacaaag cgtcgtttaa aggccacgca 600

gttgccaacg gtcacttcgg taaaaccgaa ggccacttct tcggcgacgg cgcaaccagc 660

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<210> 966

<211> 242

<212> PRT

<213> N. weaveri SLP 3a

<400> 966

Met Asn Met Lys Lys Thr Ala Leu Ala Leu Met Thr Ala Leu Val Cys

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Thr Gly Ala Tyr Ala Gly Ser Asn Tyr Tyr His Pro Asp Ala Tyr Trp
20 25 30
Val Pro Ala Lys Lys Val Lys Trp Gly Lys Ala Ala Ser Glu Glu Val
35 40 45
Gly Glu Lys Val Leu Lys Asn Ala Ala Lys Lys Ser His Val His Tyr
50 55 60
Lys Tyr Leu Asn His Tyr Asn Val Ala Ala Asp Ala Asn Asn Val Lys
65 70 75 80

Thr Ile His Ala Tyr Asn Gln Lys Arg Gly Asn Tyr Met Gly Asn Phe
85 90 95
Ala Phe Ser Thr Ile Lys Ser Gly Gly Ser Glu Val Tyr Tyr Gly Glu
100 105 110
Trp Asn Gly Thr Glu Tyr Val Lys Gly Lys Asn Arg Ala Val Tyr Tyr
115 120 125
Ser Gly Asp Lys Arg Ala Val Asn Met Pro Met Ala Gly Asn Ala Thr
130 135 140

Tyr Asn Val Gln Gly Ile Asn His Tyr Asn Gly Asn Asn Ala Met Thr
145 150 155 160
Gly Gln Leu His Ala Asp Phe Gly Lys Arg Thr Leu Thr Gly Ser Met
165 170 175
Gln Asn Ala Ala Val Lys Met Asp Val Tyr Ser Asn Ile Asn Pro Tyr
180 185 190
Lys Ala Ser Phe Lys Gly His Ala Val Ala Asn Gly His Phe Gly Lys
195 200 205

Thr Glu Gly His Phe Phe Gly Asp Gly Ala Thr Ser Leu Ala Gly Val
210 215 220
Ala Lys Phe Lys Thr Asn Arg Ala Leu Asp Thr Ala Phe Gly Gly Thr
225 230 235 240
Lys Gln

<210> 967

<211> 1005

<212> DNA

<213> N. weaveri SLP 4a

<400> 967

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aacgataaat ctgagatttc gtttgaagca ggtatgttgc acgacgatga tagcaagctg 180

gtaacgcttc atactttgga tgatccgaag caggcgaaat tgcggaagtt ggatatacat 240

catcatggta atttcggtcc aagagttgat gatgcttttg tttatcagac acctgatggg 300

aagctattca gattcggtac ttataacacg cctatacttc aggatggctt ttctccgagc 360

tacactctta aaaattctca tgagggccag gcaacagaaa atggcggacg tttgtttgcc 420

tgttgctctt tccaatggag gcaggcatct gcgacgagat tggacaacgt cggttacgga 480

gcatggattg atccgaacgg taaagtcgat ttgtttgtcg gcggtgtgcc tgcagatgta 540

gcgaaaatgc aaggtgcttg gaataatgaa ggcaagccta aaggtacggc aatctatgaa 600

gtatggggtg ttcgtgagaa aggcggaaaa tttgtgactt cttcatacac cggcttctca 660

actccgactg atggcaaata tcctcgtggc aagcctgagg cttcttatat tttagttaat 720

tttaatacca ataaattagg cggaaccatt ttgggtaatc aagattatgg tccggatgtt 780

gtgatgggta atgttgatat tgtcggtaat agttttagtg gctcggctaa gtcaggtgga 840

gttaacggca atgttgaagg taagtttttt tcttctgatg gtaaagagat tggcggcaaa 900

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<210> 968

<211> 334

<212> PRT

<213> N. weaveri SLP 4a

<400> 968

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20 25 30

Val Leu Lys Glu Thr Lys Ile Val Asn Asp Lys Ser Glu Ile Ser Phe

35 40 45

Glu Ala Gly Met Leu His Asp Asp Asp Ser Lys Leu Val Thr Leu His
50 55 60
Thr Leu Asp Asp Pro Lys Gln Ala Lys Leu Arg Lys Leu Asp Ile His
65 70 75 80
His His Gly Asn Phe Gly Pro Arg Val Asp Asp Ala Phe Val Tyr Gln
85 90 95
Thr Pro Asp Gly Lys Leu Phe Arg Phe Gly Thr Tyr Asn Thr Pro Ile
100 105 110

Leu Gln Asp Gly Phe Ser Pro Ser Tyr Thr Leu Lys Asn Ser His Glu
115 120 125
Gly Gln Ala Thr Glu Asn Gly Gly Arg Leu Phe Ala Cys Cys Ser Phe
130 135 140
Gln Trp Arg Gln Ala Ser Ala Thr Arg Leu Asp Asn Val Gly Tyr Gly
145 150 155 160
Ala Trp Ile Asp Pro Asn Gly Lys Val Asp Leu Phe Val Gly Gly Val
165 170 175

Pro Ala Asp Val Ala Lys Met Gln Gly Ala Trp Asn Asn Glu Gly Lys
180 185 190
Pro Lys Gly Thr Ala Ile Tyr Glu Val Trp Gly Val Arg Glu Lys Gly
195 200 205
Gly Lys Phe Val Thr Ser Ser Tyr Thr Gly Phe Ser Thr Pro Thr Asp
210 215 220
Gly Lys Tyr Pro Arg Gly Lys Pro Glu Ala Ser Tyr Ile Leu Val Asn
225 230 235 240

Phe Asn Thr Asn Lys Leu Gly Gly Thr Ile Leu Gly Asn Gln Asp Tyr
245 250 255
Gly Pro Asp Val Val Met Gly Asn Val Asp Ile Val Gly Asn Ser Phe
260 265 270
Ser Gly Ser Ala Lys Ser Gly Gly Val Asn Gly Asn Val Glu Gly Lys
275 280 285

Phe Phe Ser Ser Asp Gly Lys Glu Ile Gly Gly Lys Val Val Phe Asp
290 295 300

Gln Asn Arg Ser Leu Asp Thr Val Phe Gly Gly Met Arg Asp Lys Tyr
305 310 315 320
Asn Pro Ser Asp Glu Ser Leu Asp Leu Pro Thr Ile Ala Lys
325 330

<210> 969

<211> 1992

<212> DNA

<213> Neisseria sp. oral taxon 014 SLP 1a

<400> 969

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gataagggca ataccgataa gggcaatacc gataagggca ataccgataa gggcaatacc 240

gataaaggca ataccgataa aggcaatacc gataaaggca ataccgataa aggcaatacc 300

gataagggca ataccgataa gggtaataaa actaacatca acaaagaaac gtcattatta 360

aataaaggca ttcaggataa actgaccaca ctaaaactaa gtgatgtaat aaaaactgaa 420

caatttaatc aaactgaagt gaacaccggc ttcattgcaa ataacttagg tgcgactcca 480

ttattagaga cagctaaagg tccacatgat tatcctacct ctcatctttt gacatccgct 540

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attgatacgc cattaagtgc aaaaaatctg attggtgtag ataaacgcaa taaaaatggc 720

atcttagtta aaaatggcag gagcgttaac atcttagatc aaactgccag caagctagaa 780

ttagatagtg taggcggtag ccgttataca aaatggttta ataattttgc tactaatgcc 840

gataatgaaa ctgaattgga taaaggccgc cgtgtattaa cagacgtgaa atacaaatta 900

gatgcaaata ataatcctgt atggactgta actaccgaac ccagcagcgg ttatcaatat 960

gcacattctt taaatcgtta ttttaacaat aatccagacg atgaattata tgttaaccaa 1020

aacggtgaat atgcatatcg ttttacatta aaaaaatcaa ctacatttga agttagtgca 1080

gaatcagcaa aaacccatcc ggaacgtgca gaggcactca aagcattagg atggtctgct 1140

ggcaagcaat atcacttcgc accaggtagc tactttatgg ttacacaaaa agatggcagc 1200

ctaaaaattg tagccgataa cggacaaatg acgcaggtat ccttatattc agtccatgtc 1260

ggtattgatg acaataaagc attcggtgca ttccaaaata aacgtgtaat tgccgaaatg 1320

ttcagtgcat taaactatgg caagacaaat gaaattcgtg cgatttatac ctatgacgtt 1380

ggacaagcca atggcttcaa tcaacaatat ctctcattaa atgcatggcg ctataaaaat 1440

ggcgatggca cttatggact caataatcct tttaacatcg gcattttcga ccgagttgct 1500

actgaaaatg gtatagttgc caatgtctat gacatgaaga ctaaaaaagg tttatctgcc 1560

aaatatacag gcgttgccta ttctagccga gatggtaaac aagacggcat aatgaacatg 1620

actgcgcagt tccatgaacc agatatagct tacaataata ctgttttaag caataacgtt 1680

acctttaatg gcgagattac caaccgtcgc ctagatgaca aacgtaatgt atattttgcc 1740

agcggtaatg taaaaacagg gagtggaatg ccttctgcaa gcgcaggcca aaaagtttct 1800

ctagtgggta gaagccaagt tgctcaaaat gttactgtct ggatggaagg aaaaaatcca 1860

ggtgaaaata aagtaattta tggtcaaggt aacgtacgtt ttgccggtcc aaatgctgaa 1920

gaagtcggtg gtttgttaaa aatcactacc agccatggcg aaaacaatat cggtttcatc 1980

ggcaaacgct aa 1992

<210> 970

<211> 663

<212> PRT

<213> Neisseria sp. oral taxon 014 SLP 1a

<400> 970

Met Arg Thr Gln Asn Lys Leu Pro Ile Ile His Phe Val Leu Thr Gly
1 5 10 15

Ile Cys Ala Ala Val Leu Ala Ala Cys Ser Ser Ser Asn Glu Val Ser

20 25 30

Asp Ser Ala Arg Asn Leu Ser Ile Ala Ser Asn Asn Ile Asn Thr Gly
35 40 45

Asn Thr Asp Lys Gly Asn Thr Asp Lys Gly Asn Thr Asp Lys Gly Asn
50 55 60

Thr Asp Lys Gly Asn Thr Asp Lys Gly Asn Thr Asp Lys Gly Asn Thr
65 70 75 80

Asp Lys Gly Asn Thr Asp Lys Gly Asn Thr Asp Lys Gly Asn Thr Asp

85 90 95

Lys Gly Asn Thr Asp Lys Gly Asn Thr Asp Lys Gly Asn Lys Thr Asn
100 105 110
Ile Asn Lys Glu Thr Ser Leu Leu Asn Lys Gly Ile Gln Asp Lys Leu
115 120 125
Thr Thr Leu Lys Leu Ser Asp Val Ile Lys Thr Glu Gln Phe Asn Gln
130 135 140
Thr Glu Val Asn Thr Gly Phe Ile Ala Asn Asn Leu Gly Ala Thr Pro

145 150 155 160
Leu Leu Glu Thr Ala Lys Gly Pro His Asp Tyr Pro Thr Ser His Leu
165 170 175
Leu Thr Ser Ala Tyr Arg Lys Asp Lys Thr Lys Leu Leu Arg Pro Gln
180 185 190
Thr Val Ile Leu Gly Gly Val Ala Thr Arg Tyr Phe Thr Asn Tyr Thr
195 200 205
Asp Gly Tyr Val Ala Lys Arg Ala Gly Tyr Asp Glu Ile Asp Thr Pro

210 215 220
Leu Ser Ala Lys Asn Leu Ile Gly Val Asp Lys Arg Asn Lys Asn Gly
225 230 235 240
Ile Leu Val Lys Asn Gly Arg Ser Val Asn Ile Leu Asp Gln Thr Ala
245 250 255
Ser Lys Leu Glu Leu Asp Ser Val Gly Gly Ser Arg Tyr Thr Lys Trp
260 265 270
Phe Asn Asn Phe Ala Thr Asn Ala Asp Asn Glu Thr Glu Leu Asp Lys

275 280 285
Gly Arg Arg Val Leu Thr Asp Val Lys Tyr Lys Leu Asp Ala Asn Asn
290 295 300
Asn Pro Val Trp Thr Val Thr Thr Glu Pro Ser Ser Gly Tyr Gln Tyr
305 310 315 320
Ala His Ser Leu Asn Arg Tyr Phe Asn Asn Asn Pro Asp Asp Glu Leu
325 330 335
Tyr Val Asn Gln Asn Gly Glu Tyr Ala Tyr Arg Phe Thr Leu Lys Lys

340 345 350

Ser Thr Thr Phe Glu Val Ser Ala Glu Ser Ala Lys Thr His Pro Glu

355 360 365

Arg Ala Glu Ala Leu Lys Ala Leu Gly Trp Ser Ala Gly Lys Gln Tyr

370 375 380

His Phe Ala Pro Gly Ser Tyr Phe Met Val Thr Gln Lys Asp Gly Ser

385 390 395 400

Leu Lys Ile Val Ala Asp Asn Gly Gln Met Thr Gln Val Ser Leu Tyr

405 410 415

Ser Val His Val Gly Ile Asp Asp Asn Lys Ala Phe Gly Ala Phe Gln

420 425 430

Asn Lys Arg Val Ile Ala Glu Met Phe Ser Ala Leu Asn Tyr Gly Lys

435 440 445

Thr Asn Glu Ile Arg Ala Ile Tyr Thr Tyr Asp Val Gly Gln Ala Asn

450 455 460

Gly Phe Asn Gln Gln Tyr Leu Ser Leu Asn Ala Trp Arg Tyr Lys Asn

465 470 475 480

Gly Asp Gly Thr Tyr Gly Leu Asn Asn Pro Phe Asn Ile Gly Ile Phe

485 490 495

Asp Arg Val Ala Thr Glu Asn Gly Ile Val Ala Asn Val Tyr Asp Met

500 505 510

Lys Thr Lys Lys Gly Leu Ser Ala Lys Tyr Thr Gly Val Ala Tyr Ser

515 520 525

Ser Arg Asp Gly Lys Gln Asp Gly Ile Met Asn Met Thr Ala Gln Phe

530 535 540

His Glu Pro Asp Ile Ala Tyr Asn Asn Thr Val Leu Ser Asn Asn Val

545 550 555 560

Thr Phe Asn Gly Glu Ile Thr Asn Arg Arg Leu Asp Asp Lys Arg Asn

565 570 575

Val Tyr Phe Ala Ser Gly Asn Val Lys Thr Gly Ser Gly Met Pro Ser

580 585 590

Ala Ser Ala Gly Gln Lys Val Ser Leu Val Gly Arg Ser Gln Val Ala

595 600 605

Gln Asn Val Thr Val Trp Met Glu Gly Lys Asn Pro Gly Glu Asn Lys

610 615 620

Val Ile Tyr Gly Gln Gly Asn Val Arg Phe Ala Gly Pro Asn Ala Glu

625 630 635 640

Glu Val Gly Gly Leu Leu Lys Ile Thr Thr Ser His Gly Glu Asn Asn

645 650 655

Ile Gly Phe Ile Gly Lys Arg

660

<210> 971

<211> 492

<212> DNA

<213> Neisseria sp. oral taxon 014 SLP 3a

<400> 971

ttggccgtgg cggcatgcag cagtgcgggc aatgaaacgg aaatgctgaa aaaccggctc 60

tcagaggcgc agacggcagt gaagctgtcg gctgaaaaca ccaagcggct ggaagacact 120

tattcggaca tttatttcga gttaaacagc ctgacggtgg cgaacttcaa aacgaaagtg 180

gcggcggggg atactttcta cgcctacatc ggccgcccca gttgcggcga ctgcaacgca 240

ttcgaaccga tgttcaaacg ttacatcgaa aaacaccgcc taggcagcaa aatctatttt 300

gtcaacgtgc accgcctgca tcaggacaaa gaagcgtgga tggcgttccg gcagcagtac 360

aaactgagcg gtacgcccgt attggcgaaa tattccaaag gacggcaggt gaacaagctg 420

gatttggaag acaacggcgg cagcatcagc gcggccgatt tggaaaaatg gctggctttg 480

aataagttat aa 492

<210> 972

<211> 163

<212> PRT

<213> Neisseria sp. oral taxon 014 SLP 3a

<400> 972

Met Ala Val Ala Ala Cys Ser Ser Ala Gly Asn Glu Thr Glu Met Leu

1 5 10 15

Lys Asn Arg Leu Ser Glu Ala Gln Thr Ala Val Lys Leu Ser Ala Glu

20 25 30

Asn Thr Lys Arg Leu Glu Asp Thr Tyr Ser Asp Ile Tyr Phe Glu Leu

35 40 45

Asn Ser Leu Thr Val Ala Asn Phe Lys Thr Lys Val Ala Ala Gly Asp

50 55 60

Thr Phe Tyr Ala Tyr Ile Gly Arg Pro Ser Cys Gly Asp Cys Asn Ala

65 70 75 80

Phe Glu Pro Met Phe Lys Arg Tyr Ile Glu Lys His Arg Leu Gly Ser

85 90 95

Lys Ile Tyr Phe Val Asn Val His Arg Leu His Gln Asp Lys Glu Ala

100 105 110

Trp Met Ala Phe Arg Gln Gln Tyr Lys Leu Ser Gly Thr Pro Val Leu

115 120 125

Ala Lys Tyr Ser Lys Gly Arg Gln Val Asn Lys Leu Asp Leu Glu Asp

130 135 140

Asn Gly Gly Ser Ile Ser Ala Ala Asp Leu Glu Lys Trp Leu Ala Leu

145 150 155 160

Asn Lys Leu

<210> 973

<211> 885

<212> DNA

<213> Neisseria sp. oral taxon 020 SLP 3a

<400> 973

atgatgaaaa gcatcaaatt aacccttatc gccgctgccg tatgtgccgc ttcctctgct 60

ttcgccgcta attatgctgg agaaatttct caggctgacc acaagccaaa cgacaggcag 120

attaaagttg gtgaaggtaa aacagatgtt cataccggaa aagccgcaat caatgtcata 180

gatgtagctg ccacgcctga aaaccccaga aagggtttgg caaacggtaa atatatttcc 240

tttgcaaaaa tagatgaaac tgcgggtagt tttattgtaa atacgtttgc tccggatgtt 300

ttgggtaagg ataaaagtgg tgtaactgtc gcccatatgt tcaaaatgaa aggcttttg 360

tggcggaata ttcccaaaat gcccgaccac tcccatttag gccgcatgtc ttacggcaaa 420

gtcggcaatc tggatgtcta ctacggcgac tgggacaaca ccccgtctgg cgcgtctaag 480

gtgaatacag acaccaaaac caacaactac accgtgttct acagcggcac gggcaaaacc 540

accaatatgc ccaccagcgg tacggccact tatgcggtta aaggcatcaa tggtcattac 600

gagcagggca ctgccgtatt gaaaggtgat ttgaaagccg acttcggcaa gaaaacgctg 660

gcgggcactt tgagcagaac aaccggtgat ctaaaaacct tgggaattga tgcgaaaatc 720

gtaactaacg atgcttcgtt ctccggcaaa gccgttgcca acggttcggt aaacggtgca 780

accaaaggca acttcttcgg caacaacgcc gcaggcttgg ccggtatcgc ccagtttgac 840

aacaacaaaa aactcaatgc cgctttcggt ggtgcgaaga aataa 885

<210> 974

<211> 294

<212> PRT

<213> Neisseria sp. oral taxon 020 SLP 3a

<400> 974

Met Met Lys Ser Ile Lys Leu Thr Leu Ile Ala Ala Ala Val Cys Ala
1 5 10 15

Ala Ser Ser Ala Phe Ala Ala Asn Tyr Ala Gly Glu Ile Ser Gln Ala

20 25 30

Asp His Lys Pro Asn Asp Arg Gln Ile Lys Val Gly Glu Gly Lys Thr
35 40 45

Asp Val His Thr Gly Lys Ala Ala Ile Asn Val Ile Asp Val Ala Ala
50 55 60

Thr Pro Glu Asn Pro Arg Lys Gly Leu Ala Asn Gly Lys Tyr Ile Ser
65 70 75 80

Phe Ala Lys Ile Asp Glu Thr Ala Gly Ser Phe Ile Val Asn Thr Phe

85 90 95

Ala Pro Asp Val Leu Gly Lys Asp Lys Ser Gly Val Thr Val Ala His

100 105 110

Met Phe Lys Met Lys Gly Phe Leu Trp Arg Asn Ile Pro Lys Met Pro
115 120 125

Asp His Ser His Leu Gly Arg Met Ser Tyr Gly Lys Val Gly Asn Leu
130 135 140

Asp Val Tyr Tyr Gly Asp Trp Asp Asn Thr Pro Ser Gly Ala Ser Lys

145 150 155 160

Val Asn Thr Asp Thr Lys Thr Asn Asn Tyr Thr Val Phe Tyr Ser Gly

165 170 175

Thr Gly Lys Thr Thr Asn Met Pro Thr Ser Gly Thr Ala Thr Tyr Ala

180 185 190

Val Lys Gly Ile Asn Gly His Tyr Glu Gln Gly Thr Ala Val Leu Lys

195 200 205

Gly Asp Leu Lys Ala Asp Phe Gly Lys Lys Thr Leu Ala Gly Thr Leu

210 215 220

Ser Arg Thr Thr Gly Asp Leu Lys Thr Leu Gly Ile Asp Ala Lys Ile

225 230 235 240

Val Thr Asn Asp Ala Ser Phe Ser Gly Lys Ala Val Ala Asn Gly Ser

245 250 255

Val Asn Gly Ala Thr Lys Gly Asn Phe Phe Gly Asn Asn Ala Ala Gly

260 265 270

Leu Ala Gly Ile Ala Gln Phe Asp Asn Asn Lys Lys Leu Asn Ala Ala

275 280 285

Phe Gly Gly Ala Lys Lys

290

<210> 975

<211> 1590

<212> DNA

<213> Novosphingobium sp. AP12 SLP 1a

<400> 975

ttgatcaatc cgagcatcag cgaagtcttc accgccgacg ccggaaccgt ttcggcgctc 60

tatcccggcg ggggcacgag cccggaggtc gagggacgca ccaccctgac gatcgcctac 120

gatgcgacca acggcagcta tacgatcacg gctccgcagg cctctcaggt cttccgggcg 180

gcggataggg ataccgccag cagcgatcga agaataacgc gttacgtgcg aacgcaaggg 240

accgtcacag atagtctcgt cctcaccaag gcaggtgaga gcggcatctt gaccaatcgc 300

tatgtcggcg gtggcattca gcgacgcacc gacacggcgg ggggaatcca gaacaatcgc 360

ctgaacgtgt tcacctatgg cgtacagaca gccaatggcg cggttccgat cacgggaacc 420

gggaccttcg ctttcggcat catcggcatg gaggcagggg acgacgtcct cgccgatttc 480

gatggccgcg ggaccatgca agtaaacttc gcgtctgcca cgctgacagg ggtggggttg 540

aagataacgc gccgcttcaa cgataacggc tacgcggcat tagaccagtc ggtcttcacg 600

ctcgagggcg ttttgggagt gggtggaaac gccttgtccg gttcgatccg cttcagcgat 660

gctgctgcta ccttggaagg ccgcttctat ggttccgctg cggaagaggt cggcgccacg 720

ttctacggcg ccaatacgcg caaccagatg atttccggtg tactgctcgg tcgctcacgc 780

agcacacctg gatatgaaac gctcaccgat ctggtgatgc ctatcgaact ccaggcctat 840

acggcggcga ttttcgccac acgcaatgcc ggcacgaacg actacggcga cacctctctg 900

ggcagtgggg ggcagacgtc atttcttgtc gccaccgatc ctcgttcgta caagtacttc 960

tacgacttga acgacggcaa ccgcgtagca gcgcaatcgg atagccgttt cacgacgtat 1020

gtgccggcgt ctggacagat gtatcgtatc tacaatcccg ggccgggtaa cgacgaactc 1080

gcgctcacgt acacaggctt cggtctcagg gaaatgcgcg tagcgggagc ccgtgcaatg 1140

aacgagacct tcgtgttcgg cctcgaaaca ggcttctcac agttacccct tagtggccag 1200

gccagctacc ggggagtggt ctacggcagc gccatagggg ccggcagcaa cgccgacctc 1260

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tccatgcagc ccgcagccac gaatacgcgt acccaggtca cgaccgacct tggcactttg 1380

accttcatca acccatggat gccaggggca gctatgatga cgagcgcctt cgccgccgac 1440

atcggcggtc cgtctggcac aacgggccgc ataactggcc ggttctacgg gccccagggg 1500

caggaagtgg gaggaagctt ctcgctggtt accccggccg ctggaaccgt tctgactggg 1560

gtcggggttg tggccgccgt tcggagatag 1590

<210> 976

<211> 529

<212> PRT

<213> Novosphingobium sp. AP12 SLP 1a

<400> 976

Met Ile Asn Pro Ser Ile Ser Glu Val Phe Thr Ala Asp Ala Gly Thr

1 5 10 15

Val Ser Ala Leu Tyr Pro Gly Gly Gly Thr Ser Pro Glu Val Glu Gly

20 25 30

Arg Thr Thr Leu Thr Ile Ala Tyr Asp Ala Thr Asn Gly Ser Tyr Thr

35 40 45

Ile Thr Ala Pro Gln Ala Ser Gln Val Phe Arg Ala Ala Asp Arg Asp

50 55 60

Thr Ala Ser Ser Asp Arg Arg Ile Thr Arg Tyr Val Arg Thr Gln Gly

65 70 75 80

Thr Val Thr Asp Ser Leu Val Leu Thr Lys Ala Gly Glu Ser Gly Ile

85 90 95

Leu Thr Asn Arg Tyr Val Gly Gly Gly Ile Gln Arg Arg Thr Asp Thr

100 105 110

Ala Gly Gly Ile Gln Asn Asn Arg Leu Asn Val Phe Thr Tyr Gly Val

115 120 125

Gln Thr Ala Asn Gly Ala Val Pro Ile Thr Gly Thr Gly Thr Phe Ala

130 135 140

Phe Gly Ile Ile Gly Met Glu Ala Gly Asp Asp Val Leu Ala Asp Phe

145 150 155 160

Asp Gly Arg Gly Thr Met Gln Val Asn Phe Ala Ser Ala Thr Leu Thr

165 170 175

Gly Val Gly Leu Lys Ile Thr Arg Arg Phe Asn Asp Asn Gly Tyr Ala

180 185 190

Ala Leu Asp Gln Ser Val Phe Thr Leu Glu Gly Val Leu Gly Val Gly

195 200 205

Gly Asn Ala Leu Ser Gly Ser Ile Arg Phe Ser Asp Ala Ala Ala Thr

210 215 220

Leu Glu Gly Arg Phe Tyr Gly Ser Ala Ala Glu Glu Val Gly Ala Thr

225 230 235 240

Phe Tyr Gly Ala Asn Thr Arg Asn Gln Met Ile Ser Gly Val Leu Leu

245 250 255

Gly Arg Ser Arg Ser Thr Pro Gly Tyr Glu Thr Leu Thr Asp Leu Val

260 265 270

Met Pro Ile Glu Leu Gln Ala Tyr Thr Ala Ala Ile Phe Ala Thr Arg

275 280 285

Asn Ala Gly Thr Asn Asp Tyr Gly Asp Thr Ser Leu Gly Ser Gly Gly
290 295 300
Gln Thr Ser Phe Leu Val Ala Thr Asp Pro Arg Ser Tyr Lys Tyr Phe
305 310 315 320
Tyr Asp Leu Asn Asp Gly Asn Arg Val Ala Ala Gln Ser Asp Ser Arg
325 330 335
Phe Thr Thr Tyr Val Pro Ala Ser Gly Gln Met Tyr Arg Ile Tyr Asn
340 345 350

Pro Gly Pro Gly Asn Asp Glu Leu Ala Leu Thr Tyr Thr Gly Phe Gly
355 360 365
Leu Arg Glu Met Arg Val Ala Gly Ala Arg Ala Met Asn Glu Thr Phe
370 375 380
Val Phe Gly Leu Glu Thr Gly Phe Ser Gln Leu Pro Leu Ser Gly Gln
385 390 395 400
Ala Ser Tyr Arg Gly Val Val Tyr Gly Ser Ala Ile Gly Ala Gly Ser
405 410 415

Asn Ala Asp Leu Phe Ala Leu His Gly Ser Ala Ala Phe Asp Phe Asp
420 425 430
Phe Gly Arg Asn Ala Phe Thr Gly Ser Met Gln Pro Ala Ala Thr Asn
435 440 445
Thr Arg Thr Gln Val Thr Thr Asp Leu Gly Thr Leu Thr Phe Ile Asn
450 455 460
Pro Trp Met Pro Gly Ala Ala Met Met Thr Ser Ala Phe Ala Ala Asp
465 470 475 480

Ile Gly Gly Pro Ser Gly Thr Thr Gly Arg Ile Thr Gly Arg Phe Tyr
485 490 495
Gly Pro Gln Gly Gln Glu Val Gly Gly Ser Phe Ser Leu Val Thr Pro
500 505 510
Ala Ala Gly Thr Val Leu Thr Gly Val Gly Val Val Ala Ala Val Arg
515 520 525
Arg

<210> 977

<211> 543

<212> DNA

<213> Novosphingobium sp. PP1Y SLP 1a

<400> 977

atgcgcatct ggccggcagg cgggagcgcc acggacttca gctatgtatc gttcgccgaa 60

ttctatgcca gcgcgcctgc aggttccagc ctggaaaccg tggcctatgg cagcatggcg 120

atcatccagc cgacgaggcc cggtgaagtg ccgatgaccg gaagcgccag ctatcatggc 180

tttcttgtcg gctttttcgg cggagatccc ggcggaagct gggtggaagg cagaagcagg 240

ctggacttcg actttgccaa gggatcgctg tccggcgaac tgaccgccag aatggtctgc 300

atgatgggct gcgcctacga tgaccagctc tataccctgg ccgacacaca cttcgcgcac 360

ggcgcgaccg aattcggcgg tagcctcacg acagcgggcg ccccttcggc agggacgttt 420

gcgggcatgt tcgccggccc caatgccagc gagctggccg cccagttcca gcttcccttc 480

ttcaatcagg atttccgcaa gtgggtgccg gtatcgggcg tcatcatcgg caagggcccg 540

taa 543

<210> 978

<211> 180

<212> PRT

<213> Novosphingobium sp. PP1Y SLP 1a

<400> 978

Met Arg Ile Trp Pro Ala Gly Gly Ser Ala Thr Asp Phe Ser Tyr Val
1 5 10 15

Ser Phe Ala Glu Phe Tyr Ala Ser Ala Pro Ala Gly Ser Ser Leu Glu
20 25 30

Thr Val Ala Tyr Gly Ser Met Ala Ile Ile Gln Pro Thr Arg Pro Gly
35 40 45

Glu Val Pro Met Thr Gly Ser Ala Ser Tyr His Gly Phe Leu Val Gly
50 55 60

Phe Phe Gly Gly Asp Pro Gly Gly Ser Trp Val Glu Gly Arg Ser Arg
65 70 75 80

Leu Asp Phe Asp Phe Ala Lys Gly Ser Leu Ser Gly Glu Leu Thr Ala

85 90 95

Arg Met Val Cys Met Met Gly Cys Ala Tyr Asp Asp Gln Leu Tyr Thr
100 105 110
Leu Ala Asp Thr His Phe Ala His Gly Ala Thr Glu Phe Gly Gly Ser
115 120 125
Leu Thr Thr Ala Gly Ala Pro Ser Ala Gly Thr Phe Ala Gly Met Phe
130 135 140
Ala Gly Pro Asn Ala Ser Glu Leu Ala Ala Gln Phe Gln Leu Pro Phe
145 150 155 160

Phe Asn Gln Asp Phe Arg Lys Trp Val Pro Val Ser Gly Val Ile Ile
165 170 175
Gly Lys Gly Pro
180

<210> 979
<211> 1533
<212> DNA
<213> Novosphingobium sp. Rr 2-17 SLP 1a
<400> 979

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acgatgacta tcgcctataa tgcgaacacc aatggctata ccatttcgac cgacggctac 120
tcgcagacat ttctgccggc agaccagacc tcaaaggatg attacgacac agtttattcc 180
aacaacggag ccattctaac ccttacttcc aaggggtacg agaacaatct tgtcacgcaa 240

tatgttcgca tgggcctgtt gcaacgcaat accaccagcg gctcaaccca gaacacagag 300
ttgacaagct tcacgtatgg tctgccgacg gatgcagcca tgacgccgcg cacgggaacc 360
gctgcctaca acacgcaagc cttcggcgcc gtcagtgcgc cgggagcgga gccgaaggca 420
ttccaggggg ccggtcaagt cgacatcgac ttcgtgcaag gtgtgttcag cggccacagc 480
tacttgaccg aatacggcct tgtgaatggc ggcacctctt cgggcggcgg catcgaactg 540
actacggtcg gccagctttc ctctaccggt gcagggctga ctggcaccgc tgtctacgga 600
ggctgggacg gcacggtcac cgccgacctg acaggcagcc tttacggtcc gtcaggacag 660

gaactgggcg cgacgttcag cggtgagaat gccaacggaa tgaccgtgac cggttcaatc 720
gtcggccagc aagacggcac gctaaccccg gccaaccttt cgttcgcgaa catgacccac 780

caacagagtt tctacacccg catgtcggaa tattcgggag gtagcctgac ctggcagaat 840

agcgagacat tcatttattc gggctattcc tcggatgaat cgggtggtca gttcacaatt 900

gacgacaaag tggccggggc ggcgaacttc acgacctatc gcaagacctt cagcaacagc 960

tactacggca cacaggacgt cacgctggag ctttacaagc ctggtgctgc caactccgaa 1020

ctggctctta cctacgccag tttcgggcac tggcagggtt cgctgccctc cagctacgcc 1080

agcggggtga atagccagtg gttcgtctat ggcttcacga ccccgaacta tgcccttgcc 1140

aaccgaaccg gctcggccag ctacgaaggc gtcgcttatg gcacgggctt tggctccggc 1200

ggtcagcgtt acgacgtcaa cggcacctca aatctcgccg tcaatttcag ttccgacacc 1260

ttcaccggcg cgctggcact gagcggtcgc aacaccacaa ccagtgattt gaccgacttc 1320

ggatccacgg ccttctcggg caccatcgac agccgatcca atactctgaa gggcgacttc 1380

agcgcaggtg ggatattggg cagcgggatc tacggtcaat tctacggtcc gcaggggcag 1440

gaagtggcag gcaccttctc gttcaataca ccgcaaggca gcgccgcagc cggagttaac 1500

cttagcggcg ccttcgcggc caagcagaag taa 1533

<210> 980

<211> 510

<212> PRT

<213> Novosphingobium sp. Rr 2-17 SLP 1a

<400> 980

Met Ala Val Ala Trp Asp Arg Thr Thr Asn Thr Gly Ile Ser Gly Ser
1 5 10 15

Thr Lys Ser Ala Thr Met Thr Ile Ala Tyr Asn Ala Asn Thr Asn Gly
20 25 30

Tyr Thr Ile Ser Thr Asp Gly Tyr Ser Gln Thr Phe Leu Pro Ala Asp
35 40 45

Gln Thr Ser Lys Asp Asp Tyr Asp Thr Val Tyr Ser Asn Asn Gly Ala
50 55 60

Ile Leu Thr Leu Thr Ser Lys Gly Tyr Glu Asn Asn Leu Val Thr Gln
65 70 75 80

Tyr Val Arg Met Gly Leu Leu Gln Arg Asn Thr Thr Ser Gly Ser Thr
85 90 95

Gln Asn Thr Glu Leu Thr Ser Phe Thr Tyr Gly Leu Pro Thr Asp Ala

100 105 110

Ala Met Thr Pro Arg Thr Gly Thr Ala Ala Tyr Asn Thr Gln Ala Phe
115 120 125
Gly Ala Val Ser Ala Pro Gly Ala Glu Pro Lys Ala Phe Gln Gly Ala
130 135 140
Gly Gln Val Asp Ile Asp Phe Val Gln Gly Val Phe Ser Gly His Ser
145 150 155 160
Tyr Leu Thr Glu Tyr Gly Leu Val Asn Gly Gly Thr Ser Ser Gly Gly
165 170 175

Gly Ile Glu Leu Thr Thr Val Gly Gln Leu Ser Ser Thr Gly Ala Gly
180 185 190
Leu Thr Gly Thr Ala Val Tyr Gly Gly Trp Asp Gly Thr Val Thr Ala
195 200 205
Asp Leu Thr Gly Ser Leu Tyr Gly Pro Ser Gly Gln Glu Leu Gly Ala
210 215 220
Thr Phe Ser Gly Glu Asn Ala Asn Gly Met Thr Val Thr Gly Ser Ile
225 230 235 240

Val Gly Gln Gln Asp Gly Thr Leu Thr Pro Ala Asn Leu Ser Phe Ala
245 250 255
Asn Met Thr His Gln Gln Ser Phe Tyr Thr Arg Met Ser Glu Tyr Ser
260 265 270
Gly Gly Ser Leu Thr Trp Gln Asn Ser Glu Thr Phe Ile Tyr Ser Gly
275 280 285
Tyr Ser Ser Asp Glu Ser Gly Gly Gln Phe Thr Ile Asp Asp Lys Val
290 295 300

Ala Gly Ala Ala Asn Phe Thr Thr Tyr Arg Lys Thr Phe Ser Asn Ser
305 310 315 320
Tyr Tyr Gly Thr Gln Asp Val Thr Leu Glu Leu Tyr Lys Pro Gly Ala
325 330 335
Ala Asn Ser Glu Leu Ala Leu Thr Tyr Ala Ser Phe Gly His Trp Gln
340 345 350

Gly Ser Leu Pro Ser Ser Tyr Ala Ser Gly Val Asn Ser Gln Trp Phe
355 360 365

Val Tyr Gly Phe Thr Thr Pro Asn Tyr Ala Leu Ala Asn Arg Thr Gly
370 375 380
Ser Ala Ser Tyr Glu Gly Val Ala Tyr Gly Thr Gly Phe Gly Ser Gly
385 390 395 400
Gly Gln Arg Tyr Asp Val Asn Gly Thr Ser Asn Leu Ala Val Asn Phe
405 410 415
Ser Ser Asp Thr Phe Thr Gly Ala Leu Ala Leu Ser Gly Arg Asn Thr
420 425 430

Thr Thr Ser Asp Leu Thr Asp Phe Gly Ser Thr Ala Phe Ser Gly Thr
435 440 445
Ile Asp Ser Arg Ser Asn Thr Leu Lys Gly Asp Phe Ser Ala Gly Gly
450 455 460
Ile Leu Gly Ser Gly Ile Tyr Gly Gln Phe Tyr Gly Pro Gln Gly Gln
465 470 475 480
Glu Val Ala Gly Thr Phe Ser Phe Asn Thr Pro Gln Gly Ser Ala Ala
485 490 495

Ala Gly Val Asn Leu Ser Gly Ala Phe Ala Ala Lys Gln Lys
500 505 510

<210> 981
<211> 690
<212> DNA
<213> O. batsensis SLP 1a
<400> 981
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tctcccaagc ctggcggagg cggaggagga accgcgggca ccggcaaccc cggtggcacg 120
ctgagcagtt cgggatatca atcggcgctc agcgcggttc aggggcgcgg cccgacatcc 180
gacatgccga ccacgatgaa tgccaccttc accggcgcga cgcggcagga tctgcgtgag 240
accaacggcg gcgcgatcgt cggcgagatg atggccgacc tcgaactgac cgccaactgg 300

accgatggtc agagtacgaa cccctggtcg ggcaaggccg acaatttccg cgggtcgatg 360

aacgggcagg actatacgct gaccggcgaa ctgaccgtgg ccgcagccga agccaagagc 420

ctgacctcca cgatcggacg gagcgcgaat accattgccc tgcccacggg cggcacgacg 480

accgtcgcga cgggcgcggc cgcggtcaat cttgccggcg atgtcgatga cggcagcggc 540

accccgcacg aggtgatcat gtcgctcggc gggtccttct tcggtccgca gggcacggcc 600

atcagcggac cggcgacgac ccagggtttc cgggcgggag gggtccggtc cgatctgatt 660

gccgccggcg attattacgt cgagcgataa 690

<210> 982

<211> 229

<212> PRT

<213> O. batsensis SLP 1a

<400> 982

Met Met Lys Asn Phe Lys Ile Val Val Leu Ala Leu Cys Ala Leu Pro

1 5 10 15

Ile Ala Ala Cys Ser Pro Lys Pro Gly Gly Gly Gly Gly Gly Thr Ala

20 25 30

Gly Thr Gly Asn Pro Gly Gly Thr Leu Ser Ser Ser Gly Tyr Gln Ser

35 40 45

Ala Leu Ser Ala Val Gln Gly Arg Gly Pro Thr Ser Asp Met Pro Thr

50 55 60

Thr Met Asn Ala Thr Phe Thr Gly Ala Thr Arg Gln Asp Leu Arg Glu

65 70 75 80

Thr Asn Gly Gly Ala Ile Val Gly Glu Met Met Ala Asp Leu Glu Leu

85 90 95

Thr Ala Asn Trp Thr Asp Gly Gln Ser Thr Asn Pro Trp Ser Gly Lys

100 105 110

Ala Asp Asn Phe Arg Gly Ser Met Asn Gly Gln Asp Tyr Thr Leu Thr

115 120 125

Gly Glu Leu Thr Val Ala Ala Ala Glu Ala Lys Ser Leu Thr Ser Thr

130 135 140

Ile Gly Arg Ser Ala Asn Thr Ile Ala Leu Pro Thr Gly Gly Thr Thr

145 150 155 160

Thr Val Ala Thr Gly Ala Ala Ala Val Asn Leu Ala Gly Asp Val Asp

165 170 175

Asp Gly Ser Gly Thr Pro His Glu Val Ile Met Ser Leu Gly Gly Ser

180 185 190

Phe Phe Gly Pro Gln Gly Thr Ala Ile Ser Gly Pro Ala Thr Thr Gln

195 200 205

Gly Phe Arg Ala Gly Gly Val Arg Ser Asp Leu Ile Ala Ala Gly Asp

210 215 220

Tyr Tyr Val Glu Arg

225

<210> 983

<211> 1554

<212> DNA

<213> P. bermudensis SLP 1

<400> 983

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tgtagctcaa ccggcggcac ccccgaccct attttggggg aggacggaca gcccgcaccg 120

ccgcgcaacc ttgtcactaa cgccttgagc tatcgcgccg aaaaccacgg gtcggcagtc 180

agcgagacct atgatctggc cgtgacggcc atgcggacac gctatcaaac caacggggcg 240

gcggtctttg tcgggatcga acacgacgcg gtgggcgaga gcgagacgac agagtttaga 300

tatgatgccg ccgcggacac cttcaccatt gatatcgatt tgccgaatgc ggacgatgcc 360

ccgatcctgg tgaacgaaac atgggggccg ctcctattat tgaccccgaa ggatctcttc 420

ggcctcaata acggggtgtc ggcagtctat ctggccaagc aacccgactt ctacggcttc 480

gtcgacgaga ccttgatcgg ggggaacgaa tttaccgccg acgcctatat cgatgccctt 540

ggcgccgtcg atgcgacggg cagcggcagc ggctatctgg cgctgtgggt gacgatcgcc 600

aatgaccttg ggtttgaagg atcggaacgg gatgtcggct ccctgccgat ttatatcgcg 660

aacgatccgg caaccttcgg cgcgccgggc tccctcgccg gggatatcga ggccgccact 720

gcgtatgtcg aagatctcag ccccgccgcc ttcagcgacg cccaggccgc cgcccccgtc 780

cccagcagcg ccttcgaccc gatcatgagc gagctccttg ccaccgcccc cgaaagtttc 840

ggcgtcaatg ttgagggaca gatttccgac aatgatgcaa gcttcatcat tgccgtgatg 900

gacgatgtcg gcggcacagc ggtcgaggat tacatcaccg cgatcacgat cattaccgac 960

gacatcgaag cggcgcccaa ttatctctac caagccaacg gcgtcaccta ttatcagtat 1020

aaaaccgaag gggatgtcgt cgatacccgc ttcgttgccg ccggggaatg gcagaagacc 1080

gaagccagcg gcgagaccat tttcggtcat ttcgtctacg gtcaattgac cgatcccgat 1140

gagatgccga cctccggcac cgccagctac acaggcacgg tttacggctc catcctgcgg 1200

caaaaccggg tcgacagcct gcgcggcggg ctcaacctga acaccgattt tcagaccggc 1260

gccctcgaca tgaccttcaa cgccgatatc gcttaccgcg acgatgaggg gataacccaa 1320

tttatcgact atgccgactt caccggcacc ggccggatcg acgatgccaa tttcgatggc 1380

accatgcagg gggtgacctc gatcgatacc tctgaaaccg acagcccccc tgtggtggac 1440

gggtccttcg aaggccattt ctatggcccc accgcccaag aggccggggg caccttcgaa 1500

ttctcgaaca ccgaggccgc ggcgaccgga tccttcgtcg ctgtcaggga ttaa 1554

<210> 984

<211> 517

<212> PRT

<213> P. bermudensis SLP 1

<400> 984

Met Val Met Arg Leu Ser Thr Gly Leu Phe Ala Ala Ser Ser Leu Ile
1 5 10 15

Ala Leu Ala Ala Cys Ser Ser Thr Gly Gly Thr Pro Asp Pro Ile Leu
20 25 30

Gly Glu Asp Gly Gln Pro Ala Pro Pro Arg Asn Leu Val Thr Asn Ala
35 40 45

Leu Ser Tyr Arg Ala Glu Asn His Gly Ser Ala Val Ser Glu Thr Tyr
50 55 60

Asp Leu Ala Val Thr Ala Met Arg Thr Arg Tyr Gln Thr Asn Gly Ala
65 70 75 80

Ala Val Phe Val Gly Ile Glu His Asp Ala Val Gly Glu Ser Glu Thr
85 90 95

Thr Glu Phe Arg Tyr Asp Ala Ala Ala Asp Thr Phe Thr Ile Asp Ile
100 105 110

Asp Leu Pro Asn Ala Asp Asp Ala Pro Ile Leu Val Asn Glu Thr Trp
115 120 125

Gly Pro Leu Leu Leu Leu Thr Pro Lys Asp Leu Phe Gly Leu Asn Asn

130 135 140

Gly Val Ser Ala Val Tyr Leu Ala Lys Gln Pro Asp Phe Tyr Gly Phe
145 150 155 160
Val Asp Glu Thr Leu Ile Gly Gly Asn Glu Phe Thr Ala Asp Ala Tyr
165 170 175
Ile Asp Ala Leu Gly Ala Val Asp Ala Thr Gly Ser Gly Ser Gly Tyr
180 185 190
Leu Ala Leu Trp Val Thr Ile Ala Asn Asp Leu Gly Phe Glu Gly Ser
195 200 205

Glu Arg Asp Val Gly Ser Leu Pro Ile Tyr Ile Ala Asn Asp Pro Ala
210 215 220
Thr Phe Gly Ala Pro Gly Ser Leu Ala Gly Asp Ile Glu Ala Ala Thr
225 230 235 240
Ala Tyr Val Glu Asp Leu Ser Pro Ala Ala Phe Ser Asp Ala Gln Ala
245 250 255
Ala Ala Pro Val Pro Ser Ser Ala Phe Asp Pro Ile Met Ser Glu Leu
260 265 270

Leu Ala Thr Ala Pro Glu Ser Phe Gly Val Asn Val Glu Gly Gln Ile
275 280 285
Ser Asp Asn Asp Ala Ser Phe Ile Ile Ala Val Met Asp Asp Val Gly
290 295 300
Gly Thr Ala Val Glu Asp Tyr Ile Thr Ala Ile Thr Ile Ile Thr Asp
305 310 315 320
Asp Ile Glu Ala Ala Pro Asn Tyr Leu Tyr Gln Ala Asn Gly Val Thr
325 330 335

Tyr Tyr Gln Tyr Lys Thr Glu Gly Asp Val Val Asp Thr Arg Phe Val
340 345 350
Ala Ala Gly Glu Trp Gln Lys Thr Glu Ala Ser Gly Glu Thr Ile Phe
355 360 365
Gly His Phe Val Tyr Gly Gln Leu Thr Asp Pro Asp Glu Met Pro Thr
370 375 380

Ser Gly Thr Ala Ser Tyr Thr Gly Thr Val Tyr Gly Ser Ile Leu Arg
385 390 395 400

Gln Asn Arg Val Asp Ser Leu Arg Gly Gly Leu Asn Leu Asn Thr Asp
405 410 415
Phe Gln Thr Gly Ala Leu Asp Met Thr Phe Asn Ala Asp Ile Ala Tyr
420 425 430
Arg Asp Asp Glu Gly Ile Thr Gln Phe Ile Asp Tyr Ala Asp Phe Thr
435 440 445
Gly Thr Gly Arg Ile Asp Asp Ala Asn Phe Asp Gly Thr Met Gln Gly
450 455 460

Val Thr Ser Ile Asp Thr Ser Glu Thr Asp Ser Pro Leu Val Val Asp
465 470 475 480
Gly Ser Phe Glu Gly His Phe Tyr Gly Pro Thr Ala Gln Glu Ala Gly
485 490 495
Gly Thr Phe Glu Phe Ser Asn Thr Glu Ala Ala Ala Thr Gly Ser Phe
500 505 510
Val Ala Val Arg Asp
515

<210> 985
<211> 606
<212> DNA
<213> P. bettyae SLP 3a
<400
> 985

atgaaaaaac tatttctttg ctcaattgtg agtttatcca tcctattgac tgcttgtagt 60
ggtggtggcg gtagcggtag tgcacaaact ccagatgcta gcaaaataga tttaactaac 120
agtccaaaag gtgatgtggc agttaatacg gcggcaggaa ccttatatgg aaaaaatcaa 180
aatgactctt tttatggtgt atggatggat gatgctaaga cagtaaaaga attacgctat 240
caaggtacat cagcaactaa tttaccttct ggttctgcaa cttatacagg agaatcatat 300
tgggttagtg gcacaacggg tgagatatca aagggtggtg ttagcacttt aaatgttgat 360
tttgatcgaa aagcagtaga tggaaaaatc acgtattcac ttttaaatga tggtagagtt 420

caagatatta cgctacattc tacagcattg gatggtacaa aatttaatgg taatgcaagt 480

accttattag aaagtggtag ttatgaaggt gcattatttg gtaatggagc taaagaagcc 540

gctggaatag tgaatttccc aaacaatagt tcttataaca catcatttgg tggtgttaga 600

tattaa 606

<210> 986

<211> 201

<212> PRT

<213> P. bettyae SLP 3a

<400> 986

Met Lys Lys Leu Phe Leu Cys Ser Ile Val Ser Leu Ser Ile Leu Leu
1 5 10 15

Thr Ala Cys Ser Gly Gly Gly Gly Ser Gly Ser Ala Gln Thr Pro Asp
20 25 30

Ala Ser Lys Ile Asp Leu Thr Asn Ser Pro Lys Gly Asp Val Ala Val
35 40 45

Asn Thr Ala Ala Gly Thr Leu Tyr Gly Lys Asn Gln Asn Asp Ser Phe
50 55 60

Tyr Gly Val Trp Met Asp Asp Ala Lys Thr Val Lys Glu Leu Arg Tyr
65 70 75 80

Gln Gly Thr Ser Ala Thr Asn Leu Pro Ser Gly Ser Ala Thr Tyr Thr
85 90 95

Gly Glu Ser Tyr Trp Val Ser Gly Thr Thr Gly Glu Ile Ser Lys Gly
100 105 110

Gly Val Ser Thr Leu Asn Val Asp Phe Asp Arg Lys Ala Val Asp Gly
115 120 125

Lys Ile Thr Tyr Ser Leu Leu Asn Asp Gly Arg Val Gln Asp Ile Thr
130 135 140

Leu His Ser Thr Ala Leu Asp Gly Thr Lys Phe Asn Gly Asn Ala Ser
145 150 155 160

Thr Leu Leu Glu Ser Gly Ser Tyr Glu Gly Ala Leu Phe Gly Asn Gly
165 170 175

Ala Lys Glu Ala Ala Gly Ile Val Asn Phe Pro Asn Asn Ser Ser Tyr
180 185 190

Asn Thr Ser Phe Gly Gly Val Arg Tyr

195 200

<210> 987

<211> 1035

<212> DNA

<213> P. dagmatis SLP 1a

<400> 987

atgaaagagt tagttatcaa aaccagctta tttatcggat tatctagctt acttgtagct 60

tgtggcggtg gctcagatac gaatgctgaa agtagtcatg aagcacagca agttaaccca 120

actgcagtaa actctcaacc acaggttgaa cctaaaacac ataatgaaac ccaacctgaa 180

aaacaactag aaaaagaaca accgcaagat cgagaagata aaaaccaact gcaaccagaa 240

cagcctaaaa atcaaaatac gcgagaagat aaacctgcac acactccctc aagtcaacct 300

gctgtcgtta aagtatatgc ggatagcgat ataaatacag aatggtttgg aatgaaaacc 360

tctaaatatc attctcctac agtgattaac gaaaatagga ataatgtaga aatatatgat 420

ttagtgttag tggaaaatcc agatgatcaa accaaatatg ataaaactaa atctaaacaa 480

actacgatcg cattgcgtaa agaaggagaa actagtcatt atagtcatgg aaaacttaat 540

tattcattcg atttagtaaa tggcaatata tattatggct attatttaaa accagaagct 600

gattataaaa actcatatct tacatactca tatgcttttg ataagagtat agaagacaac 660

cgctccttag caaactactc tgctaagtac tcacaatatg gtggattttc attctctgta 720

aaaataggaa atgattatat acaacaattt ggagatgtgg acttaatcta cacaaatgga 780

agaattagtg gtgaaatcac aaatccacat agcagtgaag ttaataacaa aatttttgat 840

ttagaaggaa aagaaagaga attaatcatt agaccaaata aagataatga atataagcta 900

agttcaaacg gtggagataa tatgtccatg caactacacc ttattaattc taatcaaaaa 960

gaatacatta taggggcagg taaagccgaa aattattatg gtgtactttt cgcagaaaaa 1020

aaagaaaatg aataa 1035

<210> 988

<211> 344

<212> PRT

<213> P. dagmatis SLP 1a

<400> 988

Met Lys Glu Leu Val Ile Lys Thr Ser Leu Phe Ile Gly Leu Ser Ser

1 5 10 15

Leu Leu Val Ala Cys Gly Gly Gly Ser Asp Thr Asn Ala Glu Ser Ser
20 25 30
His Glu Ala Gln Gln Val Asn Pro Thr Ala Val Asn Ser Gln Pro Gln
35 40 45
Val Glu Pro Lys Thr His Asn Glu Thr Gln Pro Glu Lys Gln Leu Glu
50 55 60
Lys Glu Gln Pro Gln Asp Arg Glu Asp Lys Asn Gln Leu Gln Pro Glu
65 70 75 80

Gln Pro Lys Asn Gln Asn Thr Arg Glu Asp Lys Pro Ala His Thr Pro
85 90 95
Ser Ser Gln Pro Ala Val Val Lys Val Tyr Ala Asp Ser Asp Ile Asn
100 105 110
Thr Glu Trp Phe Gly Met Lys Thr Ser Lys Tyr His Ser Pro Thr Val
115 120 125
Ile Asn Glu Asn Arg Asn Asn Val Glu Ile Tyr Asp Leu Val Leu Val
130 135 140

Glu Asn Pro Asp Asp Gln Thr Lys Tyr Asp Lys Thr Lys Ser Lys Gln
145 150 155 160
Thr Thr Ile Ala Leu Arg Lys Glu Gly Glu Thr Ser His Tyr Ser His
165 170 175
Gly Lys Leu Asn Tyr Ser Phe Asp Leu Val Asn Gly Asn Ile Tyr Tyr
180 185 190
Gly Tyr Tyr Leu Lys Pro Glu Ala Asp Tyr Lys Asn Ser Tyr Leu Thr
195 200 205

Tyr Ser Tyr Ala Phe Asp Lys Ser Ile Glu Asp Asn Arg Ser Leu Ala
210 215 220
Asn Tyr Ser Ala Lys Tyr Ser Gln Tyr Gly Gly Phe Ser Phe Ser Val
225 230 235 240
Lys Ile Gly Asn Asp Tyr Ile Gln Gln Phe Gly Asp Val Asp Leu Ile
245 250 255

Tyr Thr Asn Gly Arg Ile Ser Gly Glu Ile Thr Asn Pro His Ser Ser
260 265 270

Glu Val Asn Asn Lys Ile Phe Asp Leu Glu Gly Lys Glu Arg Glu Leu
275 280 285
Ile Ile Arg Pro Asn Lys Asp Asn Glu Tyr Lys Leu Ser Ser Asn Gly
290 295 300
Gly Asp Asn Met Ser Met Gln Leu His Leu Ile Asn Ser Asn Gln Lys
305 310 315 320
Glu Tyr Ile Ile Gly Ala Gly Lys Ala Glu Asn Tyr Tyr Gly Val Leu
325 330 335

Phe Ala Glu Lys Lys Glu Asn Glu
340

<210> 989
<211> 711
<212> DNA
<213> P. galatheae SLP 1a
<400> 989
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gccaatattg tcggcaccca aagtgacaac actcagattc tggtgggaga atcgaatctg 120
aatgccgggc cgcatgtcgc aggtcgtgca ggtattgggg ctgcatcgat gggttccacc 180
gcgcaaaaag ttgattttca ggccctgaaa aattatggcc gcgtgcaaaa cggcgtttat 240
gtgctgggtg gcggccactc aaggatgggc aacttcaact ttgccaaagt cggggctggt 300

gatgtctggt tcggggagtg ggcgagtgat atcagcagtg atgccgatcg gacggtttat 360
tacgtgggcg ataccacggg taccacacta ccgaccagcg gcacggcgac ctatgcggtg 420
aaaggggtga acaagttctc tggcagcaat gacctgaatg ggactttcac agcgaacttc 480
accaacaata cgttgcaagg ttcgattgcc aacagccagt atacgctggg ggtgaatgcg 540
accatcaaca gtgccaccgc tgcctttaac gggacagcca cggtcggccc agccagcggc 600
acagcaaaag gtcatttctt tggcaatcat gcagcggcat tggcggggat tgcacaattt 660
tcaggggatg caaaaatctt cgacaccgct ttcggcggaa ccaagcagta a 711

<210> 990
<211> 236

<212> PRT

<213> P. galatheae SLP 1a

<400> 990

Met Lys Lys Ala Val Ile Thr Leu Ala Val Leu Ser Ala Cys Ile Ser
1 5 10 15

Gly Ala Ala Gln Ala Asn Ile Val Gly Thr Gln Ser Asp Asn Thr Gln
20 25 30

Ile Leu Val Gly Glu Ser Asn Leu Asn Ala Gly Pro His Val Ala Gly
35 40 45

Arg Ala Gly Ile Gly Ala Ala Ser Met Gly Ser Thr Ala Gln Lys Val

50 55 60

Asp Phe Gln Ala Leu Lys Asn Tyr Gly Arg Val Gln Asn Gly Val Tyr
65 70 75 80

Val Leu Gly Gly Gly His Ser Arg Met Gly Asn Phe Asn Phe Ala Lys
85 90 95

Val Gly Ala Gly Asp Val Trp Phe Gly Glu Trp Ala Ser Asp Ile Ser
100 105 110

Ser Asp Ala Asp Arg Thr Val Tyr Tyr Val Gly Asp Thr Thr Gly Thr

115 120 125

Thr Leu Pro Thr Ser Gly Thr Ala Thr Tyr Ala Val Lys Gly Val Asn
130 135 140

Lys Phe Ser Gly Ser Asn Asp Leu Asn Gly Thr Phe Thr Ala Asn Phe
145 150 155 160

Thr Asn Asn Thr Leu Gln Gly Ser Ile Ala Asn Ser Gln Tyr Thr Leu
165 170 175

Gly Val Asn Ala Thr Ile Asn Ser Ala Thr Ala Ala Phe Asn Gly Thr

180 185 190

Ala Thr Val Gly Pro Ala Ser Gly Thr Ala Lys Gly His Phe Phe Gly
195 200 205

Asn His Ala Ala Ala Leu Ala Gly Ile Ala Gln Phe Ser Gly Asp Ala
210 215 220

Lys Ile Phe Asp Thr Ala Phe Gly Gly Thr Lys Gln

225 230 235

<210> 991

<211> 963

<212> DNA

<213> P. halotolerans SLP 1a

<400> 991

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tcttcgaccg gcgggggtgg tgcaggcggc gggggcggcg gggggacgcc ctcgccggca 120

ctgtttgccg catcggcggg cacggcgagc gaggctttgg cggatgggga gacgctgatg 180

gcgtataaca gcctgatgag cgctgccgtc gagcacgatt tcgacgcggg cgagacgcgg 240

gcgctcgatg gcaccacgtt ttcgattgcc gccaatgacc agggcggcct cgatgtgatc 300

atcgacggcg ttgcctacag ctttaccgac gcggacatca gcgggaatgc cttcgagttc 360

gacgatcccg gcggaatggg gccctattac cggctcaaca gttgggacgg ggatatcgtg 420

gatgtgctcg atgtgtccaa caccgcccat caccaggtgt ggagctattt ctgggatccc 480

gcaggcgagc cgatcagcgg ctttgcggtg gtgggcaccg aaaccatgcc ggaggctctg 540

gagggcaagg ccaatgccac atattcgggc gcggcgggtg cggcgctgac cgacagcggc 600

accttcaacg acaccacgcg catcgtgggc gagctggcga tgtcggcgga tttcaacgcc 660

ggccagatat cggggcttgt cgacaatatc gcggtgatcg gtcttggggc gtgcagcggc 720

ggcgtgggtc ccgcatgcgt caacggcact gccgccctcg acagcgcggc aatcacgggg 780

acggggttca gcggaaccat caccgccgac agcgaccttc tgacggcgtt ttcgctcacc 840

gatctgggcg gcacctatag cggcaagttc tacggtgcgg acggtgagga ggtgggcggc 900

gtcatggcgc tgagcggcga ggaaacggta ggtactggct atttctcggc cacccaggac 960

tga 963

<210> 992

<211> 320

<212> PRT

<213> P. halotolerans SLP 1a

<400> 992

Met His Arg Tyr Ala Pro Phe Phe Leu Ile Gly Leu Ser Gly Thr Leu

1 5 10 15

Leu Ala Gly Cys Ser Ser Thr Gly Gly Gly Gly Ala Gly Gly Gly Gly

20 25 30

Gly Gly Gly Thr Pro Ser Pro Ala Leu Phe Ala Ala Ser Ala Gly Thr

35 40 45

Ala Ser Glu Ala Leu Ala Asp Gly Glu Thr Leu Met Ala Tyr Asn Ser

50 55 60

Leu Met Ser Ala Ala Val Glu His Asp Phe Asp Ala Gly Glu Thr Arg

65 70 75 80

Ala Leu Asp Gly Thr Thr Phe Ser Ile Ala Ala Asn Asp Gln Gly Gly

85 90 95

Leu Asp Val Ile Ile Asp Gly Val Ala Tyr Ser Phe Thr Asp Ala Asp

100 105 110

Ile Ser Gly Asn Ala Phe Glu Phe Asp Asp Pro Gly Gly Met Gly Pro

115 120 125

Tyr Tyr Arg Leu Asn Ser Trp Asp Gly Asp Ile Val Asp Val Leu Asp

130 135 140

Val Ser Asn Thr Ala His His Gln Val Trp Ser Tyr Phe Trp Asp Pro

145 150 155 160

Ala Gly Glu Pro Ile Ser Gly Phe Ala Val Val Gly Thr Glu Thr Met

165 170 175

Pro Glu Ala Leu Glu Gly Lys Ala Asn Ala Thr Tyr Ser Gly Ala Ala

180 185 190

Gly Ala Ala Leu Thr Asp Ser Gly Thr Phe Asn Asp Thr Thr Arg Ile

195 200 205

Val Gly Glu Leu Ala Met Ser Ala Asp Phe Asn Ala Gly Gln Ile Ser

210 215 220

Gly Leu Val Asp Asn Ile Ala Val Ile Gly Leu Gly Ala Cys Ser Gly

225 230 235 240

Gly Val Gly Pro Ala Cys Val Asn Gly Thr Ala Ala Leu Asp Ser Ala

245 250 255

Ala Ile Thr Gly Thr Gly Phe Ser Gly Thr Ile Thr Ala Asp Ser Asp

260 265 270

Leu Leu Thr Ala Phe Ser Leu Thr Asp Leu Gly Gly Thr Tyr Ser Gly

275 280 285

Lys Phe Tyr Gly Ala Asp Gly Glu Glu Val Gly Gly Val Met Ala Leu

290 295 300

Ser Gly Glu Glu Thr Val Gly Thr Gly Tyr Phe Ser Ala Thr Gln Asp

305 310 315 320

<210> 993

<211> 805

<212> DNA

<213> P. luminescens SLP 1a

<400> 993

aggaatatgc tatgaacaaa gttaaagtgt taattgcagt attaggtaca tgtgggttag 60

taacacaagc tatagcggcc ccaggttttg ggcaaactca aaagtttgat gagaataaac 120

ctagcgttaa cgtaggggtg actgaaccac gtggtggtgg tcacccaacc ttaggtggag 180

agccggggat tggggtgcaa tctatttcta atggtaggat tattagcttt tcaagccttg 240

ctgcttatgt caaggcggat acaaatggaa ttcataaaat ttctatgcct ggatcgggta 300

gtcatggagg catgggggta ttcaacttta gtaaagtggc tgatgctgat gtctattttg 360

gtgaatggtc acaaaccggt aaggtgaatg atactactca tactgcctat tattccggta 420

aagatgtcac gactaatttg cctaccggtg gtattgcaac ttatacggtt aaaggaatta 480

accaatatag tggtagcaat gctctacatg gaacatttac tgctgatttc ggtcagaaaa 540

gacttactgg ttcaatagca aatagcgcac tcactgtcgg tattaattct gttattaaat 600

ctgatggctc atttgttggt agtgcgactg ctggaggtgc tgttggtaga aatagcggac 660

atttctttgg tgataatgcc gctagtttag cagggactgc tacgtttgct gcggaccata 720

gtaaagatac cgcctttggt ggaactaaga acccgtaata tgcgttctta gtaactggat 780

aaggcaaagc catgtgggct ttgtc 805

<210> 994

<211> 248

<212> PRT

<213> P. luminescens SLP 1a

<400> 994

Met Asn Lys Val Lys Val Leu Ile Ala Val Leu Gly Thr Cys Gly Leu

1 5 10 15

Val Thr Gln Ala Ile Ala Ala Pro Gly Phe Gly Gln Thr Gln Lys Phe

20 25 30

Asp Glu Asn Lys Pro Ser Val Asn Val Gly Val Thr Glu Pro Arg Gly

35 40 45

Gly Gly His Pro Thr Leu Gly Gly Glu Pro Gly Ile Gly Val Gln Ser

50 55 60

Ile Ser Asn Gly Arg Ile Ile Ser Phe Ser Ser Leu Ala Ala Tyr Val

65 70 75 80

Lys Ala Asp Thr Asn Gly Ile His Lys Ile Ser Met Pro Gly Ser Gly

85 90 95

Ser His Gly Gly Met Gly Val Phe Asn Phe Ser Lys Val Ala Asp Ala

100 105 110

Asp Val Tyr Phe Gly Glu Trp Ser Gln Thr Gly Lys Val Asn Asp Thr

115 120 125

Thr His Thr Ala Tyr Tyr Ser Gly Lys Asp Val Thr Thr Asn Leu Pro

130 135 140

Thr Gly Gly Ile Ala Thr Tyr Thr Val Lys Gly Ile Asn Gln Tyr Ser

145 150 155 160

Gly Ser Asn Ala Leu His Gly Thr Phe Thr Ala Asp Phe Gly Gln Lys

165 170 175

Arg Leu Thr Gly Ser Ile Ala Asn Ser Ala Leu Thr Val Gly Ile Asn

180 185 190

Ser Val Ile Lys Ser Asp Gly Ser Phe Val Gly Ser Ala Thr Ala Gly

195 200 205

Gly Ala Val Gly Arg Asn Ser Gly His Phe Phe Gly Asp Asn Ala Ala

210 215 220

Ser Leu Ala Gly Thr Ala Thr Phe Ala Ala Asp His Ser Lys Asp Thr

225 230 235 240

Ala Phe Gly Gly Thr Lys Asn Pro

245

<210> 995

<211> 801

<212> DNA

<213> P. mirabilis SLP 1a

<400> 995

atgaaaaaaa taaacatttt tacgggtact ctatttgttt tatctagcat aagtatggca 60

caagcagaaa tccattctaa tcaaagtggc cctttaacca ccatgagtgt gggggcgagt 120

gatcccgtga ctcatggccc tcatcaatca gcaggtgggg agccgggtgt tggtatttct 180

aatctatatg ggggtaaaaa aattggtttt gcgtcattaa caccaaataa tatgagtggt 240

ggggcggata gccatggtgt ttatactgtc caatctaatc atcatcataa taatcttggc 300

gtttttcatt tttcacaggt gactgatgcc aatgtctatt ttggtacttg ggcaaaaaca 360

gcctctgtta cagatatcac tcatcagtct tattatgtag gtaaagaggt tactagtacg 420

ctaccgacag acagtgcaac ttataccgta acaggtatca gtcaatatag tggtgataat 480

ttactgtctg gtacttttga tgttgatttt tcacaaaaga caattggtgg ttcactggct 540

aatagcctac gtactgtcga gttagaacgt ggcaatattt ataccgcaaa taaccaagta 600

actttctctg cagatgcaaa agaagatacc acatccggta ttgttgaagg ggcgttcttt 660

ggtgaaaatg ctgaaacatt ggctggtatt gtcgtcttcc acaccgatca tactaaagat 720

attggttttg gaggaagcaa aaatagtgct gaagtagata ctgcaacaga tagcgtaaca 780

gatagtgcag aagcctctta a 801

<210> 996

<211> 266

<212> PRT

<213> P. mirabilis SLP 1a

<400> 996

Met Lys Lys Ile Asn Ile Phe Thr Gly Thr Leu Phe Val Leu Ser Ser
1 5 10 15

Ile Ser Met Ala Gln Ala Glu Ile His Ser Asn Gln Ser Gly Pro Leu
20 25 30

Thr Thr Met Ser Val Gly Ala Ser Asp Pro Val Thr His Gly Pro His
35 40 45

Gln Ser Ala Gly Gly Glu Pro Gly Val Gly Ile Ser Asn Leu Tyr Gly
50 55 60

Gly Lys Lys Ile Gly Phe Ala Ser Leu Thr Pro Asn Asn Met Ser Gly
65 70 75 80
Gly Ala Asp Ser His Gly Val Tyr Thr Val Gln Ser Asn His His His
85 90 95
Asn Asn Leu Gly Val Phe His Phe Ser Gln Val Thr Asp Ala Asn Val
100 105 110
Tyr Phe Gly Thr Trp Ala Lys Thr Ala Ser Val Thr Asp Ile Thr His
115 120 125

Gln Ser Tyr Tyr Val Gly Lys Glu Val Thr Ser Thr Leu Pro Thr Asp
130 135 140
Ser Ala Thr Tyr Thr Val Thr Gly Ile Ser Gln Tyr Ser Gly Asp Asn
145 150 155 160
Leu Leu Ser Gly Thr Phe Asp Val Asp Phe Ser Gln Lys Thr Ile Gly
165 170 175
Gly Ser Leu Ala Asn Ser Leu Arg Thr Val Glu Leu Glu Arg Gly Asn
180 185 190

Ile Tyr Thr Ala Asn Asn Gln Val Thr Phe Ser Ala Asp Ala Lys Glu
195 200 205
Asp Thr Thr Ser Gly Ile Val Glu Gly Ala Phe Phe Gly Glu Asn Ala
210 215 220
Glu Thr Leu Ala Gly Ile Val Val Phe His Thr Asp His Thr Lys Asp
225 230 235 240
Ile Gly Phe Gly Gly Ser Lys Asn Ser Ala Glu Val Asp Thr Ala Thr
245 250 255

Asp Ser Val Thr Asp Ser Ala Glu Ala Ser
260 265

<210> 997
<211> 942
<212> DNA
<213> P. multocida SLP 1a
<400> 997
atgcagtatt ttgacatcaa aaaatctctc cctgtttttt gttctcttct gattaccgct 60

tgtagtggtg gtgggggtgg taataatcca tcacaatatc ctaaagaagt acgccctgtg 120

gtaactgaac aagccaaaac agctaaagaa gtgattttac ctacaccctc tattggatca 180

gaacagtcat ctcaaaacgt aatagctaaa gatgctttca atgtgagcga aaaaacgcat 240

caacactcca aaccagaaaa aattgcaaaa gatattaatt ggacaggtag tgctgtgtcg 300

tctataggct ctacttggtg gcaacataaa ccaaataata ttcctgtttt tacactaatt 360

cttaatgaaa accaaattta ctccgatgaa aaaaacttca ctctagaaca aaaacatatt 420

gatcttacaa agaataatat tttggatgaa aagtactttc atttcacatt attagactcc 480

ggaatttatt atggaaatta tttaagttca tacgatcaga tgaacgcaga atctaattat 540

gtttttgcat ttgataaaga tcgtgaatat acaggaaaag atatcaccgc aaattattat 600

ggtaatgaag gatttaaata ttctgtaaaa ttaggtaata catacctatc acaggtgggt 660

gatgttcact taatctatcg agaagggaaa gtatcaggag aaatttttgg tcaaaataac 720

gtaaaacact ttagctttat gaatagcaat aaaattgacc caaatagcat tgttattgtc 780

ccagaagaag cacatcgata tctatccaga aatgataaaa tgttcttaga aatgcatttc 840

attaatgggg aaaatggaga aaaatataaa tatattgtgg gtagtggtaa aacggacaaa 900

tactacggcg cattatttgc aactaaacaa gaaaaccagt ga 942

<210> 998

<211> 313

<212> PRT

<213> P. multocida SLP 1a

<400> 998

Met Gln Tyr Phe Asp Ile Lys Lys Ser Leu Pro Val Phe Cys Ser Leu
1 5 10 15

Leu Ile Thr Ala Cys Ser Gly Gly Gly Gly Gly Asn Asn Pro Ser Gln
20 25 30

Tyr Pro Lys Glu Val Arg Pro Val Val Thr Glu Gln Ala Lys Thr Ala
35 40 45

Lys Glu Val Ile Leu Pro Thr Pro Ser Ile Gly Ser Glu Gln Ser Ser
50 55 60

Gln Asn Val Ile Ala Lys Asp Ala Phe Asn Val Ser Glu Lys Thr His
65 70 75 80

Gln His Ser Lys Pro Glu Lys Ile Ala Lys Asp Ile Asn Trp Thr Gly

85 90 95

Ser Ala Val Ser Ser Ile Gly Ser Thr Trp Trp Gln His Lys Pro Asn

100 105 110

Asn Ile Pro Val Phe Thr Leu Ile Leu Asn Glu Asn Gln Ile Tyr Ser

115 120 125

Asp Glu Lys Asn Phe Thr Leu Glu Gln Lys His Ile Asp Leu Thr Lys

130 135 140

Asn Asn Ile Leu Asp Glu Lys Tyr Phe His Phe Thr Leu Leu Asp Ser

145 150 155 160

Gly Ile Tyr Tyr Gly Asn Tyr Leu Ser Ser Tyr Asp Gln Met Asn Ala

165 170 175

Glu Ser Asn Tyr Val Phe Ala Phe Asp Lys Asp Arg Glu Tyr Thr Gly

180 185 190

Lys Asp Ile Thr Ala Asn Tyr Tyr Gly Asn Glu Gly Phe Lys Tyr Ser

195 200 205

Val Lys Leu Gly Asn Thr Tyr Leu Ser Gln Val Gly Asp Val His Leu

210 215 220

Ile Tyr Arg Glu Gly Lys Val Ser Gly Glu Ile Phe Gly Gln Asn Asn

225 230 235 240

Val Lys His Phe Ser Phe Met Asn Ser Asn Lys Ile Asp Pro Asn Ser

245 250 255

Ile Val Ile Val Pro Glu Glu Ala His Arg Tyr Leu Ser Arg Asn Asp

260 265 270

Lys Met Phe Leu Glu Met His Phe Ile Asn Gly Glu Asn Gly Glu Lys

275 280 285

Tyr Lys Tyr Ile Val Gly Ser Gly Lys Thr Asp Lys Tyr Tyr Gly Ala

290 295 300

Leu Phe Ala Thr Lys Gln Glu Asn Gln

305 310

<210> 999

<211> 1074

<212> DNA

<213> P. pneumotropica SLP 2a

<400> 999

atggaactaa caaaaatttc attgacaaga tttggtttaa ctgccctggc tgcgttaatt 60

gtttcagctt gtggaagtag cggcggtggc agcagtagtg ataatcagcc gcaacaaaat 120

aatgcgtcaa acaattctca aataagtcaa caaacaaaca aaacatctga taataaaaca 180

tctgataaca aaacatctga taacaaaaca tctgataaca aaacatctga taacaaaaca 240

tctgataaca aaacatctga taacaaaacg tctgataaca aaacgtctga taacaaaacg 300

tctgataaca aaacgtctga taacaaaacg tctgataaca aaacgtctga taacaaaacg 360

tctgataaca aaacgactga taacaaaaca tctgataaca aaacatctaa caatcaactc 420

caacaggaga gaaacggaac aggtacggca attgtaatat caggaagtaa tgataatgtt 480

aatgcacaaa cctcaacatt aaatcattac aacacaacct ctataaatat agatggagtc 540

gatattatca ttggattgca agatcttgat attcaagatt ggacgcttac gggcttcagg 600

ggaagaaaac ttgaagtatg ttgcggtcgc tattcggata tccgctttgg tgtgagtgat 660

tctttaaatg aaagtagcaa tggctatatg ttctacaatg gaaatccaac tcaaaatatg 720

ccaacatcag gtaccgcaac ttattccggt gatgcgatta tttctgcaga aaacatttat 780

ggactagatc caaaagacta ctaccgtggc tcatctaaat ttaatgtcaa ttttggaaat 840

aaaaccttag aaggttcact cagtatccca aatgggaatc gccaacctgt aaaagtagaa 900

attaatgcca aaatttcaag taatgcattt acaggtacaa caaattcaac cacactacag 960

gatggtcaag tagaaggtaa attctatggc agtaatgcaa aagagatggc cggtcttgca 1020

caaggtaacg ataaatcttg gggtgccgct tttggtgcag caaaacaaca ataa 1074

<210> 1000

<211> 364

<212> PRT

<213> P. pneumotropica SLP 2a

<400> 1000

Met Asn Cys Thr Arg Tyr Leu Met Glu Leu Thr Lys Ile Ser Leu Thr

1 5 10 15

Arg Phe Gly Leu Thr Ala Leu Ala Ala Leu Ile Val Ser Ala Cys Gly

20 25 30

Ser Ser Gly Gly Gly Ser Ser Ser Asp Asn Gln Pro Gln Gln Asn Asn

35 40 45

Ala Ser Asn Asn Ser Gln Ile Ser Gln Gln Thr Asn Lys Thr Ser Asp

50 55 60

Asn Lys Thr Ser Asp Asn Lys Thr Ser Asp Asn Lys Thr Ser Asp Asn

65 70 75 80

Lys Thr Ser Asp Asn Lys Thr Ser Asp Asn Lys Thr Ser Asp Asn Lys

85 90 95

Thr Ser Asp Asn Lys Thr Ser Asp Asn Lys Thr Ser Asp Asn Lys Thr

100 105 110

Ser Asp Asn Lys Thr Ser Asp Asn Lys Thr Ser Asp Asn Lys Thr Ser

115 120 125

Asp Asn Lys Thr Thr Asp Asn Lys Thr Ser Asp Asn Lys Thr Ser Asn

130 135 140

Asn Gln Leu Gln Gln Glu Arg Asn Gly Thr Gly Thr Ala Ile Val Ile

145 150 155 160

Ser Gly Ser Asn Asp Asn Val Asn Ala Gln Thr Ser Thr Leu Asn His

165 170 175

Tyr Asn Thr Thr Ser Ile Asn Ile Asp Gly Val Asp Ile Ile Ile Gly

180 185 190

Leu Gln Asp Leu Asp Ile Gln Asp Trp Thr Leu Thr Gly Phe Arg Gly

195 200 205

Arg Lys Leu Glu Val Cys Cys Gly Arg Tyr Ser Asp Ile Arg Phe Gly

210 215 220

Val Ser Asp Ser Leu Asn Glu Ser Ser Asn Gly Tyr Met Phe Tyr Asn

225 230 235 240

Gly Asn Pro Thr Gln Asn Met Pro Thr Ser Gly Thr Ala Thr Tyr Ser

245 250 255

Gly Asp Ala Ile Ile Ser Ala Glu Asn Ile Tyr Gly Leu Asp Pro Lys

260 265 270

Asp Tyr Tyr Arg Gly Ser Ser Lys Phe Asn Val Asn Phe Gly Asn Lys

275 280 285

Thr Leu Glu Gly Ser Leu Ser Ile Pro Asn Gly Asn Arg Gln Pro Val

290 295 300

Lys Val Glu Ile Asn Ala Lys Ile Ser Ser Asn Ala Phe Thr Gly Thr

305 310 315 320

Thr Asn Ser Thr Thr Leu Gln Asp Gly Gln Val Glu Gly Lys Phe Tyr

325 330 335

Gly Ser Asn Ala Lys Glu Met Ala Gly Leu Ala Gln Gly Asn Asp Lys

340 345 350

Ser Trp Gly Ala Ala Phe Gly Ala Ala Lys Gln Gln

355 360

<210> 1001

<211> 747

<212> DNA

<213> P. rettgeri SLP 1a

<400> 1001

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tctgcagcaa tcggttctgg ccaaagccaa cctttcgatg ctaatcagcc ttccgtccgt 120

gttggtgcaa cagaaggaac cggtggtggt catggtggtg ctgcgggtga cccaggtatt 180

ggtgtgcaat ctgtttatgg tggaaaaacc atttctttct caggcttaac tcgaatggca 240

ccaatacagg caggaaatga agcacatgtt atttccatgc ctaatggacc tggttcacat 300

gacaaaatgg gcgtttttaa ctttgccaaa attgcagatg cagaagtcta cttcggcgaa 360

tggtcatcga caggacaagt tagtgacacc acacataccg cttactattc tggcaaggat 420

gtcaccacca atatgcctac agctggcaca gcggaatact ccgttaaagg aataagccaa 480

tacaatggag gcgcactaac cgcagggact ctgacagcca actttggtac taaatcctta 540

gcagggaata ttggtgcaac caatattgat gccaccatta aaaacaatgc cactttcgcc 600

ggggcggcca ctcttaatgg tgaatcaggc tcaacaaatg gacacttctt tggcgatcaa 660

gctaagcata ttgctggtgt cactcaattt gaagatcaca gcaaagatat ggcctttggt 720

ggaagccgtg ggaatatttc ccagtaa 747

<210> 1002

<211> 248

<212> PRT

<213> P. rettgeri SLP 1a

<400> 1002

Met Lys Lys Leu Asn Ile Ile Ala Leu Ala Leu Ala Thr Cys Thr Val
1 5 10 15
Thr Phe Gly Ala Ser Ala Ala Ile Gly Ser Gly Gln Ser Gln Pro Phe
20 25 30
Asp Ala Asn Gln Pro Ser Val Arg Val Gly Ala Thr Glu Gly Thr Gly
35 40 45

Gly Gly His Gly Gly Ala Ala Gly Asp Pro Gly Ile Gly Val Gln Ser
50 55 60
Val Tyr Gly Gly Lys Thr Ile Ser Phe Ser Gly Leu Thr Arg Met Ala
65 70 75 80
Pro Ile Gln Ala Gly Asn Glu Ala His Val Ile Ser Met Pro Asn Gly
85 90 95
Pro Gly Ser His Asp Lys Met Gly Val Phe Asn Phe Ala Lys Ile Ala
100 105 110

Asp Ala Glu Val Tyr Phe Gly Glu Trp Ser Ser Thr Gly Gln Val Ser
115 120 125
Asp Thr Thr His Thr Ala Tyr Tyr Ser Gly Lys Asp Val Thr Thr Asn
130 135 140
Met Pro Thr Ala Gly Thr Ala Glu Tyr Ser Val Lys Gly Ile Ser Gln
145 150 155 160
Tyr Asn Gly Gly Ala Leu Thr Ala Gly Thr Leu Thr Ala Asn Phe Gly
165 170 175

Thr Lys Ser Leu Ala Gly Asn Ile Gly Ala Thr Asn Ile Asp Ala Thr
180 185 190
Ile Lys Asn Asn Ala Thr Phe Ala Gly Ala Ala Thr Leu Asn Gly Glu
195 200 205
Ser Gly Ser Thr Asn Gly His Phe Phe Gly Asp Gln Ala Lys His Ile
210 215 220
Ala Gly Val Thr Gln Phe Glu Asp His Ser Lys Asp Met Ala Phe Gly
225 230 235 240

Gly Ser Arg Gly Asn Ile Ser Gln

245

<210> 1003

<211> 753

<212> DNA

<213> P. sneebia SLP 1a

<400> 1003

atgaaaggat tcaatattat tgccttagtt atagcatctt gcggtatgtc tttagcaaca 60

aacgcaattg ccagtgtagg atcaagtaaa agccaaatag ctaaaaactc tgacttaaga 120

attggtgaaa cagctaaaaa tcaaggcgct cacaaaggtc ctgctggtga acctggtatt 180

ggtgtaaaaa gtattaaaaa tggaaagtta atttcatttg cgggtttaac acgtatggca 240

ccagcaaata ctgacgatgt tcatgtcatt tccatgccaa attcacctaa tgcgcctaaa 300

tcacaccgta atatgggtgt atttaatttt gctcaagttg cagatgcaga agtttacttt 360

ggtgaatggt cacaaacagg tgagataacg gatatatctc atacttctta ctattcaggt 420

aaagatatta caaccaatat gccaacaggc ggtacagcaa catatagcat caaaggcata 480

aatcaatatg caggaggacc tttattacaa gggcatttaa atgctgattt cggtgcaaaa 540

acactaaaag ggaatatcga tgctgtcagt attaatgcaa aaattaaaga taatgcgaca 600

tttagagggt tagctgaaat cggcgaactt caaggtaaag caaaagggca tttctttggt 660

gaccaagcta aacatatttc aggtattact caatttagcg atcacagtaa agacatcgcc 720

tttgggggta gccgtggtga tattcaaaat taa 753

<210> 1004

<211> 250

<212> PRT

<213> P. sneebia SLP 1a

<400> 1004

Met Lys Gly Phe Asn Ile Ile Ala Leu Val Ile Ala Ser Cys Gly Met
1 5 10 15

Ser Leu Ala Thr Asn Ala Ile Ala Ser Val Gly Ser Ser Lys Ser Gln
20 25 30

Ile Ala Lys Asn Ser Asp Leu Arg Ile Gly Glu Thr Ala Lys Asn Gln
35 40 45

Gly Ala His Lys Gly Pro Ala Gly Glu Pro Gly Ile Gly Val Lys Ser
50 55 60

Ile Lys Asn Gly Lys Leu Ile Ser Phe Ala Gly Leu Thr Arg Met Ala
65 70 75 80
Pro Ala Asn Thr Asp Asp Val His Val Ile Ser Met Pro Asn Ser Pro
85 90 95
Asn Ala Pro Lys Ser His Arg Asn Met Gly Val Phe Asn Phe Ala Gln
100 105 110

Val Ala Asp Ala Glu Val Tyr Phe Gly Glu Trp Ser Gln Thr Gly Glu
115 120 125
Ile Thr Asp Ile Ser His Thr Ser Tyr Tyr Ser Gly Lys Asp Ile Thr
130 135 140
Thr Asn Met Pro Thr Gly Gly Thr Ala Thr Tyr Ser Ile Lys Gly Ile
145 150 155 160
Asn Gln Tyr Ala Gly Gly Pro Leu Leu Gln Gly His Leu Asn Ala Asp
165 170 175

Phe Gly Ala Lys Thr Leu Lys Gly Asn Ile Asp Ala Val Ser Ile Asn
180 185 190
Ala Lys Ile Lys Asp Asn Ala Thr Phe Arg Gly Leu Ala Glu Ile Gly
195 200 205
Glu Leu Gln Gly Lys Ala Lys Gly His Phe Phe Gly Asp Gln Ala Lys
210 215 220
His Ile Ser Gly Ile Thr Gln Phe Ser Asp His Ser Lys Asp Ile Ala
225 230 235 240

Phe Gly Gly Ser Arg Gly Asp Ile Gln Asn
245 250

<210> 1005

<211> 747

<212> DNA

<213> Photorhabdus temperata J3 SLP 1a

<400> 1005

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atagctgcgc ctggttctgg acaaacccaa agttttaatc ctgagaatca aagtattaca 120

gtcggtgtaa ctgaaccgcg tggtggtggt catccgaccc caggtgggga gcctggaatt 180

ggagtgcaat ctgttgctag aggtcaaatt accagctttg caagtcttgc tcgttatgtc 240

gaggcggatg cgaatggcat tcataagatt tctgtgcctg gatcgagtag ccataaaggc 300

atgggggtat ttaactttag caaagtggct aatgctgatg tctattttgg tgaatggtca 360

caaaccggtc aggtgcatga tactacgcac accgcctatt actccggtaa agatgttaca 420

accaatttac caactggtgg catagcgacc tatacagtta aagggattaa ccaatatagt 480

ggcagcaatg ctctgcaagg gacattcact gctgatttcg gccagaaaag actttctggt 540

tcaatagcga atagcgcatt gactgttgat attaattcca gaattagagc agatggctca 600

tttgtgggta gggcaaccgc tggaaatgtt gtcggtacaa acaacggcca cttctttggt 660

gataatgcgt cgagtttagc tggggtggct aaatttaatt cggatcatag taaagatacc 720

gcctttggtg ggactaagaa tccatga 747

<210> 1006

<211> 248

<212> PRT

<213> Photorhabdus temperata J3 SLP 1a

<400> 1006

Met Asn Lys Val Lys Val Leu Ile Ala Val Leu Gly Thr Cys Gly Leu
1 5 10 15

Val Thr Gln Ala Ile Ala Ala Pro Gly Ser Gly Gln Thr Gln Ser Phe
20 25 30

Asn Pro Glu Asn Gln Ser Ile Thr Val Gly Val Thr Glu Pro Arg Gly
35 40 45

Gly Gly His Pro Thr Pro Gly Gly Glu Pro Gly Ile Gly Val Gln Ser
50 55 60

Val Ala Arg Gly Gln Ile Thr Ser Phe Ala Ser Leu Ala Arg Tyr Val
65 70 75 80

Glu Ala Asp Ala Asn Gly Ile His Lys Ile Ser Val Pro Gly Ser Ser
85 90 95

Ser His Lys Gly Met Gly Val Phe Asn Phe Ser Lys Val Ala Asn Ala
100 105 110

Asp Val Tyr Phe Gly Glu Trp Ser Gln Thr Gly Gln Val His Asp Thr
115 120 125

Thr His Thr Ala Tyr Tyr Ser Gly Lys Asp Val Thr Thr Asn Leu Pro
130 135 140
Thr Gly Gly Ile Ala Thr Tyr Thr Val Lys Gly Ile Asn Gln Tyr Ser
145 150 155 160
Gly Ser Asn Ala Leu Gln Gly Thr Phe Thr Ala Asp Phe Gly Gln Lys
165 170 175

Arg Leu Ser Gly Ser Ile Ala Asn Ser Ala Leu Thr Val Asp Ile Asn
180 185 190
Ser Arg Ile Arg Ala Asp Gly Ser Phe Val Gly Arg Ala Thr Ala Gly
195 200 205
Asn Val Val Gly Thr Asn Asn Gly His Phe Phe Gly Asp Asn Ala Ser
210 215 220
Ser Leu Ala Gly Val Ala Lys Phe Asn Ser Asp His Ser Lys Asp Thr
225 230 235 240

Ala Phe Gly Gly Thr Lys Asn Pro
245

<210> 1007
<211> 930
<212> DNA
<213> Phyllobacterium sp. YR531 SLP 1a
<400> 1007
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tcttcagaga aaactgtttc cacatcgtca gctggcagcg aacccgtttc cgtacagccc 120
actgtcgcaa aaccagagtc gacaaaatcc gtagcagaat atgaccttaa aggtcatggt 180
tttgtgacag gagctgatgg aaagttggtg gcggtcaatg ttggtgccaa ggtcagcggt 240
ctatcggaaa cagagtctgc tatgtttaaa ggcaatacgc ctctggtaaa gctggcttat 300

agtggtgata agccatttac gggtacaacc acggggacgc ggcgcgacag cggtgaggac 360
tatgggcctt atggcaatga tacccgtttt ctcatgagtg atacatctat caattccaag 420
gatgcgccga cggcatttgg tgtgttccgc gaccaatcca gtaaagacaa gtttaatgca 480
gctgcttatt atggtggcgt gaatgcaacg aatgtgccca cttccggtca ggctagctat 540
cgtggcaagt ttgccggcgg gattaatgag agcggcgttg tgggcggcga gcaaaggcac 600
gtttctggaa agtttaatct cgctgctgac tttggagcag gtaccgtcaa gggcactgtg 660

tccgagctta atgccaccca tcgagatcct ataatagcgg ccggtaacct caatgcaacc 720

gacctgacat tcgacggtac aatagccaag gacaagccaa cctactcagc agataaggtc 780

actttcgagg gcgaaaccct cgcagctaat gttgagggcg gtttctacaa tgccaatgca 840

agcgagacag ctggtattat cagcgccacg accgatgctg aagacacctc aacaataatt 900

ggtacgttcc atggtgaaaa gcaaccgtag 930

<210> 1008

<211> 309

<212> PRT

<213> Phyllobacterium sp. YR531 SLP 1a

<400> 1008

Met Ala Val Lys Leu Leu Phe Val Ala Gly Leu Cys Ala Thr Leu Val
1 5 10 15

Gly Cys Gly His Ser Ser Glu Lys Thr Val Ser Thr Ser Ser Ala Gly
20 25 30

Ser Glu Pro Val Ser Val Gln Pro Thr Val Ala Lys Pro Glu Ser Thr
35 40 45

Lys Ser Val Ala Glu Tyr Asp Leu Lys Gly His Gly Phe Val Thr Gly
50 55 60

Ala Asp Gly Lys Leu Val Ala Val Asn Val Gly Ala Lys Val Ser Gly
65 70 75 80

Leu Ser Glu Thr Glu Ser Ala Met Phe Lys Gly Asn Thr Pro Leu Val
85 90 95

Lys Leu Ala Tyr Ser Gly Asp Lys Pro Phe Thr Gly Thr Thr Thr Gly
100 105 110

Thr Arg Arg Asp Ser Gly Glu Asp Tyr Gly Pro Tyr Gly Asn Asp Thr
115 120 125

Arg Phe Leu Met Ser Asp Thr Ser Ile Asn Ser Lys Asp Ala Pro Thr
130 135 140

Ala Phe Gly Val Phe Arg Asp Gln Ser Ser Lys Asp Lys Phe Asn Ala
145 150 155 160

Ala Ala Tyr Tyr Gly Gly Val Asn Ala Thr Asn Val Pro Thr Ser Gly

165 170 175

Gln Ala Ser Tyr Arg Gly Lys Phe Ala Gly Gly Ile Asn Glu Ser Gly

180 185 190

Val Val Gly Gly Glu Gln Arg His Val Ser Gly Lys Phe Asn Leu Ala

195 200 205

Ala Asp Phe Gly Ala Gly Thr Val Lys Gly Thr Val Ser Glu Leu Asn

210 215 220

Ala Thr His Arg Asp Pro Ile Ile Ala Ala Gly Asn Leu Asn Ala Thr

225 230 235 240

Asp Leu Thr Phe Asp Gly Thr Ile Ala Lys Asp Lys Pro Thr Tyr Ser

245 250 255

Ala Asp Lys Val Thr Phe Glu Gly Glu Thr Leu Ala Ala Asn Val Glu

260 265 270

Gly Gly Phe Tyr Asn Ala Asn Ala Ser Glu Thr Ala Gly Ile Ile Ser

275 280 285

Ala Thr Thr Asp Ala Glu Asp Thr Ser Thr Ile Ile Gly Thr Phe His

290 295 300

Gly Glu Lys Gln Pro

305

<210> 1009

<211> 1449

<212> DNA

<213> Psychrobacter sp. 1501(2011) SLP 1a

<400> 1009

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gatgaaacag accctactga tcctgtagat gcaacagacc ctactgatcc tacggataat 180

gcaggtgatg cagctgaagc atttgatatt tctaaaaaat catctgtagt gggtcaaaat 240

tatatccgtg gcagtagttc tgattttgat aaatcaccag atacaaatgt aaaaggcact 300

gataatggta actctacagt attaggcgct gagacactgc aaaacaaaaa aatgaccaac 360

attgttgttg ctcagtatga cgatgtttct gttactgatg ctgaaggcaa tgctaacaac 420

gttaaatata tcttgggtga aaaaccaaaa gctaccccag atgtaaatgc tctagactct 480

atccaaacta ataatgatgc aagtcatgct agtggaacac tttctccatt tataatggtt 540

actaaagata tagacgataa atttgtatca acaggtcaag agtctaaagt agattctaaa 600
aactctaagt tcactcagac tggaacggca tttgttgctt ctacagacac tgataatgat 660
gcaagagttt acggtaaact ttctaataaa aacaacacct taaacaacag ttcaagatat 720
atttacaatg atacaaacac tgtagattta ggtactaata gtcagtttaa agttacccct 780
attaaactta atcatgttca atatggtcga gttacgggta atttagaagg cgtaacagca 840
gataccatcg ctggtcgcag ctatatccaa gcagatttcg ccaataagaa ctttaatggc 900
aataccactc aaacggatat ctacttctac cgtggcttaa gtcaaactgc cattgctgct 960

atgcctaaat caggtacctt cgagtacgct ggacatgcct taatgtacgg tatcgataat 1020
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gaagcaatag gtaactttgt aaatgcgact tatgatgctg ataacaaaac tgtagacggt 1140
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Val Asp Ala Thr Asp Pro Thr Asp Pro Thr Asp Asn Ala Gly Asp Ala
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Tyr Ile Arg Gly Ser Ser Ser Asp Phe Asp Lys Ser Pro Asp Thr Asn

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Val Lys Gly Thr Asp Asn Gly Asn Ser Thr Val Leu Gly Ala Glu Thr

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Leu Gln Asn Lys Lys Met Thr Asn Ile Val Val Ala Gln Tyr Asp Asp

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Val Ser Val Thr Asp Ala Glu Gly Asn Ala Asn Asn Val Lys Tyr Ile

130 135 140

Leu Gly Glu Lys Pro Lys Ala Thr Pro Asp Val Asn Ala Leu Asp Ser

145 150 155 160

Ile Gln Thr Asn Asn Asp Ala Ser His Ala Ser Gly Thr Leu Ser Pro

165 170 175

Phe Ile Met Val Thr Lys Asp Ile Asp Asp Lys Phe Val Ser Thr Gly

180 185 190

Gln Glu Ser Lys Val Asp Ser Lys Asn Ser Lys Phe Thr Gln Thr Gly

195 200 205

Thr Ala Phe Val Ala Ser Thr Asp Thr Asp Asn Asp Ala Arg Val Tyr

210 215 220

Gly Lys Leu Ser Asn Lys Asn Asn Thr Leu Asn Asn Ser Ser Arg Tyr

225 230 235 240

Ile Tyr Asn Asp Thr Asn Thr Val Asp Leu Gly Thr Asn Ser Gln Phe

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Lys Val Thr Pro Ile Lys Leu Asn His Val Gln Tyr Gly Arg Val Thr

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Gly Asn Leu Glu Gly Val Thr Ala Asp Thr Ile Ala Gly Arg Ser Tyr

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Thr Asp Ile Tyr Phe Tyr Arg Gly Leu Ser Gln Thr Ala Ile Ala Ala

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Met Pro Lys Ser Gly Thr Phe Glu Tyr Ala Gly His Ala Leu Met Tyr
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Ala Thr Tyr Asp Ala Asp Asn Lys Thr Val Asp Gly Ser Ile Tyr Asn
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Tyr Gly His Asn Ala Lys Glu Met Gly Gly Ser Phe Asn Ser Ile Ser
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<213> Psychrobacter sp. PRwf-1 SLP 1a

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Pro Thr Asn Pro Asp Val Ala Ala Gln Ser Asn Leu Thr Gly Val Gln
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Ser Asn Ala Ile Gly Lys Ser Gly Leu Gly Thr Ser Ile Arg Tyr Thr
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Glu Ile Leu Asp Asn Glu Ser Asp Ser Tyr Asn Gln Leu Ala Val Arg
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Ala Asp Gln Val Ala Ser Lys Met Ala Lys Gln Gly Pro Ile Asp Ile

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Gln Leu Thr Asp Leu Asn Asp Ser Asp Leu Glu Asn Gly Phe Lys Gln

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His Ser Gly Phe Thr Glu Val Val Gly Gln Asp Ser Ala Gly Ile Ala

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Ile Asn Val Asp Glu Tyr Arg Leu Ser Asn Val Tyr Val Gln Gly Asn

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His Gln Asp Thr Asn Leu Ser Glu Gly Val Val Gln Tyr Thr Gly Asp

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Ala Thr Tyr Met Glu Asn Leu His Leu Lys Asp Gly Gln Gln Ser Ser

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Pro Val Val Asn Gly Thr Ser Glu Phe Asn Val Asp Phe Val Lys Ala

245 250 255

Leu Leu Glu Gly Thr Leu Ser Phe Gln Asp Gly Asp Tyr Lys Tyr Met

260 265 270

Pro Glu Gly Asn Lys Ile Gly Ile Lys Ala Gly Ile Thr Gly Asn Thr

275 280 285

Phe Lys Gly Asn Asn Asn Gly Ile Asp Thr Ala Gly Ser Phe Tyr Gly

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Phe Gly Ala Ser Lys Thr Thr Lys Thr Leu Asp Pro Val Ala Asn Pro

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            420                 425                 430
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Pro Phe Gly Leu Gly Lys Leu Asp Asn Ala Val Gly Tyr Val Ala Ile

675 680 685

Arg Asp Asp Gln Ser Asp Phe Thr Thr Thr Val Asp Lys Asp Gly Ser

690 695 700

Leu Val Pro Val Asp Asn Arg Lys Gly Asp Asn Phe Lys Ser Phe Asp

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Lys Gly Val Val Arg Ala Asp Met Val Lys Pro Asp Ser Val Leu Lys

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Pro Ile Asp Val Ser Leu Lys Gln Ser Gly Ser Val Lys Val Asp Ala

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Gly Lys Gly Ser Phe Asn Pro Thr Phe Asn Tyr Lys Ser Val Tyr Glu

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Asn Phe Asp Ser Gln Met Gln Val Gly His Val Tyr Gly Asn Phe Asp

770 775 780

Ser Ala Ala Gly Glu Val Ser Arg Ala Thr Asn Val Tyr Val Gln Gly

785 790 795 800

Tyr Leu Thr Ala Thr Glu Ala Met Asp Arg Leu Lys Asp Ile Asn Glu

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<212> PRT

<213> Psychrobacter sp. PRwf-1 SLP 1b

<400> 1014

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Asp Asn Ala Gln Ile Asn Asn Ala Pro Glu Ser Ala Lys Ser Gly Val
        35                  40                  45

Gln Thr Leu Asn Val Asp Val Val Pro Leu Gly Lys Val Phe Lys Thr
    50                  55                  60
Thr Thr Arg Asp Phe Glu Ala Asp Ser Thr Ser Val Val Ala Arg Ala
65                  70                  75                  80
Asp Leu Ala Ser Glu Ser Ala Pro Gly Ala Gly Asp Gly Leu Leu Gly
                85                  90                  95
Gln Val Pro Val Thr Ile Ser Gly Asp Asn Asp Ala Asp Ile Ala Gly
            100                 105                 110

Thr Asn Gly Phe Lys Ala His Glu Asp Thr Ala Glu Val Asp Ala Leu
        115                 120                 125
Gly Asn Lys Leu Pro Leu Thr Tyr Thr Ser Thr Tyr Lys Asp Phe Gly
    130                 135                 140
Asp Asp Met Arg Ile Gly His Ile Asp Gly Lys Ala Val Phe Ser Gly
145                 150                 155                 160
Leu Glu Leu Pro Val Asn Gly Ala Ala Val Ile Gly Asn Ala Thr Lys
                165                 170                 175

Ala Glu Asn Met Pro Thr Glu Gly Thr Val Gly Tyr Thr Gly Asp Ala
            180                 185                 190
Thr His Arg Lys Leu Gly Leu Gly Asn Ala Ile Glu Phe Gly Ser Ser
        195                 200                 205
Val Phe Thr Ala Asp Phe Val Lys Lys Ala Leu Asp Gly Lys Leu Ser
    210                 215                 220
Phe Ala Lys Ala Gly Asp Ile Asn Leu Lys Ala Asn Ile Ser Gly Asn
225                 230                 235                 240

Lys Phe Ser Gly Gly Ala Ala Asp Asn Ala Gly Tyr Ala Thr Glu Gly
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Gly Phe Tyr Gly Gly Asp Ala Gln Tyr Leu Gly Gly Val Tyr Glu Gly

260 265 270

Asn Gly Ala Gln Gly Thr Tyr Gly Ala Lys Ser Asp Lys Gln Thr Ala

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Ala Glu Gln Ala Ala Val Asp Ala Gln Ala Ala Ala Asp Ala Val Gln

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Lys Glu Ile Glu Ala Leu Lys Val Glu Ala Glu Lys Ala Lys Ala Asp

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Ala Val Gln Ala Lys Ala Ala Ala Asp Lys Ala Gln Ala Glu Ala Asp

325 330 335

Lys Ala Lys Glu Lys Ala Glu Asn Ala Gly Gly Ser Asp Ala Leu Lys

340 345 350

Asp Ala Leu Ala Glu Ala Glu Ala Ala Asp Lys Ala Arg Gln Ala Ala

355 360 365

Glu Ala Ala Lys Ala Ala Ala Glu Leu Ala Ala Ser Lys Ala Glu Ala

370 375 380

Ala Lys Lys Ala Ala Glu Asn Ala Leu Ala Ala Glu Lys Ser Ala Ala

385 390 395 400

Glu Lys Ala Val Gly Glu Ala Lys Ala Glu Ala Asp Lys Arg Val Glu

405 410 415

Ala Ala Glu Lys Gln Leu Ala Asp Ala Lys Ala Ala Ala Ala Lys Ala

420 425 430

Lys Ala Asp Ala Asp Lys Ala Lys Ala Asp Ala Asp Ile Ala Val Gln

435 440 445

Asp Ala Lys Asp Arg Ala Asp Lys Ala Glu Ala Glu Ala Val Lys Ala

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Lys Ala Asp Ala Asp Ala Ala Asn Asn Leu Ala Ala Ser Glu Lys Ala

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Lys Ala Glu Ala Ala Gln Lys Glu Ala Glu Thr Ala Lys Ser Glu Leu

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Asp Arg Arg Gln Ala Ala Leu Asp Ala Ala Asn Asp Lys Ala Ala Ala
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Ala Gln Ile Lys Asn Ala Pro Glu Ser Ala Lys Ser Gly Val Gln Thr
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Leu Asn Val Asp Val Val Pro Leu Gly Lys Val Phe Lys Thr Thr Thr
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Glu Leu Pro Leu Thr Tyr Thr Ser Thr Tyr Lys Asp Phe Gly Asp Asp
675 680 685

Met Arg Ile Gly His Ile Asp Gly Lys Ala Val Phe Ser Gly Leu Glu
690 695 700
Leu Pro Val Asn Gly Ala Ala Val Ile Gly Asn Ala Thr Lys Ala Glu
705 710 715 720
Asn Met Pro Thr Glu Gly Thr Val Gly Tyr Thr Gly Asp Ala Thr His
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740 745 750

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900 905 910

Ala Ala Glu Ala Ala Ala Lys Thr Ala Ala Glu Thr Ala Lys Ala Ala
915 920 925

Glu Asn Ala Ala Lys Glu Ala Leu Val Ala Ala Gln Ala Ala Ala Asp
930 935 940

Lys Ala Ile Gly Asp Ala Lys Ala Glu Ala Gln Lys Gln Val Asp Ala
945 950 955 960

Ala Lys Ala Ala Glu Ala Ala Ala Lys Gln Glu Ala Val Thr Ala Gln
965 970 975

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995 1000 1005

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Gln Ala Ala Val Asp Ala Gln Ala Ala Ala Asp Ala Ala Gln Ala

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Gly Asp Asp Met Arg Ile Gly His Ile Asp Gly Lys Ala Val Phe

1790 1795 1800

Ser Gly Leu Glu Leu Pro Val Asn Gly Ala Ala Val Ile Gly Asn

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Ala Thr Lys Ala Glu Asn Met Pro Thr Glu Gly Thr Val Gly Tyr

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Thr Gly Asp Ala Thr His Arg Lys Leu Gly Leu Gly Asn Ala Ile

1835 1840 1845

Glu Phe Gly Ser Ser Val Phe Thr Ala Asp Phe Val Lys Lys Ala

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1865 1870 1875

Lys Ala Asn Ile Ser Gly Asn Lys Phe Ser Gly Gly Ala Ala Asp

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1895 1900 1905

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1940 1945 1950
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Phe Ala Gly Asn Val Asn Gly Ile Asp Thr Ala Gly Gly Phe Tyr

3170 3175 3180

Gly Asp Asp Ala Gln Phe Leu Gly Gly Ile Tyr Gln Asp Ala Ser

3185 3190 3195

Val Thr Gly Gly Lys Gly Asp Leu Pro Gly Thr Gly Thr Arg Phe

3200 3205 3210

Gln Gly Thr Phe Gly Ala Glu Lys Gln Pro Val Lys

3215 3220 3225

<210> 1015

<211> 2259

<212> DNA

<213> Psychrobacter sp. PRwf-1 SLP 2a

<400> 1015

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gaacaacagg cgcaaaaaat cgaagctaat cgtgtggctt tagtagcaaa agctaaaaaa 180

gcaggtctaa cagaggttca agcgaatgct tatgcagaag ctaacaaaga ggccagtgtc 240

aacgatgctg aaagtgcttt aaataaaatt ctagcggata ttgaggcaga gcgtttagag 300

aaaatcgaag cgaatcgtgt agccttagta gcaaaagcta aaaaagcagg tctaacagag 360

gctcaagcga atgcttatgc tcaagctaac aaagaagtca gtaccaaaga tgctgaaagt 420

gctttgaata aaattctagc ggatattgag gcagagcgtt tagagaaaat cgaagcgaat 480

cgtgtagcat tagtagctaa agcgaaaaaa gcaggtctaa cagaggctca agcaaatgct 540

tatgctcaaa ctaacaaaga agtcagtacc aaagatgctg aaagtgcttt gaataaaatt 600

ctagcggata ttgaggcaga gcgtttagag aaaatcgaag cgaatcgtgt agcattagta 660

gctaaagcga aaaaagcagg tctaacagag gctcaagcga acgcttatgc tcaagctaac 720

aaagaagtca gtaccaaaga tgccgaaagc gctctaagca aaattttagc tgatattgca 780

gaagcacagc gtttagagaa gattgaagcg aatcgtgtag cgttagtagc aaaagcgaaa 840

aaagcaggct taacagaggc tcaagcgaac gcttatgctc aagctaacaa agaaggcaat 900

accaaagatg ctgaaagcgc tctaaacaaa attttagctg atattgcaga agcacagcgt 960

ttagagaaga ttgaagcaaa tcgtgtagcg ttagtagcaa aagcgaaaaa agcaggttta 1020

acagaggctc aagcaaatgc ttatgctcaa gctaacaaag aagccaatac caaagatgct 1080

gaaagtgctt taaataaaat cctagctgat attacagaag cacagcgttt agagaagatt 1140

gaagcaaatc gtgtagcgtt agtagcaaaa gcgaaaaaag caggtttaac agaggctcaa 1200

gcaaatgctt atgctcaagc taacaaagaa gccaatacca aagatgctga aagtgcttta 1260

aataaaattt tagccgatat tgaggcagag cgtttagaga agatcgaagc gaatcgtgta 1320

gcgttaatag caaaagcgaa aaaagcaggc ttaacagatg ctcaagcgaa cgcctatgct 1380

caagctaata aagaagcgag tactaaagat gctgatagtg ctttaaacaa aattttggct 1440

gatattgcag aaacaaagcg tctagagaaa atcgaagcta accgtgtagc gttagtagca 1500

aaagctaaaa aagcaggttt aacggatgct caagcagagt cctatgcaga agctaacaaa 1560

gaagccagtg ccaaagatgc tgatactgct ttaaacaata ttttggctga gattaaagag 1620

catgaaagac ttgctttaga agctgcagtt tctttagaaa aaggccatta tgataatcca 1680

gcacgctatc ctgaatattt agttacggca catcagttat cttatagtga tagcacactg 1740

aataatgata gaacaatcaa tattgagcat gaagtagttt acaatcagcc ttattctgtt 1800

gttattggga gctactctag ctggacgaaa ggaataggtt cgtatatttt tagctcaggc 1860

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ggaaaggcga attactctgg acttgcattt agtagtgaag aaaatcctat ttttgcttca 1980

acttcgggtt actataaaga agggctatta tcatatgatg tagactttgg aagtcgcaaa 2040

ggctctggaa caattaccgg gttaggggat gtggttgagc tacatgaagg gactatctcc 2100

ggttctggta tatcttcatt ggccactcag tcatataaaa ctggagatta ttcgttaggg 2160

ttctatggta aaaaagctga agaaatcgtt ggtaccattg cgtttgaagg taaagatact 2220

attggttttg gtggtacgcg tggcgaaatc actaaatag 2259

<210> 1016

<211> 752

<212> PRT

<213> Psychrobacter sp. PRwf-1 SLP 2a

<400> 1016

Met Ser Leu Val Asn Leu Ser Lys Leu Ser Phe Val Val Val Leu Gly
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Leu Gly Val Val Ala Cys Ser Ser Gly Gly Ser Ser Ser Ser Phe Gly
20 25 30

Gly Ser Ser Pro Ile Ile Thr Pro Glu Gln Gln Ala Gln Lys Ile Glu
35 40 45

Ala Asn Arg Val Ala Leu Val Ala Lys Ala Lys Lys Ala Gly Leu Thr
50 55 60

Glu Val Gln Ala Asn Ala Tyr Ala Glu Ala Asn Lys Glu Ala Ser Val
65 70 75 80

Asn Asp Ala Glu Ser Ala Leu Asn Lys Ile Leu Ala Asp Ile Glu Ala
85 90 95

Glu Arg Leu Glu Lys Ile Glu Ala Asn Arg Val Ala Leu Val Ala Lys
100 105 110

Ala Lys Lys Ala Gly Leu Thr Glu Ala Gln Ala Asn Ala Tyr Ala Gln
115 120 125

Ala Asn Lys Glu Val Ser Thr Lys Asp Ala Glu Ser Ala Leu Asn Lys
130 135 140

Ile Leu Ala Asp Ile Glu Ala Glu Arg Leu Glu Lys Ile Glu Ala Asn
145 150 155 160

Arg Val Ala Leu Val Ala Lys Ala Lys Lys Ala Gly Leu Thr Glu Ala
165 170 175

Gln Ala Asn Ala Tyr Ala Gln Thr Asn Lys Glu Val Ser Thr Lys Asp
180 185 190

Ala Glu Ser Ala Leu Asn Lys Ile Leu Ala Asp Ile Glu Ala Glu Arg
195 200 205

Leu Glu Lys Ile Glu Ala Asn Arg Val Ala Leu Val Ala Lys Ala Lys
210 215 220
Lys Ala Gly Leu Thr Glu Ala Gln Ala Asn Ala Tyr Ala Gln Ala Asn
225 230 235 240
Lys Glu Val Ser Thr Lys Asp Ala Glu Ser Ala Leu Ser Lys Ile Leu
245 250 255
Ala Asp Ile Ala Glu Ala Gln Arg Leu Glu Lys Ile Glu Ala Asn Arg
260 265 270

Val Ala Leu Val Ala Lys Ala Lys Lys Ala Gly Leu Thr Glu Ala Gln
275 280 285
Ala Asn Ala Tyr Ala Gln Ala Asn Lys Glu Gly Asn Thr Lys Asp Ala
290 295 300
Glu Ser Ala Leu Asn Lys Ile Leu Ala Asp Ile Ala Glu Ala Gln Arg
305 310 315 320
Leu Glu Lys Ile Glu Ala Asn Arg Val Ala Leu Val Ala Lys Ala Lys
325 330 335

Lys Ala Gly Leu Thr Glu Ala Gln Ala Asn Ala Tyr Ala Gln Ala Asn
340 345 350
Lys Glu Ala Asn Thr Lys Asp Ala Glu Ser Ala Leu Asn Lys Ile Leu
355 360 365
Ala Asp Ile Thr Glu Ala Gln Arg Leu Glu Lys Ile Glu Ala Asn Arg
370 375 380
Val Ala Leu Val Ala Lys Ala Lys Lys Ala Gly Leu Thr Glu Ala Gln
385 390 395 400

Ala Asn Ala Tyr Ala Gln Ala Asn Lys Glu Ala Asn Thr Lys Asp Ala
405 410 415
Glu Ser Ala Leu Asn Lys Ile Leu Ala Asp Ile Glu Ala Glu Arg Leu
420 425 430
Glu Lys Ile Glu Ala Asn Arg Val Ala Leu Ile Ala Lys Ala Lys Lys
435 440 445
Ala Gly Leu Thr Asp Ala Gln Ala Asn Ala Tyr Ala Gln Ala Asn Lys

450 455 460

Glu Ala Ser Thr Lys Asp Ala Asp Ser Ala Leu Asn Lys Ile Leu Ala
465 470 475 480
Asp Ile Ala Glu Thr Lys Arg Leu Glu Lys Ile Glu Ala Asn Arg Val
485 490 495
Ala Leu Val Ala Lys Ala Lys Lys Ala Gly Leu Thr Asp Ala Gln Ala
500 505 510
Glu Ser Tyr Ala Glu Ala Asn Lys Glu Ala Ser Ala Lys Asp Ala Asp
515 520 525

Thr Ala Leu Asn Asn Ile Leu Ala Glu Ile Lys Glu His Glu Arg Leu
530 535 540
Ala Leu Glu Ala Ala Val Ser Leu Glu Lys Gly His Tyr Asp Asn Pro
545 550 555 560
Ala Arg Tyr Pro Glu Tyr Leu Val Thr Ala His Gln Leu Ser Tyr Ser
565 570 575
Asp Ser Thr Leu Asn Asn Asp Arg Thr Ile Asn Ile Glu His Glu Val
580 585 590

Val Tyr Asn Gln Pro Tyr Ser Val Val Ile Gly Ser Tyr Ser Ser Trp
595 600 605
Thr Lys Gly Ile Gly Ser Tyr Ile Phe Ser Ser Gly Met Asp Ser Ser
610 615 620
Phe Thr Thr Lys Gly Leu Lys Thr Lys Ala Asp Ala Ile Pro Ser Leu
625 630 635 640
Gly Lys Ala Asn Tyr Ser Gly Leu Ala Phe Ser Ser Glu Glu Asn Pro
645 650 655

Ile Phe Ala Ser Thr Ser Gly Tyr Tyr Lys Glu Gly Leu Leu Ser Tyr
660 665 670
Asp Val Asp Phe Gly Ser Arg Lys Gly Ser Gly Thr Ile Thr Gly Leu
675 680 685
Gly Asp Val Val Glu Leu His Glu Gly Thr Ile Ser Gly Ser Gly Ile
690 695 700

Ser Ser Leu Ala Thr Gln Ser Tyr Lys Thr Gly Asp Tyr Ser Leu Gly
705 710 715 720

Phe Tyr Gly Lys Lys Ala Glu Glu Ile Val Gly Thr Ile Ala Phe Glu
725 730 735
Gly Lys Asp Thr Ile Gly Phe Gly Gly Thr Arg Gly Glu Ile Thr Lys
740 745 750

<210> 1017
<211> 693
<212> DNA
<213> Rhodobacteraceae bacterium PD-2 SLP 1a
<400> 1017
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acgtcgaaca tgccgaccga gatcaacgcc tcctatgccg gacggctgaa ggtggacgtg 240
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tccatcagcc gggtggtcaa tcccgcgatg gaggtggccg gcgtctcggt ccccgagaca 480
cagatcgggg cgctgaccgt caccctcacc ggcgaactga gtcagggcgg caccacggcc 540

gacacgaata tcatgctcgg cgggtcgttc ttcggcgatg ccggtgaagc cgcgcttggg 600
ccggtggtcg gtggttacaa cctgccggac tcggccaatc cggcgatatt cgacggcgcc 660
atcgcaggca cctactacat cgaacaggaa tga 693
<210> 1018
<211> 230
<212> PRT
<213> Rhodobacteraceae bacterium PD-2 SLP 1a
<400> 1018
Met Arg Ile Ala Asn Leu Gly Arg Leu Gly Leu Val Leu Val Leu Gly
1 5 10 15
Thr Ser Leu Ser Gly Cys Leu Gly Ser Ser Ser Gly Gly Gly Gly Gly

20 25 30

Gly Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Ser Phe

35 40 45

Asp Thr Glu Phe Asp Arg Val Thr Ala Lys Ala Pro Thr Ser Asn Met

50 55 60

Pro Thr Glu Ile Asn Ala Ser Tyr Ala Gly Arg Leu Lys Val Asp Val

65 70 75 80

Thr Asp Pro Thr Thr Thr Ile Gly Glu Val Glu Gly Asn Leu Asn Leu

85 90 95

Asp Val Ala Trp Arg Asp Gly Gln Thr Thr Asn Pro Phe Thr Gly Thr

100 105 110

Ala Ser Asp Phe Thr Gly Thr Leu Val Thr Gly Glu Thr Gly Ala Ile

115 120 125

Asp Gly Thr Leu Thr Val Asp Asp Ser Phe Gly Gly Ser Ile Ser Arg

130 135 140

Val Val Asn Pro Ala Met Glu Val Ala Gly Val Ser Val Pro Glu Thr

145 150 155 160

Gln Ile Gly Ala Leu Thr Val Thr Leu Thr Gly Glu Leu Ser Gln Gly

165 170 175

Gly Thr Thr Ala Asp Thr Asn Ile Met Leu Gly Gly Ser Phe Phe Gly

180 185 190

Asp Ala Gly Glu Ala Ala Leu Gly Pro Val Val Gly Gly Tyr Asn Leu

195 200 205

Pro Asp Ser Ala Asn Pro Ala Ile Phe Asp Gly Ala Ile Ala Gly Thr

210 215 220

Tyr Tyr Ile Glu Gln Glu

225 230

<210> 1019

<211> 1131

<212> DNA

<213> S. bongori SLP 1a

<400> 1019

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tctggtaata atactgttga gttaaatgaa actgtcggta cagcaggaac tcactccgcc 120

agtaacacgg ggatacctgt cgctaatgaa gccacagctc cgtcgtgcgg cccatcaatt 180

gcgtgcggtg gcggaggaaa tagcaataaa gcacccagta caaccacggg tgaaacctcc 240

caggtcgaaa gtatcggtac atcagggacc tccggttcat ctgataataa ttcgggtgag 300

gtaactgaaa cagtcgattc tgtagaaaat aactctactg tcaataccgg aacaccggta 360

attaatgagg ctacactaca ggataaacct gcaatatcaa caccgacgaa caagactcat 420

atttcagagg ctaagtatga cacaggtacg atcctcaccc gtacagtaaa tgatattgac 480

tccgccatga ttcataaaag taatgtagta gacgatcctg atgtctttgc tatcaaaatg 540

aaagacggtg aggtcattgt ggatgtcaaa ccactcaata ccggcgatcc agaagactat 600

cgtaagcttg tatccaaaaa tcttaatatt ctgcgggata agagtggtga agctatcggg 660

ttttacggcc ttgtggaaac gtatacgaat caaaccgatc tgaggactct gacaggtaaa 720

aatagatatg gcagagttga ttatattgtt gccatgaacg gagaagaaaa gaagcttcct 780

tctgtcacag ctgactatat cggtaaactt tactacgatc aggagcaggc tccagcaaaa 840

gaagctgata ttagtcttca ctatgaagaa cgtcagatta gtggaacaat aatagataaa 900

gatcgcccac atttcagcct ggaaattgat acccgaaaac ctcacaaagt ggatgaggat 960

ggcagtttca tggctgcgtt agtgggtagg aatgatcgta cagatgaaaa aatgcacgga 1020

tacattgatg gtaattttta tggaaaggat ggcgaaattg tcgccggttc ggtacgttcc 1080

aaagctgata acagctgggg aggtgtattt gggggagaaa agcaggaata a 1131

<210> 1020

<211> 376

<212> PRT

<213> S. bongori SLP 1a

<400> 1020

Met Ala Thr Asn Glu Thr Ser Gln Val Glu Ser Ile Ser Ala Ser Ala
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Pro Pro Asn Ser Ser Gly Asn Asn Thr Val Glu Leu Asn Glu Thr Val
20 25 30

Gly Thr Ala Gly Thr His Ser Ala Ser Asn Thr Gly Ile Pro Val Ala
35 40 45

Asn Glu Ala Thr Ala Pro Ser Cys Gly Pro Ser Ile Ala Cys Gly Gly

50 55 60

Gly Gly Asn Ser Asn Lys Ala Pro Ser Thr Thr Thr Gly Glu Thr Ser

65 70 75 80

Gln Val Glu Ser Ile Gly Thr Ser Gly Thr Ser Gly Ser Ser Asp Asn

85 90 95

Asn Ser Gly Glu Val Thr Glu Thr Val Asp Ser Val Glu Asn Asn Ser

100 105 110

Thr Val Asn Thr Gly Thr Pro Val Ile Asn Glu Ala Thr Leu Gln Asp

115 120 125

Lys Pro Ala Ile Ser Thr Pro Thr Asn Lys Thr His Ile Ser Glu Ala

130 135 140

Lys Tyr Asp Thr Gly Thr Ile Leu Thr Arg Thr Val Asn Asp Ile Asp

145 150 155 160

Ser Ala Met Ile His Lys Ser Asn Val Val Asp Asp Pro Asp Val Phe

165 170 175

Ala Ile Lys Met Lys Asp Gly Glu Val Ile Val Asp Val Lys Pro Leu

180 185 190

Asn Thr Gly Asp Pro Glu Asp Tyr Arg Lys Leu Val Ser Lys Asn Leu

195 200 205

Asn Ile Leu Arg Asp Lys Ser Gly Glu Ala Ile Gly Phe Tyr Gly Leu

210 215 220

Val Glu Thr Tyr Thr Asn Gln Thr Asp Leu Arg Thr Leu Thr Gly Lys

225 230 235 240

Asn Arg Tyr Gly Arg Val Asp Tyr Ile Val Ala Met Asn Gly Glu Glu

245 250 255

Lys Lys Leu Pro Ser Val Thr Ala Asp Tyr Ile Gly Lys Leu Tyr Tyr

260 265 270

Asp Gln Glu Gln Ala Pro Ala Lys Glu Ala Asp Ile Ser Leu His Tyr

275 280 285

Glu Glu Arg Gln Ile Ser Gly Thr Ile Ile Asp Lys Asp Arg Pro His

290 295 300

Phe Ser Leu Glu Ile Asp Thr Arg Lys Pro His Lys Val Asp Glu Asp

305 310 315 320

Gly Ser Phe Met Ala Ala Leu Val Gly Arg Asn Asp Arg Thr Asp Glu

325 330 335

Lys Met His Gly Tyr Ile Asp Gly Asn Phe Tyr Gly Lys Asp Gly Glu

340 345 350

Ile Val Ala Gly Ser Val Arg Ser Lys Ala Asp Asn Ser Trp Gly Gly

355 360 365

Val Phe Gly Gly Glu Lys Gln Glu

370 375

<210> 1021

<211> 1242

<212> DNA

<213> S. japonicum SLP 1a

<400> 1021

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ggctcgcgcg agcaaattct gctcgcaggc atcattgcgg tggctcaagg taatttgtct 180

ttggctgaag cgggcttccg aaccctccta ttgcgggatc ctcacgacac cagagtccgg 240

ctcgaacttg cacgggtact ttttttgctg caccgatatg cagctgcaga ttatcatttt 300

aggctcagcg ctgcgcgaag cccaaagtct gtgcaacata atatttcact tttccgccgc 360

gcaatacagg cacaacgaac atggcgtgtt tcggtggaag ggggaattgc cccggatacc 420

aacgtgaact cagcaggtcg tgaccgaatt gtcgatttgt tcgggttgcc ctttaacgtg 480

gacaacgatg ctcgcgaaaa atcaggggtc ggtgtttttg caaatgccga tgttgaactt 540

cggttgcggc gctctgaagc agtgggattg tccatccgcg cattcggaaa cgctcgggaa 600

taccgtcgtt cggcttttaa tgatgaggtc gcgggcatcg aaatcggacc acaatttcgg 660

tttggcaacg cgcaagtgac cgttgcggga acaggtctgt ttcggtggta tggccgagag 720

atatactcgc gagctctagg agcagcgcta cgcgttgaac tgcccatctc aacgcaatgg 780

caggtcgatc tgaagcctca attcagatca gtcaattatc tccaaaaccc aagccaaaac 840

gggccttta tgagcttgaa cggtcagatt agccgctccc tcggaagtca tgccttaggg 900

caaatcgatt ttctcgcgtc gcgacagtct gctcgcgctc ctggctacgc ttatcgagaa 960

gcagggctag gtgtgagtgc atttgctgaa cttggaaatg gaattactgt aggaggaagt 1020

atcgaggcag cgcggacggt attcgatgct ccactcttcg gctttgcaaa gacacgccgc 1080

gactggagag ccgcaacaac catttctgtt ctcaatcgga actggatttt gttaggattc 1140

tcgcctgtca cgcggctgag ttttgcacag tcgaaatcta caattagttt ttttgaatat 1200

cgtcgaacac gactggaact tgcattgcag cggccattct aa 1242

<210> 1022

<211> 413

<212> PRT

<213> S. japonicum SLP 1a

<400> 1022

Met Leu Ser Thr Glu Gly Val Ser Ala Ser Gln Met Leu Asp Leu Gly
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Glu His Leu Ala Val Ala Gly Lys Ile Gly Asp Ala Asn Leu Ile Leu
20 25 30

Asp Ala Leu Lys Gln Asn Asp Glu Gly Ser Arg Glu Gln Ile Leu Leu
35 40 45

Ala Gly Ile Ile Ala Val Ala Gln Gly Asn Leu Ser Leu Ala Glu Ala
50 55 60

Gly Phe Arg Thr Leu Leu Leu Arg Asp Pro His Asp Thr Arg Val Arg
65 70 75 80

Leu Glu Leu Ala Arg Val Leu Phe Leu Leu His Arg Tyr Ala Ala Ala
85 90 95

Asp Tyr His Phe Arg Leu Ser Ala Ala Arg Ser Pro Lys Ser Val Gln
100 105 110

His Asn Ile Ser Leu Phe Arg Arg Ala Ile Gln Ala Gln Arg Thr Trp
115 120 125

Arg Val Ser Val Glu Gly Gly Ile Ala Pro Asp Thr Asn Val Asn Ser
130 135 140

Ala Gly Arg Asp Arg Ile Val Asp Leu Phe Gly Leu Pro Phe Asn Val
145 150 155 160

Asp Asn Asp Ala Arg Glu Lys Ser Gly Val Gly Val Phe Ala Asn Ala

165 170 175

Asp Val Glu Leu Arg Leu Arg Arg Ser Glu Ala Val Gly Leu Ser Ile
180 185 190
Arg Ala Phe Gly Asn Ala Arg Glu Tyr Arg Arg Ser Ala Phe Asn Asp
195 200 205
Glu Val Ala Gly Ile Glu Ile Gly Pro Gln Phe Arg Phe Gly Asn Ala
210 215 220
Gln Val Thr Val Ala Gly Thr Gly Leu Phe Arg Trp Tyr Gly Arg Glu
225 230 235 240

Ile Tyr Ser Arg Ala Leu Gly Ala Ala Leu Arg Val Glu Leu Pro Ile
245 250 255
Ser Thr Gln Trp Gln Val Asp Leu Lys Pro Gln Phe Arg Ser Val Asn
260 265 270
Tyr Leu Gln Asn Pro Ser Gln Asn Gly Pro Phe Met Ser Leu Asn Gly
275 280 285
Gln Ile Ser Arg Ser Leu Gly Ser His Ala Leu Gly Gln Ile Asp Phe
290 295 300

Leu Ala Ser Arg Gln Ser Ala Arg Ala Pro Gly Tyr Ala Tyr Arg Glu
305 310 315 320
Ala Gly Leu Gly Val Ser Ala Phe Ala Glu Leu Gly Asn Gly Ile Thr
325 330 335
Val Gly Gly Ser Ile Glu Ala Ala Arg Thr Val Phe Asp Ala Pro Leu
340 345 350
Phe Gly Phe Ala Lys Thr Arg Arg Asp Trp Arg Ala Ala Thr Thr Ile
355 360 365

Ser Val Leu Asn Arg Asn Trp Ile Leu Leu Gly Phe Ser Pro Val Thr
370 375 380
Arg Leu Ser Phe Ala Gln Ser Lys Ser Thr Ile Ser Phe Phe Glu Tyr
385 390 395 400
Arg Arg Thr Arg Leu Glu Leu Ala Leu Gln Arg Pro Phe
405 410

<210> 1023

<211> 1371

<212> DNA

<213> S. lithotrophicus SLP 1a

<400> 1023

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gcggcttttc cggtgacggc atattgtgct gccggtcgtg tggatttcac gatcggcaat 120

gtggaggcga tcgcagcaaa tggcagccgg catccggtct acaaaggcac cgagatcaat 180

tccggcgaga cgatcaacac tgcggcgggt gcgcgagcac aggtgcgttt tgccgacggc 240

ggtttcgttt cgctgcaacc cggtaccgta ttccgggtgg atgaattcaa ctacaagggc 300

aaggcggatg gcgaggaaaa gggtttcttc agcctgctga aaggcgggtt cagggcgatc 360

accggcgtga tcggccatct caacaaggac acttaccggg tcaagacacc ggcggccacc 420

ctcggcatcc gcggtaccgg atacaacatg gcgctgcgtg atgacggcct gttcgtgaac 480

gtcggagaag gagcgatttc gctgaacaat aacggcgggc tgctggtggt cacggccggc 540

aatgcggcct atgtggcgaa cttcaatact gcaccggtgc ccactaccga gcagccgctt 600

acgccgccga acgggttgca ggagccgact ttcacggtgg ctgaccagcg cgacaactcg 660

gggagcctgg ctttgatcag tctgccgtcg gggcctggct atgcgatggc cgatgcgtat 720

acgacaacgg ctgctgcctt cggtaccaat ctgctgaccg gcgtcaccgc ccttttcagt 780

ggcgccagcc agttgaccca atataactgg atcgatgtta acggagcgcc gcaaaccgga 840

tcgcttggcg gagccgcggt ctccttttcc gcgactgacg gcatcatcgg ctgggggcgc 900

tgggtcggca ctacggcagg aaccgcagca ccgaaccctt tgaccggcgt cttcgactac 960

gtgatcggta ttcccaccgc agccatgccg acaacaggca cggcaaccta cagcctgatg 1020

ggctatacca gtccgacagc tacggatgga tcgaccgggt atagtgtgaa tggaactctc 1080

gcggttaatt tcgctgcgac ctcaggacag gtcggcgtga acatgacagt ggcgaacagt 1140

tcaaccaata catacgggat caatggcgca ctgacaataa caccgggcac tgcgactttt 1200

gccggggtca ccaattacac caacctgacc aattgcacag caggatgttc cacgtcagtc 1260

aacgggttct ttgccggagc cagcgcgtcg cgagccgggc tgtcctactc gatcaccaat 1320

aacctcacag ctaatcacat tcagggtgtg gcggctttcg cgaagaatta a 1371

<210> 1024

<211> 456

<212> PRT

<213> S. lithotrophicus SLP 1a

<400> 1024

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Ala Thr Ile Ser Ala Ala Phe Pro Val Thr Ala Tyr Cys Ala Ala Gly
20 25 30

Arg Val Asp Phe Thr Ile Gly Asn Val Glu Ala Ile Ala Ala Asn Gly
35 40 45

Ser Arg His Pro Val Tyr Lys Gly Thr Glu Ile Asn Ser Gly Glu Thr
50 55 60

Ile Asn Thr Ala Ala Gly Ala Arg Ala Gln Val Arg Phe Ala Asp Gly
65 70 75 80

Gly Phe Val Ser Leu Gln Pro Gly Thr Val Phe Arg Val Asp Glu Phe
85 90 95

Asn Tyr Lys Gly Lys Ala Asp Gly Glu Glu Lys Gly Phe Phe Ser Leu
100 105 110

Leu Lys Gly Gly Phe Arg Ala Ile Thr Gly Val Ile Gly His Leu Asn
115 120 125

Lys Asp Thr Tyr Arg Val Lys Thr Pro Ala Ala Thr Leu Gly Ile Arg
130 135 140

Gly Thr Gly Tyr Asn Met Ala Leu Arg Asp Asp Gly Leu Phe Val Asn
145 150 155 160

Val Gly Glu Gly Ala Ile Ser Leu Asn Asn Asn Gly Gly Leu Leu Val
165 170 175

Val Thr Ala Gly Asn Ala Ala Tyr Val Ala Asn Phe Asn Thr Ala Pro
180 185 190

Val Pro Thr Thr Glu Gln Pro Leu Thr Pro Pro Asn Gly Leu Gln Glu
195 200 205

Pro Thr Phe Thr Val Ala Asp Gln Arg Asp Asn Ser Gly Ser Leu Ala
210 215 220

Leu Ile Ser Leu Pro Ser Gly Pro Gly Tyr Ala Met Ala Asp Ala Tyr

225 230 235 240

Thr Thr Thr Ala Ala Ala Phe Gly Thr Asn Leu Leu Thr Gly Val Thr
245 250 255
Ala Leu Phe Ser Gly Ala Ser Gln Leu Thr Gln Tyr Asn Trp Ile Asp
260 265 270
Val Asn Gly Ala Pro Gln Thr Gly Ser Leu Gly Gly Ala Ala Val Ser
275 280 285
Phe Ser Ala Thr Asp Gly Ile Ile Gly Trp Gly Arg Trp Val Gly Thr
290 295 300

Thr Ala Gly Thr Ala Ala Pro Asn Pro Leu Thr Gly Val Phe Asp Tyr
305 310 315 320
Val Ile Gly Ile Pro Thr Ala Ala Met Pro Thr Thr Gly Thr Ala Thr
325 330 335
Tyr Ser Leu Met Gly Tyr Thr Ser Pro Thr Ala Thr Asp Gly Ser Thr
340 345 350
Gly Tyr Ser Val Asn Gly Thr Leu Ala Val Asn Phe Ala Ala Thr Ser
355 360 365

Gly Gln Val Gly Val Asn Met Thr Val Ala Asn Ser Ser Thr Asn Thr
370 375 380
Tyr Gly Ile Asn Gly Ala Leu Thr Ile Thr Pro Gly Thr Ala Thr Phe
385 390 395 400
Ala Gly Val Thr Asn Tyr Thr Asn Leu Thr Asn Cys Thr Ala Gly Cys
405 410 415
Ser Thr Ser Val Asn Gly Phe Phe Ala Gly Ala Ser Ala Ser Arg Ala
420 425 430

Gly Leu Ser Tyr Ser Ile Thr Asn Asn Leu Thr Ala Asn His Ile Gln
435 440 445
Gly Val Ala Ala Phe Ala Lys Asn
450 455

<210> 1025

<211> 921

<212> DNA

<213> S. muelleri SLP 1a

<400> 1025

atggtaaatt taaagctttc agtaatcgct accgcaatgg tttttgcatt aacggcatgt 60

ggtagtagtg gcgatagcag tggtgctggt tttggaagag tgaattttaa ttcaaatagc 120

caatctgctg ccaatagtgc aaccaataat ggtacaacta aaacgtcagg ttttacattg 180

aataaaggca aaaccaccaa tacggcaaat acaagtacca atacagtagg taaaacaacc 240

acgcctaccc cagctaatac agcaaccaca aagccagcag tacaagcaaa tacaaataat 300

ggtttggcat taatcggtta cgatagaaat ggtgtaaatg tgagtccagt tgccatcagc 360

agtgcagatt taaacaaagt aacgattgat ggtactgagg ttactttgtc gcaaccaggt 420

atttcagcag gtacatttac cactatcagc aacaatacaa aagagactat tgccagtggt 480

cgtgccttga gttatagccg tattggtgcg tatcgtgatt ttaatgatgc acaaggcaga 540

aacccatctt ttacttttgt agtaggtagc gttacaccaa ctgcacaagt gccaacttct 600

ggtcaagcaa cgtatgatgg tttatcttta gtgagcattg taggaggtgg agcattttca 660

aaagggacat ctaatttcaa tgtggatttt ggtagcaaaa aaattatggg tacagtgaaa 720

gcgaattcgg atgtgactat tgtgccatta gaaggtaaaa ttgatggcgc atctttcagt 780

ggtaccaaag atggtgttaa tatgagtggt cagttctatg gtccgcaagc ggctgagttg 840

ggtggtgtat tcaatggtac acaacaaaat ggtagtacat ttaatgagtt aatgggtgtg 900

tttggtgcca caaaacaata a 921

<210> 1026

<211> 306

<212> PRT

<213> S. muelleri SLP 1a

<400> 1026

Met Val Asn Leu Lys Leu Ser Val Ile Ala Thr Ala Met Val Phe Ala
1 5 10 15

Leu Thr Ala Cys Gly Ser Ser Gly Asp Ser Ser Gly Ala Gly Phe Gly
20 25 30

Arg Val Asn Phe Asn Ser Asn Ser Gln Ser Ala Ala Asn Ser Ala Thr
35 40 45

Asn Asn Gly Thr Thr Lys Thr Ser Gly Phe Thr Leu Asn Lys Gly Lys

50 55 60

Thr Thr Asn Thr Ala Asn Thr Ser Thr Asn Thr Val Gly Lys Thr Thr
65 70 75 80
Thr Pro Thr Pro Ala Asn Thr Ala Thr Thr Lys Pro Ala Val Gln Ala
85 90 95
Asn Thr Asn Asn Gly Leu Ala Leu Ile Gly Tyr Asp Arg Asn Gly Val
100 105 110
Asn Val Ser Pro Val Ala Ile Ser Ser Ala Asp Leu Asn Lys Val Thr
115 120 125

Ile Asp Gly Thr Glu Val Thr Leu Ser Gln Pro Gly Ile Ser Ala Gly
130 135 140
Thr Phe Thr Thr Ile Ser Asn Asn Thr Lys Glu Thr Ile Ala Ser Gly
145 150 155 160
Arg Ala Leu Ser Tyr Ser Arg Ile Gly Ala Tyr Arg Asp Phe Asn Asp
165 170 175
Ala Gln Gly Arg Asn Pro Ser Phe Thr Phe Val Val Gly Ser Val Thr
180 185 190

Pro Thr Ala Gln Val Pro Thr Ser Gly Gln Ala Thr Tyr Asp Gly Leu
195 200 205
Ser Leu Val Ser Ile Val Gly Gly Gly Ala Phe Ser Lys Gly Thr Ser
210 215 220
Asn Phe Asn Val Asp Phe Gly Ser Lys Lys Ile Met Gly Thr Val Lys
225 230 235 240
Ala Asn Ser Asp Val Thr Ile Val Pro Leu Glu Gly Lys Ile Asp Gly
245 250 255

Ala Ser Phe Ser Gly Thr Lys Asp Gly Val Asn Met Ser Gly Gln Phe
260 265 270
Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Val Phe Asn Gly Thr Gln
275 280 285
Gln Asn Gly Ser Thr Phe Asn Glu Leu Met Gly Val Phe Gly Ala Thr
290 295 300

Lys Gln

305

<210> 1027

<211> 543

<212> DNA

<213> S. pontiacus SLP 1a

<400> 1027

atgcgcatct ggccggcagg cgggagcgcc acggacttca gctatgtatc gttcgccgaa 60

ttctatgcca gcgcgcctgc aggttccagc ctggaaaccg tggcctatgg cagcatggcg 120

atcatccagc cgacgaggcc cggtgaagtg ccgatgaccg gaagcgccag ctatcatggc 180

tttcttgtcg gctttttcgg cggagatccc ggcggaagct gggtggaagg cagaagcagg 240

ctggacttcg actttgccaa gggatcgctg tccggcgaac tgaccgccag aatggtctgc 300

atgatgggct gcgcctacga tgaccagctc tataccctgg ccgacacaca cttcgcgcac 360

ggcgcgaccg aattcggcgg tagcctcacg acagcgggcg ccccttcggc agggacgttt 420

gcgggcatgt tcgccggccc caatgccagc gagctggccg cccagttcca gcttcccttc 480

ttcaatcagg atttccgcaa gtgggtgccg gtatcgggcg tcatcatcgg caagggcccg 540

taa 543

<210> 1028

<211> 334

<212> PRT

<213> S. pontiacus SLP 1a

<400> 1028

Met Lys Leu Tyr Met Gln Leu Met Thr Thr Thr Ala Leu Ala Leu Ser

1 5 10 15

Val Ala Ala Cys Gly Ser Ser Asn Gly Val Asp Lys Val Ile Asp Val

20 25 30

Thr Asp Ile Thr Glu Glu Ala Gln Ala Lys Arg Thr Phe Ala Thr Asp

35 40 45

Glu Asp Gly Asp Pro Val Asp Ala Gly Ala Ala Ile Ala Ser Gly Lys

50 55 60

Thr Leu Thr Ala Arg Ala Val Gly Val Ala Leu Gln Asn Leu Asn Tyr

65 70 75 80

His Thr Gly Glu Thr Ser Thr Thr Thr Asp Val Thr Ala Ser Ile Lys
85 90 95
Arg Asn Asp Asp Gly Ala Leu Thr Val Thr Ile Asp Gly Glu Glu Leu

100 105 110
Ala Phe Thr Pro Ala Asp Val Asn Gly Glu Gly Asp Gly Tyr Glu Val
115 120 125
Glu Val Asp Gly Lys Phe Ala Gly Val Tyr Asn Phe Asn Gly Pro Val
130 135 140
Glu Glu Leu Leu Thr Ala Gly Asn Gly Phe Ala Gln Val Val Ser Ile
145 150 155 160
Phe Arg Thr Ser Glu Asn Ala Glu Gly His Val Ser Gly Asp Asn Thr

165 170 175
Phe Ala Ile Phe Gly Thr Glu Thr Ala Asp Glu Asp Leu Lys Asp Leu
180 185 190
Pro Lys Ala Glu Tyr Thr Gly Arg Ser Arg Ile Asn Val Val Pro Asn
195 200 205
Ser Gly Phe Glu Ser Asn Ser Glu Ser Arg Tyr Lys Val Arg Ser Glu
210 215 220
Ile Ala Met Thr Ala Asp Phe Gly Ala Gly Glu Ile Trp Gly Thr Ile

225 230 235 240
Gly Asn Thr Thr Ile Glu Asp Pro Glu Asp Gly Glu Arg Asp Ala Val
245 250 255
Glu Gly Thr Ile Ala Met Asp Lys Thr Thr Phe Asp Asn Asn Gly Phe
260 265 270
Ala Gly Thr Leu Thr Ala Asp Ala Asp Phe Ile Ser Asp Ile Asp Val
275 280 285
Asn Ser Ala Glu Gly Thr Tyr Ser Gly Ala Phe Tyr Gly Pro Asn Ala

290 295 300
Glu Gln Val Ala Gly Ala Leu Thr Phe Gly Ile Gly Ala Asp Asp Gly
305 310 315 320
Ser Leu Asn Gly Asn Gly Tyr Phe Ser Ala Asp Lys Val Asp

325 330

<210> 1029

<211> 705

<212> DNA

<213> S. pontiacus SLP 2a

<400> 1029

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ggttgcaatg gaagcagctc cgccggcggg cttgttggcg gcggcgcagg cggcgggcag 120

gattttgaaa cagcctttaa cgctgtcagt caaaaggccc ccacttcgga tatgcccacg 180

tcgctgaaag ccagctacga aggtcagatg aaggtcggcg tgaacagcgg atcggcccag 240

attttcggca ccgatatgga tgcgaatagc gcggaaatca ttggcgatct ggcagtcgat 300

gtggattgga ccgacgggca gaccaccaat ccgttcaccg gaaccgcctc caacatcgtc 360

gcgacagagg cgggcacctc gaactccgtc aaactggacg ggacgctgac ggtcgatcaa 420

ggtttgccag cctcactcag ccgcaccacc attccggcgc aggtcgtcgc gggcgtcaat 480

atccccgagc agaacaccgg cgcgatgctg ttccatatgt ccggtcggct tagcagtggc 540

gagaacgaag gggacgccac cttgcagttc ggcggcaact tcatgggacc gggtgcagaa 600

tcgatgcttg gaccggtatc tggcggtatc aacgatgtga acaatccctc gccgcagatt 660

ttcgatgcgg gcgtcggtgg tacattctac gccaacaaga aatag 705

<210> 1030

<211> 234

<212> PRT

<213> S. pontiacus SLP 2a

<400> 1030

Met Lys His Ala Arg Leu Ser Ile Val Ile Ala Ser Leu Gly Ala Ala

1 5 10 15

Thr Val Leu Ser Gly Cys Asn Gly Ser Ser Ser Ala Gly Gly Leu Val

20 25 30

Gly Gly Gly Ala Gly Gly Gly Gln Asp Phe Glu Thr Ala Phe Asn Ala

35 40 45

Val Ser Gln Lys Ala Pro Thr Ser Asp Met Pro Thr Ser Leu Lys Ala

50 55 60

Ser Tyr Glu Gly Gln Met Lys Val Gly Val Asn Ser Gly Ser Ala Gln

65 70 75 80

Ile Phe Gly Thr Asp Met Asp Ala Asn Ser Ala Glu Ile Ile Gly Asp

85 90 95

Leu Ala Val Asp Val Asp Trp Thr Asp Gly Gln Thr Thr Asn Pro Phe

100 105 110

Thr Gly Thr Ala Ser Asn Ile Val Ala Thr Glu Ala Gly Thr Ser Asn

115 120 125

Ser Val Lys Leu Asp Gly Thr Leu Thr Val Asp Gln Gly Leu Pro Ala

130 135 140

Ser Leu Ser Arg Thr Thr Ile Pro Ala Gln Val Val Ala Gly Val Asn

145 150 155 160

Ile Pro Glu Gln Asn Thr Gly Ala Met Leu Phe His Met Ser Gly Arg

165 170 175

Leu Ser Ser Gly Glu Asn Glu Gly Asp Ala Thr Leu Gln Phe Gly Gly

180 185 190

Asn Phe Met Gly Pro Gly Ala Glu Ser Met Leu Gly Pro Val Ser Gly

195 200 205

Gly Ile Asn Asp Val Asn Asn Pro Ser Pro Gln Ile Phe Asp Ala Gly

210 215 220

Val Gly Gly Thr Phe Tyr Ala Asn Lys Lys

225 230

<210> 1031

<211> 696

<212> DNA

<213> S. stellata SLP 1a

<400> 1031

atgcgcattg caaatcttgg gcggcttagc ctcgccctgg tgcttggcac atcgctgtcc 60

ggctgcctgc agggcagcag tggtggcgga gctggcggtg gtggaactgg cggtggcggc 120

ggaggaggcg gtggcagctc aagcttcgac accgagttcg atcgcgtcac ggccaaggcg 180

ccgacgtcga acatgccgac cgcgatcaac gcatcctacg ccggacggct taaggttgac 240

gtgaccgatc cttccagcac catcggtgag gtcgagggcg atctggacct cgatgtggcc 300

tggaatgatg gacaggccac caacccgttc accgggaccg cgtcgaattt caccggcacg 360

ctggtgaccg gccaaacagg caccattgac ggcactctga ccgtagacaa cagcttcggc 420

gggtccatca gccgggtggt caatccctcg atgaacgtgg gcggggtcac catccccgag 480

acacagatcg gggcgctgag cgtcactctc accggtgagt tgagccaggg cgggaccgct 540

gccgacacgc agataacgct cggcgggtcg ttcttcggcg atgccggtga ggccgcgctt 600

gggccggtgg tcggcggtta caacctgccg aactcgggca atccggcggt gttcgacggt 660

gccatcgcag gcacctatta tatcgaacaa aaatga 696

<210> 1032

<211> 231

<212> PRT

<213> S. stellata SLP 1a

<400> 1032

Met Arg Ile Ala Asn Leu Gly Arg Leu Ser Leu Ala Leu Val Leu Gly
1 5 10 15

Thr Ser Leu Ser Gly Cys Leu Gln Gly Ser Ser Gly Gly Gly Ala Gly
20 25 30

Gly Gly Gly Thr Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Ser Ser
35 40 45

Phe Asp Thr Glu Phe Asp Arg Val Thr Ala Lys Ala Pro Thr Ser Asn
50 55 60

Met Pro Thr Ala Ile Asn Ala Ser Tyr Ala Gly Arg Leu Lys Val Asp
65 70 75 80

Val Thr Asp Pro Ser Ser Thr Ile Gly Glu Val Glu Gly Asp Leu Asp
85 90 95

Leu Asp Val Ala Trp Asn Asp Gly Gln Ala Thr Asn Pro Phe Thr Gly
100 105 110

Thr Ala Ser Asn Phe Thr Gly Thr Leu Val Thr Gly Gln Thr Gly Thr
115 120 125

Ile Asp Gly Thr Leu Thr Val Asp Asn Ser Phe Gly Gly Ser Ile Ser
130 135 140

Arg Val Val Asn Pro Ser Met Asn Val Gly Gly Val Thr Ile Pro Glu
145 150 155 160

Thr Gln Ile Gly Ala Leu Ser Val Thr Leu Thr Gly Glu Leu Ser Gln
165 170 175

Gly Gly Thr Ala Ala Asp Thr Gln Ile Thr Leu Gly Gly Ser Phe Phe
180 185 190
Gly Asp Ala Gly Glu Ala Ala Leu Gly Pro Val Val Gly Gly Tyr Asn
195 200 205
Leu Pro Asn Ser Gly Asn Pro Ala Val Phe Asp Gly Ala Ile Ala Gly
210 215 220
Thr Tyr Tyr Ile Glu Gln Lys
225 230

<210> 1033

<211> 1863

<212> DNA

<213> S. yanoikuyae SLP 2a

<400> 1033

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tgtggcgggg gtggtggcgt gaacagtacg cccactccca cgccagcacc tactccgact 120

ccgacgccca cacccacacc cacaccgagc gccaatgcgg atctggtcgc accgcttgtt 180

tcggaaactt tcgtcaataa tgcggtggct ggcacagcca gcttcccggc aaatggagca 240

ggtacggcga cagccgccaa gtctgcgctg acgttccgtt atgatgcgtc gagcaatcgc 300

tattcggtgt cggcggccga ccgttcgcag aattttgctg tatcgagcag ggatgctgcg 360

ctcagcaatg cggacctcga cgtttatgtc gataaatcgg gtaaccgcac agacacgttg 420

gccgttcgta agaacgcagc cgagaagggg acgcctgaca gcccgcaatt ccaatatgcc 480

ggcgctgccg tgtggcaacg caccacagca aatagcagcg cagtgagcgc cacagcggat 540

gcctttacct atggcgtgga aacaaaggct tcggccatgc cgctcggcgg caccgcaact 600

tttgtggcat cgctgaacgg cattgccacc tatgccgaca cggcactggg cctcaaggga 660

ggcggcactc tcaacatcga tttctcctct ggcggcctga ccggcaatgg tgatttttcc 720

acctatggaa cggatggcgg aaaggtggac accagcaact ggtatgccag cgccaggatc 780

gcgtccggat ccaatgcctt cagcggtagt ttcacgatcg gggcgcccag caacccggcc 840

gggtcgttcg atggacgctt ttatggcccc aaccatgagg agcttggtgc ggcctggagc 900

tggaacacgc cgacaggagg gcgcgcctat ttgggtacgc tgctggggcg cgacctggca 960

acattgccgg ccaatggcgg gctggatgcg ctgcgcgtca atgaggcgtt tgagaccacg 1020

ggcatgcagg cgcaatatat cctgacctcg cccaccaaca gctatatgca gcgcatcacc 1080

agcctgacga caccgcccgt caccatgcgc tattcggaag atagcgatag tctggtggtc 1140

aatcagtttg cggtggtcag cgatgtcgcc ttgaccgacg cgatcaggga tgctgcggcc 1200

agcaatgcgt ccttcgacgt ctatcggacc acgaagacgg aaacatttgg tggggtcgcc 1260

agcgaatatc cgatcgagat ccgtgtcctg aaaccgggcg ccggaaaccc gacgattgcg 1320

ctgacctata ccagctttgc aacctggtcg gttggtcccg ttcccagtct gtatcagtcc 1380

gacgtcaacg aaactgtgct ggcctatggc cgcaagacgc cggatggcgc gatgccgcgg 1440

tctggttcgg ccagctatgc ggcgatcatc caggggatca cgactgtgcc cgtaagtgcc 1500

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gcggcccgaa tgtcgggcgt gatgcgcccc gtggcaaccg atcgcgatag cgggcagcgc 1620

tacgaactgg gggcgcagaa ttttgccgga agttccattg tcggctcatc cagcttttcg 1680

ggacagttcg aaaaggaaat gaccattcgt ggcattggca ccactaatgg cagcatcaac 1740

ggccagttta ccggcccgca ggcgcaggaa ttctttgcgc gctggaatta tggcatgatc 1800

gatccggtca atggcggcac gctcaacatg ggcggcgtca tggtcggcaa gcagacgcag 1860

tag 1863

<210> 1034

<211> 620

<212> PRT

<213> S. yanoikuyae SLP 2a

<400> 1034

Met Thr Lys Gln Ala Leu Arg Gly Ala Ser Ala Ile Ala Phe Met Leu
1 5 10 15

Ala Leu Ser Ala Cys Gly Gly Gly Gly Gly Val Asn Ser Thr Pro Thr
20 25 30

Pro Thr Pro Ala Pro Thr Pro Thr Pro Thr Pro Thr Pro Thr Pro Thr
35 40 45

Pro Ser Ala Asn Ala Asp Leu Val Ala Pro Leu Val Ser Glu Thr Phe
50 55 60

Val Asn Asn Ala Val Ala Gly Thr Ala Ser Phe Pro Ala Asn Gly Ala
65 70 75 80

Gly Thr Ala Thr Ala Ala Lys Ser Ala Leu Thr Phe Arg Tyr Asp Ala
85 90 95
Ser Ser Asn Arg Tyr Ser Val Ser Ala Ala Asp Arg Ser Gln Asn Phe
100 105 110
Ala Val Ser Ser Arg Asp Ala Ala Leu Ser Asn Ala Asp Leu Asp Val
115 120 125
Tyr Val Asp Lys Ser Gly Asn Arg Thr Asp Thr Leu Ala Val Arg Lys
130 135 140

Asn Ala Ala Glu Lys Gly Thr Pro Asp Ser Pro Gln Phe Gln Tyr Ala
145 150 155 160
Gly Ala Ala Val Trp Gln Arg Thr Thr Ala Asn Ser Ser Ala Val Ser
165 170 175
Ala Thr Ala Asp Ala Phe Thr Tyr Gly Val Glu Thr Lys Ala Ser Ala
180 185 190
Met Pro Leu Gly Gly Thr Ala Thr Phe Val Ala Ser Leu Asn Gly Ile
195 200 205

Ala Thr Tyr Ala Asp Thr Ala Leu Gly Leu Lys Gly Gly Gly Thr Leu
210 215 220
Asn Ile Asp Phe Ser Ser Gly Gly Leu Thr Gly Asn Gly Asp Phe Ser
225 230 235 240
Thr Tyr Gly Thr Asp Gly Gly Lys Val Asp Thr Ser Asn Trp Tyr Ala
245 250 255
Ser Ala Arg Ile Ala Ser Gly Ser Asn Ala Phe Ser Gly Ser Phe Thr
260 265 270

Ile Gly Ala Pro Ser Asn Pro Ala Gly Ser Phe Asp Gly Arg Phe Tyr
275 280 285
Gly Pro Asn His Glu Glu Leu Gly Ala Ala Trp Ser Trp Asn Thr Pro
290 295 300
Thr Gly Gly Arg Ala Tyr Leu Gly Thr Leu Leu Gly Arg Asp Leu Ala
305 310 315 320
Thr Leu Pro Ala Asn Gly Gly Leu Asp Ala Leu Arg Val Asn Glu Ala

325 330 335

Phe Glu Thr Thr Gly Met Gln Ala Gln Tyr Ile Leu Thr Ser Pro Thr
340 345 350
Asn Ser Tyr Met Gln Arg Ile Thr Ser Leu Thr Thr Pro Pro Val Thr
355 360 365
Met Arg Tyr Ser Glu Asp Ser Asp Ser Leu Val Val Asn Gln Phe Ala
370 375 380
Val Val Ser Asp Val Ala Leu Thr Asp Ala Ile Arg Asp Ala Ala Ala
385 390 395 400

Ser Asn Ala Ser Phe Asp Val Tyr Arg Thr Thr Lys Thr Glu Thr Phe
405 410 415
Gly Gly Val Ala Ser Glu Tyr Pro Ile Glu Ile Arg Val Leu Lys Pro
420 425 430
Gly Ala Gly Asn Pro Thr Ile Ala Leu Thr Tyr Thr Ser Phe Ala Thr
435 440 445
Trp Ser Val Gly Pro Val Pro Ser Leu Tyr Gln Ser Asp Val Asn Glu
450 455 460

Thr Val Leu Ala Tyr Gly Arg Lys Thr Pro Asp Gly Ala Met Pro Arg
465 470 475 480
Ser Gly Ser Ala Ser Tyr Ala Ala Ile Ile Gln Gly Ile Thr Thr Val
485 490 495
Pro Val Ser Ala Ser Ala Thr Gln Arg Pro Tyr Val Ile Thr Gly Asp
500 505 510
Ala Ser Leu Ser Tyr Asp Phe Ala Ala Ala Arg Met Ser Gly Val Met
515 520 525

Arg Pro Val Ala Thr Asp Arg Asp Ser Gly Gln Arg Tyr Glu Leu Gly
530 535 540
Ala Gln Asn Phe Ala Gly Ser Ser Ile Val Gly Ser Ser Ser Phe Ser
545 550 555 560
Gly Gln Phe Glu Lys Glu Met Thr Ile Arg Gly Ile Gly Thr Thr Asn
565 570 575

Gly Ser Ile Asn Gly Gln Phe Thr Gly Pro Gln Ala Gln Glu Phe Phe
580 585 590

Ala Arg Trp Asn Tyr Gly Met Ile Asp Pro Val Asn Gly Gly Thr Leu
595 600 605

Asn Met Gly Gly Val Met Val Gly Lys Gln Thr Gln
610 615 620

<210> 1035

<211> 1284

<212> DNA

<213> Salmonella enterica subsp diarizonae SLP 1a

<400> 1035

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gcctgtagct ctacgccacc cgatcaaatc ccttccgatc aaaccgcgcc tggcaccgcc 120

tcgcgcccga ttctgtcggc aaatgaagcg aaaaacttcg ttgcggcgca ctatttcgcc 180

tctctgacgc cgaataccgc gccgtggtcg ccgtcaccga ttactttgcc cgcgcagcct 240

gactttgtgg tcggtccggc aggcacgcct ggcgttacgc acacctcgat tcaggccgcc 300

gtcgatgcgg caatggttaa acgcacgaat aaacgccagt acatcgctat tatgccgggc 360

gcctatcagg gtaccgtcta cattcccgcc gcgccgggaa gtctgacgct gtatgggaca 420

ggtgaaaaac cgatcgatgt aaaaatcggt atggcgattg atggtgaaat gagcatcgcc 480

gactggcgcc gcgcggtgaa tcccggaggg aaatatatgc cgggtaaacc cgcgtggtat 540

atgttcgata actgccaaag caaacgtgca gcaacgatcg gcgtgatgtg ttctgctgcg 600

ttctggtcgc aaaataacgg actgcagcta caaaacctga ccatcgaaaa cacgttgggc 660

gacagcgtcg atgccggaaa ccatcctgcg gtggcgctgc gtaccgatgg cgataaggtc 720

cagattaaca aggtcaatat ccttggccgt cagaatacct tctttgtgac caatagtggc 780

gtgcagaacc gtctgcaaac cgatcgccag ccgcgtacgc tggtgacgaa cagctatatt 840

gaaggcgatg tagatatggt ttccggacgc ggcgccgtgg tgttcgataa cactaacttc 900

caggtcgtca actcccgcac gcaacaggaa gcctacgtgt tcgcccctgc gacgctatcc 960

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gacagtgtga ttaacgaggg ctttaacatc gccaaaccgt gggccgacgc ggtcatctcg 1140

aaacgtccgt ttgccggaaa tacgggaacc gtggatgaca aaggcgaggt gcagcgtaat 1200

ctgaacgaca ctaactacaa ccgcatgtgg gaatacaaca accgcgggcc aggcagtaaa 1260

gtggtaacgg agcctaagca gtaa 1284

<210> 1036

<211> 427

<212> PRT

<213> Salmonella enterica subsp diarizonae SLP 1a

<400> 1036

Met Asn Thr Leu Ser Val Ser Arg Leu Ala Leu Ala Leu Ala Phe Gly

1 5 10 15

Val Thr Leu Ser Ala Cys Ser Ser Thr Pro Pro Asp Gln Ile Pro Ser

20 25 30

Asp Gln Thr Ala Pro Gly Thr Ala Ser Arg Pro Ile Leu Ser Ala Asn

35 40 45

Glu Ala Lys Asn Phe Val Ala Ala His Tyr Phe Ala Ser Leu Thr Pro

50 55 60

Asn Thr Ala Pro Trp Ser Pro Ser Pro Ile Thr Leu Pro Ala Gln Pro

65 70 75 80

Asp Phe Val Val Gly Pro Ala Gly Thr Pro Gly Val Thr His Thr Ser

85 90 95

Ile Gln Ala Ala Val Asp Ala Ala Met Val Lys Arg Thr Asn Lys Arg

100 105 110

Gln Tyr Ile Ala Ile Met Pro Gly Ala Tyr Gln Gly Thr Val Tyr Ile

115 120 125

Pro Ala Ala Pro Gly Ser Leu Thr Leu Tyr Gly Thr Gly Glu Lys Pro

130 135 140

Ile Asp Val Lys Ile Gly Met Ala Ile Asp Gly Glu Met Ser Ile Ala

145 150 155 160

Asp Trp Arg Arg Ala Val Asn Pro Gly Gly Lys Tyr Met Pro Gly Lys

165 170 175

Pro Ala Trp Tyr Met Phe Asp Asn Cys Gln Ser Lys Arg Ala Ala Thr

180 185 190

Ile Gly Val Met Cys Ser Ala Ala Phe Trp Ser Gln Asn Asn Gly Leu

195 200 205

Gln Leu Gln Asn Leu Thr Ile Glu Asn Thr Leu Gly Asp Ser Val Asp

210 215 220

Ala Gly Asn His Pro Ala Val Ala Leu Arg Thr Asp Gly Asp Lys Val

225 230 235 240

Gln Ile Asn Lys Val Asn Ile Leu Gly Arg Gln Asn Thr Phe Phe Val

245 250 255

Thr Asn Ser Gly Val Gln Asn Arg Leu Gln Thr Asp Arg Gln Pro Arg

260 265 270

Thr Leu Val Thr Asn Ser Tyr Ile Glu Gly Asp Val Asp Met Val Ser

275 280 285

Gly Arg Gly Ala Val Val Phe Asp Asn Thr Asn Phe Gln Val Val Asn

290 295 300

Ser Arg Thr Gln Gln Glu Ala Tyr Val Phe Ala Pro Ala Thr Leu Ser

305 310 315 320

Asn Ile Tyr Tyr Gly Phe Leu Ala Ile Asn Ser Arg Phe Ser Ala Ser

325 330 335

Gly Asp Gly Val Ala Gln Leu Gly Arg Ser Leu Asp Val Asp Ala Asn

340 345 350

Thr Asn Gly Gln Val Val Ile Arg Asp Ser Val Ile Asn Glu Gly Phe

355 360 365

Asn Ile Ala Lys Pro Trp Ala Asp Ala Val Ile Ser Lys Arg Pro Phe

370 375 380

Ala Gly Asn Thr Gly Thr Val Asp Asp Lys Gly Glu Val Gln Arg Asn

385 390 395 400

Leu Asn Asp Thr Asn Tyr Asn Arg Met Trp Glu Tyr Asn Asn Arg Gly

405 410 415

Pro Gly Ser Lys Val Val Thr Glu Pro Lys Gln

420 425

<210> 1037

<211> 930

<212> DNA

<213> Simonsiella muelleri ATCC 29453 SLP 2a

<400> 1037

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gctggtaatg aactccgtaa acctaaatct gataatactt cgattgttgg tcaaatgtac 120

ggtgcgaaaa tcactaatgt taaagaagat ggtgaagaaa caaatgcgcc atttacccaa 180

aaaccttata agaatgttca gtatggtagt ttgacttctg ctttacatgc ccaagatatt 240

tcaacattag aaaatgggga cgaggtggat actaaaattg ctaagtatgg ttacactggc 300

actctaggta ctgaagataa ttacttctac cgtttaaatg agaataacat ggatgtagct 360

ggattgaaaa aacttaaaaa tgataatcca aacacagtgt tgaaatacga tggtcatgcg 420

gtaacttatg gtattgataa tagctgggtt ggtccagcta aagccaaagt caatagtgta 480

cctacagcca ttgtggctgc tgagaaagca gctgactcag gtttagtgag tggtacacat 540

gttactgcta aaattaactt gaataccaat gctgtagaag gtaacttgta caataaatgg 600

tatgatggtg cgttgaaagg cgttaaagat gttcgtttag tagattttac tggttctatg 660

tctgagaatg gtaatattgc tggtacatcg cataacaaca tcgataatac tggtggttta 720

tttggtgcat ctttaaataa agaggcaaca gaaatgggcg gtgtggtttc atctaatgac 780

catacagcag gaaataaatg gggtgctgta tttggtgctc agttgacagg tcgcgaaact 840

gttgtacctg ctaaaacagg aactcctgct gatccggtta agcctgctga tgaaccaagt 900

attaatagtt ctggtaatgt tactagataa 930

<210> 1038

<211> 309

<212> PRT

<213> Simonsiella muelleri ATCC 29453 SLP 2a

<400> 1038

Met Ser Leu Ala Pro Lys Ser Lys Leu Lys Val Leu Asn Ala Lys Gly
1 5 10 15

Glu Asp Ala Ser Ala Gly Asn Glu Leu Arg Lys Pro Lys Ser Asp Asn
20 25 30

Thr Ser Ile Val Gly Gln Met Tyr Gly Ala Lys Ile Thr Asn Val Lys
35 40 45

Glu Asp Gly Glu Glu Thr Asn Ala Pro Phe Thr Gln Lys Pro Tyr Lys

50 55 60

Asn Val Gln Tyr Gly Ser Leu Thr Ser Ala Leu His Ala Gln Asp Ile

65 70 75 80

Ser Thr Leu Glu Asn Gly Asp Glu Val Asp Thr Lys Ile Ala Lys Tyr

85 90 95

Gly Tyr Thr Gly Thr Leu Gly Thr Glu Asp Asn Tyr Phe Tyr Arg Leu

100 105 110

Asn Glu Asn Asn Met Asp Val Ala Gly Leu Lys Lys Leu Lys Asn Asp

115 120 125

Asn Pro Asn Thr Val Leu Lys Tyr Asp Gly His Ala Val Thr Tyr Gly

130 135 140

Ile Asp Asn Ser Trp Val Gly Pro Ala Lys Ala Lys Val Asn Ser Val

145 150 155 160

Pro Thr Ala Ile Val Ala Ala Glu Lys Ala Ala Asp Ser Gly Leu Val

165 170 175

Ser Gly Thr His Val Thr Ala Lys Ile Asn Leu Asn Thr Asn Ala Val

180 185 190

Glu Gly Asn Leu Tyr Asn Lys Trp Tyr Asp Gly Ala Leu Lys Gly Val

195 200 205

Lys Asp Val Arg Leu Val Asp Phe Thr Gly Ser Met Ser Glu Asn Gly

210 215 220

Asn Ile Ala Gly Thr Ser His Asn Asn Ile Asp Asn Thr Gly Gly Leu

225 230 235 240

Phe Gly Ala Ser Leu Asn Lys Glu Ala Thr Glu Met Gly Gly Val Val

245 250 255

Ser Ser Asn Asp His Thr Ala Gly Asn Lys Trp Gly Ala Val Phe Gly

260 265 270

Ala Gln Leu Thr Gly Arg Glu Thr Val Val Pro Ala Lys Thr Gly Thr

275 280 285

Pro Ala Asp Pro Val Lys Pro Ala Asp Glu Pro Ser Ile Asn Ser Ser

290 295 300

Gly Asn Val Thr Arg

305

<210

> 1039

<211> 1005

<212> DNA

<213> Sulfitobacter sp. CB2047 SLP 1a

<400> 1039

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gccaaacgga cctttgcaac agacgaggat ggtgatccgg tcgatgccgg tgcagcgatt 180

gcgtccggca agacgctgac cgcgcgcgcc gtgggcgtcg ccttgcagaa cctgaactat 240

cacaccgggg aaaccagcac gacgactgat gtcaccgcgt cgatcaagcg caataatgat 300

ggcgcgctga ccgtgaccat cgacggcgaa gagctggcgt tcacccctgc cgacgtgaat 360

ggcgaaggtg acggctacga ggtcgaagtg gatggcaaat tcgccggggt ctataacttt 420

aatggtccgg tcgaagaact gctgacggcg ggcaatggct ttgcccaggt ggtaagcatt 480

ttccggacat ccgagaacgc cgaaggtcac gtctccggcg acagtacctt tgcgatcttt 540

ggcacagaga cggcggatga agatctgaag gatctgccaa aagccgaata tacgggccgg 600

tcgcggatca atgttgtgcc aaacagcggc ttcgaatcga acagcgaaag ccggtacaag 660

gtgcgtagcg agattgcgat gacggcagac tttggcgccg gcgagatctg gggcaccatc 720

gggaacacca ccatcgaaga ccccgaagac ggtgaacgtg acgccgttga agggaccatc 780

gcgatggata aaaccacgtt cgataacaac ggttttgccg ggacattgac ggcagatgcg 840

gacttcatca gcgatatcga cgtcaatagc gccgaaggga cgtactccgg tgcgttctat 900

gggccaaacg ccgaacaggt tgccggtgcg ctgacatttg gtatcggcgc tgacgacggg 960

tcgctgaacg ggaacggcta cttctcggcc gacaaagtcg actaa 1005

<210> 1040

<211> 334

<212> PRT

<213> Sulfitobacter sp. CB2047 SLP 1a

<400> 1040

Met Lys Leu Tyr Met Gln Leu Met Thr Thr Thr Ala Leu Ala Leu Ser

1 5 10 15

Val Ala Ala Cys Gly Ser Ser Asn Gly Val Asp Lys Val Ile Asp Val
20 25 30
Thr Asp Ile Thr Glu Glu Ala Gln Ala Lys Arg Thr Phe Ala Thr Asp
35 40 45
Glu Asp Gly Asp Pro Val Asp Ala Gly Ala Ala Ile Ala Ser Gly Lys
50 55 60
Thr Leu Thr Ala Arg Ala Val Gly Val Ala Leu Gln Asn Leu Asn Tyr
65 70 75 80

His Thr Gly Glu Thr Ser Thr Thr Thr Asp Val Thr Ala Ser Ile Lys
85 90 95
Arg Asn Asn Asp Gly Ala Leu Thr Val Thr Ile Asp Gly Glu Glu Leu
100 105 110
Ala Phe Thr Pro Ala Asp Val Asn Gly Glu Gly Asp Gly Tyr Glu Val
115 120 125
Glu Val Asp Gly Lys Phe Ala Gly Val Tyr Asn Phe Asn Gly Pro Val
130 135 140

Glu Glu Leu Leu Thr Ala Gly Asn Gly Phe Ala Gln Val Val Ser Ile
145 150 155 160
Phe Arg Thr Ser Glu Asn Ala Glu Gly His Val Ser Gly Asp Ser Thr
165 170 175
Phe Ala Ile Phe Gly Thr Glu Thr Ala Asp Glu Asp Leu Lys Asp Leu
180 185 190
Pro Lys Ala Glu Tyr Thr Gly Arg Ser Arg Ile Asn Val Val Pro Asn
195 200 205

Ser Gly Phe Glu Ser Asn Ser Glu Ser Arg Tyr Lys Val Arg Ser Glu
210 215 220
Ile Ala Met Thr Ala Asp Phe Gly Ala Gly Glu Ile Trp Gly Thr Ile
225 230 235 240
Gly Asn Thr Thr Ile Glu Asp Pro Glu Asp Gly Glu Arg Asp Ala Val
245 250 255

Glu Gly Thr Ile Ala Met Asp Lys Thr Thr Phe Asp Asn Asn Gly Phe
260 265 270

Ala Gly Thr Leu Thr Ala Asp Ala Asp Phe Ile Ser Asp Ile Asp Val
275 280 285
Asn Ser Ala Glu Gly Thr Tyr Ser Gly Ala Phe Tyr Gly Pro Asn Ala
290 295 300
Glu Gln Val Ala Gly Ala Leu Thr Phe Gly Ile Gly Ala Asp Asp Gly
305 310 315 320
Ser Leu Asn Gly Asn Gly Tyr Phe Ser Ala Asp Lys Val Asp
325 330

<210> 1041
<211> 705
<212> DNA
<213> Sulfitobacter sp. CB2047 SLP 2a
<400> 1041
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ggttgcaatg gaagcagctc cgccggcggg cttgttggcg gcgtcgcagg cggcgggcag 120
gattttgaaa cagcctttaa cgctgtcagt caaaaggccc ctacttcgga tatgcccacg 180
tcgctgaaag ccagctacga aggtcagatg aaggtcggcg tgaacagcgg atcggcccag 240
attttcggca ccgatatcga tgcgaatagc gcggaaatca ttggcgatct ggcagtcgat 300
gtggattgga ccgacgggca gaccaccaat ccgttcaccg gaaccgcctc caacatcgtc 360

gcgacagagg cgggcacctc gaactccgtc aaactggacg ggacgctgac ggtcgatcaa 420
ggcttgccag cctcgctcag ccgcaccacc attccggcgc aggtcgtcgc gggcgtcaat 480
atccccgagc agaacaccgg cgcgatgctg ttccacatgt ccggtcggct cagcaatggc 540
gagaatgaag gagacgccac cttgcagttc ggcggcaact tcatgggtcc gggtgcagaa 600
tcgatgcttg gaccggtatc tggcggtatc aacgatgtga acaatccctc gccgcagatt 660
ttcgatgcgg gcgtcggtgg tacattctac gccaacaaga aatag 705
<210> 1042
<211> 234
<212> PRT
<213> Sulfitobacter sp. CB2047 SLP 2a

<400> 1042

Met Lys His Ala Arg Leu Ser Ile Val Ile Ala Ser Leu Gly Ala Ala
1 5 10 15
Thr Val Leu Ser Gly Cys Asn Gly Ser Ser Ser Ala Gly Gly Leu Val
20 25 30
Gly Gly Val Ala Gly Gly Gly Gln Asp Phe Glu Thr Ala Phe Asn Ala
35 40 45
Val Ser Gln Lys Ala Pro Thr Ser Asp Met Pro Thr Ser Leu Lys Ala
50 55 60

Ser Tyr Glu Gly Gln Met Lys Val Gly Val Asn Ser Gly Ser Ala Gln
65 70 75 80
Ile Phe Gly Thr Asp Ile Asp Ala Asn Ser Ala Glu Ile Ile Gly Asp
85 90 95
Leu Ala Val Asp Val Asp Trp Thr Asp Gly Gln Thr Thr Asn Pro Phe
100 105 110
Thr Gly Thr Ala Ser Asn Ile Val Ala Thr Glu Ala Gly Thr Ser Asn
115 120 125

Ser Val Lys Leu Asp Gly Thr Leu Thr Val Asp Gln Gly Leu Pro Ala
130 135 140
Ser Leu Ser Arg Thr Thr Ile Pro Ala Gln Val Val Ala Gly Val Asn
145 150 155 160
Ile Pro Glu Gln Asn Thr Gly Ala Met Leu Phe His Met Ser Gly Arg
165 170 175
Leu Ser Asn Gly Glu Asn Glu Gly Asp Ala Thr Leu Gln Phe Gly Gly
180 185 190

Asn Phe Met Gly Pro Gly Ala Glu Ser Met Leu Gly Pro Val Ser Gly
195 200 205
Gly Ile Asn Asp Val Asn Asn Pro Ser Pro Gln Ile Phe Asp Ala Gly
210 215 220
Val Gly Gly Thr Phe Tyr Ala Asn Lys Lys
225 230

<210> 1043

<211> 1005

<212> DNA

<213> Sulfitobacter sp. NAS-14.1 SLP 1a

<400> 1043

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gccaaacgga cctttgctac agacgaggac ggtgatccgg tcgatgccgg tgctgcgatt 180

gcgtcaggca agacactgac cgcgcgcgcc gtgggcgtcg ccttgcagaa cctgaactat 240

cacaccgggg aaaccagcac gaccaataat gtcaccgcat cgatcaagcg caatgatgac 300

ggcgcgttga ccgtgaccat cgacggcgaa gagctgtcgt tcacccctgc cgatgtgaat 360

ggcgacggtg acggctacga ggtcgaagtg gatgggaaat tcgcgggcgt ctacaactat 420

aatggtccgg ttgaagatct gctgacggcg ggcaacggct ttgcccaggt ggtgcagatt 480

ttccggtcgt ccgagaacgc cgaaggtcac gtgtccggcg acagcacctt tgcgatcttt 540

ggcaccgaga cggcagatga agatctgaaa gatctgccga aagccgaata tacgggccgg 600

tcgcggatca atgttgtgcc aaacagcggc ttcgagtcga acagcgaaag ccggtacaag 660

gtgcgcagcg agatcgcgat gacggcagac tttggcgcgg gcgagatctg gggcaccatc 720

gggaacacca ccatcgaaga ccccgaagac ggtgtacgtg atgccgttga ggggaccatc 780

gcgatggata aaaccacgtt cgacaacaac ggttttgccg ggacgttgac ggctgatgcg 840

gatttcatca gcgatatcga cgtcaatagt gccgaaggga cgtattccgg tgcgttctat 900

gggccaaatg ccgaacaggt tgccggtgcg ctgacatttg gtatcggcgc tgacgacggg 960

tcgctgaacg ggaacggcta cttctcggcc gacaaagtcg actaa 1005

<210> 1044

<211> 334

<212> PRT

<213> Sulfitobacter sp. NAS-14.1 SLP 1a

<400> 1044

Met Lys Leu Tyr Met Gln Leu Met Thr Thr Thr Ala Leu Ala Leu Ser
1 5 10 15

Val Ala Ala Cys Gly Ser Ser Asn Gly Val Asp Lys Val Ile Asp Val
20 25 30

Thr Asp Ile Thr Glu Glu Ala Gln Ala Lys Arg Thr Phe Ala Thr Asp

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        35                  40                  45
Glu Asp Gly Asp Pro Val Asp Ala Gly Ala Ala Ile Ala Ser Gly Lys
    50                  55                  60
Thr Leu Thr Ala Arg Ala Val Gly Val Ala Leu Gln Asn Leu Asn Tyr
65                  70                  75                  80
His Thr Gly Glu Thr Ser Thr Thr Asn Asn Val Thr Ala Ser Ile Lys
                85                  90                  95

Arg Asn Asp Asp Gly Ala Leu Thr Val Thr Ile Asp Gly Glu Glu Leu
            100                 105                 110
Ser Phe Thr Pro Ala Asp Val Asn Gly Asp Gly Asp Gly Tyr Glu Val
        115                 120                 125
Glu Val Asp Gly Lys Phe Ala Gly Val Tyr Asn Tyr Asn Gly Pro Val
    130                 135                 140
Glu Asp Leu Leu Thr Ala Gly Asn Gly Phe Ala Gln Val Val Gln Ile
145                 150                 155                 160

Phe Arg Ser Ser Glu Asn Ala Glu Gly His Val Ser Gly Asp Ser Thr
                165                 170                 175
Phe Ala Ile Phe Gly Thr Glu Thr Ala Asp Glu Asp Leu Lys Asp Leu
            180                 185                 190
Pro Lys Ala Glu Tyr Thr Gly Arg Ser Arg Ile Asn Val Val Pro Asn
        195                 200                 205
Ser Gly Phe Glu Ser Asn Ser Glu Ser Arg Tyr Lys Val Arg Ser Glu
    210                 215                 220

Ile Ala Met Thr Ala Asp Phe Gly Ala Gly Glu Ile Trp Gly Thr Ile
225                 230                 235                 240
Gly Asn Thr Thr Ile Glu Asp Pro Glu Asp Gly Val Arg Asp Ala Val
                245                 250                 255
Glu Gly Thr Ile Ala Met Asp Lys Thr Thr Phe Asp Asn Asn Gly Phe
            260                 265                 270
Ala Gly Thr Leu Thr Ala Asp Ala Asp Phe Ile Ser Asp Ile Asp Val
        275                 280                 285
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Asn Ser Ala Glu Gly Thr Tyr Ser Gly Ala Phe Tyr Gly Pro Asn Ala
290 295 300

Glu Gln Val Ala Gly Ala Leu Thr Phe Gly Ile Gly Ala Asp Asp Gly
305 310 315 320

Ser Leu Asn Gly Asn Gly Tyr Phe Ser Ala Asp Lys Val Asp
325 330

<210> 1045

<211> 705

<212> DNA

<213> Sulfitobacter sp. NAS-14.1 SLP 2a

<400> 1045

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ggttgcaatg gaagcagctc cgccggcggg cttgttggcg gcgtcgcagg cggcgggcag 120

gattttgaaa cagcctttaa cgctgtcagt caaaaggccc ccacttcgga tatgcccacg 180

tcgctgaaag ccagctacga aggtcagatg aaggtcggcg tgaacagcgg atcggcccag 240

attttcggca ccgatatcga tgcgaatagc gcggaaatca ttggcgatct ggcagtcgat 300

gtggattgga ccgacgggca gaccaccaat ccgttcaccg gaacggcctc caacatcgtc 360

gcgaccgagg cgggcacctc gaactccgtc aaactggacg ggacgctgac ggtcgatcag 420

ggcctgccag cctcactcag ccgtaccacc attccggcgc aggtcgtcgc gggcgtcaat 480

atccccgagc agaacaccgg cgcgatgctg ttccacatgt ccggtcggct tagcagtggc 540

aagaacgaag gggacgccac cttgcagttc ggcggcaact tcatggggcc gggtgcagaa 600

tcgatgcttg gaccggtatc tggcggtatc aacgatgtga acaatccctc gccgcagatt 660

ttcgacgcgg gcgtcggtgg tacattctac gccaacaaga aatag 705

<210> 1046

<211> 234

<212> PRT

<213> Sulfitobacter sp. NAS-14.1 SLP 2a

<400> 1046

Met Lys His Ala Arg Leu Ser Ile Val Ile Ala Ser Leu Gly Ala Ala
1 5 10 15

Thr Val Leu Ser Gly Cys Asn Gly Ser Ser Ser Ala Gly Gly Leu Val
20 25 30

Gly Gly Val Ala Gly Gly Gly Gln Asp Phe Glu Thr Ala Phe Asn Ala
35 40 45
Val Ser Gln Lys Ala Pro Thr Ser Asp Met Pro Thr Ser Leu Lys Ala
50 55 60
Ser Tyr Glu Gly Gln Met Lys Val Gly Val Asn Ser Gly Ser Ala Gln
65 70 75 80

Ile Phe Gly Thr Asp Ile Asp Ala Asn Ser Ala Glu Ile Ile Gly Asp
85 90 95
Leu Ala Val Asp Val Asp Trp Thr Asp Gly Gln Thr Thr Asn Pro Phe
100 105 110
Thr Gly Thr Ala Ser Asn Ile Val Ala Thr Glu Ala Gly Thr Ser Asn
115 120 125
Ser Val Lys Leu Asp Gly Thr Leu Thr Val Asp Gln Gly Leu Pro Ala
130 135 140

Ser Leu Ser Arg Thr Thr Ile Pro Ala Gln Val Val Ala Gly Val Asn
145 150 155 160
Ile Pro Glu Gln Asn Thr Gly Ala Met Leu Phe His Met Ser Gly Arg
165 170 175
Leu Ser Ser Gly Lys Asn Glu Gly Asp Ala Thr Leu Gln Phe Gly Gly
180 185 190
Asn Phe Met Gly Pro Gly Ala Glu Ser Met Leu Gly Pro Val Ser Gly
195 200 205

Gly Ile Asn Asp Val Asn Asn Pro Ser Pro Gln Ile Phe Asp Ala Gly
210 215 220
Val Gly Gly Thr Phe Tyr Ala Asn Lys Lys
225 230
<210> 1047
<211> 2037
<212> DNA
<213> T. equigenitalis SLP 1a
<400> 1047
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cgaggcagtt ttgatactct atcaattaaa gaaaatattg acactgttaa accaggaaag 120

caaaacaatc aagataataa accatcagaa tcagacgtaa taaaacctga agctaaagga 180

gttatgagac cttcattagg ttatgcagtt gccgtgcctg tcagggatgt agcaaaacga 240

gacgaatctg gtaaattttt ggaaccactt actgttgaag gtaagacagt ggctcaggaa 300

agagaaatca gaaagcctat agatgattct aaagccatac cgcttttaga tggtgacctt 360

gagtatattt atattgatgg caaagaaaaa tttcctgtag ttagagattt tgagaaaggt 420

agtaatcagt ttgattataa gtatgtcaga gctggaatcg taaaacgcaa aggcaattca 480

acaattgata aatacaatga aaatgaagat ctcatcagca gtcttaataa tattgaagcc 540

tatgcttatt acaaaggatc ggaagctgct agtgcattgc caacagataa atctgtagtt 600

tatgacgggc attgggagta tatgactgat gctagattgt atagaaacaa taaaggcgat 660

gtgcgtaagg gaattccaga aggctttaat acaacctcag ctcaaggcta tgaacatggt 720

gctatgtcta tatcacatga atatagacct ttgtttgggt caaaccaaaa accagaacac 780

cgaattacaa ataatgccca ttttgaagtt aattttgcag aaaagtcatt gaaaggaaaa 840

ttagatttcg gcacacaaac tacaagattc acaggcgatg ttacatatac tcctaaatat 900

gatattgtcg ctaaacttta tggaaatcgc ttcgtaggtt ctgctttggc acttgatgag 960

ccaggaaatg aaattaaagc aacatatgca aatgcgacaa ataagctgga gggtggcttc 1020

tttggaccca aagctgaaga actagcaggt aactttatta ctgatgataa ttctttatat 1080

ggggtatttg cagctaaaca aaaaaatgct tcacaaaata tagagagcgt tgttcttgca 1140

cagtttcttg atacgactta cggaaaaatt aagcagtcag cggatataaa ggaagtcact 1200

ttcgatgaag agggaaagga gacaacaaaa caatacaaaa aagaattgga agatctagat 1260

gttcctggag cgcaaacaac gaaaaatctt tcactatttg aaaatattga taagttgata 1320

atagatggca gagagttgaa cttagtgcca ggtcgaacag tatccataga aaaagatgga 1380

cgcagactga acgtgacagc ttacaaaggg gattttgaat atttgcgatt aggtaaagtt 1440

tttaaatctg gattcaccaa ggttggagaa gaggaacaag tagaaagtgg agattcagag 1500

gaagaagatt caaataagga aatcacgcaa aaaataacta ctgtatatcc agatcaagat 1560

ggctattttg tccaaggagc cttaacagag tctaaaaatg tgcctaatca aggtgtagct 1620

aagtatgacg gtgtgtgggg cggaaaaatc tactacttta atcgtgcaat tggaacaaat 1680

cataatactg ctcattttga tgttgatttt ggcgaaagaa aaattaaagg cgacctcaaa 1740

gactttggag caaaggtgtt tgaaatcgat gcctcaatag ataaaaacac cttcacaggt 1800

aaggtgactt cagttggcga aatcaaactc gataatgcag ttggaggaac tacccataca 1860

tcaagtgcaa gatttgatat taaggatagg gatattgctg taacaggtgc tttctttggt 1920

cctaaagcag atgagcttgc aggatcattt tcaggaaaag gaaatttaaa aggggattct 1980

aacggcaaaa cagaagctga tattggagta gttttcggtg ctaaaaaaac aaactaa 2037

<210> 1048

<211> 678

<212> PRT

<213> T. equigenitalis SLP 1a

<400> 1048

Met Asn Lys Lys Ile Phe Tyr Ala Ser Leu Leu Ala Leu Gly Leu Thr
1 5 10 15

Ala Cys Gly Gly Arg Gly Ser Phe Asp Thr Leu Ser Ile Lys Glu Asn
20 25 30

Ile Asp Thr Val Lys Pro Gly Lys Gln Asn Asn Gln Asp Asn Lys Pro
35 40 45

Ser Glu Ser Asp Val Ile Lys Pro Glu Ala Lys Gly Val Met Arg Pro
50 55 60

Ser Leu Gly Tyr Ala Val Ala Val Pro Val Arg Asp Val Ala Lys Arg
65 70 75 80

Asp Glu Ser Gly Lys Phe Leu Glu Pro Leu Thr Val Glu Gly Lys Thr
85 90 95

Val Ala Gln Glu Arg Glu Ile Arg Lys Pro Ile Asp Asp Ser Lys Ala
100 105 110

Ile Pro Leu Leu Asp Gly Asp Leu Glu Tyr Ile Tyr Ile Asp Gly Lys
115 120 125

Glu Lys Phe Pro Val Val Arg Asp Phe Glu Lys Gly Ser Asn Gln Phe
130 135 140

Asp Tyr Lys Tyr Val Arg Ala Gly Ile Val Lys Arg Lys Gly Asn Ser

145 150 155 160

Thr Ile Asp Lys Tyr Asn Glu Asn Glu Asp Leu Ile Ser Ser Leu Asn
165 170 175

Asn Ile Glu Ala Tyr Ala Tyr Tyr Lys Gly Ser Glu Ala Ala Ser Ala
180 185 190
Leu Pro Thr Asp Lys Ser Val Val Tyr Asp Gly His Trp Glu Tyr Met
195 200 205
Thr Asp Ala Arg Leu Tyr Arg Asn Asn Lys Gly Asp Val Arg Lys Gly

210 215 220
Ile Pro Glu Gly Phe Asn Thr Thr Ser Ala Gln Gly Tyr Glu His Gly
225 230 235 240
Ala Met Ser Ile Ser His Glu Tyr Arg Pro Leu Phe Gly Ser Asn Gln
245 250 255
Lys Pro Glu His Arg Ile Thr Asn Asn Ala His Phe Glu Val Asn Phe
260 265 270
Ala Glu Lys Ser Leu Lys Gly Lys Leu Asp Phe Gly Thr Gln Thr Thr

275 280 285
Arg Phe Thr Gly Asp Val Thr Tyr Thr Pro Lys Tyr Asp Ile Val Ala
290 295 300
Lys Leu Tyr Gly Asn Arg Phe Val Gly Ser Ala Leu Ala Leu Asp Glu
305 310 315 320
Pro Gly Asn Glu Ile Lys Ala Thr Tyr Ala Asn Ala Thr Asn Lys Leu
325 330 335
Glu Gly Gly Phe Phe Gly Pro Lys Ala Glu Glu Leu Ala Gly Asn Phe

340 345 350
Ile Thr Asp Asp Asn Ser Leu Tyr Gly Val Phe Ala Ala Lys Gln Lys
355 360 365
Asn Ala Ser Gln Asn Ile Glu Ser Val Val Leu Ala Gln Phe Leu Asp
370 375 380
Thr Thr Tyr Gly Lys Ile Lys Gln Ser Ala Asp Ile Lys Glu Val Thr
385 390 395 400
Phe Asp Glu Glu Gly Lys Glu Thr Thr Lys Gln Tyr Lys Lys Glu Leu

405 410 415
Glu Asp Leu Asp Val Pro Gly Ala Gln Thr Thr Lys Asn Leu Ser Leu

420 425 430

Phe Glu Asn Ile Asp Lys Leu Ile Ile Asp Gly Arg Glu Leu Asn Leu

435 440 445

Val Pro Gly Arg Thr Val Ser Ile Glu Lys Asp Gly Arg Arg Leu Asn

450 455 460

Val Thr Ala Tyr Lys Gly Asp Phe Glu Tyr Leu Arg Leu Gly Lys Val

465 470 475 480

Phe Lys Ser Gly Phe Thr Lys Val Gly Glu Glu Glu Gln Val Glu Ser

485 490 495

Gly Asp Ser Glu Glu Glu Asp Ser Asn Lys Glu Ile Thr Gln Lys Ile

500 505 510

Thr Thr Val Tyr Pro Asp Gln Asp Gly Tyr Phe Val Gln Gly Ala Leu

515 520 525

Thr Glu Ser Lys Asn Val Pro Asn Gln Gly Val Ala Lys Tyr Asp Gly

530 535 540

Val Trp Gly Gly Lys Ile Tyr Tyr Phe Asn Arg Ala Ile Gly Thr Asn

545 550 555 560

His Asn Thr Ala His Phe Asp Val Asp Phe Gly Glu Arg Lys Ile Lys

565 570 575

Gly Asp Leu Lys Asp Phe Gly Ala Lys Val Phe Glu Ile Asp Ala Ser

580 585 590

Ile Asp Lys Asn Thr Phe Thr Gly Lys Val Thr Ser Val Gly Glu Ile

595 600 605

Lys Leu Asp Asn Ala Val Gly Gly Thr Thr His Thr Ser Ser Ala Arg

610 615 620

Phe Asp Ile Lys Asp Arg Asp Ile Ala Val Thr Gly Ala Phe Phe Gly

625 630 635 640

Pro Lys Ala Asp Glu Leu Ala Gly Ser Phe Ser Gly Lys Gly Asn Leu

645 650 655

Lys Gly Asp Ser Asn Gly Lys Thr Glu Ala Asp Ile Gly Val Val Phe

660 665 670

Gly Ala Lys Lys Thr Asn

675

<210> 1049

<211> 750

<212> DNA

<213> T. linaloolentis SLP 1a

<400> 1049

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ctgtcgttgg ggatctgctt gtccttcatt gtcaggccgc tgctcagggg cattttctgg 120

ctctggggca agattacccg tgccgatgtg agacccggtt atgagctggc tgggttcaat 180

tggtttgcgc ttcccttcgc gctttttgcg gtgttgctcg tgctggacct gggacgggaa 240

gatgtaacgc tttactgggg tcttccgctg ctgtccgttg ggctctacct gttctattcg 300

gcggcaaggg atgccggtgt gcgtttccgt catggagaac gtttgcttgc tagcgccatt 360

gccatgccgg aaaaggacgt attccggcgt tcgggagagg tgaacaagta caagaatgtc 420

cagttgatgg gtatcgccgt ggtggcgttg ctgccgcttt tcttgagcgg agcgttcggc 480

taccttctgg aaggcgccat gcgcatggcc caggtgcgca tcgaagcccc cgccatctac 540

gtgaaggcac catacgccac gctgttgccg gaggcacttg ccagtcgcca cccacgcgtt 600

ccagaaggct atacggccta catcggcacc acggtgctgt tcaagggctt cggcaacatg 660

acggtagtgg ccttcccgga tgcgaacggt acccggcaac tggccattcc caacgagcag 720

atcatcgtgg agcgccagtc tggcggctag 750

<210> 1050

<211> 249

<212> PRT

<213> T. linaloolentis SLP 1a

<400> 1050

Met Phe Leu Leu Ala Ala Ala Cys Phe Gly Ala Val Tyr Ala Leu Phe

1 5 10 15

Val Gly Cys Leu Leu Ser Leu Gly Ile Cys Leu Ser Phe Ile Val Arg

20 25 30

Pro Leu Leu Arg Gly Ile Phe Trp Leu Trp Gly Lys Ile Thr Arg Ala

35 40 45

Asp Val Arg Pro Gly Tyr Glu Leu Ala Gly Phe Asn Trp Phe Ala Leu

50 55 60

Pro Phe Ala Leu Phe Ala Val Leu Leu Val Leu Asp Leu Gly Arg Glu

65 70 75 80

Asp Val Thr Leu Tyr Trp Gly Leu Pro Leu Leu Ser Val Gly Leu Tyr

85 90 95

Leu Phe Tyr Ser Ala Ala Arg Asp Ala Gly Val Arg Phe Arg His Gly

100 105 110

Glu Arg Leu Leu Ala Ser Ala Ile Ala Met Pro Glu Lys Asp Val Phe

115 120 125

Arg Arg Ser Gly Glu Val Asn Lys Tyr Lys Asn Val Gln Leu Met Gly

130 135 140

Ile Ala Val Val Ala Leu Leu Pro Leu Phe Leu Ser Gly Ala Phe Gly

145 150 155 160

Tyr Leu Leu Glu Gly Ala Met Arg Met Ala Gln Val Arg Ile Glu Ala

165 170 175

Pro Ala Ile Tyr Val Lys Ala Pro Tyr Ala Thr Leu Leu Pro Glu Ala

180 185 190

Leu Ala Ser Arg His Pro Arg Val Pro Glu Gly Tyr Thr Ala Tyr Ile

195 200 205

Gly Thr Thr Val Leu Phe Lys Gly Phe Gly Asn Met Thr Val Val Ala

210 215 220

Phe Pro Asp Ala Asn Gly Thr Arg Gln Leu Ala Ile Pro Asn Glu Gln

225 230 235 240

Ile Ile Val Glu Arg Gln Ser Gly Gly

245

<210> 1051

<211> 846

<212> DNA

<213> V. cholerae SLP 1a

<400> 1051

atgaaaaata aaatatctac tattttgggt ttagttagta tacttgttgg atgtagtagt 60

ggaggtcaga gtaattataa tattccgcta gagcagccgt tgatagaggg tccggtagtg 120

gagagtccgg tagtggacaa agcagatagc gaggtttttg ctgtagacaa aaataactta 180

gaatcgcaga tgataggtac tatcatatct agagatacat atattgatag tgattttcta 240

aataaaaaca gttttgatgg taaaaatgac ttatatactg tttcaattga taatgatgaa 300

gtatcattta aagatatagc gaaagataat gaagtaatta ctgttaaaga tataagaaaa 360

atatcatcga ataataatat aataggatac tatggttatg tactaagtta tgcagacaag 420

gaaattctag gtaataatga caagtatact agatcagatt atatttttgc gataaatgcc 480

agtgagcaaa gaaagcctga atatacagct acctataaag gcacaatttt ttatgattat 540

gatggttcag ctggtaaaga agcaaatctg actatgtttt atgacaacac taaatcaatg 600

ttaacaggaa caattgaagg taattcacaa cagggattta atttttcat taataataag 660

atgcaggagg gcaatgttta tgatgatggt tcatttattg cggagctaac actgccaaat 720

aaaaataatg ttgagggtgt aatgtctggt gcattttatg gagataaagg ccaaacagcg 780

gttggaaccg ttgagtctat taatgaaaaa tcatggggtg gagtattcag tgctcaggta 840

gagtaa 846

<210> 1052

<211> 281

<212> PRT

<213> V. cholerae SLP 1a

<400> 1052

Met Lys Asn Lys Ile Ser Thr Ile Leu Gly Leu Val Ser Ile Leu Val
1 5 10 15

Gly Cys Ser Ser Gly Gly Gln Ser Asn Tyr Asn Ile Pro Leu Glu Gln
20 25 30

Pro Leu Ile Glu Gly Pro Val Val Glu Ser Pro Val Val Asp Lys Ala
35 40 45

Asp Ser Glu Val Phe Ala Val Asp Lys Asn Asn Leu Glu Ser Gln Met
50 55 60

Ile Gly Thr Ile Ile Ser Arg Asp Thr Tyr Ile Asp Ser Asp Phe Leu
65 70 75 80

Asn Lys Asn Ser Phe Asp Gly Lys Asn Asp Leu Tyr Thr Val Ser Ile
85 90 95

Asp Asn Asp Glu Val Ser Phe Lys Asp Ile Ala Lys Asp Asn Glu Val

100 105 110

Ile Thr Val Lys Asp Ile Arg Lys Ile Ser Ser Asn Asn Asn Ile Ile

115 120 125

Gly Tyr Tyr Gly Tyr Val Leu Ser Tyr Ala Asp Lys Glu Ile Leu Gly

130 135 140

Asn Asn Asp Lys Tyr Thr Arg Ser Asp Tyr Ile Phe Ala Ile Asn Ala

145 150 155 160

Ser Glu Gln Arg Lys Pro Glu Tyr Thr Ala Thr Tyr Lys Gly Thr Ile

165 170 175

Phe Tyr Asp Tyr Asp Gly Ser Ala Gly Lys Glu Ala Asn Leu Thr Met

180 185 190

Phe Tyr Asp Asn Thr Lys Ser Met Leu Thr Gly Thr Ile Glu Gly Asn

195 200 205

Ser Gln Gln Gly Phe Asn Phe Phe Ile Asn Asn Lys Met Gln Glu Gly

210 215 220

Asn Val Tyr Asp Asp Gly Ser Phe Ile Ala Glu Leu Thr Leu Pro Asn

225 230 235 240

Lys Asn Asn Val Glu Gly Val Met Ser Gly Ala Phe Tyr Gly Asp Lys

245 250 255

Gly Gln Thr Ala Val Gly Thr Val Glu Ser Ile Asn Glu Lys Ser Trp

260 265 270

Gly Gly Val Phe Ser Ala Gln Val Glu

275 280

<210> 1053

<211> 729

<212> DNA

<213> V. fortis SLP 1a

<400> 1053

atgaaaccag ttcaactttc atggatcgcg gctgcaatga ttggccttag cccacttgtt 60

caagcaggtt ttgatggcgc gattagcgac gactctctac gccaagttgg tgaatctgaa 120

gtttacgtcc cactgtttca ctcgaaaggt aaagccggca ttggcagctc aacaggtaag 180

cgtgtcgatt tcgatggtct agctaacagc tttttcagtg ctgatccacg cgatggcgtt 240

catacttctg gcagtaaaca ctttggctca acgcactaca actttgcgca agcggctaac 300

caagacgttt ggtttggcga atggtatgaa gggaaacaag atgaaacata caacaaccgt 360
actgtttact atgtaggcga caacactggt accactgtac ctacctcagg tagcgcgacg 420
tacaacatta ctggtattaa ccactttagc ggtaataaca aactgtcagg tacgtttact 480
gctgatttcg ctcaacaaac actaacaggc gacattgcta atgcgtctct atctatcaat 540
gtggatagca cgattgatgc agcaagcgct tcgttcaatg gtacggcaac agctaaccaa 600
gcaggtgtga caactcaagg tatttctcaa ggtcacttct ttggcgcaga tgcagcaaca 660
cttgctggta ttgcgacttt tgctggcaac tctgatcttg atactgcatt cggcggtgca 720

aaacagtaa 729

<210> 1054

<211> 242

<212> PRT

<213> V. fortis SLP 1a

<400> 1054

Met Lys Pro Val Gln Leu Ser Trp Ile Ala Ala Ala Met Ile Gly Leu
1 5 10 15
Ser Pro Leu Val Gln Ala Gly Phe Asp Gly Ala Ile Ser Asp Asp Ser
20 25 30
Leu Arg Gln Val Gly Glu Ser Glu Val Tyr Val Pro Leu Phe His Ser
35 40 45

Lys Gly Lys Ala Gly Ile Gly Ser Ser Thr Gly Lys Arg Val Asp Phe
50 55 60
Asp Gly Leu Ala Asn Ser Phe Phe Ser Ala Asp Pro Arg Asp Gly Val
65 70 75 80
His Thr Ser Gly Ser Lys His Phe Gly Ser Thr His Tyr Asn Phe Ala
85 90 95
Gln Ala Ala Asn Gln Asp Val Trp Phe Gly Glu Trp Tyr Glu Gly Lys
100 105 110

Gln Asp Glu Thr Tyr Asn Asn Arg Thr Val Tyr Tyr Val Gly Asp Asn
115 120 125
Thr Gly Thr Thr Val Pro Thr Ser Gly Ser Ala Thr Tyr Asn Ile Thr

130 135 140

Gly Ile Asn His Phe Ser Gly Asn Asn Lys Leu Ser Gly Thr Phe Thr
145 150 155 160

Ala Asp Phe Ala Gln Gln Thr Leu Thr Gly Asp Ile Ala Asn Ala Ser
165 170 175

Leu Ser Ile Asn Val Asp Ser Thr Ile Asp Ala Ala Ser Ala Ser Phe
180 185 190

Asn Gly Thr Ala Thr Ala Asn Gln Ala Gly Val Thr Thr Gln Gly Ile
195 200 205

Ser Gln Gly His Phe Phe Gly Ala Asp Ala Ala Thr Leu Ala Gly Ile
210 215 220

Ala Thr Phe Ala Gly Asn Ser Asp Leu Asp Thr Ala Phe Gly Gly Ala
225 230 235 240

Lys Gln

<210> 1055

<211> 1380

<212> DNA

<213> V. fortis SLP 1b

<400> 1055

atgcatggct atacttacaa gtttccaata attctctctt tcgctttcat tacggcgtgt 60

aatgaaagcg cttctgattc atcgccgaca agcgatccga ataatcaaac tccgatcgct 120

atcgctggta tcaatcaaca agttaaagtt aatcaagtcg tccacttaga cggcacgcgt 180

agtgttgatt atgacaacga cttcatctct tattcgtggt cattctcaga aaaacccgca 240

ggtagcgaag cacaactttc cagcttggag gccatcaaac cgactttcgt tgcggatcag 300

attggtacgt attatctctc gttggtggtc aacgatggcc aagtcaacag tcgcccaaat 360

caagtgaaaa tagtggctaa atccaaccaa gacaactcgc caccggtggt ctctcttacc 420

ccaacgtaca gcgcatccct gtctcaatcc gttaagctgt ttgacacatc cacagatgct 480

gacggcgatg agctttaccg tcaatggaaa attatcaacc agccagacga gagtcagcct 540

agtctcagta aatatgaggg caaatacccc gacttaaccg ctgatgtggc gggtgactat 600

gtggtggaat taaccgtcac cgatggtttc ttatcgacca aggcgaccac aaccgtcacc 660

tttaatgaaa accatcagaa ccgacctcca attgcttata aaaaccagca catgttagcc 720

attgaaggta tgacgatccc tctagatgcc agtgtaagta ctgacccgga cggcgatcca 780

ctcaccttta attggttttt tgtgtcaaaa ccacaaggga gcaacgctac tatcgctgat 840
cctaatgcgg taatcacaag ttttattgcc gatgtgagcg gacaatatac tttcaatatc 900
gaagtaagtg acggtgagtt caccgattta ggttacaaac ccacgtacgt aaatgtggct 960
tcgttaaatg gcccgcacgc aaaagtcttt ctgagagatg aaaccgaacc tttacttcta 1020
ccctttgatg aagataagaa catagatcta accaatgata ccggagaaat acctgagtac 1080
tacactttag gatcctttac gtttgaagcc gtcgaaaaag acattactct taccgtgact 1140
tccttgactg atgttaaaga catcgtacag cccatcataa gaacctcttt tggtgagctc 1200

gctgaatctg atgtttatgt gattccagca ggtacccgtg aaaccctaac tttgtattca 1260
cctccaaccc agagcaaacc cactcgagtt gttctcggat ttgcgtggag tttaaatgga 1320
cccaacgatt tctcgtatat agagcgtgct ggcggtaact acaatttcat gagtcgataa 1380

<210> 1056
<211> 459
<212> PRT
<213> V. fortis SLP 1b
<400> 1056

Met His Gly Tyr Thr Tyr Lys Phe Pro Ile Ile Leu Ser Phe Ala Phe
1 5 10 15
Ile Thr Ala Cys Asn Glu Ser Ala Ser Asp Ser Ser Pro Thr Ser Asp
20 25 30

Pro Asn Asn Gln Thr Pro Ile Ala Ile Ala Gly Ile Asn Gln Gln Val
35 40 45
Lys Val Asn Gln Val Val His Leu Asp Gly Thr Arg Ser Val Asp Tyr
50 55 60
Asp Asn Asp Phe Ile Ser Tyr Ser Trp Ser Phe Ser Glu Lys Pro Ala
65 70 75 80
Gly Ser Glu Ala Gln Leu Ser Ser Leu Glu Ala Ile Lys Pro Thr Phe
85 90 95

Val Ala Asp Gln Ile Gly Thr Tyr Tyr Leu Ser Leu Val Val Asn Asp
100 105 110
Gly Gln Val Asn Ser Arg Pro Asn Gln Val Lys Ile Val Ala Lys Ser

115 120 125

Asn Gln Asp Asn Ser Pro Pro Val Val Ser Leu Thr Pro Thr Tyr Ser

130 135 140

Ala Ser Leu Ser Gln Ser Val Lys Leu Phe Asp Thr Ser Thr Asp Ala

145 150 155 160

Asp Gly Asp Glu Leu Tyr Arg Gln Trp Lys Ile Ile Asn Gln Pro Asp

165 170 175

Glu Ser Gln Pro Ser Leu Ser Lys Tyr Glu Gly Lys Tyr Pro Asp Leu

180 185 190

Thr Ala Asp Val Ala Gly Asp Tyr Val Val Glu Leu Thr Val Thr Asp

195 200 205

Gly Phe Leu Ser Thr Lys Ala Thr Thr Thr Val Thr Phe Asn Glu Asn

210 215 220

His Gln Asn Arg Pro Pro Ile Ala Tyr Lys Asn Gln His Met Leu Ala

225 230 235 240

Ile Glu Gly Met Thr Ile Pro Leu Asp Ala Ser Val Ser Thr Asp Pro

245 250 255

Asp Gly Asp Pro Leu Thr Phe Asn Trp Phe Phe Val Ser Lys Pro Gln

260 265 270

Gly Ser Asn Ala Thr Ile Ala Asp Pro Asn Ala Val Ile Thr Ser Phe

275 280 285

Ile Ala Asp Val Ser Gly Gln Tyr Thr Phe Asn Ile Glu Val Ser Asp

290 295 300

Gly Glu Phe Thr Asp Leu Gly Tyr Lys Pro Thr Tyr Val Asn Val Ala

305 310 315 320

Ser Leu Asn Gly Pro His Ala Lys Val Phe Leu Arg Asp Glu Thr Glu

325 330 335

Pro Leu Leu Leu Pro Phe Asp Glu Asp Lys Asn Ile Asp Leu Thr Asn

340 345 350

Asp Thr Gly Glu Ile Pro Glu Tyr Tyr Thr Leu Gly Ser Phe Thr Phe

355 360 365

Glu Ala Val Glu Lys Asp Ile Thr Leu Thr Val Thr Ser Leu Thr Asp
370 375 380

Val Lys Asp Ile Val Gln Pro Ile Ile Arg Thr Ser Phe Gly Glu Leu
385 390 395 400

Ala Glu Ser Asp Val Tyr Val Ile Pro Ala Gly Thr Arg Glu Thr Leu
405 410 415

Thr Leu Tyr Ser Pro Pro Thr Gln Ser Lys Pro Thr Arg Val Val Leu
420 425 430

Gly Phe Ala Trp Ser Leu Asn Gly Pro Asn Asp Phe Ser Tyr Ile Glu
435 440 445

Arg Ala Gly Gly Asn Tyr Asn Phe Met Ser Arg
450 455

<210> 1057

<211> 1323

<212> DNA

<213> V. fortis SLP 1c

<400> 1057

atgacttcaa aactaaaatg gaccttactt gctgccgcta tgccagcgct tatcgcatgc 60

ggtagtggga gcagcgacag cagttcagac tcttcaaaca acgcaactgt agaaaaatct 120

tatgccaaac taggcaagcg tgtgcgctta gatgtaaccc aaggtttaga tacctacaac 180

gaaaacatga ctttcgaatg gaaggtcaca agcaaacctg atggcagtaa cgttgcactt 240

aacgcaagca aggccatttc accttatttc actccagatg ttgttggtga ttacacattt 300

gaactagaaa gtgcagtatc tggcacttca agtaccacaa agcaaaccat tgaagtcact 360

gacgcatcac aaaacgtggc gccaatcatc gatattgcga caccaccaag tgttgctcta 420

gccaaatcta tcgaaattcc gtctaacgcc gtcgaccttg atggcgatgt tttaacttat 480

caatgggcgc ttttatcaac accggataat gcgacaatga aacttacggg cagcggagca 540

tcaacagcag tactactttc taatacagcc ggtgactaca aactgaaatt aacagtaagc 600

gacggttacg agagcgctag ccaagaagtg actgtgtcat attcagcaga aaacattgct 660

cctgtggcta atgcgggtgg cgtaaagtct ttagagatta gagaaacagc aaccttagat 720

ggcagcggca gctacgacgg caatgaagat gcgattacgt acacgtggaa actactttct 780

aaacctgaaa atagtacagc tgagctttca gactctacag tcgcgaaacc tgatttcaca 840

cccgaccaag tgggtgatta cctcttctcg ctaactgtaa atgacggtga attaaccagt 900

gaagccgata tggttcgctt gagcgcaagt gccacaggca gcagcgaaat catctttacc 960

tttggagatg aaaaaacaat acatgcccta cctttcgcta ttccgcctat taccttagat 1020

aaaaccatca caggtgatgc acccgattac gttctagtgg gaacttatac tctagaggcg 1080

gttggtaagg actacacaat cagtgaaatt actgaaatgg acttcagagg tgaagattat 1140

gcaccgaaaa tgacagggat agaactaaac caagtcctac atgcagggga tgtggcttac 1200

gtgaaaatgt gggcaaaacc gacgaatggc gcgcgaacca acgttgtata ttcgttcatc 1260

cttgatagtg atttcacaaa ctacatgggc gttgcttacg acttaagtgc tgaggcgaac 1320

taa 1323

<210> 1058

<211> 440

<212> PRT

<213> V. fortis SLP 1c

<400> 1058

Met Thr Ser Lys Leu Lys Trp Thr Leu Leu Ala Ala Ala Met Pro Ala
1 5 10 15

Leu Ile Ala Cys Gly Ser Gly Ser Ser Asp Ser Ser Ser Asp Ser Ser
20 25 30

Asn Asn Ala Thr Val Glu Lys Ser Tyr Ala Lys Leu Gly Lys Arg Val
35 40 45

Arg Leu Asp Val Thr Gln Gly Leu Asp Thr Tyr Asn Glu Asn Met Thr
50 55 60

Phe Glu Trp Lys Val Thr Ser Lys Pro Asp Gly Ser Asn Val Ala Leu
65 70 75 80

Asn Ala Ser Lys Ala Ile Ser Pro Tyr Phe Thr Pro Asp Val Val Gly
85 90 95

Asp Tyr Thr Phe Glu Leu Glu Ser Ala Val Ser Gly Thr Ser Ser Thr
100 105 110

Thr Lys Gln Thr Ile Glu Val Thr Asp Ala Ser Gln Asn Val Ala Pro
115 120 125

Ile Ile Asp Ile Ala Thr Pro Pro Ser Val Ala Leu Ala Lys Ser Ile

130 135 140

Glu Ile Pro Ser Asn Ala Val Asp Leu Asp Gly Asp Val Leu Thr Tyr
145 150 155 160
Gln Trp Ala Leu Leu Ser Thr Pro Asp Asn Ala Thr Met Lys Leu Thr
165 170 175

Gly Ser Gly Ala Ser Thr Ala Val Leu Leu Ser Asn Thr Ala Gly Asp
180 185 190
Tyr Lys Leu Lys Leu Thr Val Ser Asp Gly Tyr Glu Ser Ala Ser Gln
195 200 205
Glu Val Thr Val Ser Tyr Ser Ala Glu Asn Ile Ala Pro Val Ala Asn
210 215 220
Ala Gly Gly Val Lys Ser Leu Glu Ile Arg Glu Thr Ala Thr Leu Asp
225 230 235 240

Gly Ser Gly Ser Tyr Asp Gly Asn Glu Asp Ala Ile Thr Tyr Thr Trp
245 250 255
Lys Leu Leu Ser Lys Pro Glu Asn Ser Thr Ala Glu Leu Ser Asp Ser
260 265 270
Thr Val Ala Lys Pro Asp Phe Thr Pro Asp Gln Val Gly Asp Tyr Leu
275 280 285
Phe Ser Leu Thr Val Asn Asp Gly Glu Leu Thr Ser Glu Ala Asp Met
290 295 300

Val Arg Leu Ser Ala Ser Ala Thr Gly Ser Ser Glu Ile Ile Phe Thr
305 310 315 320
Phe Gly Asp Glu Lys Thr Ile His Ala Leu Pro Phe Ala Ile Pro Pro
325 330 335
Ile Thr Leu Asp Lys Thr Ile Thr Gly Asp Ala Pro Asp Tyr Val Leu
340 345 350
Val Gly Thr Tyr Thr Leu Glu Ala Val Gly Lys Asp Tyr Thr Ile Ser
355 360 365

Glu Ile Thr Glu Met Asp Phe Arg Gly Glu Asp Tyr Ala Pro Lys Met
370 375 380

Thr Gly Ile Glu Leu Asn Gln Val Leu His Ala Gly Asp Val Ala Tyr
385 390 395 400
Val Lys Met Trp Ala Lys Pro Thr Asn Gly Ala Arg Thr Asn Val Val
405 410 415
Tyr Ser Phe Ile Leu Asp Ser Asp Phe Thr Asn Tyr Met Gly Val Ala
420 425 430

Tyr Asp Leu Ser Ala Glu Ala Asn
435 440

<210> 1059
<211> 750
<212> DNA
<213> V. nigripulchritudo SLP 1a
<400> 1059

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cacgcaggtt ttaacggcgc aatcagcgac aacactcacc gccacgttgg cgaatctcaa 120
gttgacgcat cactattctt cggcaccgta atcatccatg aaagtggtta cgcgggtatc 180
ggtgccacag gaaaagaacg tgttgatttc aaaaacctgg cgaagcgttc ctcatggccg 240
tttggtgtaa cacgtgaagg tatacatact cgcggaagcc gccactctac aacttctcaa 300

tacaactttg ccagcgttgc aagtcaggac gtttggtttg gtgagtggta cgaaggcagc 360
cgtgactctg gctacgcaaa ccgtgcggta ttctacgtag gtgataacac aggtactaca 420
gtaccaacaa ctggaacagc aacttacagt gtagctggcg taaacaaatt caacggttcg 480
aacaaactta gcggtacttt tacagctaac tttggcactc aaaaactaac tggttctatt 540
aacaatgcct ctctgactgt tggtgtaaac gcaaacatca atgcttctac tgctgcattt 600
aacggtacag caacagcaac aactggtggt gcgactacaa acggtacgtc tcagggtcac 660
ttctttggtg caaacgcatc tgctctggca ggtattgcga ccttcactaa caaagaccta 720

gacacggcat ttggcggcag caaaaactaa 750

<210> 1060
<211> 249
<212> PRT
<213> V. nigripulchritudo SLP 1a
<400> 1060

Met Lys Pro Val Lys Leu Thr Leu Ile Ser Ala Ala Leu Leu Gly Leu

1 5 10 15

Ser Ser Met Ala His Ala Gly Phe Asn Gly Ala Ile Ser Asp Asn Thr

20 25 30

His Arg His Val Gly Glu Ser Gln Val Asp Ala Ser Leu Phe Phe Gly

35 40 45

Thr Val Ile Ile His Glu Ser Gly Tyr Ala Gly Ile Gly Ala Thr Gly

50 55 60

Lys Glu Arg Val Asp Phe Lys Asn Leu Ala Lys Arg Ser Ser Trp Pro

65 70 75 80

Phe Gly Val Thr Arg Glu Gly Ile His Thr Arg Gly Ser Arg His Ser

85 90 95

Thr Thr Ser Gln Tyr Asn Phe Ala Ser Val Ala Ser Gln Asp Val Trp

100 105 110

Phe Gly Glu Trp Tyr Glu Gly Ser Arg Asp Ser Gly Tyr Ala Asn Arg

115 120 125

Ala Val Phe Tyr Val Gly Asp Asn Thr Gly Thr Thr Val Pro Thr Thr

130 135 140

Gly Thr Ala Thr Tyr Ser Val Ala Gly Val Asn Lys Phe Asn Gly Ser

145 150 155 160

Asn Lys Leu Ser Gly Thr Phe Thr Ala Asn Phe Gly Thr Gln Lys Leu

165 170 175

Thr Gly Ser Ile Asn Asn Ala Ser Leu Thr Val Gly Val Asn Ala Asn

180 185 190

Ile Asn Ala Ser Thr Ala Ala Phe Asn Gly Thr Ala Thr Ala Thr Thr

195 200 205

Gly Gly Ala Thr Thr Asn Gly Thr Ser Gln Gly His Phe Phe Gly Ala

210 215 220

Asn Ala Ser Ala Leu Ala Gly Ile Ala Thr Phe Thr Asn Lys Asp Leu

225 230 235 240

Asp Thr Ala Phe Gly Gly Ser Lys Asn

245

<210> 1061

<211> 1368

<212> DNA

<213> V. nigripulchritudo SLP 1b

<400> 1061

atgataaagc tgacccaaat cctgagctta gcctttacag cggtcattct tgcgggatgt 60

aatgaaagtc tgaaactcga tctggcatct accaagtcga ataccctcc tattgctatc 120

gcgggtacca atcaactggt ttatgtgggt gagccagctc aactgaatgg gaaaaaaagc 180

ttcgataaag accttcagcc gctgaccttt gaatggaaaa tacaacctga tcaatacacg 240

cagctggatc gtaacgccaa gctccttcaa ccaaattcaa ttaaaccgtc gttcgttgcc 300

catgaagcgg gagagttcta catagacctg acggtcaatg atggcattga aaacagccgg 360

gtaaacacca tcaagctcac tgctataatt aaaggggcaa acagcccaac agttatcata 420

ttaaatgaaa ttattgaagg ctctttgcaa cacggagctt ccattagacc aagctatgaa 480

gacgccgata atgatgagct gttttataca tgggaaattt tagaaaaacc cctaaatagc 540

tccccaacca ttgaaaatac taattccaca tacggttggg gtagcctcaa aacagatgtt 600

gaaggggatt atttgatcaa gcttaccgta ttcgacggga cacaccattc gtccgctacg 660

acaacggttc aaattcgcta tgttgataca aacgcaagac cctatgccaa cctagatcct 720

gatgtatgga taagttttgt aggaaactca gtcactcttg atggaacaaa gagctcagat 780

gcagatggag acccattaaa ctaccactgg acaatgacgc caccaaatgg ttctaacgcg 840

acctttgatg accctagttc agccacgcca actgtaactg gtgacgtacc gggcatttac 900

ttctatgaat tggtagttga cgatggtgaa ttgtttagca ttcctaatga gcaagcactg 960

gaatttctcg cgccaagttc accaggctta cgaatctacc acagcaacag ctcttctccg 1020

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gttgccagtg acagggccaa tattatcacc ccttattttg atggcttgga gcaaactcaa 1200

ttattcacac taaaaaaagg tgagagcata tcttttaact tggtatcccc tgccactggc 1260

ggaaaaacaa gccagcccat atttagcttt aactggataa tggggcgcgc tacggactac 1320

cacaatgcct atcactttga cgctaaatat actttcacca gtaattaa 1368

<210> 1062

<211> 455

<212> PRT

<213> V. nigripulchritudo SLP 1b

<400> 1062

Met Ile Lys Leu Thr Gln Ile Leu Ser Leu Ala Phe Thr Ala Val Ile
1 5 10 15

Leu Ala Gly Cys Asn Glu Ser Leu Lys Leu Asp Leu Ala Ser Thr Lys
20 25 30

Ser Asn Thr Pro Pro Ile Ala Ile Ala Gly Thr Asn Gln Leu Val Tyr
35 40 45

Val Gly Glu Pro Ala Gln Leu Asn Gly Lys Lys Ser Phe Asp Lys Asp
50 55 60

Leu Gln Pro Leu Thr Phe Glu Trp Lys Ile Gln Pro Asp Gln Tyr Thr
65 70 75 80

Gln Leu Asp Arg Asn Ala Lys Leu Leu Gln Pro Asn Ser Ile Lys Pro
85 90 95

Ser Phe Val Ala His Glu Ala Gly Glu Phe Tyr Ile Asp Leu Thr Val
100 105 110

Asn Asp Gly Ile Glu Asn Ser Arg Val Asn Thr Ile Lys Leu Thr Ala
115 120 125

Ile Ile Lys Gly Ala Asn Ser Pro Thr Val Ile Ile Leu Asn Glu Ile
130 135 140

Ile Glu Gly Ser Leu Gln His Gly Ala Ser Ile Arg Pro Ser Tyr Glu
145 150 155 160

Asp Ala Asp Asn Asp Glu Leu Phe Tyr Thr Trp Glu Ile Leu Glu Lys
165 170 175

Pro Leu Asn Ser Ser Pro Thr Ile Glu Asn Thr Asn Ser Thr Tyr Gly
180 185 190

Trp Gly Ser Leu Lys Thr Asp Val Glu Gly Asp Tyr Leu Ile Lys Leu
195 200 205

Thr Val Phe Asp Gly Thr His His Ser Ser Ala Thr Thr Thr Val Gln
210 215 220

Ile Arg Tyr Val Asp Thr Asn Ala Arg Pro Tyr Ala Asn Leu Asp Pro
225 230 235 240

Asp Val Trp Ile Ser Phe Val Gly Asn Ser Val Thr Leu Asp Gly Thr
245 250 255
Lys Ser Ser Asp Ala Asp Gly Asp Pro Leu Asn Tyr His Trp Thr Met
260 265 270

Thr Pro Pro Asn Gly Ser Asn Ala Thr Phe Asp Asp Pro Ser Ser Ala
275 280 285
Thr Pro Thr Val Thr Gly Asp Val Pro Gly Ile Tyr Phe Tyr Glu Leu
290 295 300
Val Val Asp Asp Gly Glu Leu Phe Ser Ile Pro Asn Glu Gln Ala Leu
305 310 315 320
Glu Phe Leu Ala Pro Ser Ser Pro Gly Leu Arg Ile Tyr His Ser Asn
325 330 335

Ser Ser Ser Pro Val Asp Met Pro His Ser Pro Asp Gln Thr Ile Ile
340 345 350
Glu Thr Gln Ser Asn Ser Thr Tyr Tyr Val Leu Gly Ser Tyr Arg Ile
355 360 365
Glu Ala Val Gly Ala Asp Val Tyr Ile Arg Asp Val Val Ala Ser Asp
370 375 380
Arg Ala Asn Ile Ile Thr Pro Tyr Phe Asp Gly Leu Glu Gln Thr Gln
385 390 395 400

Leu Phe Thr Leu Lys Lys Gly Glu Ser Ile Ser Phe Asn Leu Val Ser
405 410 415
Pro Ala Thr Gly Gly Lys Thr Ser Gln Pro Ile Phe Ser Phe Asn Trp
420 425 430
Ile Met Gly Arg Ala Thr Asp Tyr His Asn Ala Tyr His Phe Asp Ala
435 440 445
Lys Tyr Thr Phe Thr Ser Asn
450 455

<210> 1063
<211> 1536
<212> DNA

<213> V. nigripulchritudo SLP 1c

<400> 1063

atgaacaaca aaaatacatg gatgcttctg gctttgagtc tgccgacatt agtcgcatgc 60

ggtggcggtt cgagctccaa cgattccaac ggttccaacg gttccaacga caacacagta 120

aaaccacctg tcgttgcacc agcaccagca ccagcaccag caccagcacc agctaaaaaa 180

ccacaaatca acgccaagat gaacaacact gttcatctaa atggtttgga tattttcgct 240

caggcagctc agaaaaaagc actgaactcg gcagtagctg acactgcaaa cactcaacca 300

ttcacttggg tcattagcaa aaaaccagca ggcagcaaca gtgcaattaa aaacgccaat 360

gcattagtga cgtcgttcca accagacctg gcgggtgaat acaccattca gcttaccgca 420

acgaatcctg cagcgacgat agaaaaacac tataaagtga caggtgccgc tgagaacgca 480

gcaccaaatg tcttcccagt cgagtcagta atgacgcgaa tcgacacgaa cattactctg 540

tcagcaaacg ctgaggatcc agacaataac gctctgactt accagtggtc tgtggcaaat 600

aaacctagta atgcaacggt aacactaact aatgaaacga cagaaaatgc cacattctct 660

gccaatgcag caggtgagta tgagttaagc attgcggttt cagattcaaa agagacagta 720

aagcgtgcag ttactgtgaa gatagatgaa agtgtagtgc cttacacgtc tgagacgtct 780

gtttatttag aaagaaccaa cgcctttacc caagaaaacg taaaaccaat caataaactg 840

aactttgcga cgcttgagtt aaataagaag gtaaaattgg atgccagctc gaacacagac 900

aaagacagca caaatttcca ataccaatgg gcggttgttt ctaaacctac tgcaagctca 960

ggcacaatca cactagattc ggcgcaagtt gccgaattta ctccagatgt aattggtgat 1020

tatgtctttt ctgttacggt aaacgaaggc aataagcaac gtgctattga atatgtgggt 1080

ataacagcgg tagaaaatgt aacatcagca actgctctta tcagtgtggt aaactctaca 1140

ggattgactt atacctataa atcttccaat tacattccag aaggcgaccc gaggtttaat 1200

tatgtagaag accctatgta tggaagacac aaagtcattg ctgtttccaa aaacggagct 1260

tcaactgatt atattaaagt tgattccatt accattacgc caactgtagc agatgtattt 1320

gtctttgact ttgtaaccgt gaatactcca ccacctgtat cgggaattaa attcgaagga 1380

atcaaaaaga atcaattaat ttcagtggga gaatcggtag tttttgatgt ttatatggat 1440

gcttcgcttc cattaaataa gttcacagaa atagctatcg atttttctgg aagatatacc 1500

cattccttct caaatattta tgcgtttaca gagtaa 1536

<210> 1064

<211> 511

<212> PRT

<213> V. nigripulchritudo SLP 1c

<400> 1064

Met Asn Asn Lys Asn Thr Trp Met Leu Leu Ala Leu Ser Leu Pro Thr

1 5 10 15

Leu Val Ala Cys Gly Gly Gly Ser Ser Ser Asn Asp Ser Asn Gly Ser

20 25 30

Asn Gly Ser Asn Asp Asn Thr Val Lys Pro Pro Val Val Ala Pro Ala

35 40 45

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Lys Lys Pro Gln Ile Asn

50 55 60

Ala Lys Met Asn Asn Thr Val His Leu Asn Gly Leu Asp Ile Phe Ala

65 70 75 80

Gln Ala Ala Gln Lys Lys Ala Leu Asn Ser Ala Val Ala Asp Thr Ala

85 90 95

Asn Thr Gln Pro Phe Thr Trp Val Ile Ser Lys Lys Pro Ala Gly Ser

100 105 110

Asn Ser Ala Ile Lys Asn Ala Asn Ala Leu Val Thr Ser Phe Gln Pro

115 120 125

Asp Leu Ala Gly Glu Tyr Thr Ile Gln Leu Thr Ala Thr Asn Pro Ala

130 135 140

Ala Thr Ile Glu Lys His Tyr Lys Val Thr Gly Ala Ala Glu Asn Ala

145 150 155 160

Ala Pro Asn Val Phe Pro Val Glu Ser Val Met Thr Arg Ile Asp Thr

165 170 175

Asn Ile Thr Leu Ser Ala Asn Ala Glu Asp Pro Asp Asn Asn Ala Leu

180 185 190

Thr Tyr Gln Trp Ser Val Ala Asn Lys Pro Ser Asn Ala Thr Val Thr

195 200 205

Leu Thr Asn Glu Thr Thr Glu Asn Ala Thr Phe Ser Ala Asn Ala Ala

210 215 220

Gly Glu Tyr Glu Leu Ser Ile Ala Val Ser Asp Ser Lys Glu Thr Val

225 230 235 240

Lys Arg Ala Val Thr Val Lys Ile Asp Glu Ser Val Val Pro Tyr Thr

245 250 255

Ser Glu Thr Ser Val Tyr Leu Glu Arg Thr Asn Ala Phe Thr Gln Glu

260 265 270

Asn Val Lys Pro Ile Asn Lys Leu Asn Phe Ala Thr Leu Glu Leu Asn

275 280 285

Lys Lys Val Lys Leu Asp Ala Ser Ser Asn Thr Asp Lys Asp Ser Thr

290 295 300

Asn Phe Gln Tyr Gln Trp Ala Val Val Ser Lys Pro Thr Ala Ser Ser

305 310 315 320

Gly Thr Ile Thr Leu Asp Ser Ala Gln Val Ala Glu Phe Thr Pro Asp

325 330 335

Val Ile Gly Asp Tyr Val Phe Ser Val Thr Val Asn Glu Gly Asn Lys

340 345 350

Gln Arg Ala Ile Glu Tyr Val Gly Ile Thr Ala Val Glu Asn Val Thr

355 360 365

Ser Ala Thr Ala Leu Ile Ser Val Val Asn Ser Thr Gly Leu Thr Tyr

370 375 380

Thr Tyr Lys Ser Ser Asn Tyr Ile Pro Glu Gly Asp Pro Arg Phe Asn

385 390 395 400

Tyr Val Glu Asp Pro Met Tyr Gly Arg His Lys Val Ile Ala Val Ser

405 410 415

Lys Asn Gly Ala Ser Thr Asp Tyr Ile Lys Val Asp Ser Ile Thr Ile

420 425 430

Thr Pro Thr Val Ala Asp Val Phe Val Phe Asp Phe Val Thr Val Asn

435 440 445

Thr Pro Pro Pro Val Ser Gly Ile Lys Phe Glu Gly Ile Lys Lys Asn

450 455 460

Gln Leu Ile Ser Val Gly Glu Ser Val Val Phe Asp Val Tyr Met Asp

465 470 475 480

Ala Ser Leu Pro Leu Asn Lys Phe Thr Glu Ile Ala Ile Asp Phe Ser
485 490 495
Gly Arg Tyr Thr His Ser Phe Ser Asn Ile Tyr Ala Phe Thr Glu
500 505 510

<210> 1065
<211> 729
<212> DNA
<213> V. splendidus SLP 1a

<400> 1065
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caagccggtt ttgacggtgc tatcagcgac aattcacttc gccaagttgg tgaatcagaa 120
gtttatgtgc catttttcca ctcaaaaggc aaagcaggaa tcggcagtgc tactggtaaa 180
cgcgtcgact tcgacggctt agctggaaat attttcagca gtaaagagcg agacagtgtt 240
catacatcag gcagtaaaca cttcagtaac tctcactaca attttgtaca agttgcgaac 300
caagacattt ggtttgggga atggtatgaa ggcaaccaag acgcagattt caataaccga 360
acggtttact acgtagggaa cgatgcaggc acaactgtac caactaacgg tactgcaact 420

tacaacatca ccggcattaa taagtttagt ggcagcaata aattgtctgg aacatttgat 480
gctgatttca ataaccaaac tttagagggt agtatctcga atgcaaccct aactgttggt 540
gtgaatagca ctattgactc tgcaacggcg tcgttcaacg gaagtgcaac cgcgacacaa 600
gctggttctg taacccaagg ttcgtctcaa ggtcacttct tcggtgcgga tgcggcttcc 660
cttgctggta tcgcgacatt cactaacaat agtgatcttg atactgcctt cggtggtgaa 720
aagcagtaa 729

<210> 1066
<211> 242
<212> PRT
<213> V. splendidus SLP 1a

<400> 1066
Met Lys Pro Val Gln Leu Ser Trp Ile Ala Ala Ala Phe Leu Gly Leu
1 5 10 15
Ser Pro Val Val Gln Ala Gly Phe Asp Gly Ala Ile Ser Asp Asn Ser
20 25 30
Leu Arg Gln Val Gly Glu Ser Glu Val Tyr Val Pro Phe Phe His Ser

35 40 45

Lys Gly Lys Ala Gly Ile Gly Ser Ala Thr Gly Lys Arg Val Asp Phe
50 55 60

Asp Gly Leu Ala Gly Asn Ile Phe Ser Ser Lys Glu Arg Asp Ser Val
65 70 75 80
His Thr Ser Gly Ser Lys His Phe Ser Asn Ser His Tyr Asn Phe Val
85 90 95
Gln Val Ala Asn Gln Asp Ile Trp Phe Gly Glu Trp Tyr Glu Gly Asn
100 105 110
Gln Asp Ala Asp Phe Asn Asn Arg Thr Val Tyr Tyr Val Gly Asn Asp
115 120 125

Ala Gly Thr Thr Val Pro Thr Asn Gly Thr Ala Thr Tyr Asn Ile Thr
130 135 140
Gly Ile Asn Lys Phe Ser Gly Ser Asn Lys Leu Ser Gly Thr Phe Asp
145 150 155 160
Ala Asp Phe Asn Asn Gln Thr Leu Glu Gly Ser Ile Ser Asn Ala Thr
165 170 175
Leu Thr Val Gly Val Asn Ser Thr Ile Asp Ser Ala Thr Ala Ser Phe
180 185 190

Asn Gly Ser Ala Thr Ala Thr Gln Ala Gly Ser Val Thr Gln Gly Ser
195 200 205
Ser Gln Gly His Phe Phe Gly Ala Asp Ala Ala Ser Leu Ala Gly Ile
210 215 220
Ala Thr Phe Thr Asn Asn Ser Asp Leu Asp Thr Ala Phe Gly Gly Glu
225 230 235 240
Lys Gln

<210> 1067
<211> 1395
<212> DNA
<213> V. splendidus SLP 1b
<400> 1067

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aacagtggtg gggatagcaa cactccaagt accgacccag gtttacagaa caaccagaga 120

ccgattgcga ttgcaggcat aaatcagcaa gtgaaagaag gcgatcgggt acaactcgat 180

ggaacctcaa gcattgatta tgataaagac gaaattacct atcaatggtc tttgagttca 240

accccgcttc aaagcctagc ggaactgtct caggtcgatg caatcaagcc cacatttata 300

gcagacaagt taggaaccta tgttgttgat cttgtcgttc atgatggaac caccagcagc 360

cgaaccaacc aagtaaaagt tgttgcggtt tctgatggag aaaactcacc accgacggtt 420

tcgatatctc gggaccatta tcgtgctaat ctaattgatt ttgttacgat ttttggcaag 480

gcaagcgatg ctgacgatga cgatgacgag ttaatatatc gctggaaaat catacaacaa 540

ccagaaaaca gtaacccaag tctggataat acttcttcta aatatccaag gttaacgaca 600

gatactatcg gcgattacat tgtggagctt actgtatccg atggtttagc atccgccagt 660

gatacagcca ctgtttcttt ctactatgag aacgtcccac caattgttag agggacagga 720

agccctatcg gtgccattga aggcatgacc attccattag acgcaagtac aagcgaagat 780

ccaaatggtg acccgatcac tttccaatgg tcattcatct caaaacctca agcatcaaac 840

actgtcattg ttaacccaag ctcagcaaaa cctcattttt tagcagacgt agctggtgac 900

tatggcatta ctgtcgaagt cagtgatgga gagttgtcat catttccatc aaaagctgcc 960

tatgtgcgcg tggcttcgct gacgggcccc catgcaaagg taatgattga tgatgacccc 1020

aaccctgttc tattaccgta tcgcaataca tggaccattg ataagacaca agatagcggt 1080

gacctcccag actattatga actgggcact tatacatttg aagccgtaac caatgacatc 1140

actctaacgg ttagtaccct ccgagatcga tcgaatactg tacaaccaat agctcgaacg 1200

ccctttggtg atttaaagga aagagaaata tacgttattc ctgctggcac aaaagaagtc 1260

attacaatcc tttcccctcc aacttcaggt caaaccacgg atatagacct tgattttgcc 1320

tggagcctct acggcttggg tgattacagt ccaatccgaa gagctggtgg gaattacata 1380

ttcactagtc gatag 1395

<210> 1068

<211> 464

<212> PRT

<213> V. splendidus SLP 1b

<400> 1068

Met His Ile Asn Phe His Trp Ala Pro Ile Leu Leu Phe Ala Ala Leu

1 5 10 15

Ser Thr Gly Cys Asn Ser Gly Gly Asp Ser Asn Thr Pro Ser Thr Asp
20 25 30
Pro Gly Leu Gln Asn Asn Gln Arg Pro Ile Ala Ile Ala Gly Ile Asn

35 40 45
Gln Gln Val Lys Glu Gly Asp Arg Val Gln Leu Asp Gly Thr Ser Ser
50 55 60
Ile Asp Tyr Asp Lys Asp Glu Ile Thr Tyr Gln Trp Ser Leu Ser Ser
65 70 75 80
Thr Pro Leu Gln Ser Leu Ala Glu Leu Ser Gln Val Asp Ala Ile Lys
85 90 95
Pro Thr Phe Ile Ala Asp Lys Leu Gly Thr Tyr Val Val Asp Leu Val

100 105 110
Val His Asp Gly Thr Thr Ser Ser Arg Thr Asn Gln Val Lys Val Val
115 120 125
Ala Val Ser Asp Gly Glu Asn Ser Pro Pro Thr Val Ser Ile Ser Arg
130 135 140
Asp His Tyr Arg Ala Asn Leu Ile Asp Phe Val Thr Ile Phe Gly Lys
145 150 155 160
Ala Ser Asp Ala Asp Asp Asp Asp Asp Glu Leu Ile Tyr Arg Trp Lys

165 170 175
Ile Ile Gln Gln Pro Glu Asn Ser Asn Pro Ser Leu Asp Asn Thr Ser
180 185 190
Ser Lys Tyr Pro Arg Leu Thr Thr Asp Thr Ile Gly Asp Tyr Ile Val
195 200 205
Glu Leu Thr Val Ser Asp Gly Leu Ala Ser Ala Ser Asp Thr Ala Thr
210 215 220
Val Ser Phe Tyr Tyr Glu Asn Val Pro Pro Ile Val Arg Gly Thr Gly

225 230 235 240
Ser Pro Ile Gly Ala Ile Glu Gly Met Thr Ile Pro Leu Asp Ala Ser
245 250 255
Thr Ser Glu Asp Pro Asn Gly Asp Pro Ile Thr Phe Gln Trp Ser Phe

260 265 270

Ile Ser Lys Pro Gln Ala Ser Asn Thr Val Ile Val Asn Pro Ser Ser

275 280 285

Ala Lys Pro His Phe Leu Ala Asp Val Ala Gly Asp Tyr Gly Ile Thr

290 295 300

Val Glu Val Ser Asp Gly Glu Leu Ser Ser Phe Pro Ser Lys Ala Ala

305 310 315 320

Tyr Val Arg Val Ala Ser Leu Thr Gly Pro His Ala Lys Val Met Ile

325 330 335

Asp Asp Asp Pro Asn Pro Val Leu Leu Pro Tyr Arg Asn Thr Trp Thr

340 345 350

Ile Asp Lys Thr Gln Asp Ser Gly Asp Leu Pro Asp Tyr Tyr Glu Leu

355 360 365

Gly Thr Tyr Thr Phe Glu Ala Val Thr Asn Asp Ile Thr Leu Thr Val

370 375 380

Ser Thr Leu Arg Asp Arg Ser Asn Thr Val Gln Pro Ile Ala Arg Thr

385 390 395 400

Pro Phe Gly Asp Leu Lys Glu Arg Glu Ile Tyr Val Ile Pro Ala Gly

405 410 415

Thr Lys Glu Val Ile Thr Ile Leu Ser Pro Pro Thr Ser Gly Gln Thr

420 425 430

Thr Asp Ile Asp Leu Asp Phe Ala Trp Ser Leu Tyr Gly Leu Gly Asp

435 440 445

Tyr Ser Pro Ile Arg Arg Ala Gly Gly Asn Tyr Ile Phe Thr Ser Arg

450 455 460

<210> 1069

<211> 1344

<212> DNA

<213> V. splendidus SLP 1c

<400> 1069

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ttagcggtga tctccgcgca aagtgtcgcg aaggttaaca gtcgagttcg agttgatggg 180
cttcagagtg aaggattaga tggagaatct cttagctacc aatgggaaat cagtaataaa 240
ccggaaggga gcacagcttc acttaataac gccaatgctg tctctccata cttcactccg 300
gatatagctg gtaactacac cttagatttg gtcacaaaaa gtggtagtaa agacagtgaa 360
aaagtctctt atgtaatcga tgtaagtgat gcgagcacta atacgcagcc gattgtcgat 420
ctagattttc ctgacagtgt cgctattggt aaaaccgtcg atctacattc acaagcttat 480
gatgcagacg gtgatgtgct gacttaccaa tgggcactac tttcatcgcc aagtaatgcc 540

acaatgaaat taacaaacag tgccactcca acagcaaatc tcctttccaa cactgccgga 600
gattaccaat taaagctaac agtgagtgat ggctacgaaa caatatctga agaaatgact 660
gtttcatatt ctgctgaaaa tgtagcgcct aaagctagcg taaaaaacaa gcaaacattt 720
gaattaggta caagtgcact gcttgacgca acagcaagta ctgacggaaa cgatgaccaa 780
ataacctacg aatggaaagt ggtttctcaa ccagaaaaca gcacggcaac gctaagtagc 840
acaacagatg aaaaaccgaa ttttacccct gatttaattg gcgactatgt attgtccctt 900
accgtttctg atggcgaatt aaccagtaaa aaagagtaca ttcgtttatc tgcaacagaa 960

gtcggaacca gtgaccttat tcttaagtat gcggaagata ccacggctag agtatggcca 1020
tttgctgaac aattcacttc gaatatttcg actacgggcg atgcaccagc tcatgttcta 1080
ctaggcactt ttagccttga agctgtaggt aaggactata caattaatga gacaaccgct 1140
atcgattata ttggtaatgt tgatgcggta atgacaggaa tgaatgctgg tcaggtacta 1200
aatgctggcg ataaaattaa cgtaaaaatg tgggcagagc caacccaagg tcaattatca 1260
atgatttcat atggtttcat tgttgataca actttagagc aatatatggg actggggtat 1320
atgtatactt caacggctga ataa 1344

<210> 1070
<211> 447
<212> PRT
<213> V. splendidus SLP 1c
<400> 1070
Met Lys Ser Asn Phe Lys Trp Thr Leu Leu Ala Leu Thr Ile Pro Thr
1 5 10 15
Leu Ile Ala Cys Gly Gly Gly Ser Ser Ser Ser Ser Ser Ser Thr
20 25 30

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Pro Ala Ala Gln Asp Pro Leu Gly Leu Ala Val Ile Ser Ala Gln Ser
        35                  40                  45
Val Ala Lys Val Asn Ser Arg Val Arg Val Asp Gly Leu Gln Ser Glu

    50                  55                  60
Gly Leu Asp Gly Glu Ser Leu Ser Tyr Gln Trp Glu Ile Ser Asn Lys
65                  70                  75                  80
Pro Glu Gly Ser Thr Ala Ser Leu Asn Asn Ala Asn Ala Val Ser Pro
                85                  90                  95
Tyr Phe Thr Pro Asp Ile Ala Gly Asn Tyr Thr Leu Asp Leu Val Thr
            100                 105                 110
Lys Ser Gly Ser Lys Asp Ser Glu Lys Val Ser Tyr Val Ile Asp Val

        115                 120                 125
Ser Asp Ala Ser Thr Asn Thr Gln Pro Ile Val Asp Leu Asp Phe Pro
    130                 135                 140
Asp Ser Val Ala Ile Gly Lys Thr Val Asp Leu His Ser Gln Ala Tyr
145                 150                 155                 160
Asp Ala Asp Gly Asp Val Leu Thr Tyr Gln Trp Ala Leu Leu Ser Ser
                165                 170                 175
Pro Ser Asn Ala Thr Met Lys Leu Thr Asn Ser Ala Thr Pro Thr Ala

            180                 185                 190
Asn Leu Leu Ser Asn Thr Ala Gly Asp Tyr Gln Leu Lys Leu Thr Val
        195                 200                 205
Ser Asp Gly Tyr Glu Thr Ile Ser Glu Glu Met Thr Val Ser Tyr Ser
    210                 215                 220
Ala Glu Asn Val Ala Pro Lys Ala Ser Val Lys Asn Lys Gln Thr Phe
225                 230                 235                 240
Glu Leu Gly Thr Ser Ala Leu Leu Asp Ala Thr Ala Ser Thr Asp Gly

                245                 250                 255
Asn Asp Asp Gln Ile Thr Tyr Glu Trp Lys Val Val Ser Gln Pro Glu
            260                 265                 270
Asn Ser Thr Ala Thr Leu Ser Ser Thr Thr Asp Glu Lys Pro Asn Phe
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275 280 285

Thr Pro Asp Leu Ile Gly Asp Tyr Val Leu Ser Leu Thr Val Ser Asp

290 295 300

Gly Glu Leu Thr Ser Lys Lys Glu Tyr Ile Arg Leu Ser Ala Thr Glu

305 310 315 320

Val Gly Thr Ser Asp Leu Ile Leu Lys Tyr Ala Glu Asp Thr Thr Ala

325 330 335

Arg Val Trp Pro Phe Ala Glu Gln Phe Thr Ser Asn Ile Ser Thr Thr

340 345 350

Gly Asp Ala Pro Ala His Val Leu Leu Gly Thr Phe Ser Leu Glu Ala

355 360 365

Val Gly Lys Asp Tyr Thr Ile Asn Glu Thr Thr Ala Ile Asp Tyr Ile

370 375 380

Gly Asn Val Asp Ala Val Met Thr Gly Met Asn Ala Gly Gln Val Leu

385 390 395 400

Asn Ala Gly Asp Lys Ile Asn Val Lys Met Trp Ala Glu Pro Thr Gln

405 410 415

Gly Gln Leu Ser Met Ile Ser Tyr Gly Phe Ile Val Asp Thr Thr Leu

420 425 430

Glu Gln Tyr Met Gly Leu Gly Tyr Met Tyr Thr Ser Thr Ala Glu

435 440 445

<210> 1071

<211> 1317

<212> DNA

<213> Vibrio sp. HENC-01 SLP 1a

<400> 1071

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ggtggttcag actcaaacac tgcagattca cataaagcgc ctgtatccgt tgtctcaggt 120

tacgaaacag caaaagtcgg aaacagaatt cgtgtagatg gactgggtag ctacggtgta 180

gatgccagta tcgcaacgta cacttggtct atcagcaaaa aaccacaagg cagtaacgtc 240

aagttaaata acgttaatgc agtctctcca tacttcacac cagacgtggc aggagactac 300

accgttcagt tggtaaccaa cgatggcaaa aaagacagta gcgcacaatc gctgactatc 360

accgcaacag aagtaaatac caacgtggcg cccgttattt atgcatcgga aacctacacg 420

gcagcgcttg atcaaaccct gaaattagac gcgaaagctt acgacgctga taatgatatg 480

ctcagctacc aatgggctct taactcagca ccaaaaaaca ccacgatgtc gttgagcaac 540

gcaagcacca aacaagcagc gctaaaagca aacgttgcgg gtgaatacaa actaactcta 600

accgtctcag acggtaaaga agagacaact aaagagatca ccatcaacta ctctgccgat 660

aacgtagcac cggttgccat ggcaggacga gataccacat tcgaattggg tggaaccgca 720

accttagacg ctagcgcaag cattgatggc aatgattcag gtatcacgta ccagtgggaa 780

tttgtgtcca agccttcggc aagtactgca gaattgtcgg atgctacgtc agcaaaacca 840

acattcaccc ccgatgtcga gggtgattat gcgcttgctc taaccgtaag tgatggtgct 900

ctaagcagtg aaaaagattt tgttcgagta acggcatcga aagcaggaac aagcgacctc 960

gtattgcact tcaacggtga gaaaaaacga tggccgttcg cagaagaggt tactctgaat 1020

gaagaaatta aaggtgaagc gcccaaatac gtactcctag ggtcattaac tcttgaagcc 1080

gttggacacg attatgaggt tcagcagatc tttgcaatgg acgcagtcag cctcactcac 1140

gacgttaaat taagcggcat tgaagatggt agcgtgctac ctgtcggcga tgaaatagtt 1200

gttaagcttt ggtcggcgcc aacgcaagga aatactgtta cattgtctta cggttttatg 1260

atcaaagatc aaacaaactt ttatgcaggt cttggctacc acttccaaac aaactga 1317

<210> 1072

<211> 438

<212> PRT

<213> Vibrio sp. HENC-01 SLP 1a

<400> 1072

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1 5 10 15

Leu Ile Ala Cys Gly Gly Ser Asp Ser Asn Thr Ala Asp Ser His Lys

20 25 30

Ala Pro Val Ser Val Val Ser Gly Tyr Glu Thr Ala Lys Val Gly Asn

35 40 45

Arg Ile Arg Val Asp Gly Leu Gly Ser Tyr Gly Val Asp Ala Ser Ile

50 55 60

Ala Thr Tyr Thr Trp Ser Ile Ser Lys Lys Pro Gln Gly Ser Asn Val

65 70 75 80

Lys Leu Asn Asn Val Asn Ala Val Ser Pro Tyr Phe Thr Pro Asp Val

85 90 95

Ala Gly Asp Tyr Thr Val Gln Leu Val Thr Asn Asp Gly Lys Lys Asp

100 105 110

Ser Ser Ala Gln Ser Leu Thr Ile Thr Ala Thr Glu Val Asn Thr Asn

115 120 125

Val Ala Pro Val Ile Tyr Ala Ser Glu Thr Tyr Thr Ala Ala Leu Asp

130 135 140

Gln Thr Leu Lys Leu Asp Ala Lys Ala Tyr Asp Ala Asp Asn Asp Met

145 150 155 160

Leu Ser Tyr Gln Trp Ala Leu Asn Ser Ala Pro Lys Asn Thr Thr Met

165 170 175

Ser Leu Ser Asn Ala Ser Thr Lys Gln Ala Ala Leu Lys Ala Asn Val

180 185 190

Ala Gly Glu Tyr Lys Leu Thr Leu Thr Val Ser Asp Gly Lys Glu Glu

195 200 205

Thr Thr Lys Glu Ile Thr Ile Asn Tyr Ser Ala Asp Asn Val Ala Pro

210 215 220

Val Ala Met Ala Gly Arg Asp Thr Thr Phe Glu Leu Gly Gly Thr Ala

225 230 235 240

Thr Leu Asp Ala Ser Ala Ser Ile Asp Gly Asn Asp Ser Gly Ile Thr

245 250 255

Tyr Gln Trp Glu Phe Val Ser Lys Pro Ser Ala Ser Thr Ala Glu Leu

260 265 270

Ser Asp Ala Thr Ser Ala Lys Pro Thr Phe Thr Pro Asp Val Glu Gly

275 280 285

Asp Tyr Ala Leu Ala Leu Thr Val Ser Asp Gly Ala Leu Ser Ser Glu

290 295 300

Lys Asp Phe Val Arg Val Thr Ala Ser Lys Ala Gly Thr Ser Asp Leu

305 310 315 320

Val Leu His Phe Asn Gly Glu Lys Lys Arg Trp Pro Phe Ala Glu Glu

325 330 335

Val Thr Leu Asn Glu Glu Ile Lys Gly Glu Ala Pro Lys Tyr Val Leu

340 345 350

Leu Gly Ser Leu Thr Leu Glu Ala Val Gly His Asp Tyr Glu Val Gln

355 360 365

Gln Ile Phe Ala Met Asp Ala Val Ser Leu Thr His Asp Val Lys Leu

370 375 380

Ser Gly Ile Glu Asp Gly Ser Val Leu Pro Val Gly Asp Glu Ile Val

385 390 395 400

Val Lys Leu Trp Ser Ala Pro Thr Gln Gly Asn Thr Val Thr Leu Ser

405 410 415

Tyr Gly Phe Met Ile Lys Asp Gln Thr Asn Phe Tyr Ala Gly Leu Gly

420 425 430

Tyr His Phe Gln Thr Asn

435

<210> 1073

<211> 1413

<212> DNA

<213> Vibrio sp. HENC-01 SLP 1b

<400> 1073

atgagtctaa gctcgaaata tactctcaca ccattgctat tattacttct taatggttgt 60

aatggtggcg gtgggaatga tgcctctgaa ccccaaacgc ctaacaatca ccccctatt 120

gcgatagctg ggatcaatca acatgtaaag ctgagtgaaa aagtggtgca tctcgatggc 180

acgggtagcg tcgactacga tcaagactca atagccttct cttggaaaat ggtatcgaaa 240

cccttcaaga gtaaagcgga gctcattaat ccagaatcca gaactccgcg ctttgagcca 300

gacttattgg gcacttacct tgtagaattg gtggtgaacg atggcaaaac agacagccgc 360

cctaaccaag taaagataga agtcatcagg gaagacgaaa atacaccacc aacgattaaa 420

tttaccaaag ataagtacac cggtaaccta actcagcaaa ttaacctaaa cacaagacct 480

caagatattg atggcgataa attgtcgttt acatgggaag tgttgtccca cccacaaggc 540

agcaattact ctatagcgaa atcgactgtg tatgatttca actcaatcaa ggctgatacg 600

gagggcaatt atgtggttaa agtgactgca ttcgatggct tttctgaagc ttccgctacg 660

accaccgctt ccttttttta taaaaatgtc cctccacatg cggaggtaga tggttcaatg 720

ttttgggttc ttgataacat gagtgtccca ttgaatggca cacccagtgg tgatgccaac 780

ggcgatgtac tcacttatga atggcacttc actaaaaaac caaacggctc atccgccgtc 840

atcgatgatc cttatgctgt gctaacttca ttttcgccag atatctccgg ggattacgtc 900

gtcagtttaa ccgtaaatga tggcgagttt tcagatagcc attctgtggg agttagagta 960

agagcgattt ctgaatccca accgcacacc aaactcacac gcggctcaga taccactcct 1020

ttgcgactgc ctcacaagca aaatgacgtc atcgataaaa catccgatac gggtcctatt 1080

cctaactatt acactctcga tagctatact tttgaagcag taggaaagcc aatcaccatt 1140

actctcggaa agtatacgct tagtagtagc agcgacgatg taacaccaag gatattagtt 1200

ggctctcaaa gctactttag taaagacctc caagataacg atgttattat tgttatcccc 1260

gctggtgaca gcttaacctt ccaactacaa agtccaccga ccaacggcaa agtggcaaaa 1320

gcctcaatgg gcttcagctg gagtcttaac ggtcctaatg actttagtat ggttgaaaga 1380

atttccacaa cgattgaatt taccagccgt taa 1413

<210> 1074

<211> 470

<212> PRT

<213> Vibrio sp. HENC-01 SLP 1b

<400> 1074

Met Ser Leu Ser Ser Lys Tyr Thr Leu Thr Pro Leu Leu Leu Leu Leu

1 5 10 15

Leu Asn Gly Cys Asn Gly Gly Gly Gly Asn Asp Ala Ser Glu Pro Gln

20 25 30

Thr Pro Asn Asn His Pro Pro Ile Ala Ile Ala Gly Ile Asn Gln His

35 40 45

Val Lys Leu Ser Glu Lys Val Val His Leu Asp Gly Thr Gly Ser Val

50 55 60

Asp Tyr Asp Gln Asp Ser Ile Ala Phe Ser Trp Lys Met Val Ser Lys

65 70 75 80

Pro Phe Lys Ser Lys Ala Glu Leu Ile Asn Pro Glu Ser Arg Thr Pro

85 90 95

Arg Phe Glu Pro Asp Leu Leu Gly Thr Tyr Leu Val Glu Leu Val Val

100 105 110

Asn Asp Gly Lys Thr Asp Ser Arg Pro Asn Gln Val Lys Ile Glu Val

115 120 125

Ile Arg Glu Asp Glu Asn Thr Pro Pro Thr Ile Lys Phe Thr Lys Asp

130 135 140

Lys Tyr Thr Gly Asn Leu Thr Gln Gln Ile Asn Leu Asn Thr Arg Pro

145 150 155 160

Gln Asp Ile Asp Gly Asp Lys Leu Ser Phe Thr Trp Glu Val Leu Ser

165 170 175

His Pro Gln Gly Ser Asn Tyr Ser Ile Ala Lys Ser Thr Val Tyr Asp

180 185 190

Phe Asn Ser Ile Lys Ala Asp Thr Glu Gly Asn Tyr Val Val Lys Val

195 200 205

Thr Ala Phe Asp Gly Phe Ser Glu Ala Ser Ala Thr Thr Thr Ala Ser

210 215 220

Phe Phe Tyr Lys Asn Val Pro Pro His Ala Glu Val Asp Gly Ser Met

225 230 235 240

Phe Trp Val Leu Asp Asn Met Ser Val Pro Leu Asn Gly Thr Pro Ser

245 250 255

Gly Asp Ala Asn Gly Asp Val Leu Thr Tyr Glu Trp His Phe Thr Lys

260 265 270

Lys Pro Asn Gly Ser Ser Ala Val Ile Asp Asp Pro Tyr Ala Val Leu

275 280 285

Thr Ser Phe Ser Pro Asp Ile Ser Gly Asp Tyr Val Val Ser Leu Thr

290 295 300

Val Asn Asp Gly Glu Phe Ser Asp Ser His Ser Val Gly Val Arg Val

305 310 315 320

Arg Ala Ile Ser Glu Ser Gln Pro His Thr Lys Leu Thr Arg Gly Ser

325 330 335

Asp Thr Thr Pro Leu Arg Leu Pro His Lys Gln Asn Asp Val Ile Asp

340 345 350

Lys Thr Ser Asp Thr Gly Pro Ile Pro Asn Tyr Tyr Thr Leu Asp Ser

355 360 365

Tyr Thr Phe Glu Ala Val Gly Lys Pro Ile Thr Ile Thr Leu Gly Lys

370 375 380

Tyr Thr Leu Ser Ser Ser Ser Asp Asp Val Thr Pro Arg Ile Leu Val

385 390 395 400

Gly Ser Gln Ser Tyr Phe Ser Lys Asp Leu Gln Asp Asn Asp Val Ile

405 410 415

Ile Val Ile Pro Ala Gly Asp Ser Leu Thr Phe Gln Leu Gln Ser Pro

420 425 430

Pro Thr Asn Gly Lys Val Ala Lys Ala Ser Met Gly Phe Ser Trp Ser

435 440 445

Leu Asn Gly Pro Asn Asp Phe Ser Met Val Glu Arg Ile Ser Thr Thr

450 455 460

Ile Glu Phe Thr Ser Arg

465 470

<210> 1075

<211> 726

<212> DNA

<213> Vibrio sp. HENC-01 SLP 1c

<400> 1075

atgaaaccac ttcaactttc atggattgca gcagcaatga ttggtctaag cccacttgtt 60

catgcaggat ttgatggcgc gatcagtgat gattcgcttc gccaagtagg agaatcagaa 120

gtttgggtcc catttattca ctctaaaggc aatgcaggca tcggtaaaac aggtggcaaa 180

cgagtggact ttgaaggtct agctggtggt atttttgatg acgagcgaaa tggtgttcac 240

acatcaggca gcaaacattt tcaagacaat ttttacagtt ttgtccaagt agcgaatcaa 300

gatgtgtggt ttggagaatg gtacgaaggt aagaaagatt ctgagtttaa caaccgtacc 360

gtttactacg tcggtaatga tgcaggaacg actgtaccaa ccagcggcaa ggcgacctac 420

aacattactg gtattaacaa gctctctggc gcaaacaaac tttcaggtac gtttaacgct 480

gatttcggag ccaaaacgct agacggttca atcaacaata gcaacctaac ggtaagtgta 540

gacgcaacga ttaatgcagc aaccgcagca tttaatggcg ctgctcaagc tgtacagaat 600

ggcacaacca cgaatggcgc ttctcaaggt cacttctttg gtgcgaatgc tgctggcttg 660

gctggtatcg ccacctttac caacaatagc gatctagaca ctgcttttgg cggcgagaaa 720

aaataa 726

<210> 1076

<211> 241

<212> PRT

<213> Vibrio sp. HENC-01 SLP 1c

<400> 1076

Met Lys Pro Leu Gln Leu Ser Trp Ile Ala Ala Ala Met Ile Gly Leu
1 5 10 15

Ser Pro Leu Val His Ala Gly Phe Asp Gly Ala Ile Ser Asp Asp Ser
20 25 30

Leu Arg Gln Val Gly Glu Ser Glu Val Trp Val Pro Phe Ile His Ser
35 40 45

Lys Gly Asn Ala Gly Ile Gly Lys Thr Gly Gly Lys Arg Val Asp Phe
50 55 60

Glu Gly Leu Ala Gly Gly Ile Phe Asp Asp Glu Arg Asn Gly Val His
65 70 75 80

Thr Ser Gly Ser Lys His Phe Gln Asp Asn Phe Tyr Ser Phe Val Gln
85 90 95

Val Ala Asn Gln Asp Val Trp Phe Gly Glu Trp Tyr Glu Gly Lys Lys
100 105 110

Asp Ser Glu Phe Asn Asn Arg Thr Val Tyr Tyr Val Gly Asn Asp Ala
115 120 125

Gly Thr Thr Val Pro Thr Ser Gly Lys Ala Thr Tyr Asn Ile Thr Gly
130 135 140

Ile Asn Lys Leu Ser Gly Ala Asn Lys Leu Ser Gly Thr Phe Asn Ala
145 150 155 160

Asp Phe Gly Ala Lys Thr Leu Asp Gly Ser Ile Asn Asn Ser Asn Leu
165 170 175

Thr Val Ser Val Asp Ala Thr Ile Asn Ala Ala Thr Ala Ala Phe Asn
180 185 190

Gly Ala Ala Gln Ala Val Gln Asn Gly Thr Thr Thr Asn Gly Ala Ser

195 200 205

Gln Gly His Phe Phe Gly Ala Asn Ala Ala Gly Leu Ala Gly Ile Ala

210 215 220

Thr Phe Thr Asn Asn Ser Asp Leu Asp Thr Ala Phe Gly Gly Glu Lys

225 230 235 240

Lys

<210> 1077

<211> 714

<212> DNA

<213> X. doucetiae SLP 2a

<400> 1077

atgaaaaaga tcaatatatt cattgccatg ttaggcattt ttggacttat cacacaggtt 60

caggcaaaag ttgcgtatgg tataagccaa caagaaactg acccacatct tctcatcgga 120

gaggtagatg gtgaacccgg tttaggtatc actttaccaa taacagggaa taaattattt 180

tctgcctctt acctgaaaaa gttagctaca cgcgataata atggtgttta tcgtttcaaa 240

ctggagaata atcctattgc tgagaaccaa tatctcgaca tctttcaaat tcccaatacg 300

gatatttact ttggggaatg ggcacaaaaa acgcctgata aatcggatat tacccacact 360

gtttttttatg caggtaaaga tgtgacaacc aatctgccaa ctggcggcac tgcgacctat 420

acagtaacag gacttaaccg atataacgat aacaatctcc tctctggtaa attcaccgca 480

gactttggta acaaaaaact gaatggttca ctcagtaatg actcattaaa tatcgatatt 540

gatgccaata taaataatga tgccggattt tcaggtaaag ccacggccaa tggaaatatt 600

aacggcgtca ccgatgggaa attttatggt aattccgcct cctctctggc agggtatgcc 660

aaatttgcta gtgacagaaa caaagatacg gctttcggtg gtactaaaca gtaa 714

<210> 1078

<211> 237

<212> PRT

<213> X. doucetiae SLP 2a

<400> 1078

Met Lys Lys Ile Asn Ile Phe Ile Ala Met Leu Gly Ile Phe Gly Leu

1 5 10 15

Ile Thr Gln Val Gln Ala Lys Val Ala Tyr Gly Ile Ser Gln Gln Glu

20 25 30

Thr Asp Pro His Leu Leu Ile Gly Glu Val Asp Gly Glu Pro Gly Leu

35 40 45

Gly Ile Thr Leu Pro Ile Thr Gly Asn Lys Leu Phe Ser Ala Ser Tyr

50 55 60

Leu Lys Lys Leu Ala Thr Arg Asp Asn Asn Gly Val Tyr Arg Phe Lys

65 70 75 80

Leu Glu Asn Asn Pro Ile Ala Glu Asn Gln Tyr Leu Asp Ile Phe Gln

85 90 95

Ile Pro Asn Thr Asp Ile Tyr Phe Gly Glu Trp Ala Gln Lys Thr Pro

100 105 110

Asp Lys Ser Asp Ile Thr His Thr Val Phe Tyr Ala Gly Lys Asp Val

115 120 125

Thr Thr Asn Leu Pro Thr Gly Gly Thr Ala Thr Tyr Thr Val Thr Gly

130 135 140

Leu Asn Arg Tyr Asn Asp Asn Asn Leu Leu Ser Gly Lys Phe Thr Ala

145 150 155 160

Asp Phe Gly Asn Lys Lys Leu Asn Gly Ser Leu Ser Asn Asp Ser Leu

165 170 175

Asn Ile Asp Ile Asp Ala Asn Ile Asn Asn Asp Ala Gly Phe Ser Gly

180 185 190

Lys Ala Thr Ala Asn Gly Asn Ile Asn Gly Val Thr Asp Gly Lys Phe

195 200 205

Tyr Gly Asn Ser Ala Ser Ser Leu Ala Gly Tyr Ala Lys Phe Ala Ser

210 215 220

Asp Arg Asn Lys Asp Thr Ala Phe Gly Gly Thr Lys Gln

225 230 235

<210> 1079

<211> 849

<212> DNA

<213> X. nematophila SLP 2a

<400> 1079

atgaatacaa aatctaaaat ctatttagct ctcgcactgg tactttctgt tacagcctgt 60

tctagaggag ggggttctca ccacggtgtc agtggtgaaa caggtaagca gcctggatat 120

aaagagaggc cgcttttgcc ctctgattat ccatcacaaa gcaaacaaaa caccgtatcg 180

ggccttaagg gatattccaa cggcagtttc tctaattatg tgtatacgac ccttactaat 240

tcccctgaag cgggtgcaaa cccagccccc ctgagcaagt attactacct ccatatacca 300

ggtgagggtg ataattatgt cccgatacaa gtgtcgaatt ttacggttgg tggagattat 360

gatatgtcat ttatggccca aaacaagaag gcagtgatag gttcttccaa taagcggata 420

taccttgcga cggatcttaa taatttaagg ccatacaccg gatcagtgaa taaagctact 480

tttagcggtc tggctcgtca cagtgaaaac ggaaaactta gtattttgaa ggtggttatg 540

gacgccacgt tcggaggtac gggggagaat ggagaaatgt ttgcccagat gaaggggagt 600

cttcagaaaa atggtaaaga ctgggctcca ttcgaaggat ataccctat aatgaacggc 660

atgagtacaa tgaagtttac cggcgatgca ccagaaggac tgcgaaaggg agatctaacg 720

ggttacttct ctgacccgga ggctggtgct tttactggaa catataattc taaggacggt 780

aaaacgtatg gtgctttcct tttggataac cagcatacat atccgtcgtc tcctaacccc 840

agcaattaa 849

<210> 1080

<211> 282

<212> PRT

<213> X. nematophila SLP 2a

<400> 1080

Met Asn Thr Lys Ser Lys Ile Tyr Leu Ala Leu Ala Leu Val Leu Ser
1 5 10 15

Val Thr Ala Cys Ser Arg Gly Gly Gly Ser His His Gly Val Ser Gly
20 25 30

Glu Thr Gly Lys Gln Pro Gly Tyr Lys Glu Arg Pro Leu Leu Pro Ser
35 40 45

Asp Tyr Pro Ser Gln Ser Lys Gln Asn Thr Val Ser Gly Leu Lys Gly
50 55 60

Tyr Ser Asn Gly Ser Phe Ser Asn Tyr Val Tyr Thr Thr Leu Thr Asn
65 70 75 80

Ser Pro Glu Ala Gly Ala Asn Pro Ala Pro Leu Ser Lys Tyr Tyr Tyr

85 90 95

Leu His Ile Pro Gly Glu Gly Asp Asn Tyr Val Pro Ile Gln Val Ser

100 105 110

Asn Phe Thr Val Gly Gly Asp Tyr Asp Met Ser Phe Met Ala Gln Asn

115 120 125

Lys Lys Ala Val Ile Gly Ser Ser Asn Lys Arg Ile Tyr Leu Ala Thr

130 135 140

Asp Leu Asn Asn Leu Arg Pro Tyr Thr Gly Ser Val Asn Lys Ala Thr

145 150 155 160

Phe Ser Gly Leu Ala Arg His Ser Glu Asn Gly Lys Leu Ser Ile Leu

165 170 175

Lys Val Val Met Asp Ala Thr Phe Gly Gly Thr Gly Glu Asn Gly Glu

180 185 190

Met Phe Ala Gln Met Lys Gly Ser Leu Gln Lys Asn Gly Lys Asp Trp

195 200 205

Ala Pro Phe Glu Gly Tyr Thr Pro Ile Met Asn Gly Met Ser Thr Met

210 215 220

Lys Phe Thr Gly Asp Ala Pro Glu Gly Leu Arg Lys Gly Asp Leu Thr

225 230 235 240

Gly Tyr Phe Ser Asp Pro Glu Ala Gly Ala Phe Thr Gly Thr Tyr Asn

245 250 255

Ser Lys Asp Gly Lys Thr Tyr Gly Ala Phe Leu Leu Asp Asn Gln His

260 265 270

Thr Tyr Pro Ser Ser Pro Asn Pro Ser Asn

275 280

<210> 1081

<211> 741

<212> DNA

<213> X. nematophilia SLP 1a

<400> 1081

atgaaaaagt tcaacgtatt agttgccgct ttaggggcat tgggatttat ggcacaggct 60

caggcagcag taggatttgg tcagagccaa gatgaaacaa cgccacacat taaggttggt 120

gcaacccaac cgggttcagg cccacacggt ggcaaaggtg gcgaacccgg cattggtgtc 180

agttccgttt atggtggtca gatcactggc tttgccggct tgactcgcat ggcacctgct 240

gacagcaatg gtatccataa catctcaatg gcaggagcac ccggctctca cggtggtatg 300

ggcgtattcc atttcagcaa agttgccaat gcagatgttt acttcggtga atggtctcag 360

acaggtcagg catcggatag cacccacacg gtttattatg caggcaagga cgtcactacc 420

aatatcccaa cagacggtac agcgacttac accgtgacgg gtattaacca atacagtggc 480

gacaatgccc tgtccggcac atttaccgca gattttggtg aaaaaacgct ggctggttca 540

ctggcaaata ctgcgatgac gatagacatt gatgccagta tcggcgctga tgccaaattt 600

gaaggtgctg ccataacgga tactttggtt gggcaaacca acggccactt ctttggtgac 660

agtgctgcca gcttggctgg atatgccaca tttgctgatg acagtaccaa ggataccgca 720

ttcggtggtt ctaaacagta a 741

<210> 1082

<211> 246

<212> PRT

<213> X. nematophilia SLP 1a

<400> 1082

Met Lys Lys Phe Asn Val Leu Val Ala Ala Leu Gly Ala Leu Gly Phe

1 5 10 15

Met Ala Gln Ala Gln Ala Ala Val Gly Phe Gly Gln Ser Gln Asp Glu

20 25 30

Thr Thr Pro His Ile Lys Val Gly Ala Thr Gln Pro Gly Ser Gly Pro

35 40 45

His Gly Gly Lys Gly Gly Glu Pro Gly Ile Gly Val Ser Ser Val Tyr

50 55 60

Gly Gly Gln Ile Thr Gly Phe Ala Gly Leu Thr Arg Met Ala Pro Ala

65 70 75 80

Asp Ser Asn Gly Ile His Asn Ile Ser Met Ala Gly Ala Pro Gly Ser

85 90 95

His Gly Gly Met Gly Val Phe His Phe Ser Lys Val Ala Asn Ala Asp

100 105 110

Val Tyr Phe Gly Glu Trp Ser Gln Thr Gly Gln Ala Ser Asp Ser Thr

115 120 125

His Thr Val Tyr Tyr Ala Gly Lys Asp Val Thr Thr Asn Ile Pro Thr

130 135 140

Asp Gly Thr Ala Thr Tyr Thr Val Thr Gly Ile Asn Gln Tyr Ser Gly

145 150 155 160

Asp Asn Ala Leu Ser Gly Thr Phe Thr Ala Asp Phe Gly Glu Lys Thr

165 170 175

Leu Ala Gly Ser Leu Ala Asn Thr Ala Met Thr Ile Asp Ile Asp Ala

180 185 190

Ser Ile Gly Ala Asp Ala Lys Phe Glu Gly Ala Ala Ile Thr Asp Thr

195 200 205

Leu Val Gly Gln Thr Asn Gly His Phe Phe Gly Asp Ser Ala Ala Ser

210 215 220

Leu Ala Gly Tyr Ala Thr Phe Ala Asp Asp Ser Thr Lys Asp Thr Ala

225 230 235 240

Phe Gly Gly Ser Lys Gln

245

<210> 1083

<211> 1017

<212> DNA

<213> P. multocida PM1514

<400> 1083

atgcagtatt ttgacatcaa aaaatctctc cctgtttttt gttctcttct gattaccgct 60

tgtagtggtg gtgggggtaa taacaatcca tctcactctc ctatggaaaa acgtaccgta 120

actataccac aagcacaaaa agtagcagaa aaaccagcgc taacaataca aacagtggta 180

acttcaccaa ctacaccaat taaagcgccc tcactcgctc cgactattga tactgcgcct 240

aaacaaaatc ccgtgccgac agcgcaaata acggctactt taccagccga acctgttaaa 300

gtgccagttc tgattcccga agtaaacaaa acacttttag aaacatcaac taatccagta 360

aaagattctt ataataaaga tgctgtattt acatacgaat taatcgcaaa tccagatgca 420

gattatagcg atcaaaaatt gattcttaaa aaagaaatta gttatatcaa acttaatcta 480

ggcataaatc aagacaataa aaatgcacca agctatattt ttaatttact agatgacaat 540

gtctattatg gtttttatcg tgatactcaa gatatgaaca gaatagaaaa taaatatact 600

tatgctttca aaaaagaagc tgaaaatttt gataaccttc aaaaatttaa tgcgacttat 660

gaaggtcaat tttggttctc tagtatagat actccaaatg tacctactgt tgcaagagca 720

ttcttaacat ataacaatgg tagagtggat ggtgaaatat tggctaaaca ttggaatgaa 780

aaattgtttc agattactgg atttgataat aatcctcgta aagtagaaat ttttcctact 840

gtagaatatt tacctaattc gggaacaaga ctaacaaaag gagccacatc acctcatcgt 900

ttccaaatgg acttacattt catcaatagt acaaatggtg aaaaaaacaa atatcttgtc 960

ggccaaggta gtactgagca gtactggggt gttttaggta tggagaaaaa acaataa 1017

<210> 1084

<211> 338

<212> PRT

<213> P. multocida

<400> 1084

Met Gln Tyr Phe Asp Ile Lys Lys Ser Leu Pro Val Phe Cys Ser Leu
1 5 10 15

Leu Ile Thr Ala Cys Ser Gly Gly Gly Gly Asn Asn Asn Pro Ser His
20 25 30

Ser Pro Met Glu Lys Arg Thr Val Thr Ile Pro Gln Ala Gln Lys Val
35 40 45

Ala Glu Lys Pro Ala Leu Thr Ile Gln Thr Val Val Thr Ser Pro Thr
50 55 60

Thr Pro Ile Lys Ala Pro Ser Leu Ala Pro Thr Ile Asp Thr Ala Pro
65 70 75 80

Lys Gln Asn Pro Val Pro Thr Ala Gln Ile Thr Ala Thr Leu Pro Ala
85 90 95

Glu Pro Val Lys Val Pro Val Leu Ile Pro Glu Val Asn Lys Thr Leu
100 105 110

Leu Glu Thr Ser Thr Asn Pro Val Lys Asp Ser Tyr Asn Lys Asp Ala
115 120 125

Val Phe Thr Tyr Glu Leu Ile Ala Asn Pro Asp Ala Asp Tyr Ser Asp

130 135 140

Gln Lys Leu Ile Leu Lys Lys Glu Ile Ser Tyr Ile Lys Leu Asn Leu
145 150 155 160
Gly Ile Asn Gln Asp Asn Lys Asn Ala Pro Ser Tyr Ile Phe Asn Leu
165 170 175
Leu Asp Asp Asn Val Tyr Tyr Gly Phe Tyr Arg Asp Thr Gln Asp Met
180 185 190
Asn Arg Ile Glu Asn Lys Tyr Thr Tyr Ala Phe Lys Lys Glu Ala Glu
195 200 205

Asn Phe Asp Asn Leu Gln Lys Phe Asn Ala Thr Tyr Glu Gly Gln Phe
210 215 220
Trp Phe Ser Ser Ile Asp Thr Pro Asn Val Pro Thr Val Ala Arg Ala
225 230 235 240
Phe Leu Thr Tyr Asn Asn Gly Arg Val Asp Gly Glu Ile Leu Ala Lys
245 250 255
His Trp Asn Glu Lys Leu Phe Gln Ile Thr Gly Phe Asp Asn Asn Pro
260 265 270

Arg Lys Val Glu Ile Phe Pro Thr Val Glu Tyr Leu Pro Asn Ser Gly
275 280 285
Thr Arg Leu Thr Lys Gly Ala Thr Ser Pro His Arg Phe Gln Met Asp
290 295 300
Leu His Phe Ile Asn Ser Thr Asn Gly Glu Lys Asn Lys Tyr Leu Val
305 310 315 320
Gly Gln Gly Ser Thr Glu Gln Tyr Trp Gly Val Leu Gly Met Glu Lys
325 330 335

Lys Gln

<210> 1085
<211> 1041
<212> DNA
<213> P. multocida PM1514-Flag

<400> 1085

atgcagtatt ttgacatcaa aaaatctctc cctgtttttt gttctcttct gattaccgct 60

tgtagtggtg gtgggggtaa taacaatcca tctcactctc ctatggaaaa acgtaccgta 120

actataccac aagcacaaaa agtagcagaa aaaccagcgc taacaataca aacagtggta 180

acttcaccaa ctacaccaat taaagcgccc tcactcgctc cgactattga tactgcgcct 240

aaacaaaatc ccgtgccgac agcgcaaata acggctactt taccagccga acctgttaaa 300

gtgccagttc tgattcccga agtaaacaaa acacttttag aaacatcaac taatccagta 360

aaagattctt ataataaaga tgctgtattt acatacgaat taatcgcaaa tccagatgca 420

gattatagcg atcaaaaatt gattcttaaa aaagaaatta gttatatcaa acttaatcta 480

ggcataaatc aagacaataa aaatgcacca agctatattt ttaatttact agatgacaat 540

gtctattatg gtttttatcg tgatactcaa gatatgaaca gaatagaaaa taaatatact 600

tatgctttca aaaaagaagc tgaaaatttt gataaccttc aaaaatttaa tgcgacttat 660

gaaggtcaat tttggttctc tagtatagat actccaaatg tacctactgt tgcaagagca 720

ttcttaacat ataacaatgg tagagtggat ggtgaaatat tggctaaaca ttggaatgaa 780

aaattgtttc agattactgg atttgataat aatcctcgta aagtagaaat ttttcctact 840

gtagaatatt tacctaattc gggaacaaga ctaacaaaag gagccacatc acctcatcgt 900

ttccaaatgg acttacattt catcaatagt acaaatggtg aaaaaaacaa atatcttgtc 960

ggccaaggta gtactgagca gtactggggt gttttaggta tggagaaaaa acaagactac 1020

aaggatgacg atgacaagta a 1041

<210> 1086

<211> 346

<212> PRT

<213> P. multocida PM1514-Flag

<400> 1086

Met Gln Tyr Phe Asp Ile Lys Lys Ser Leu Pro Val Phe Cys Ser Leu

1 5 10 15

Leu Ile Thr Ala Cys Ser Gly Gly Gly Gly Asn Asn Asn Pro Ser His

20 25 30

Ser Pro Met Glu Lys Arg Thr Val Thr Ile Pro Gln Ala Gln Lys Val

35 40 45

Ala Glu Lys Pro Ala Leu Thr Ile Gln Thr Val Val Thr Ser Pro Thr

50 55 60

Thr Pro Ile Lys Ala Pro Ser Leu Ala Pro Thr Ile Asp Thr Ala Pro

65 70 75 80

Lys Gln Asn Pro Val Pro Thr Ala Gln Ile Thr Ala Thr Leu Pro Ala

85 90 95

Glu Pro Val Lys Val Pro Val Leu Ile Pro Glu Val Asn Lys Thr Leu

100 105 110

Leu Glu Thr Ser Thr Asn Pro Val Lys Asp Ser Tyr Asn Lys Asp Ala

115 120 125

Val Phe Thr Tyr Glu Leu Ile Ala Asn Pro Asp Ala Asp Tyr Ser Asp

130 135 140

Gln Lys Leu Ile Leu Lys Lys Glu Ile Ser Tyr Ile Lys Leu Asn Leu

145 150 155 160

Gly Ile Asn Gln Asp Asn Lys Asn Ala Pro Ser Tyr Ile Phe Asn Leu

165 170 175

Leu Asp Asp Asn Val Tyr Tyr Gly Phe Tyr Arg Asp Thr Gln Asp Met

180 185 190

Asn Arg Ile Glu Asn Lys Tyr Thr Tyr Ala Phe Lys Lys Glu Ala Glu

195 200 205

Asn Phe Asp Asn Leu Gln Lys Phe Asn Ala Thr Tyr Glu Gly Gln Phe

210 215 220

Trp Phe Ser Ser Ile Asp Thr Pro Asn Val Pro Thr Val Ala Arg Ala

225 230 235 240

Phe Leu Thr Tyr Asn Asn Gly Arg Val Asp Gly Glu Ile Leu Ala Lys

245 250 255

His Trp Asn Glu Lys Leu Phe Gln Ile Thr Gly Phe Asp Asn Asn Pro

260 265 270

Arg Lys Val Glu Ile Phe Pro Thr Val Glu Tyr Leu Pro Asn Ser Gly

275 280 285

Thr Arg Leu Thr Lys Gly Ala Thr Ser Pro His Arg Phe Gln Met Asp

290 295 300

Leu His Phe Ile Asn Ser Thr Asn Gly Glu Lys Asn Lys Tyr Leu Val

305 310 315 320

Gly Gln Gly Ser Thr Glu Gln Tyr Trp Gly Val Leu Gly Met Glu Lys

325 330 335

Lys Gln Asp Tyr Lys Asp Asp Asp Asp Lys

340 345

<210> 1087

<211> 1524

<212> DNA

<213> P. multocida PM1515 (N-terminal His)

<400> 1087

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atggccatgg cccatcatca ccatcaccac aatactgtga tccccgtaga taatagccga 120

ccagatgaaa cattttccca gacgtcacct aaacagcatc tcttttctca gaaaccgaaa 180

ccgactgaac ccacatcaag tgcgagcagt cagcaaattt cgttgaccat tgaacaactt 240

gctagcagac ctgatttggt gcttcgcgcc ttaatcccgg cattaaaaaa taatgatatg 300

cgcggtgcgg aaattctgtt acccatttat gcccaacaat cgcctgatcc gctgttatta 360

aaatgggcac aggcaatggt tgctcgtaaa caaggaaaat taagtgaatc agtacgttta 420

tatcgccaaa ttattgcaga aaagcccaat ttacaacctg cacgcttaca actcgctatc 480

gccttaacgc aaaaccgtga aaatgaagcc gcgaaagcac aatttaacca actgcgttca 540

gaaaacttac ccgcgccttt actgaccctc attgatagct atattgatgc gattaaccaa 600

cgcgatagct ggaatgtgta tggcggagta aattatttgc atgagaacaa tgtcaataat 660

gcaccgccta aaggcaccaa agcggaaggc ttcacccctt caagccaacc agaaaaagca 720

catggtttaa gttattttat taatttaagt aaaaattggt cattagccca cggctttttc 780

acagaattta gtgccgatat caatggaaaa tattattggg ataatcataa gtatgatgag 840

ttttcgactc gcctcaatct aggtggtggt taccgtaatg ccaaaacaga agtgaaactt 900

ataccttttcg tggaacaatt ttggtatgtg ggcggtgaaa atgcaacaaa ggatgcacgt 960

acattacacc gttattctaa aagctcaggt atcaaccttg acgtggatta ttggttgaca 1020

cccaattgga aaatctccac ggttctggaa tataccgaac aacgttatat ccaacctcaa 1080

cggcaaagct caaatggaaa tagctattcc attagcaata ctctgatata tatgccaaat 1140

agccaacaat tttggtttgt tggattcgat tattatcaaa aaatacccgg cttaaaagcc 1200

tatgcttttg aacgtcaagg aatacgtcta ggttgggggc aagaatggcc gaaaggcatt 1260

tcaacgcgtt tacaaacaag ctatgccacg cgtacttatc gagcaccttc agcagaaaag 1320

aatatgattt tcgcgccgag tttctttaaa gttgtgcaaa aaaatcgcga atacggtgtc 1380

aattttacga tttggcatcg tagtcttcac tggttgggga tcacgcctaa aatcacttgg 1440

gcatatcaaa aaaccaccag taacaatcct ttttccgaat atgaccggaa tcggatttat 1500

ttaaccttca gtaaaacatt ttaa 1524

<210> 1088

<211> 507

<212> PRT

<213> P. multocida PM1515 (N-terminal His)

<400> 1088

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
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Ala Gln Pro Ala Met Ala Met Ala His His His His His His Asn Thr
20 25 30

Val Ile Pro Val Asp Asn Ser Arg Pro Asp Glu Thr Phe Ser Gln Thr
35 40 45

Ser Pro Lys Gln His Leu Phe Ser Gln Lys Pro Lys Pro Thr Glu Pro
50 55 60

Thr Ser Ser Ala Ser Ser Gln Gln Ile Ser Leu Thr Ile Glu Gln Leu
65 70 75 80

Ala Ser Arg Pro Asp Leu Val Leu Arg Ala Leu Ile Pro Ala Leu Lys
85 90 95

Asn Asn Asp Met Arg Gly Ala Glu Ile Leu Leu Pro Ile Tyr Ala Gln
100 105 110

Gln Ser Pro Asp Pro Leu Leu Leu Lys Trp Ala Gln Ala Met Val Ala
115 120 125

Arg Lys Gln Gly Lys Leu Ser Glu Ser Val Arg Leu Tyr Arg Gln Ile
130 135 140

Ile Ala Glu Lys Pro Asn Leu Gln Pro Ala Arg Leu Gln Leu Ala Ile
145 150 155 160

Ala Leu Thr Gln Asn Arg Glu Asn Glu Ala Ala Lys Ala Gln Phe Asn

165 170 175

Gln Leu Arg Ser Glu Asn Leu Pro Ala Pro Leu Leu Thr Leu Ile Asp
180 185 190
Ser Tyr Ile Asp Ala Ile Asn Gln Arg Asp Ser Trp Asn Val Tyr Gly
195 200 205
Gly Val Asn Tyr Leu His Glu Asn Asn Val Asn Asn Ala Pro Pro Lys
210 215 220
Gly Thr Lys Ala Glu Gly Phe Thr Pro Ser Ser Gln Pro Glu Lys Ala
225 230 235 240

His Gly Leu Ser Tyr Phe Ile Asn Leu Ser Lys Asn Trp Ser Leu Ala
245 250 255
His Gly Phe Phe Thr Glu Phe Ser Ala Asp Ile Asn Gly Lys Tyr Tyr
260 265 270
Trp Asp Asn His Lys Tyr Asp Glu Phe Ser Thr Arg Leu Asn Leu Gly
275 280 285
Gly Gly Tyr Arg Asn Ala Lys Thr Glu Val Lys Leu Ile Pro Phe Val
290 295 300

Glu Gln Phe Trp Tyr Val Gly Gly Glu Asn Ala Thr Lys Asp Ala Arg
305 310 315 320
Thr Leu His Arg Tyr Ser Lys Ser Ser Gly Ile Asn Leu Asp Val Asp
325 330 335
Tyr Trp Leu Thr Pro Asn Trp Lys Ile Ser Thr Val Leu Glu Tyr Thr
340 345 350
Glu Gln Arg Tyr Ile Gln Pro Gln Arg Gln Ser Ser Asn Gly Asn Ser
355 360 365

Tyr Ser Ile Ser Asn Thr Leu Ile Tyr Met Pro Asn Ser Gln Gln Phe
370 375 380
Trp Phe Val Gly Phe Asp Tyr Tyr Gln Lys Ile Pro Gly Leu Lys Ala
385 390 395 400
Tyr Ala Phe Glu Arg Gln Gly Ile Arg Leu Gly Trp Gly Gln Glu Trp
405 410 415

Pro Lys Gly Ile Ser Thr Arg Leu Gln Thr Ser Tyr Ala Thr Arg Thr
420 425 430

Tyr Arg Ala Pro Ser Ala Glu Lys Asn Met Ile Phe Ala Pro Ser Phe
435 440 445

Phe Lys Val Val Gln Lys Asn Arg Glu Tyr Gly Val Asn Phe Thr Ile
450 455 460

Trp His Arg Ser Leu His Trp Leu Gly Ile Thr Pro Lys Ile Thr Trp
465 470 475 480

Ala Tyr Gln Lys Thr Thr Ser Asn Asn Pro Phe Ser Glu Tyr Asp Arg
485 490 495

Asn Arg Ile Tyr Leu Thr Phe Ser Lys Thr Phe
500 505

<210> 1089

<211> 2571

<212> DNA

<213> P. multocida PM1515-PM1514-Flag

<400> 1089

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atggccatgg caaatactgt gatccccgta gataatagcc gaccagatga aacattttcc 120

cagacgtcac ctaaacagca tctcttttct cagaaaccga aaccgactga acccacatca 180

agtgcgagca gtcagcaaat ttcgttgacc attgaacaac ttgctagcag acctgatttg 240

gtgcttcgcg ccttaatccc ggcattaaaa aataatgata tgcgcggtgc ggaaattctg 300

ttacccattt atgcccaaca atcgcctgat ccgctgttat taaaatgggc acaggcaatg 360

gttgctcgta aacaaggaaa attaagtgaa tcagtacgtt tatatcgcca aattattgca 420

gaaaagccca atttacaacc tgcacgctta caactcgcta tcgccttaac gcaaaaccgt 480

gaaaatgaag ccgcgaaagc acaatttaac caactgcgtt cagaaaactt acccgcgcct 540

ttactgaccc tcattgatag ctatattgat gcgattaacc aacgcgatag ctggaatgtg 600

tatggcggag taaattattt gcatgagaac aatgtcaata atgcaccgcc taaaggcacc 660

aaagcggaag gcttcacccc ttcaagccaa ccagaaaaag cacatggttt aagttatttt 720

attaatttaa gtaaaaattg gtcattagcc cacggctttt tcacagaatt tagtgccgat 780

atcaatggaa aatattattg ggataatcat aagtatgatg agttttcgac tcgcctcaat 840

ctaggtggtg gttaccgtaa tgccaaaaca gaagtgaaac ttataccttt cgtggaacaa 900

ttttggtatg tgggcggtga aaatgcaaca aaggatgcac gtacattaca ccgttattct 960

aaaagctcag gtatcaacct tgacgtggat tattggttga cacccaattg gaaaatctcc 1020

acggttctgg aatataccga acaacgttat atccaacctc aacggcaaag caaaaatgga 1080

aatagctatt ccattagcaa tactctgata tatatgccaa atagccaaca attttggttt 1140

gttggattcg attattatca aaaaaatacc cggctaaaag cctatgcttt tgaacgtcaa 1200

ggaatacgtc taggttgggg gcaagaatgg ccgaaaggca tttcaacgcg tttacaaaca 1260

agctatgcca cgcgtactta tcgagcacct tcagcagaaa agaatatgat tttcgcgccg 1320

agtttcttta aagttgtgca aaaaaatcgc gaatacggtg tcaattttac gatttggcat 1380

cgtagtcttc actggttggg gatcacgcct aaaatcactt gggcatatca aaaaaccacc 1440

agtaacaatc ctttttccga atatgaccgg aatcggattt atttaacctt cagtaaaaca 1500

ttttaaccat tttatttaaa aggaattgtc atgcagtatt ttgacatcaa aaaatctctc 1560

cctgtttttt gttctcttct gattaccgct tgtagtggtg gtgggggtaa taacaatcca 1620

tctcactctc ctatggaaaa acgtaccgta actataccac aagcacaaaa agtagcagaa 1680

aaaccagcgc taacaataca aacagtggta acttcaccaa ctacaccaat taaagcgccc 1740

tcactcgctc cgactattga tactgcgcct aaacaaaatc ccgtgccgac agcgcaaata 1800

acggctactt taccagccga acctgttaaa gtgccagttc tgattcccga agtaaacaaa 1860

acacttttag aaacatcaac taatccagta aaagattctt ataataaaga tgctgtattt 1920

acatacgaat taatcgcaaa tccagatgca gattatagcg atcaaaaatt gattcttaaa 1980

aaagaaatta gttatatcaa acttaatcta ggcataaatc aagacaataa aaatgcacca 2040

agctatattt ttaatttact agatgacaat gtctattatg gtttttatcg tgatactcaa 2100

gatatgaaca gaatagaaaa taaatatact tatgctttca aaaaagaagc tgaaaatttt 2160

gataaccttc aaaaatttaa tgcgacttat gaaggtcaat tttggttctc tagtatagat 2220

actccaaatg tacctactgt tgcaagagca ttcttaacat ataacaatgg tagagtggat 2280

ggtgaaatat tggctaaaca ttggaatgaa aaattgtttc agattactgg atttgataat 2340

aatcctcgta aagtagaaat ttttcctact gtagaatatt tacctaattc gggaacaaga 2400

ctaacaaaag gagccacatc acctcatcgt ttccaaatgg acttacattt catcaatagt 2460

acaaatggtg aaaaaaacaa atatcttgtc ggccaaggta gtactgagca gtactggggt 2520

gttttaggta tggagaaaaa acaagactac aaggatgacg atgacaagta a 2571

<210> 1090

<211> 855

<212> PRT

<213> P. multocida PM1515-PM1514-Flag

<400> 1090

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
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Ala Gln Pro Ala Met Ala Met Ala Asn Thr Val Ile Pro Val Asp Asn
20 25 30

Ser Arg Pro Asp Glu Thr Phe Ser Gln Thr Ser Pro Lys Gln His Leu
35 40 45

Phe Ser Gln Lys Pro Lys Pro Thr Glu Pro Thr Ser Ser Ala Ser Ser
50 55 60

Gln Gln Ile Ser Leu Thr Ile Glu Gln Leu Ala Ser Arg Pro Asp Leu
65 70 75 80

Val Leu Arg Ala Leu Ile Pro Ala Leu Lys Asn Asn Asp Met Arg Gly
85 90 95

Ala Glu Ile Leu Leu Pro Ile Tyr Ala Gln Gln Ser Pro Asp Pro Leu
100 105 110

Leu Leu Lys Trp Ala Gln Ala Met Val Ala Arg Lys Gln Gly Lys Leu
115 120 125

Ser Glu Ser Val Arg Leu Tyr Arg Gln Ile Ile Ala Glu Lys Pro Asn
130 135 140

Leu Gln Pro Ala Arg Leu Gln Leu Ala Ile Ala Leu Thr Gln Asn Arg
145 150 155 160

Glu Asn Glu Ala Ala Lys Ala Gln Phe Asn Gln Leu Arg Ser Glu Asn
165 170 175

Leu Pro Ala Pro Leu Leu Thr Leu Ile Asp Ser Tyr Ile Asp Ala Ile
180 185 190

Asn Gln Arg Asp Ser Trp Asn Val Tyr Gly Gly Val Asn Tyr Leu His
195 200 205

Glu Asn Asn Val Asn Asn Ala Pro Pro Lys Gly Thr Lys Ala Glu Gly
210 215 220

Phe Thr Pro Ser Ser Gln Pro Glu Lys Ala His Gly Leu Ser Tyr Phe
225 230 235 240
Ile Asn Leu Ser Lys Asn Trp Ser Leu Ala His Gly Phe Phe Thr Glu
245 250 255
Phe Ser Ala Asp Ile Asn Gly Lys Tyr Tyr Trp Asp Asn His Lys Tyr
260 265 270
Asp Glu Phe Ser Thr Arg Leu Asn Leu Gly Gly Gly Tyr Arg Asn Ala

275 280 285
Lys Thr Glu Val Lys Leu Ile Pro Phe Val Glu Gln Phe Trp Tyr Val
290 295 300
Gly Gly Glu Asn Ala Thr Lys Asp Ala Arg Thr Leu His Arg Tyr Ser
305 310 315 320
Lys Ser Ser Gly Ile Asn Leu Asp Val Asp Tyr Trp Leu Thr Pro Asn
325 330 335
Trp Lys Ile Ser Thr Val Leu Glu Tyr Thr Glu Gln Arg Tyr Ile Gln

340 345 350
Pro Gln Arg Gln Ser Lys Asn Gly Asn Ser Tyr Ser Ile Ser Asn Thr
355 360 365
Leu Ile Tyr Met Pro Asn Ser Gln Gln Phe Trp Phe Val Gly Phe Asp
370 375 380
Tyr Tyr Gln Lys Asn Thr Arg Leu Lys Ala Tyr Ala Phe Glu Arg Gln
385 390 395 400
Gly Ile Arg Leu Gly Trp Gly Gln Glu Trp Pro Lys Gly Ile Ser Thr

405 410 415
Arg Leu Gln Thr Ser Tyr Ala Thr Arg Thr Tyr Arg Ala Pro Ser Ala
420 425 430
Glu Lys Asn Met Ile Phe Ala Pro Ser Phe Phe Lys Val Val Gln Lys
435 440 445
Asn Arg Glu Tyr Gly Val Asn Phe Thr Ile Trp His Arg Ser Leu His
450 455 460
Trp Leu Gly Ile Thr Pro Lys Ile Thr Trp Ala Tyr Gln Lys Thr Thr

465 470 475 480

Ser Asn Asn Pro Phe Ser Glu Tyr Asp Arg Asn Arg Ile Tyr Leu Thr

485 490 495

Phe Ser Lys Thr Phe Pro Phe Tyr Leu Lys Gly Ile Val Met Gln Tyr

500 505 510

Phe Asp Ile Lys Lys Ser Leu Pro Val Phe Cys Ser Leu Leu Ile Thr

515 520 525

Ala Cys Ser Gly Gly Gly Gly Asn Asn Asn Pro Ser His Ser Pro Met

530 535 540

Glu Lys Arg Thr Val Thr Ile Pro Gln Ala Gln Lys Val Ala Glu Lys

545 550 555 560

Pro Ala Leu Thr Ile Gln Thr Val Val Thr Ser Pro Thr Thr Pro Ile

565 570 575

Lys Ala Pro Ser Leu Ala Pro Thr Ile Asp Thr Ala Pro Lys Gln Asn

580 585 590

Pro Val Pro Thr Ala Gln Ile Thr Ala Thr Leu Pro Ala Glu Pro Val

595 600 605

Lys Val Pro Val Leu Ile Pro Glu Val Asn Lys Thr Leu Leu Glu Thr

610 615 620

Ser Thr Asn Pro Val Lys Asp Ser Tyr Asn Lys Asp Ala Val Phe Thr

625 630 635 640

Tyr Glu Leu Ile Ala Asn Pro Asp Ala Asp Tyr Ser Asp Gln Lys Leu

645 650 655

Ile Leu Lys Lys Glu Ile Ser Tyr Ile Lys Leu Asn Leu Gly Ile Asn

660 665 670

Gln Asp Asn Lys Asn Ala Pro Ser Tyr Ile Phe Asn Leu Leu Asp Asp

675 680 685

Asn Val Tyr Tyr Gly Phe Tyr Arg Asp Thr Gln Asp Met Asn Arg Ile

690 695 700

Glu Asn Lys Tyr Thr Tyr Ala Phe Lys Lys Glu Ala Glu Asn Phe Asp

705 710 715 720

Asn Leu Gln Lys Phe Asn Ala Thr Tyr Glu Gly Gln Phe Trp Phe Ser

725 730 735

Ser Ile Asp Thr Pro Asn Val Pro Thr Val Ala Arg Ala Phe Leu Thr

740 745 750

Tyr Asn Asn Gly Arg Val Asp Gly Glu Ile Leu Ala Lys His Trp Asn

755 760 765

Glu Lys Leu Phe Gln Ile Thr Gly Phe Asp Asn Asn Pro Arg Lys Val

770 775 780

Glu Ile Phe Pro Thr Val Glu Tyr Leu Pro Asn Ser Gly Thr Arg Leu

785 790 795 800

Thr Lys Gly Ala Thr Ser Pro His Arg Phe Gln Met Asp Leu His Phe

805 810 815

Ile Asn Ser Thr Asn Gly Glu Lys Asn Lys Tyr Leu Val Gly Gln Gly

820 825 830

Ser Thr Glu Gln Tyr Trp Gly Val Leu Gly Met Glu Lys Lys Gln Asp

835 840 845

Tyr Lys Asp Asp Asp Asp Lys

850 855

<210> 1091

<211> 24

<212> DNA

<213> Artificial Sequence

<220><223> Flag sequence

<400> 1091

gactacaagg atgacgatga caag 24

<210> 1092

<211> 8

<212> PRT

<213> Artificial Sequence

<220><223> Flag sequene

<400> 1092

Asp Tyr Lys Asp Asp Asp Asp Lys

1 5

<210> 1093

<211> 1800

<212> DNA

<213> N. meningitidis TbpB

<400> 1093

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tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 180

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 240

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 300

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 360

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 420

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 480

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 540

ccatcggaaa agataactta taaaggtact tgggattatg ttactgatgc tatggaaaaa 600

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 660

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 720

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 780

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 840

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 900

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 960

gggccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 1020

gtgtttggtg cgaagcagaa agataagaag gatggggaaa acgcggcagg gcctgcaacg 1080

gaaaccgtga tagatgcata ccgtattacc ggcgaggagt ttaagaaaga gcaaatagac 1140

agttttggag atgtgaaaaa gctgctggtt gacggagtgg agctttcact gctgccgtct 1200

gagggcaata aggcggcatt tcagcacgag attgagcaaa acggcgtgaa ggcaacggtg 1260

tgttgttcca acttggatta catgagtttt gggaagctgt caaaagaaaa taaagacgat 1320

atgttcctgc aaggtgtccg cactccagta tccgatgtgg cggcaaggac ggaggcaaac 1380

gccaaatatc gcggtacttg gtacggatat attgccaacg gcacaagctg gagcggcgaa 1440

gcctccaatc aggaaggtgg taatagggca gagtttgacg tggatttttc cactaaaaaa 1500

atcagtggca cactgacggc aaaagaccgt acgtctcctg cgtttactat tactgccatg 1560

attaaggaca acggtttttc aggtgtggcg aaaaccggtg aaaacggctt tgcgctggat 1620

ccgcaaaata ccggaaattc ccactatacg catattgaag ccactgtatc cggcggtttc 1680

tacggcaaaa acgccatcga gatgggcgga tcgttctcat ttccgggaaa tgcaccagag 1740

ggaaaacaag aaaaagcatc ggtggtattc ggtgcgaaac gccaacagct tgtgcaataa 1800

<210> 1094

<211> 599

<212> PRT

<213> N. meningitidis TbpB

<400> 1094

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Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
20 25 30

Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
35 40 45

Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala
50 55 60

Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn
65 70 75 80

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys
85 90 95

Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu
100 105 110

Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp
115 120 125

Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser
130 135 140

Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile
145 150 155 160

Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro

165 170 175

Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp
180 185 190
Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser
195 200 205
Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly
210 215 220
Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly
225 230 235 240

Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly
245 250 255
Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys
260 265 270
Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn
275 280 285
Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly
290 295 300

Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr
305 310 315 320
Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn
325 330 335
Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly
340 345 350
Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg
355 360 365

Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp
370 375 380
Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser
385 390 395 400
Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val
405 410 415

Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys
420 425 430

Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr
435 440 445
Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg
450 455 460
Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu
465 470 475 480
Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe
485 490 495

Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser
500 505 510
Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly
515 520 525
Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr
530 535 540
Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
545 550 555 560

Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly
565 570 575
Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala
580 585 590
Lys Arg Gln Gln Leu Val Gln
595

<210> 1095
<211> 1053
<212> DNA
<213> N. meningitidis TbpB N lobe
<400> 1095
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tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 180

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 240

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 300

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 360

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 420

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 480

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 540

ccatcggaaa agataactta taaaggtact tgggattatg ttactgatgc tatggaaaaa 600

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 660

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 720

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 780

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 840

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 900

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 960

gggccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 1020

gtgtttggtg cgaagcagaa agataagaag gat 1053

<210> 1096

<211> 351

<212> PRT

<213> N. meningitidis TbpB N lobe

<400> 1096

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe

1 5 10 15

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser

20 25 30

Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu

35 40 45

Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala

50 55 60

Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn

65 70 75 80

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys

85 90 95

Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu

100 105 110

Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp

115 120 125

Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser

130 135 140

Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile

145 150 155 160

Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro

165 170 175

Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp

180 185 190

Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser

195 200 205

Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly

210 215 220

Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly

225 230 235 240

Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly

245 250 255

Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys

260 265 270

Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn

275 280 285

Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly

290 295 300

Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr

305 310 315 320

Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn

325 330 335

Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp

340 345 350

<210> 1097

<211> 927

<212> DNA

<213> N. meningitidis TbpB C lobe

<400> 1097

atgaacaatc cattggtaaa tcaggctgct atggtgctgc ctgtgttttt gttgagtgct 60

tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 180

ggggaaaacg cggcagggcc tgcaacggaa accgtgatag atgcataccg tattaccggc 240

gaggagttta agaaagagca aatagacagt tttggagatg tgaaaaagct gctggttgac 300

ggagtggagc tttcactgct gccgtctgag ggcaataagg cggcatttca gcacgagatt 360

gagcaaaacg gcgtgaaggc aacggtgtgt tgttccaact tggattacat gagttttggg 420

aagctgtcaa aagaaaataa agacgatatg ttcctgcaag gtgtccgcac tccagtatcc 480

gatgtggcgg caaggacgga ggcaaacgcc aaatatcgcg gtacttggta cggatatatt 540

gccaacggca caagctggag cggcgaagcc tccaatcagg aaggtggtaa tagggcagag 600

tttgacgtgg atttttccac taaaaaaatc agtggcacac tgacggcaaa agaccgtacg 660

tctcctgcgt ttactattac tgccatgatt aaggacaacg gtttttcagg tgtggcgaaa 720

accggtgaaa acggctttgc gctggatccg caaaataccg gaaattccca ctatacgcat 780

attgaagcca ctgtatccgg cggtttctac ggcaaaaacg ccatcgagat gggcggatcg 840

ttctcatttc cgggaaatgc accagaggga aaacaagaaa aagcatcggt ggtattcggt 900

gcgaaacgcc aacagcttgt gcaataa 927

<210> 1098

<211> 308

<212> PRT

<213> N. meningitidis TbpB C lobe

<400> 1098

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe

1 5 10 15

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser

20 25 30

Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu

35 40 45

Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Gly Glu Asn Ala

50 55 60

Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg Ile Thr Gly

65 70 75 80

Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp Val Lys Lys

85 90 95

Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser Glu Gly Asn

100 105 110

Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val Lys Ala Thr

115 120 125

Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys Leu Ser Lys

130 135 140

Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr Pro Val Ser

145 150 155 160

Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg Gly Thr Trp

165 170 175

Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu Ala Ser Asn

180 185 190

Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe Ser Thr Lys

195 200 205

Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser Pro Ala Phe

210 215 220

Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly Val Ala Lys

225 230 235 240

Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr Gly Asn Ser

245 250 255

His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe Tyr Gly Lys

260 265 270

Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly Asn Ala Pro

275 280 285

Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala Lys Arg Gln

290 295 300

Gln Leu Val Gln

305

<210> 1099

<211> 1026

<212> DNA

<213> N. meningitidis HpuA

<400> 1099

atgaaataca aagccctgtc cttactgccg cttgtcgctg cccttgccgc ctgtgccggg 60

ggggggggtag ccgaaccgca cgtccccgtg tccatcccca ccgccacccc gctgcccacc 120

ggcgaggtaa agttatcaga cgacaatagc aaaatcgaaa acatcaacac cgccgacacc 180

ggaagcacat ccggcatttc cattcagcag cggaaatatg aagtagaaag ttacggcatc 240

aaaagagaag aaaaagcatt catcttccaa acacccggcg gcgcgcaata cgccctttca 300

tcctacgccg accccataac cgtcagctac tcctcccccg atttcaaaat tcccgaccgc 360

cacgcagggc agcggcttgc cgacggcagc cgcatcttta tctgttgcag cgaatccggg 420

gctacttcgt atgcggaaat caccaaacaa gattatatga aattcggggc gtggataggt 480

cccaacggcg aaatcgacct cttcgccggc ggcttccccg tcggcaaaac gccgaagcct 540

aaatactctt ggggcaacac cgaacccgaa accaaaggca agggcaaaat cacttatcag 600

gtttggggca tccgcgtcag aaacaggcaa tttgttactt cctcttatac gccgccgaaa 660

agcggttctt attatgggac acttgccaac acccccgtcc tttccctttat cactgccaat 720

ttcaacagca acaaactggc aggcgaaatc cgcggcaaca gcgattacgg accgagtgtg 780

aaaattgaaa acgcaacgat taacagttta tccttttccg gcactgccac gtccggcggg 840

aaaaccggca atttggaagg caagtttttt ggaaaattca acggctaccg ggacactgaa 900

accagcatag gcggcaaaat cacctttgac ggcgaccgct ccctcgatac cgtattcggc 960

ggtgtgagtt ataaaaaaga acttgaaaac aacactgata caagtaccac ccatctcaca 1020

aaataa 1026

<210> 1100

<211> 341

<212> PRT

<213> N. meningitidis HpuA

<400> 1100

Met Lys Tyr Lys Ala Leu Ser Leu Leu Pro Leu Val Ala Ala Leu Ala
1 5 10 15
Ala Cys Ala Gly Gly Gly Val Ala Glu Pro His Val Pro Val Ser Ile
20 25 30
Pro Thr Ala Thr Pro Leu Pro Thr Gly Glu Val Lys Leu Ser Asp Asp
35 40 45
Asn Ser Lys Ile Glu Asn Ile Asn Thr Ala Asp Thr Gly Ser Thr Ser
50 55 60

Gly Ile Ser Ile Gln Gln Arg Lys Tyr Glu Val Glu Ser Tyr Gly Ile
65 70 75 80
Lys Arg Glu Glu Lys Ala Phe Ile Phe Gln Thr Pro Gly Gly Ala Gln
85 90 95
Tyr Ala Leu Ser Ser Tyr Ala Asp Pro Ile Thr Val Ser Tyr Ser Ser
100 105 110
Pro Asp Phe Lys Ile Pro Asp Arg His Ala Gly Gln Arg Leu Ala Asp
115 120 125

Gly Ser Arg Ile Phe Ile Cys Cys Ser Glu Ser Gly Ala Thr Ser Tyr
130 135 140
Ala Glu Ile Thr Lys Gln Asp Tyr Met Lys Phe Gly Ala Trp Ile Gly
145 150 155 160
Pro Asn Gly Glu Ile Asp Leu Phe Ala Gly Gly Phe Pro Val Gly Lys
165 170 175
Thr Pro Lys Pro Lys Tyr Ser Trp Gly Asn Thr Glu Pro Glu Thr Lys
180 185 190

Gly Lys Gly Lys Ile Thr Tyr Gln Val Trp Gly Ile Arg Val Arg Asn
195 200 205
Arg Gln Phe Val Thr Ser Ser Tyr Thr Pro Pro Lys Ser Gly Ser Tyr
210 215 220
Tyr Gly Thr Leu Ala Asn Thr Pro Val Leu Ser Phe Ile Thr Ala Asn

225 230 235 240

Phe Asn Ser Asn Lys Leu Ala Gly Glu Ile Arg Gly Asn Ser Asp Tyr

245 250 255

Gly Pro Ser Val Lys Ile Glu Asn Ala Thr Ile Asn Ser Leu Ser Phe

260 265 270

Ser Gly Thr Ala Thr Ser Gly Gly Lys Thr Gly Asn Leu Glu Gly Lys

275 280 285

Phe Phe Gly Lys Phe Asn Gly Tyr Arg Asp Thr Glu Thr Ser Ile Gly

290 295 300

Gly Lys Ile Thr Phe Asp Gly Asp Arg Ser Leu Asp Thr Val Phe Gly

305 310 315 320

Gly Val Ser Tyr Lys Lys Glu Leu Glu Asn Asn Thr Asp Thr Ser Thr

325 330 335

Thr His Leu Thr Lys

340

<210> 1101

<211> 2025

<212> DNA

<213> N. meningitidis TbpB N lobe-HpuA fusion

<400> 1101

atgaacaatc cattggtaaa tcaggctgct atggtgctgc ctgtgttttt gttgagtgct 60

tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 180

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 240

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 300

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 360

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 420

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 480

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 540

ccatcggaaa agataactta taaaggtact tgggattatg ttactgatgc tatggaaaaa 600

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 660

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 720

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 780

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 840

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 900

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 960

gggccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 1020

gtgtttggtg cgaagcagaa agataagaag gatgccgggg gaggggtagc cgaaccgcac 1080

gtccccgtgt ccatccccac cgccacccca ctgcccaccg gcgaggtaaa gttatcagac 1140

gacaatagca aaatcgaaaa catcaacacc gccgacaccg gaagcacatc cggcatttcc 1200

attcagcagc ggaaatatga agtagaaagt tacggcatca aaagagaaga aaaagcattc 1260

atcttccaaa cacccggcgg cgcgcaatac gccctttcat cctacgccga ccccataacc 1320

gtcagctact cctcccccga tttcaaaatt cccgaccgcc acgcagggca gcggcttgcc 1380

gacggcagcc gcatctttat ctgttgcagc gaatccgggg ctacttcgta tgcggaaatc 1440

accaaacaag attatatgaa attcggggcg tggataggtc ccaacggcga aatcgacctc 1500

ttcgccggcg gcttccccgt cggcaaaacg ccgaagccta aatactcttg gggcaacacc 1560

gaacccgaaa ccaaaggcaa gggcaaaatc acttatcagg tttggggcat ccgcgtcaga 1620

aacaggcaat ttgttacttc ctcttatacg ccgccgaaaa gcggttctta ttatgggaca 1680

cttgccaaca cccccgtcct ttcctttatc actgccaatt tcaacagcaa caaactggca 1740

ggcgaaatcc gcggcaacag cgattacgga ccgagtgtga aaattgaaaa cgcaacgatt 1800

aacagtttat ccttttccgg cactgccacg tccggcggga aaaccggcaa tttggaaggc 1860

aagttttttg gaaaattcaa cggctaccgg gacactgaaa ccagcatagg cggcaaaatc 1920

acctttgacg gcgaccgctc cctcgatacc gtattcggcg gtgtgagtta taaaaaagaa 1980

cttgaaaaca acactgatac aagtaccacc catctcacaa aataa 2025

<210> 1102

<211> 674

<212> PRT

<213> N. meningitidis TbpB N lobe-HpuA fusion

<400> 1102

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe

1 5 10 15

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser

20 25 30

Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu

35 40 45

Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala

50 55 60

Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn

65 70 75 80

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys

85 90 95

Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu

100 105 110

Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp

115 120 125

Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser

130 135 140

Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile

145 150 155 160

Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro

165 170 175

Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp

180 185 190

Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser

195 200 205

Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly

210 215 220

Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly

225 230 235 240

Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly

245 250 255

Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys

260 265 270

Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn

275 280 285

Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly

290 295 300

Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr

305 310 315 320

Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn

325 330 335

Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Ala

340 345 350

Gly Gly Gly Val Ala Glu Pro His Val Pro Val Ser Ile Pro Thr Ala

355 360 365

Thr Pro Leu Pro Thr Gly Glu Val Lys Leu Ser Asp Asp Asn Ser Lys

370 375 380

Ile Glu Asn Ile Asn Thr Ala Asp Thr Gly Ser Thr Ser Gly Ile Ser

385 390 395 400

Ile Gln Gln Arg Lys Tyr Glu Val Glu Ser Tyr Gly Ile Lys Arg Glu

405 410 415

Glu Lys Ala Phe Ile Phe Gln Thr Pro Gly Gly Ala Gln Tyr Ala Leu

420 425 430

Ser Ser Tyr Ala Asp Pro Ile Thr Val Ser Tyr Ser Ser Pro Asp Phe

435 440 445

Lys Ile Pro Asp Arg His Ala Gly Gln Arg Leu Ala Asp Gly Ser Arg

450 455 460

Ile Phe Ile Cys Cys Ser Glu Ser Gly Ala Thr Ser Tyr Ala Glu Ile

465 470 475 480

Thr Lys Gln Asp Tyr Met Lys Phe Gly Ala Trp Ile Gly Pro Asn Gly

485 490 495

Glu Ile Asp Leu Phe Ala Gly Gly Phe Pro Val Gly Lys Thr Pro Lys

500 505 510

Pro Lys Tyr Ser Trp Gly Asn Thr Glu Pro Glu Thr Lys Gly Lys Gly

515 520 525

Lys Ile Thr Tyr Gln Val Trp Gly Ile Arg Val Arg Asn Arg Gln Phe

530 535 540

Val Thr Ser Ser Tyr Thr Pro Pro Lys Ser Gly Ser Tyr Tyr Gly Thr

545 550 555 560

Leu Ala Asn Thr Pro Val Leu Ser Phe Ile Thr Ala Asn Phe Asn Ser

565 570 575

Asn Lys Leu Ala Gly Glu Ile Arg Gly Asn Ser Asp Tyr Gly Pro Ser

580 585 590

Val Lys Ile Glu Asn Ala Thr Ile Asn Ser Leu Ser Phe Ser Gly Thr

595 600 605

Ala Thr Ser Gly Gly Lys Thr Gly Asn Leu Glu Gly Lys Phe Phe Gly

610 615 620

Lys Phe Asn Gly Tyr Arg Asp Thr Glu Thr Ser Ile Gly Gly Lys Ile

625 630 635 640

Thr Phe Asp Gly Asp Arg Ser Leu Asp Thr Val Phe Gly Gly Val Ser

645 650 655

Tyr Lys Lys Glu Leu Glu Asn Asn Thr Asp Thr Ser Thr Thr His Leu

660 665 670

Thr Lys

<210> 1103

<211> 1800

<212> DNA

<213> N. meningitidis TbpB polyalanine mutant B22

<400> 1103

atgaacaatc cattggtaaa tcaggctgct atggtgctgc ctgtgttttt gttgagtgct 60

tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 180

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 240

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 300

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 360

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 420

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 480

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 540

ccatcggaaa agataactta taaaggtact tgggattatg ttactgatgc tatggaaaaa 600

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 660

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 720

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 780

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 840

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 900

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 960

gggccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 1020

gtgtttggtg cgaagcagaa agataagaag gatggggaaa acgcggcagg gcctgcaacg 1080

gaaaccgtga tagatgcata ccgtattacc ggcgaggagt ttaagaaaga gcaaatagac 1140

agttttggag atgtgaaaaa gctgctggtt gacggagtgg agctttcact gctgccgtct 1200

gagggcaata aggcggcatt tcagcacgag attgagcaaa acggcgtgaa ggcaacggtg 1260

tgttgttcca acttggatta catggctgca gcagctgcag ctgcagcaaa taaagacgat 1320

atgttcctgc aaggtgtccg cactccagta tccgatgtgg cggcaaggac ggaggcaaac 1380

gccaaatatc gcggtacttg gtacggatat attgccaacg gcacaagctg gagcggcgaa 1440

gcctccaatc aggaaggtgg taatagggca gagtttgacg tggatttttc cactaaaaaa 1500

atcagtggca cactgacggc aaaagaccgt acgtctcctg cgtttactat tactgccatg 1560

attaaggaca acggtttttc aggtgtggcg aaaaccggtg aaaacggctt tgcgctggat 1620

ccgcaaaata ccggaaattc ccactatacg catattgaag ccactgtatc cggcggtttc 1680

tacggcaaaa acgccatcga gatgggcgga tcgttctcat ttccgggaaa tgcaccagag 1740

ggaaaacaag aaaaagcatc ggtggtattc ggtgcgaaac gccaacagct tgtgcaataa 1800

<210> 1104

<211> 599

<212> PRT

<213> N. meningitidis TbpB polyalanine mutant B22

<400> 1104

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe

1 5 10 15

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
20 25 30
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
35 40 45
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala
50 55 60
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn
65 70 75 80

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys
85 90 95
Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu
100 105 110
Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp
115 120 125
Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser
130 135 140

Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile
145 150 155 160
Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro
165 170 175
Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp
180 185 190
Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser
195 200 205

Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly
210 215 220
Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly
225 230 235 240
Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly
245 250 255

Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys
260 265 270

Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn
275 280 285

Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly
290 295 300

Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr
305 310 315 320

Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn
325 330 335

Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly
340 345 350

Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg
355 360 365

Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp
370 375 380

Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser
385 390 395 400

Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val
405 410 415

Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ala Ala Ala Ala
420 425 430

Ala Ala Ala Ala Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr
435 440 445

Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg
450 455 460

Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu
465 470 475 480

Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe
485 490 495

Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser

500 505 510

Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly

515 520 525

Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr

530 535 540

Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe

545 550 555 560

Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly

565 570 575

Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala

580 585 590

Lys Arg Gln Gln Leu Val Gln

595

<210> 1105

<211> 1800

<212> DNA

<213> N. meningitidis TbpB polyalanine mutant B23

<400> 1105

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tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 180

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 240

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 300

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 360

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 420

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 480

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 540

ccatcggaaa agataactta taaaggtact tgggattatg ttactgatgc tatggaaaaa 600

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 660

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 720

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 780

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 840

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 900

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 960

gggccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 1020

gtgtttggtg cgaagcagaa agataagaag gatggggaaa acgcggcagg gcctgcaacg 1080

gaaaccgtga tagatgcata ccgtattacc ggcgaggagt ttaagaaaga gcaaatagac 1140

agttttggag atgtgaaaaa gctgctggtt gacggagtgg agctttcact gctgccgtct 1200

gagggcaata aggcggcatt tcagcacgag attgagcaaa acggcgtgaa ggcaacggtg 1260

tgttgttcca acttggatta catgagtttt gggaagctgt caaaagaaaa taaagacgct 1320

gcagcagctg cagctgcacg cactccagta tccgatgtgg cggcaaggac ggaggcaaac 1380

gccaaatatc gcggtacttg gtacggatat attgccaacg gcacaagctg gagcggcgaa 1440

gcctccaatc aggaaggtgg taatagggca gagtttgacg tggatttttc cactaaaaaa 1500

atcagtggca cactgacggc aaaagaccgt acgtctcctg cgtttactat tactgccatg 1560

attaaggaca acggtttttc aggtgtggcg aaaaccggtg aaaacggctt tgcgctggat 1620

ccgcaaaata ccggaaattc ccactatacg catattgaag ccactgtatc cggcggtttc 1680

tacggcaaaa acgccatcga gatgggcgga tcgttctcat ttccgggaaa tgcaccagag 1740

ggaaaacaag aaaaagcatc ggtggtattc ggtgcgaaac gccaacagct tgtgcaataa 1800

<210> 1106

<211> 599

<212> PRT

<213> N. meningitidis TbpB polyalanine mutant B23

<400> 1106

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
1 5 10 15

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
20 25 30

Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
35 40 45

Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala
50 55 60

Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn

65 70 75 80

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys
85 90 95

Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu
100 105 110

Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp
115 120 125

Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser
130 135 140

Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile
145 150 155 160

Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro
165 170 175

Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp
180 185 190

Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser
195 200 205

Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly
210 215 220

Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly
225 230 235 240

Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly
245 250 255

Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys
260 265 270

Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn
275 280 285

Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly
290 295 300

Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr
305 310 315 320

Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn
325 330 335

Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly
340 345 350

Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg
355 360 365

Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp
370 375 380

Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser
385 390 395 400

Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val
405 410 415

Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys
420 425 430

Leu Ser Lys Glu Asn Lys Asp Ala Ala Ala Ala Ala Ala Ala Arg Thr
435 440 445

Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg
450 455 460

Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu
465 470 475 480

Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe
485 490 495

Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser
500 505 510

Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly
515 520 525

Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr
530 535 540

Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
545 550 555 560

Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly

565 570 575

Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala

580 585 590

Lys Arg Gln Gln Leu Val Gln

595

<210> 1107

<211> 1800

<212> DNA

<213> N. meningitidis TbpB polyalanine mutant B30

<400> 1107

atgaacaatc cattggtaaa tcaggctgct atggtgctgc ctgtgttttt gttgagtgct 60

tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 180

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 240

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 300

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 360

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 420

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 480

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 540

ccatcggaaa agataactta taaaggtact tgggattatg ttactgatgc tatggaaaaa 600

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 660

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 720

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 780

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 840

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 900

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggatttac 960

gggccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 1020

gtgtttggtg cgaagcagaa agataagaag gatggggaaa acgcggcagg gcctgcaacg 1080

gaaaccgtga tagatgcata ccgtattacc ggcgaggagt ttaagaaaga gcaaatagac 1140

agttttggag atgtgaaaaa gctgctggtt gacggagtgg agctttcact gctgccgtct 1200

gagggcaata aggcggcatt tcagcacgag attgagcaaa acggcgtgaa ggcaacggtg 1260

tgttgttcca acttggatta catgagtttt gggaagctgt caaaagaaaa taaagacgat 1320

atgttcctgc aaggtgtccg cactccagta tccgatgtgg cggcaaggac ggaggcaaac 1380

gccaaatatc gcggtacttg gtacggatat attgccaacg gcacaagctg gagcggcgaa 1440

gcctccaatc aggaaggtgg taatagggca gagtttgacg tggatttttc cactaaaaaa 1500

atcagtggca cactgacggc aaaagaccgt acgtctcctg cgtttactat tactgccatg 1560

attaaggaca acggtttttc aggtgtggcg aaaaccggtg aaaacggctt tgcgctggat 1620

ccgcaaaata ccggaaattc ccactatacg catattgaag ccactgtatc cggcggtttc 1680

tacggcaaaa acgccatcga ggcagcagct gcagctgcat ttccgggaaa tgcaccagag 1740

ggaaaacaag aaaaagcatc ggtggtattc ggtgcgaaac gccaacagct tgtgcaataa 1800

<210> 1108

<211> 599

<212> PRT

<213> N. meningitidis TbpB polyalanine mutant B30

<400> 1108

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
1 5 10 15

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
20 25 30

Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
35 40 45

Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala
50 55 60

Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn
65 70 75 80

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys
85 90 95

Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu
100 105 110

Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp
115 120 125

Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser

130 135 140

Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile
145 150 155 160
Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro
165 170 175
Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp
180 185 190
Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser
195 200 205

Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly
210 215 220
Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly
225 230 235 240
Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly
245 250 255
Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys
260 265 270

Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn
275 280 285
Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly
290 295 300
Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr
305 310 315 320
Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn
325 330 335

Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly
340 345 350
Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg
355 360 365
Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp
370 375 380

Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser
385 390 395 400

Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val
405 410 415
Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys
420 425 430
Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr
435 440 445
Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg
450 455 460

Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu
465 470 475 480
Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe
485 490 495
Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser
500 505 510
Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly
515 520 525

Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr
530 535 540
Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
545 550 555 560
Tyr Gly Lys Asn Ala Ile Glu Ala Ala Ala Ala Ala Ala Phe Pro Gly
565 570 575
Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala
580 585 590

Lys Arg Gln Gln Leu Val Gln
595

<210> 1109
<211> 1800
<212> DNA

<213> N. meningitidis TbpB polyalanine mutant B31

<400> 1109

atgaacaatc cattggtaaa tcaggctgct atggtgctgc ctgtgttttt gttgagtgct 60

tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 180

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 240

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 300

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 360

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 420

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 480

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 540

ccatcggaaa agataactta taaaggtact tgggattatg ttactgatgc tatggaaaaa 600

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 660

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 720

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 780

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 840

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 900

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 960

gggccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 1020

gtgtttggtg cgaagcagaa agataagaag gatggggaaa acgcggcagg gcctgcaacg 1080

gaaaccgtga tagatgcata ccgtattacc ggcgaggagt ttaagaaaga gcaaatagac 1140

agttttggag atgtgaaaaa gctgctggtt gacggagtgg agctttcact gctgccgtct 1200

gagggcaata aggcggcatt tcagcacgag attgagcaaa acggcgtgaa ggcaacggtg 1260

tgttgttcca acttggatta catgagtttt gggaagctgt caaaagaaaa taaagacgat 1320

atgttcctgc aaggtgtccg cactccagta tccgatgtgg cggcaaggac ggaggcaaac 1380

gccaaatatc gcggtacttg gtacggatat attgccaacg gcacaagctg gagcggcgaa 1440

gcctccaatc aggaaggtgg taatagggca gagtttgacg tggatttttc cactaaaaaa 1500

atcagtggca cactgacggc aaaagaccgt acgtctcctg cgtttactat tactgccatg 1560

attaaggaca acggtttttc aggtgtggcg aaaaccggtg aaaacggctt tgcgctggat 1620

ccgcaaaata ccggaaattc ccactatacg catattgaag ccactgtatc cggcggtttc 1680

tacggcaaaa acgccatcga gatgggcgga tcgttctcat ttccgggaaa tgcaccagag 1740

ggaaaacaag aaaaagcagc tgcagcagct gcagctgcac gccaacagct tgtgcaataa 1800

<210> 1110

<211> 599

<212> PRT

<213> N. meningitidis TbpB polyalanine mutant B31

<400> 1110

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
1 5 10 15

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
20 25 30

Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
35 40 45

Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala
50 55 60

Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn
65 70 75 80

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys
85 90 95

Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu
100 105 110

Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp
115 120 125

Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser
130 135 140

Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile
145 150 155 160

Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro
165 170 175

Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp
180 185 190

Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser

195 200 205

Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly
210 215 220
Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly
225 230 235 240
Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly
245 250 255
Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys
260 265 270

Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn
275 280 285
Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly
290 295 300
Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr
305 310 315 320
Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn
325 330 335

Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly
340 345 350
Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg
355 360 365
Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp
370 375 380
Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser
385 390 395 400

Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val
405 410 415
Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys
420 425 430
Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr
435 440 445

Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg
450 455 460

Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu
465 470 475 480
Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe
485 490 495
Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser
500 505 510
Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly
515 520 525

Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr
530 535 540
Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
545 550 555 560
Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly
565 570 575
Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ala Ala Ala Ala Ala Ala
580 585 590

Ala Arg Gln Gln Leu Val Gln
595

<210> 1111
<211> 857
<212> DNA
<213> N. meningitidis SLAM1 truncated version
<400> 1111
ggaaggtaaa tggcggcttc agcgtcaccc gcgaacacaa tatcaaccaa gccccgaaac 60
ggcagcagta cggcaaatgg actttcccga aacaggtgga cggcacggcg gtcaattacc 120
ggctcggcgc ggagaaaaaa tggtcgctga aaaacggctg gtacacgacg gctggcggcg 180
acgtgtccgg cagggtttat ccggggaata agaaattcaa cgatatgacg gcaggcgttt 240
ccggcggcat cggttttgcc gaccggcgca aagatgccgg gctggcagtg ttccacgaac 300

gccgcaccta cggcaacgac gcttattctt acaccaacgg cgcacgcctt tatttcaacc 360

gttggcaaac cccgaaatgg caaacgttgt cttcggcgga gtgggggcgt ttgaagaata 420

cgcgccgggc gcgttccgac aatacccatt tgcaaatttc caattcgctg gtgttttacc 480

ggaatgcgcg ccaatattgg atgggcggtt tggattttta ccgcgagcgc aaccccgccg 540

accggggcga caatttcaac cgttacggcc tgcgctttgc ctgggggcag gaatggggcg 600

gcagcggcct gtcttcgctg ttgcgcctcg gcgcggcgaa acggcattat gaaaaacccg 660

gctttttcag cggttttaaa ggggaaaggc gcagggataa agaattgaac acatccttga 720

gcctttggca ccgggcattg catttcaaag gcatcacgcc gcgcctgacg ttgtcgcacc 780

gcgaaacgcg gagtaacgat gtgttcaacg aatacgagaa aaatcgggcg tttgtcgagt 840

ttaataaaac gttctga 857

<210> 1112

<211> 284

<212> PRT

<213> N. meningitidis SLAM1 truncated version

<400> 1112

Lys Val Asn Gly Gly Phe Ser Val Thr Arg Glu His Asn Ile Asn Gln
1 5 10 15

Ala Pro Lys Arg Gln Gln Tyr Gly Lys Trp Thr Phe Pro Lys Gln Val

20 25 30

Asp Gly Thr Ala Val Asn Tyr Arg Leu Gly Ala Glu Lys Lys Trp Ser
35 40 45

Leu Lys Asn Gly Trp Tyr Thr Thr Ala Gly Gly Asp Val Ser Gly Arg
50 55 60

Val Tyr Pro Gly Asn Lys Lys Phe Asn Asp Met Thr Ala Gly Val Ser
65 70 75 80

Gly Gly Ile Gly Phe Ala Asp Arg Arg Lys Asp Ala Gly Leu Ala Val

85 90 95

Phe His Glu Arg Arg Thr Tyr Gly Asn Asp Ala Tyr Ser Tyr Thr Asn
100 105 110

Gly Ala Arg Leu Tyr Phe Asn Arg Trp Gln Thr Pro Lys Trp Gln Thr
115 120 125

Leu Ser Ser Ala Glu Trp Gly Arg Leu Lys Asn Thr Arg Arg Ala Arg
130 135 140

Ser Asp Asn Thr His Leu Gln Ile Ser Asn Ser Leu Val Phe Tyr Arg

145 150 155 160

Asn Ala Arg Gln Tyr Trp Met Gly Gly Leu Asp Phe Tyr Arg Glu Arg

165 170 175

Asn Pro Ala Asp Arg Gly Asp Asn Phe Asn Arg Tyr Gly Leu Arg Phe

180 185 190

Ala Trp Gly Gln Glu Trp Gly Gly Ser Gly Leu Ser Ser Leu Leu Arg

195 200 205

Leu Gly Ala Ala Lys Arg His Tyr Glu Lys Pro Gly Phe Phe Ser Gly

210 215 220

Phe Lys Gly Glu Arg Arg Arg Asp Lys Glu Leu Asn Thr Ser Leu Ser

225 230 235 240

Leu Trp His Arg Ala Leu His Phe Lys Gly Ile Thr Pro Arg Leu Thr

245 250 255

Leu Ser His Arg Glu Thr Arg Ser Asn Asp Val Phe Asn Glu Tyr Glu

260 265 270

Lys Asn Arg Ala Phe Val Glu Phe Asn Lys Thr Phe

275 280

<210> 1113

<211> 1566

<212> DNA

<213> K. denitrificans SLAM5 codon optimized

<400> 1113

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atggccatgg cccatcatca ccatcaccac gaaccgctgc cgcagaccgc agcagaacag 120

gcaggcgaaa gcctgcagca gcagccgtgg ctgcagagcc tggaagcaga tggtgccggt 180

gaaaaacagc ctgcactgga acgtaaaggt gcagcaccgg ttgttgttcg taatcaggat 240

ctgcgtgaac atccggaact gctggcagca atgctgcgtc aggcagttga tgcacgtcat 300

gaacctctgc tgggtgcact gctgccgacc tatctgaccc tgccgcaaga acagcaggat 360

gcaaaactgc gtcagcatgc acaggcagaa ctggcacgtc tgcgtggtga ttatccgacc 420

gcaaccgcac attatcaggc cgttcagcgt cagtatccgg atgatgttcg tctgcagctg 480

gatagcgcag caaccctggc cgaagatcgt cagtggcgtg aagcagaagc actgtttgcc 540

caggcagcac agacccctga actgccggat accgttgcag aaaatattcg tctgtatcgt 600

aatggcattc gtcagaatac ccagtggcag gttcagggtg gtgttcagct gagctatgat 660

aaaaacatta atgatgcacc gcaggcctat tgtacaccgc tgggttgtgt tcgtgaacgt 720

caagaaaatg catggggtct gcgttatcgt gtttatgcag aaaaaaacac cccgattcgt 780

ggtcatcata atctgctgtt tcgtatgaat gcaagcggca ccacctatta tctgagccag 840

cgtagcgcat atgattatgc cctggcacgt gcaagcctgg gttatcgttt tcaggatgcc 900

cgtcagagtc tggaaattct gccgttttat caggcacagt ttagcggtag ccgtcagttt 960

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gttcaggcag catttgaacg tcagctggca ccgaaatgga ccggttttgt tagtctggaa 1080

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ggttggggta gcctgcatcc agataatgat atggttggtg gtcgtgcaaa tagcagcggt 1260

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aataccgaag tgcgtggcca gtatacccag cgtcgttatc gcggtagcgc actggatacc 1380

gcatttctgc gtcgtccgca gcgtaataat gaacgtagcc tgaccgttgc actgagttat 1440

ccgaaatggc gtgtttgggg tgcagttccg aaactggttt ggcaagaaaa tcgtattgat 1500

agcacccatg attgggcaga tcgtcgtcag cgtaatgttt ggctggaatg ggaaaaacgc 1560

ttttaa 1566

<210> 1114

<211> 521

<212> PRT

<213> K. denitrificans SLAM5 codon optimized

<400> 1114

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Met Ala His His His His His His Glu Pro
20 25 30

Leu Pro Gln Thr Ala Ala Glu Gln Ala Gly Glu Ser Leu Gln Gln Gln
35 40 45

Pro Trp Leu Gln Ser Leu Glu Ala Asp Gly Ala Gly Glu Lys Gln Pro

50 55 60

Ala Leu Glu Arg Lys Gly Ala Ala Pro Val Val Val Arg Asn Gln Asp
65 70 75 80
Leu Arg Glu His Pro Glu Leu Leu Ala Ala Met Leu Arg Gln Ala Val
85 90 95
Asp Ala Arg His Glu Pro Leu Leu Gly Ala Leu Leu Pro Thr Tyr Leu
100 105 110

Thr Leu Pro Gln Glu Gln Gln Asp Ala Lys Leu Arg Gln His Ala Gln
115 120 125
Ala Glu Leu Ala Arg Leu Arg Gly Asp Tyr Pro Thr Ala Thr Ala His
130 135 140
Tyr Gln Ala Val Gln Arg Gln Tyr Pro Asp Asp Val Arg Leu Gln Leu
145 150 155 160
Asp Ser Ala Ala Thr Leu Ala Glu Asp Arg Gln Trp Arg Glu Ala Glu
165 170 175

Ala Leu Phe Ala Gln Ala Ala Gln Thr Pro Glu Leu Pro Asp Thr Val
180 185 190
Ala Glu Asn Ile Arg Leu Tyr Arg Asn Gly Ile Arg Gln Asn Thr Gln
195 200 205
Trp Gln Val Gln Gly Gly Val Gln Leu Ser Tyr Asp Lys Asn Ile Asn
210 215 220
Asp Ala Pro Gln Ala Tyr Cys Thr Pro Leu Gly Cys Val Arg Glu Arg
225 230 235 240

Gln Glu Asn Ala Trp Gly Leu Arg Tyr Arg Val Tyr Ala Glu Lys Asn
245 250 255
Thr Pro Ile Arg Gly His His Asn Leu Leu Phe Arg Met Asn Ala Ser
260 265 270
Gly Thr Thr Tyr Tyr Leu Ser Gln Arg Ser Ala Tyr Asp Tyr Ala Leu
275 280 285
Ala Arg Ala Ser Leu Gly Tyr Arg Phe Gln Asp Ala Arg Gln Ser Leu
290 295 300

Glu Ile Leu Pro Phe Tyr Gln Ala Gln Phe Ser Gly Ser Arg Gln Phe
305 310 315 320
Pro Asp Lys Ala Pro Arg Gln Lys Arg Val Leu Pro Tyr Met Leu Gly
325 330 335
His Ala Val Gly Val Gln Ala Ala Phe Glu Arg Gln Leu Ala Pro Lys
340 345 350
Trp Thr Gly Phe Val Ser Leu Glu Gly Met Arg Gln Asp Phe Arg Glu
355 360 365

Ala Glu Arg Ala Arg His Gln Asn Gly Met Val Trp Asn Ala Phe Ala
370 375 380
Ser Leu Ser Tyr Arg Ile Arg Pro Gln His Leu Leu Phe Ala Gly Tyr
385 390 395 400
Gly Trp Gly Ser Leu His Pro Asp Asn Asp Met Val Gly Gly Arg Ala
405 410 415
Asn Ser Ser Gly Tyr Val Arg His Ser Val Gln Ala Gly Trp Leu Ala
420 425 430

Gln Trp Thr Ala Leu Gly Asn Leu Asn Thr Glu Val Arg Gly Gln Tyr
435 440 445
Thr Gln Arg Arg Tyr Arg Gly Ser Ala Leu Asp Thr Ala Phe Leu Arg
450 455 460
Arg Pro Gln Arg Asn Asn Glu Arg Ser Leu Thr Val Ala Leu Ser Tyr
465 470 475 480
Pro Lys Trp Arg Val Trp Gly Ala Val Pro Lys Leu Val Trp Gln Glu
485 490 495

Asn Arg Ile Asp Ser Thr His Asp Trp Ala Asp Arg Arg Gln Arg Asn
500 505 510
Val Trp Leu Glu Trp Glu Lys Arg Phe
515 520

<210> 1115
<211> 849
<212> DNA
<213> N. meningitidis FHbp

<400> 1115

gtgaaccgaa ctaccttctg ctgcctttct ctgaccgccg ccctgattct gaccgcctgc 60

agcagcggag gcggcggaag cggaggcggc ggtgtcgccg ccgacatcgg cgcggggctt 120

gccgatgcac taaccgcacc gctcgaccat aaagacaaag gtttgaaatc cctgacattg 180

gaagactcca tttcccaaaa cggaacactg accctgtcgg cacaaggtgc ggaaagaact 240

ttcaaagccg gcgacaaaga caacagtctc aacacaggca aactgaagaa cgacaaaatc 300

agccgcttcg actttatccg tcaaatcgaa gtggacgggc agctcattac cttggagagc 360

ggagagttcc aagtgtacaa acaaagccat tccgccttaa ccgcccttca gaccgagcaa 420

gtacaagact cggagcattc cgggaagatg gttgcgaaac gccagttcag aatcggcgac 480

atagtgggcg aacatacatc ttttggcaag cttcccaaag acgtcatggc gacatatcgc 540

gggacggcgt tcggttcaga cgatgccggc ggaaaactga cctacaccat agatttcgcc 600

gccaagcagg gacacggcaa aatcgaacat ttgaaatcgc cagaactcaa tgttgacctg 660

gccgccgccg atatcaagcc ggatgaaaaa caccatgccg tcatcagcgg ttccgtcctt 720

tacaaccaag ccgagaaagg cagttactct ctaggcatct ttggcgggca agcccaggaa 780

gttgccggca gcgcggaagt ggaaaccgca aacggcatac gccatatcgg tcttgccgcc 840

aagcaataa 849

<210> 1116

<211> 282

<212> PRT

<213> N. meningitidis FHbp

<400> 1116

Val Asn Arg Thr Thr Phe Cys Cys Leu Ser Leu Thr Ala Ala Leu Ile

1 5 10 15

Leu Thr Ala Cys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val

20 25 30

Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu

35 40 45

Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile

50 55 60

Ser Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Arg Thr

65 70 75 80

Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys
85 90 95
Asn Asp Lys Ile Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp
100 105 110
Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln
115 120 125
Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu Gln Val Gln Asp Ser

130 135 140
Glu His Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp
145 150 155 160
Ile Val Gly Glu His Thr Ser Phe Gly Lys Leu Pro Lys Asp Val Met
165 170 175
Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys
180 185 190
Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile

195 200 205
Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp
210 215 220
Ile Lys Pro Asp Glu Lys His His Ala Val Ile Ser Gly Ser Val Leu
225 230 235 240
Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly
245 250 255
Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val Glu Thr Ala Asn Gly

260 265 270
Ile Arg His Ile Gly Leu Ala Ala Lys Gln
275 280

<210> 1117
<211> 798
<212> DNA
<213> N. lactamica FHbp
<400> 1117
atgagaaccc tccgcatttc tgctttgact gcttccctgt ctttgatgtt ggctgcctgc 60

ggtggcgcaa caagcggctt gtcgaatgcc ctgaccaaac cgctcaatcc gcatccgaaa 120

ggcgtgttgt ccattgaatt gaacgaatct gtccctgaaa acggtacgtt ggagctgacg 180

gccaacggta aaacgcaaac cctacaaaaa ggcagcaaac tcgataccgg ctttttgaaa 240

actgataaag tatcctctta cgactacgcc caaaaaatta aggtaaacgg ccaagtcatc 300

actttggaaa cgggcgactt ccaagtgtat aaacaaaatt attccgctgt tgccgcgcgt 360

tacgccaaac aaaaagccga tgacgcgggc aagctgcaaa acctcgatac atacacattc 420

accgtcggcg aagtccaagg cgatgaaacc gcttatcgca atttgcccaa acaaggcagc 480

tatcagtatt cgggtattgc gtttaacggc gatgaccgca gcggccgcct gaaatacacc 540

gtcgatttcg ataaaaaaca aggttacggc aaaatcagca gcatggcttc ccacaataat 600

gtcgacctgc ttgcagcagg cattgccaat aacaatggta aagccgccat cagcggtaaa 660

accagtttaa acggtatcga aaacggtcgt tatgatttaa aactcttcgg cccgcaggct 720

caagaaattg ccggtaaggc gcaaatcaaa gttggcgatt ccaccaaaga aatcggtttg 780

gccggtaaga aagagtag 798

<210> 1118

<211> 265

<212> PRT

<213> N. lactamica FHbp

<400> 1118

Met Arg Thr Leu Arg Ile Ser Ala Leu Thr Ala Ser Leu Ser Leu Met
1 5 10 15

Leu Ala Ala Cys Gly Gly Ala Thr Ser Gly Leu Ser Asn Ala Leu Thr
20 25 30

Lys Pro Leu Asn Pro His Pro Lys Gly Val Leu Ser Ile Glu Leu Asn
35 40 45

Glu Ser Val Pro Glu Asn Gly Thr Leu Glu Leu Thr Ala Asn Gly Lys
50 55 60

Thr Gln Thr Leu Gln Lys Gly Ser Lys Leu Asp Thr Gly Phe Leu Lys
65 70 75 80

Thr Asp Lys Val Ser Ser Tyr Asp Tyr Ala Gln Lys Ile Lys Val Asn
85 90 95

Gly Gln Val Ile Thr Leu Glu Thr Gly Asp Phe Gln Val Tyr Lys Gln

100 105 110

Asn Tyr Ser Ala Val Ala Ala Arg Tyr Ala Lys Gln Lys Ala Asp Asp

115 120 125

Ala Gly Lys Leu Gln Asn Leu Asp Thr Tyr Thr Phe Thr Val Gly Glu

130 135 140

Val Gln Gly Asp Glu Thr Ala Tyr Arg Asn Leu Pro Lys Gln Gly Ser

145 150 155 160

Tyr Gln Tyr Ser Gly Ile Ala Phe Asn Gly Asp Asp Arg Ser Gly Arg

165 170 175

Leu Lys Tyr Thr Val Asp Phe Asp Lys Lys Gln Gly Tyr Gly Lys Ile

180 185 190

Ser Ser Met Ala Ser His Asn Asn Val Asp Leu Leu Ala Ala Gly Ile

195 200 205

Ala Asn Asn Asn Gly Lys Ala Ala Ile Ser Gly Lys Thr Ser Leu Asn

210 215 220

Gly Ile Glu Asn Gly Arg Tyr Asp Leu Lys Leu Phe Gly Pro Gln Ala

225 230 235 240

Gln Glu Ile Ala Gly Lys Ala Gln Ile Lys Val Gly Asp Ser Thr Lys

245 250 255

Glu Ile Gly Leu Ala Gly Lys Lys Glu

260 265

<210> 1119

<211> 825

<212> DNA

<213> N. cinerea FHbp

<400> 1119

gtgaaccgaa ctaccttctg ttgcctttct ttgaccgccg ccctgattct gaccgcctgc 60

agcagcggag gaggcggtgt cgccgccgac atcggtgcgg ggcttgccga tgcactaacc 120

gcaccgctcg accataaaga caaaggtttg cagtctttga cgctggatca gtccgtcagg 180

aaaaacgaga aactgaagct ggcggcacaa ggtgcggaaa aaacttatgg aaacggcgac 240

agcctcaata cgggcaaatt gaagaacgac aaggtcagcc gtttcgactt tatccgccaa 300

atcgaagtgg acgggcagct cattaccttg gagagtggag agttccaagt gtacaaacaa 360

agccattccg ccttaaccgc ccttcagaca gagcaagtac aagattcgga gcattcaggg 420

aagatggttg cgaaacgcca gttcagaatc ggcgatatag cgggcgaaca tacatctttt 480

gacaagcttc ccgaaggcgt cagggcgaca tatcgcggga cggcattcgg ttcagacgat 540

gccggtggaa aactgaccta caccatagat ttcgccgcca agcagggaca cggcaaaatc 600

gaacatttga aatcgccaga actcaatgtc gacctggccg ccgccgatat caagccggat 660

gaaaaacacc atgccgtcat cagcggttcc gtcctttaca accaagacga gaaaggcagt 720

tactccctcg gtatctttgg cggaaaagcc caggaagttg ccggcagcgc ggaagtgaaa 780

accgtaaacg gcatacgcca tatcggcctt gccgccaagc aataa 825

<210> 1120

<211> 274

<212> PRT

<213> N. cinerea FHbp

<400> 1120

Val Asn Arg Thr Thr Phe Cys Cys Leu Ser Leu Thr Ala Ala Leu Ile

1 5 10 15

Leu Thr Ala Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly

20 25 30

Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys

35 40 45

Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys

50 55 60

Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp

65 70 75 80

Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp

85 90 95

Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser

100 105 110

Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu

115 120 125

Gln Thr Glu Gln Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala

130 135 140

Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe
145 150 155 160
Asp Lys Leu Pro Glu Gly Val Arg Ala Thr Tyr Arg Gly Thr Ala Phe
165 170 175
Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
180 185 190
Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu

195 200 205
Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Glu Lys His His
210 215 220
Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser
225 230 235 240
Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser
245 250 255
Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala

260 265 270
Lys Gln

<210> 1121
<211> 798
<212> DNA
<213> N. flavescens FHbp
<400> 1121
atgagaactt tccatgtttc tgctttgact gcttccctgt ctttgatgtt ggctgcctgc 60
ggtggcgcaa caagcggctt gtcgaatgcc gtgaccgaac cgctcaatcc gcatccgaaa 120
ggcgtgttgt ccattgaatt gaacgaatcc gtccctgaaa acggtacgtt ggagctgacg 180
gccaacggta aaacgcaaac cctgaaaaaa ggcggcaaac tcgataccgg ctttttgaaa 240
accgataaag tatcctctta cgactacgcc caaaaaatta aggtaaaagg ccaagtcatc 300

actttggaaa cgggcgactt ccaagtgtat aaacaaaatt attccactgt tgccgcgcgt 360
tacgccaaac aaaaagccga tgacgcaggc aagctgcaaa acctcgatac atacacattc 420
accgtcggcg aagtccaagg cgatgaaacc gcttaccgca atttgcccaa acaaggcagc 480
tatcagtatt cgggcattgc gtttaacggc gatgaccgca gcggccgtct gaaatacacc 540

gtcgatttcg ataaaaaaca aggttacggc aaaatcagca gcatggcttc ccacaataat 600

gtcgacctgc ttgcagcagg cattgccaat aacaatggta aagccgccat cagcggtaaa 660

accagtttga acggcgtgga aaacggccgt tatgatttga aactcttcgg tccgcaggct 720

gaagaaattg ccggtaaggc gcaaatcaaa gttggtgact ctaccaaaga aattggtttg 780

gccggtaaga aagaatag 798

<210> 1122

<211> 265

<212> PRT

<213> N. flavescens FHbp

<400> 1122

Met Arg Thr Phe His Val Ser Ala Leu Thr Ala Ser Leu Ser Leu Met
1 5 10 15

Leu Ala Ala Cys Gly Gly Ala Thr Ser Gly Leu Ser Asn Ala Val Thr
20 25 30

Glu Pro Leu Asn Pro His Pro Lys Gly Val Leu Ser Ile Glu Leu Asn
35 40 45

Glu Ser Val Pro Glu Asn Gly Thr Leu Glu Leu Thr Ala Asn Gly Lys
50 55 60

Thr Gln Thr Leu Lys Lys Gly Gly Lys Leu Asp Thr Gly Phe Leu Lys
65 70 75 80

Thr Asp Lys Val Ser Ser Tyr Asp Tyr Ala Gln Lys Ile Lys Val Lys
85 90 95

Gly Gln Val Ile Thr Leu Glu Thr Gly Asp Phe Gln Val Tyr Lys Gln
100 105 110

Asn Tyr Ser Thr Val Ala Ala Arg Tyr Ala Lys Gln Lys Ala Asp Asp
115 120 125

Ala Gly Lys Leu Gln Asn Leu Asp Thr Tyr Thr Phe Thr Val Gly Glu
130 135 140

Val Gln Gly Asp Glu Thr Ala Tyr Arg Asn Leu Pro Lys Gln Gly Ser
145 150 155 160

Tyr Gln Tyr Ser Gly Ile Ala Phe Asn Gly Asp Asp Arg Ser Gly Arg

165 170 175

Leu Lys Tyr Thr Val Asp Phe Asp Lys Lys Gln Gly Tyr Gly Lys Ile

180 185 190

Ser Ser Met Ala Ser His Asn Asn Val Asp Leu Leu Ala Ala Gly Ile

195 200 205

Ala Asn Asn Asn Gly Lys Ala Ala Ile Ser Gly Lys Thr Ser Leu Asn

210 215 220

Gly Val Glu Asn Gly Arg Tyr Asp Leu Lys Leu Phe Gly Pro Gln Ala

225 230 235 240

Glu Glu Ile Ala Gly Lys Ala Gln Ile Lys Val Gly Asp Ser Thr Lys

245 250 255

Glu Ile Gly Leu Ala Gly Lys Lys Glu

260 265

<210> 1123

<211> 798

<212> DNA

<213> N. mucosa FHbp

<400> 1123

atgagaaccc tccgcatttc tgctttgacg gcttccctgt ctttgatgtt ggctgcctgc 60

ggcggcgcaa caagcggctt gtcaaatgcc gttaccgagc cgctcaatcc gcatccgaaa 120

ggcgtgttgt ccgttgaatt gaacgaatcc gtccctgaaa acggtacgtt ggacctgaca 180

gccaacggta aaacgcaaac cctgcaaaaa ggtgacaaac tcgataccgg ctttttgaaa 240

accgataaag tatcctctta cgactacgcc caaaaaatca aggtaaacgg ccaagtcatc 300

actttggaaa caggcgactt ccaagtgtat aaacaaaatt attcctctgt tgccgcgcgt 360

tacgccaaac aaaaagccga tgacgcaggc aagctgcaaa acctcgatac atacacattt 420

accgtcggcg aagtccaagg cgatgaaaca gcgtatagca atttgcccaa acaaggcagc 480

tatcagtatt cgggtatcgc gtttaacggc gacgaccgca gcggccgtct gaaatacacc 540

gtcgatttcg ataaaaaaca aggttacggc aacatcagca gcatggcttc ccacaataat 600

gtcaacctgc ttgccgcagg cattgccaat aacaacggca aagccgccat cagcggtaaa 660

accagtttga acggtgtcga aaacggccgt tacgatttga aactcttcgg tccgcaggct 720

gaagaaattg ccggtaaggc gcaaatcaaa attggcgatt ccaccaaaga aatcggtttg 780

gccggtaaga aagaatag 798

<210> 1124

<211> 265

<212> PRT

<213> N. mucosa FHbp

<400> 1124

Met Arg Thr Leu Arg Ile Ser Ala Leu Thr Ala Ser Leu Ser Leu Met
1 5 10 15

Leu Ala Ala Cys Gly Gly Ala Thr Ser Gly Leu Ser Asn Ala Val Thr
20 25 30

Glu Pro Leu Asn Pro His Pro Lys Gly Val Leu Ser Val Glu Leu Asn
35 40 45

Glu Ser Val Pro Glu Asn Gly Thr Leu Asp Leu Thr Ala Asn Gly Lys
50 55 60

Thr Gln Thr Leu Gln Lys Gly Asp Lys Leu Asp Thr Gly Phe Leu Lys
65 70 75 80

Thr Asp Lys Val Ser Ser Tyr Asp Tyr Ala Gln Lys Ile Lys Val Asn
85 90 95

Gly Gln Val Ile Thr Leu Glu Thr Gly Asp Phe Gln Val Tyr Lys Gln
100 105 110

Asn Tyr Ser Ser Val Ala Ala Arg Tyr Ala Lys Gln Lys Ala Asp Asp
115 120 125

Ala Gly Lys Leu Gln Asn Leu Asp Thr Tyr Thr Phe Thr Val Gly Glu
130 135 140

Val Gln Gly Asp Glu Thr Ala Tyr Ser Asn Leu Pro Lys Gln Gly Ser
145 150 155 160

Tyr Gln Tyr Ser Gly Ile Ala Phe Asn Gly Asp Asp Arg Ser Gly Arg
165 170 175

Leu Lys Tyr Thr Val Asp Phe Asp Lys Lys Gln Gly Tyr Gly Asn Ile
180 185 190

Ser Ser Met Ala Ser His Asn Asn Val Asn Leu Leu Ala Ala Gly Ile
195 200 205

Ala Asn Asn Asn Gly Lys Ala Ala Ile Ser Gly Lys Thr Ser Leu Asn
210 215 220

Gly Val Glu Asn Gly Arg Tyr Asp Leu Lys Leu Phe Gly Pro Gln Ala
225 230 235 240

Glu Glu Ile Ala Gly Lys Ala Gln Ile Lys Ile Gly Asp Ser Thr Lys
245 250 255

Glu Ile Gly Leu Ala Gly Lys Lys Glu
260 265

<210> 1125

<211> 801

<212> DNA

<213> N. macacae FHbp

<400> 1125

atgaaagccg tccgcttggt tcttgccgca tctttggttt ctacgcttgc cgcctgcggc 60

agctcctctt ccgcgctgtc cgatgcgata ggcaaaggct ttgatcctaa ggctaagggc 120

gtgaaataca ttaccgtttt cgagagcgtt cccgaaaacg gcacgatgca gctgagtgcc 180

aacaataagg tgcaaacgct taaaaaaggc gataatttgg acaccgcctt tctgaagcgc 240

gacaagattt cctattatga ctacgtcggc aaaatcaacg tcaacggaca ggtcatcgat 300

ttagaacgcg gcgactttat ggtttacaaa caagacaatt cggctgtcgc tgccaaatat 360

atcaagcaga aagccgatcc tgccgacggc aacaagctga aagacttgca ggcgtatgaa 420

tttaaagtcg gcgaagtgca aggtaaggaa attgccttta aagacctgcc gcaactgggc 480

cgctatacct accgcggtat cgcgtttaac ggcgacgata atagcggccg cctgacgtac 540

accattgatt tcgagaaaaa acaaggtcag ggcaaaatca gcggcatggc acctgattac 600

aatgtcgatt tggctgccgc caacattgcc gcagcaggtg cgggttcggc aatcaacgga 660

cgcgcgacgc tcaataatga agacaaaggc agctaccgtt tgaacatttt cggcagcaaa 720

gccgaagaga ttgccggtaa agcgcaagtg aaagtcggcg ataaagaaaa agacatcgga 780

cttgccggta aaaaagaata a 801

<210> 1126

<211> 266

<212> PRT

<213> N. macacae FHbp

<400> 1126

Met Lys Ala Val Arg Leu Val Leu Ala Ala Ser Leu Val Ser Thr Leu
1 5 10 15
Ala Ala Cys Gly Ser Ser Ser Ser Ala Leu Ser Asp Ala Ile Gly Lys
20 25 30
Gly Phe Asp Pro Lys Ala Lys Gly Val Lys Tyr Ile Thr Val Phe Glu
35 40 45
Ser Val Pro Glu Asn Gly Thr Met Gln Leu Ser Ala Asn Asn Lys Val

50 55 60
Gln Thr Leu Lys Lys Gly Asp Asn Leu Asp Thr Ala Phe Leu Lys Arg
65 70 75 80
Asp Lys Ile Ser Tyr Tyr Asp Tyr Val Gly Lys Ile Asn Val Asn Gly
85 90 95
Gln Val Ile Asp Leu Glu Arg Gly Asp Phe Met Val Tyr Lys Gln Asp
100 105 110
Asn Ser Ala Val Ala Ala Lys Tyr Ile Lys Gln Lys Ala Asp Pro Ala

115 120 125
Asp Gly Asn Lys Leu Lys Asp Leu Gln Ala Tyr Glu Phe Lys Val Gly
130 135 140
Glu Val Gln Gly Lys Glu Ile Ala Phe Lys Asp Leu Pro Gln Leu Gly
145 150 155 160
Arg Tyr Thr Tyr Arg Gly Ile Ala Phe Asn Gly Asp Asp Asn Ser Gly
165 170 175
Arg Leu Thr Tyr Thr Ile Asp Phe Glu Lys Lys Gln Gly Gln Gly Lys

180 185 190
Ile Ser Gly Met Ala Pro Asp Tyr Asn Val Asp Leu Ala Ala Ala Asn
195 200 205
Ile Ala Ala Ala Gly Ala Gly Ser Ala Ile Asn Gly Arg Ala Thr Leu
210 215 220
Asn Asn Glu Asp Lys Gly Ser Tyr Arg Leu Asn Ile Phe Gly Ser Lys
225 230 235 240
Ala Glu Glu Ile Ala Gly Lys Ala Gln Val Lys Val Gly Asp Lys Glu

245 250 255

Lys Asp Ile Gly Leu Ala Gly Lys Lys Glu

260 265

<210> 1127

<211> 840

<212> DNA

<213> N. subflava FHbp

<400> 1127

atgataaata tcataccaaa taaaaaagga aaggaaaaaa tgatgagaac cctccgtatt 60

cctgctttga cggcttccct gtctttgatg ttggctgcct gcggtggcgc aacaagcggc 120

ttgtcgaatg ccgttaccga gccgctcaat ccgcatccga aaggcgtgtt gtctgttgaa 180

ttgaacgaat ccgtccctga aaacggtacg ttggacctga cagccaacgg taaaacgcaa 240

atcctgcaaa aaggtgacaa actcgatacc ggctttttga aaaccgataa agtatcttct 300

tacgactacg cccaaaaaat caaggtaaac ggccaagtca tcactttgga aacgggcgac 360

ttccaagtgt ataaacaaaa ttattccact gttgccgcgc gttacgccaa acaaaaagcc 420

gatgacgcag gcaagctgca aaacctcgat acatacacat tcaccgtcgg cgaaatccaa 480

ggcgacgaaa ctgcatatcg caatttgccc aaacaaggca gctatcagta ttcgggcatt 540

gcatttaacg gcgacgaccg cagcggccgt ctgaaataca ccattgattt cgataaaaaa 600

caaggttacg gcaacatcag cagcatggct tcctacaata atgtcgacct gcttgccgca 660

ggcattgcca ataacaacgg caaagccgcc atcagcggta aaaccagttt gaacggtatc 720

gaaaacggcc attacgattt gaaactcttc ggcccgcagg ctgaagaaat tgccggtaag 780

gcgcaaatca aagttggcga ttccaccaaa gaaatcggtt tggccggtaa gaaagaatag 840

<210> 1128

<211> 279

<212> PRT

<213> N. subflava FHbp

<400> 1128

Met Ile Asn Ile Ile Pro Asn Lys Lys Gly Lys Glu Lys Met Met Arg

1 5 10 15

Thr Leu Arg Ile Pro Ala Leu Thr Ala Ser Leu Ser Leu Met Leu Ala

20 25 30

Ala Cys Gly Gly Ala Thr Ser Gly Leu Ser Asn Ala Val Thr Glu Pro

35 40 45

Leu Asn Pro His Pro Lys Gly Val Leu Ser Val Glu Leu Asn Glu Ser

50 55 60

Val Pro Glu Asn Gly Thr Leu Asp Leu Thr Ala Asn Gly Lys Thr Gln

65 70 75 80

Ile Leu Gln Lys Gly Asp Lys Leu Asp Thr Gly Phe Leu Lys Thr Asp

85 90 95

Lys Val Ser Ser Tyr Asp Tyr Ala Gln Lys Ile Lys Val Asn Gly Gln

100 105 110

Val Ile Thr Leu Glu Thr Gly Asp Phe Gln Val Tyr Lys Gln Asn Tyr

115 120 125

Ser Thr Val Ala Ala Arg Tyr Ala Lys Gln Lys Ala Asp Asp Ala Gly

130 135 140

Lys Leu Gln Asn Leu Asp Thr Tyr Thr Phe Thr Val Gly Glu Ile Gln

145 150 155 160

Gly Asp Glu Thr Ala Tyr Arg Asn Leu Pro Lys Gln Gly Ser Tyr Gln

165 170 175

Tyr Ser Gly Ile Ala Phe Asn Gly Asp Asp Arg Ser Gly Arg Leu Lys

180 185 190

Tyr Thr Ile Asp Phe Asp Lys Lys Gln Gly Tyr Gly Asn Ile Ser Ser

195 200 205

Met Ala Ser Tyr Asn Asn Val Asp Leu Leu Ala Ala Gly Ile Ala Asn

210 215 220

Asn Asn Gly Lys Ala Ala Ile Ser Gly Lys Thr Ser Leu Asn Gly Ile

225 230 235 240

Glu Asn Gly His Tyr Asp Leu Lys Leu Phe Gly Pro Gln Ala Glu Glu

245 250 255

Ile Ala Gly Lys Ala Gln Ile Lys Val Gly Asp Ser Thr Lys Glu Ile

260 265 270

Gly Leu Ala Gly Lys Lys Glu

275

<210> 1129

<211> 801

<212> DNA

<213> N. sicca FHbp

<400> 1129

atgaaagccg tccgcttggt tcttgccgca tttttggttt ctacgcttgc cgcctgcggc 60

agctcctctt ccgcgctgtc cgatgcgata ggcaaaggct ttgatcctaa ggctaagggc 120

gtgaaataca ttaccgtttt cgagagcgtt cccgaaaacg gtacgatgca gctgagtgcc 180

aacaataagg tgcaaacgct taaaaaaggc gacaatttgg acaccgcctt tctgaagcgc 240

gacaagattt cctattatga ctacgtcggc aaaatcaacg tcaacggaca ggtcatcgat 300

ttggaacgcg gcgactttat ggtttacaaa caagacaatt cggctgtcgc tgccaaatat 360

atcaagcaga aagccgatcc tgccgacggc aacaagctga aagacttgca ggcgtatgaa 420

tttaaagtcg gcgaagtgca aggtaaggaa attgccttta aagacctgcc gcaactgggc 480

cgctatacct accgcggcat cgcgtttaac ggcgacgata tagcggccg tctgacgtac 540

accattgatt tcgagaaaaa acaaggtcag ggcaaaatca gcggcatggc acctgattac 600

aatgtcgatt tggctgccgc caacattgcc gcagcagggg cgggttcggc aatcaacgga 660

cgcgcgacgc tcaacaatga agacaaaggt agctaccgtt tgaacatttt cggcagcaag 720

gctgaagaga ttgccggtaa ggcgcaagtg aaagtcggcg ataaagagaa agacatcgga 780

cttgccggta aaaaagaata a 801

<210> 1130

<211> 266

<212> PRT

<213> N. sicca FHbp

<400> 1130

Met Lys Ala Val Arg Leu Val Leu Ala Ala Phe Leu Val Ser Thr Leu

1 5 10 15

Ala Ala Cys Gly Ser Ser Ser Ser Ala Leu Ser Asp Ala Ile Gly Lys

20 25 30

Gly Phe Asp Pro Lys Ala Lys Gly Val Lys Tyr Ile Thr Val Phe Glu

35 40 45

Ser Val Pro Glu Asn Gly Thr Met Gln Leu Ser Ala Asn Asn Lys Val

50 55 60

Gln Thr Leu Lys Lys Gly Asp Asn Leu Asp Thr Ala Phe Leu Lys Arg
65 70 75 80
Asp Lys Ile Ser Tyr Tyr Asp Tyr Val Gly Lys Ile Asn Val Asn Gly
85 90 95
Gln Val Ile Asp Leu Glu Arg Gly Asp Phe Met Val Tyr Lys Gln Asp
100 105 110
Asn Ser Ala Val Ala Ala Lys Tyr Ile Lys Gln Lys Ala Asp Pro Ala

115 120 125
Asp Gly Asn Lys Leu Lys Asp Leu Gln Ala Tyr Glu Phe Lys Val Gly
130 135 140
Glu Val Gln Gly Lys Glu Ile Ala Phe Lys Asp Leu Pro Gln Leu Gly
145 150 155 160
Arg Tyr Thr Tyr Arg Gly Ile Ala Phe Asn Gly Asp Asp Asn Ser Gly
165 170 175
Arg Leu Thr Tyr Thr Ile Asp Phe Glu Lys Lys Gln Gly Gln Gly Lys

180 185 190
Ile Ser Gly Met Ala Pro Asp Tyr Asn Val Asp Leu Ala Ala Ala Asn
195 200 205
Ile Ala Ala Ala Gly Ala Gly Ser Ala Ile Asn Gly Arg Ala Thr Leu
210 215 220
Asn Asn Glu Asp Lys Gly Ser Tyr Arg Leu Asn Ile Phe Gly Ser Lys
225 230 235 240
Ala Glu Glu Ile Ala Gly Lys Ala Gln Val Lys Val Gly Asp Lys Glu

245 250 255
Lys Asp Ile Gly Leu Ala Gly Lys Lys Glu
260 265
<210> 1131
<211> 801
<212> DNA
<213> Neisseria sp. GT4A CT1 FHbp
<400> 1131
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agctcctctt ccgcgctgtc cgatgcgata ggcaaaggct ttgatcctaa ggctaagggc 120

gtgaaataca ttaccgtttt cgagagcgtt cccgaaaacg gcacgatgca gctgagtgcc 180

aacaataagg tgcaaacgct taaaaaaggc gacaatttgg acaccgcctt tctgaagcgc 240

gacaagattt cctattatga ttacgtcggc aaaatcaacg tcaacggaca ggtcatcgat 300

ttggaacgcg gcgattttat ggtttacaaa caagacaatt cggctgtcgc tgccaaatat 360

atcaagcaga aagccgattc tgccgacggc aacaagctga aagacttgca ggcgtatgaa 420

tttaaagtcg gcgaagtgca aggtaaggaa attgccttta aagacctgcc gcaactgggc 480

cgctatacct accgtggtat cgcatttaac ggcgacgata atagcggccg cctgacgtac 540

accattgatt ttgagaaaaa acaaggtcag ggcaaaatca gcggcatggc gcctgattac 600

aatgtcgatt tggctgccgc taacattgcc gcagcaggta cgggttcggc aatcaacgga 660

cgcgcgacgc tcaacaatga agacaaaggc agctaccgtt tgaacatttt cggcagcaag 720

gctgaagaga ttgccggtaa agcgcaagtg aaagttggcg ataaagagaa agacatcgga 780

cttgccggta aaaaagaata a 801

<210> 1132

<211> 266

<212> PRT

<213> Neisseria sp. GT4A CT1 FHbp

<400> 1132

Met Lys Ala Val Arg Leu Val Leu Ala Ala Ser Leu Val Ser Thr Leu

1 5 10 15

Ala Ala Cys Gly Ser Ser Ser Ser Ala Leu Ser Asp Ala Ile Gly Lys

20 25 30

Gly Phe Asp Pro Lys Ala Lys Gly Val Lys Tyr Ile Thr Val Phe Glu

35 40 45

Ser Val Pro Glu Asn Gly Thr Met Gln Leu Ser Ala Asn Asn Lys Val

50 55 60

Gln Thr Leu Lys Lys Gly Asp Asn Leu Asp Thr Ala Phe Leu Lys Arg

65 70 75 80

Asp Lys Ile Ser Tyr Tyr Asp Tyr Val Gly Lys Ile Asn Val Asn Gly

85 90 95

Gln Val Ile Asp Leu Glu Arg Gly Asp Phe Met Val Tyr Lys Gln Asp

100 105 110

Asn Ser Ala Val Ala Ala Lys Tyr Ile Lys Gln Lys Ala Asp Ser Ala

115 120 125

Asp Gly Asn Lys Leu Lys Asp Leu Gln Ala Tyr Glu Phe Lys Val Gly

130 135 140

Glu Val Gln Gly Lys Glu Ile Ala Phe Lys Asp Leu Pro Gln Leu Gly

145 150 155 160

Arg Tyr Thr Tyr Arg Gly Ile Ala Phe Asn Gly Asp Asp Asn Ser Gly

165 170 175

Arg Leu Thr Tyr Thr Ile Asp Phe Glu Lys Lys Gln Gly Gln Gly Lys

180 185 190

Ile Ser Gly Met Ala Pro Asp Tyr Asn Val Asp Leu Ala Ala Ala Asn

195 200 205

Ile Ala Ala Ala Gly Thr Gly Ser Ala Ile Asn Gly Arg Ala Thr Leu

210 215 220

Asn Asn Glu Asp Lys Gly Ser Tyr Arg Leu Asn Ile Phe Gly Ser Lys

225 230 235 240

Ala Glu Glu Ile Ala Gly Lys Ala Gln Val Lys Val Gly Asp Lys Glu

245 250 255

Lys Asp Ile Gly Leu Ala Gly Lys Lys Glu

260 265

<210> 1133

<211> 753

<212> DNA

<213> M. haemolytica FHbp

<400> 1133

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ggtagcggtg gttcaggtag cagttctaat aatgctaaat cgaaaccaca agttgagtta 120

aaaaaaactg aagaggataa aaaggctgaa gaagcaaaaa aaattgcaga ggcaaaagga 180

attggcaata aagaatataa agatggatta aatgagttag aagaaaaaaa tgaaacaggt 240

aaaaacggag aagagattcg aacctatggt tatctctata acagccatta ttccgttgta 300

actgccaaaa tgaaacaaac tttacaggaa aatggtcgtc aaatggaacc tacggttgaa 360

gtgaaagggc ttaaaactga gaatttaccg acagagggca aagcaacata taaaggagaa 420

gcctttgatt ctcacggtaa taacagcaat tcagtagtag gtggagaatt aatctataat 480

gttgatttct ctagtcgtac cggatcaggt ctagttaaaa atgtacaggg cggttctatc 540

gagttagcac aaggcgaaat aaaaaatgat agtattatag cttctgctca ccaaaagtat 600

aatgatcagg ctgttggaaa tggtagttac aatatccaat tctttggtcc aaatgcagaa 660

gaaattggag ggaaaattga gcttaatggt gagggcgaag gctcaatgaa gcagatgtta 720

ggtattgcag gaacccgaga agaacaaaaa taa 753

<210> 1134

<211> 250

<212> PRT

<213> M. haemolytica FHbp

<400> 1134

Met Lys Ser Ile Lys Lys Leu Thr Leu Ala Thr Leu Ile Leu Val Gly

1 5 10 15

Leu Thr Ala Cys Gly Ser Gly Gly Ser Gly Ser Ser Ser Asn Asn Ala

20 25 30

Lys Ser Lys Pro Gln Val Glu Leu Lys Lys Thr Glu Glu Asp Lys Lys

35 40 45

Ala Glu Glu Ala Lys Lys Ile Ala Glu Ala Lys Gly Ile Gly Asn Lys

50 55 60

Glu Tyr Lys Asp Gly Leu Asn Glu Leu Glu Glu Lys Asn Glu Thr Gly

65 70 75 80

Lys Asn Gly Glu Glu Ile Arg Thr Tyr Gly Tyr Leu Tyr Asn Ser His

85 90 95

Tyr Ser Val Val Thr Ala Lys Met Lys Gln Thr Leu Gln Glu Asn Gly

100 105 110

Arg Gln Met Glu Pro Thr Val Glu Val Lys Gly Leu Lys Thr Glu Asn

115 120 125

Leu Pro Thr Glu Gly Lys Ala Thr Tyr Lys Gly Glu Ala Phe Asp Ser

130 135 140

His Gly Asn Asn Ser Asn Ser Val Val Gly Gly Glu Leu Ile Tyr Asn

145 150 155 160

Val Asp Phe Ser Ser Arg Thr Gly Ser Gly Leu Val Lys Asn Val Gln

165 170 175

Gly Gly Ser Ile Glu Leu Ala Gln Gly Glu Ile Lys Asn Asp Ser Ile

180 185 190

Ile Ala Ser Ala His Gln Lys Tyr Asn Asp Gln Ala Val Gly Asn Gly

195 200 205

Ser Tyr Asn Ile Gln Phe Phe Gly Pro Asn Ala Glu Glu Ile Gly Gly

210 215 220

Lys Ile Glu Leu Asn Gly Glu Gly Glu Gly Ser Met Lys Gln Met Leu

225 230 235 240

Gly Ile Ala Gly Thr Arg Glu Glu Gln Lys

245 250

<210> 1135

<211> 792

<212> DNA

<213> A. actinomycetemcomitans FHbp

<400> 1135

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caagctgccg gggggttggc ggatggtcta ctgaaaccgt tcgatccgaa agcaaaagac 120

tggaagcagt taaccatctc cgaatctgtt cccgataacg gcactttgga actaaccgac 180

cgcggcggca aaacccagat cttgcgtaaa ggcggcgttc tggatacagg ccatttgaga 240

tccgataaga tctctgacta cgattacgtc aaaaaaatca acgtgaacgg tcaaataatc 300

gagttggaac gaggcgattt tctgatatat aaacagagta attccatcat cgccgctacg 360

ttagcgaaac agaaaaccaa cgcagatggt acacgctcct ctgcctttga tttccatgtc 420

aacgagattc aagggcgaga catcgccttt aataatctgc cggcttcggg acaggtaaac 480

tatcgcggca tcgcatttac cggcgatgac cgtagaggtc gtttatccta cactatcgac 540

ttcgctaaaa aacaaggcag cggtcgcatc agtgatctac gtggtgacta taacgtagat 600

ttggcgcaaa cagacgtccg cgcaatgggg aacggttccg ggttgagtgg taaggctatg 660

aaaaatggtg tggaaagagg aaattacacg ctaaaaatct tcggtaacaa ggcagaagaa 720

atcgccggta aagctgagat caaaaccggt aagggaactc aagaaatcgg tttggcaggt 780

aaaaaagaat aa 792

<210> 1136

<211> 263

<212> PRT

<213> A. actinomycetemcomitans FHbp

<400> 1136

Met Lys Thr Lys Tyr Leu Leu Ala Ala Leu Thr Val Ala Cys Thr Leu
1 5 10 15

Ser Ala Cys Ser Gln Ala Ala Gly Gly Leu Ala Asp Gly Leu Leu Lys
20 25 30

Pro Phe Asp Pro Lys Ala Lys Asp Trp Lys Gln Leu Thr Ile Ser Glu
35 40 45

Ser Val Pro Asp Asn Gly Thr Leu Glu Leu Thr Asp Arg Gly Gly Lys
50 55 60

Thr Gln Ile Leu Arg Lys Gly Gly Val Leu Asp Thr Gly His Leu Arg
65 70 75 80

Ser Asp Lys Ile Ser Asp Tyr Asp Tyr Val Lys Lys Ile Asn Val Asn
85 90 95

Gly Gln Ile Ile Glu Leu Glu Arg Gly Asp Phe Leu Ile Tyr Lys Gln
100 105 110

Ser Asn Ser Ile Ile Ala Ala Thr Leu Ala Lys Gln Lys Thr Asn Ala
115 120 125

Asp Gly Thr Arg Ser Ser Ala Phe Asp Phe His Val Asn Glu Ile Gln
130 135 140

Gly Arg Asp Ile Ala Phe Asn Asn Leu Pro Ala Ser Gly Gln Val Asn
145 150 155 160

Tyr Arg Gly Ile Ala Phe Thr Gly Asp Asp Arg Arg Gly Arg Leu Ser
165 170 175

Tyr Thr Ile Asp Phe Ala Lys Lys Gln Gly Ser Gly Arg Ile Ser Asp
180 185 190

Leu Arg Gly Asp Tyr Asn Val Asp Leu Ala Gln Thr Asp Val Arg Ala
195 200 205

Met Gly Asn Gly Ser Gly Leu Ser Gly Lys Ala Met Lys Asn Gly Val
210 215 220

Glu Arg Gly Asn Tyr Thr Leu Lys Ile Phe Gly Asn Lys Ala Glu Glu
225 230 235 240

Ile Ala Gly Lys Ala Glu Ile Lys Thr Gly Lys Gly Thr Gln Glu Ile
245 250 255

Gly Leu Ala Gly Lys Lys Glu
260

<210> 1137

<211> 2214

<212> DNA

<213> N. meningitidis LbpB

<400> 1137

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ggcggcaatt tcggcgtgca gcctgttgtc gaatcaacgc cgaccgcgta ccccgtcacc 120

ttcaaatcta aggacgttcc cactccgccc cctgccgggt cttcggtaga aaccacgccg 180

gtcaaccggc ccgccgtcgg tgcggcaatg cggctgccaa ggcggaatat tgcttcctat 240

aaacaagacg gtacggaaat tcccgacaag catcaggcag aggagcatct gccgcttaaa 300

gagaaggata tcctgttttt agacggtacg ctgaaagaac aggctgacaa acttaaaaag 360

aaaatcaacg aacggtattc tgatgtgagg gttatcacat cgaaaaaaga agaagaaaaa 420

tatcaatatc aatttgtccg tgcgggctat gtgtttacca gggcggaagg aaaggataat 480

gaaaaagaaa agacttctga tggtaaggag tttgttaacc gatttagtta tgacggtttt 540

gtatattatt ccggagaacg tccttcccaa tctttaccga gcgcgggaac ggtgcaatat 600

tccggtaact ggcaatatat gaccgatgcc aaacgtcatc ggacaggtaa ggcggtttcc 660

agtacggatt tgggttatac cacatattat ggtaatgaaa ttggggcaac ttcttatgag 720

gctagggatg ccgacgacag ggaaaagcat cctgccgaat atacggttga ttttgataac 780

aaaaccctga atggcaagct gattaaaaat cagtatgtgc aaaataaaag taatccaaat 840

gagcccaaaa aaccgctgac catttacgac attaccgcaa cattggacgg caaccgcttt 900

accggcagtg ccaaagttag caccgaggtg aagacgcaac acgctgataa agaatatttg 960

tttttccata ccgatgccga tcagcggctt gagggcggtt ttttcggcga taacggagaa 1020

gagcttgccg gacggtttat cagcaacgac aacagcgtat tcggcgtatt cgcaggcaaa 1080

caaaaaacag agacagaaaa cgcagcagat acaaaacctg ccctgtcgtc tggaaaacac 1140

accaaaatct tggattctct gaaaatttcc gttgacgagg caagtgataa aaatccccgt 1200
gagtttgcca tttcctctat gcccgatttt ggtcatcccg acaaacttct tgtcgaaggg 1260
cgtgaaattc ctttggtaaa caaagaacaa accatcgagc ttgccgatgg taggaaaacg 1320
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cgtcccgccg ccaaaccgaa ggcgcaggac gaagagaggg acgaagagga tacaggcgtt 1440
gatagcgtcg aagaaggcga agacgaaatc gacgatgaag aaggcaccga agacgcagcc 1500
gtaaaagacg aaggcagcga agaagacgaa gccgtagaag gtgaagatga agctgaagaa 1560

cccgaagaag aatcgccgac agaagaaggc ggcagcggtt cagacggcat cctgcccgct 1620
ccggaagccc ctaaaggcag gaacatcgac cttttcctga aaggtatccg cacggcggaa 1680
acggatattc cgaaaactgg agaagcacac tataccggca cttgggaagc gcgtatcggc 1740
aaacccattc aatgggacaa tcaggcggat aaagaagcgg caaaagcagt atttaccgtt 1800
gatttcggca agaaatcgat ttccggaacg ctgacggagg aaaacggtgt agaacctgct 1860
ttccatattg aaaacggcaa gattgagggc aacggtttct acgcgacagc acgcactcgg 1920
gagaacggca tcaatctttc gggaaatggt tcgaccgacc ccaaaacctt ccaagctagt 1980

aatcttcgtg tagaaggggg attttacggc ccgcaggcgg aggaattggg cggtattatt 2040
ttcaataatg atgggaaatc tcttggtata actgaaggta ctgaaaataa agttgatgtt 2100
gaagctgaag ttgatgctga agttgatgtt ggcaaacagt tagaatctga agttaaacac 2160
caattcggcg tggtattcgg tgcgaagaaa gatatgcagg aggtggaaaa atga 2214

<210> 1138
<211> 737
<212> PRT
<213> N. meningitidis LbpB
<400> 1138

Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
1 5 10 15

Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
20 25 30

Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
35 40 45

Pro Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Arg Pro

50 55 60

Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn Ile Ala Ser Tyr
65 70 75 80

Lys Gln Asp Gly Thr Glu Ile Pro Asp Lys His Gln Ala Glu Glu His
85 90 95

Leu Pro Leu Lys Glu Lys Asp Ile Leu Phe Leu Asp Gly Thr Leu Lys
100 105 110

Glu Gln Ala Asp Lys Leu Lys Lys Lys Ile Asn Glu Arg Tyr Ser Asp
115 120 125

Val Arg Val Ile Thr Ser Lys Lys Glu Glu Glu Lys Tyr Gln Tyr Gln
130 135 140

Phe Val Arg Ala Gly Tyr Val Phe Thr Arg Ala Glu Gly Lys Asp Asn
145 150 155 160

Glu Lys Glu Lys Thr Ser Asp Gly Lys Glu Phe Val Asn Arg Phe Ser
165 170 175

Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln Ser Leu
180 185 190

Pro Ser Ala Gly Thr Val Gln Tyr Ser Gly Asn Trp Gln Tyr Met Thr
195 200 205

Asp Ala Lys Arg His Arg Thr Gly Lys Ala Val Ser Ser Thr Asp Leu
210 215 220

Gly Tyr Thr Thr Tyr Tyr Gly Asn Glu Ile Gly Ala Thr Ser Tyr Glu
225 230 235 240

Ala Arg Asp Ala Asp Asp Arg Glu Lys His Pro Ala Glu Tyr Thr Val
245 250 255

Asp Phe Asp Asn Lys Thr Leu Asn Gly Lys Leu Ile Lys Asn Gln Tyr
260 265 270

Val Gln Asn Lys Ser Asn Pro Asn Glu Pro Lys Lys Pro Leu Thr Ile
275 280 285

Tyr Asp Ile Thr Ala Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala
290 295 300

Lys Val Ser Thr Glu Val Lys Thr Gln His Ala Asp Lys Glu Tyr Leu
305 310 315 320
Phe Phe His Thr Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly
325 330 335

Asp Asn Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser
340 345 350
Val Phe Gly Val Phe Ala Gly Lys Gln Lys Thr Glu Thr Glu Asn Ala
355 360 365
Ala Asp Thr Lys Pro Ala Leu Ser Ser Gly Lys His Thr Lys Ile Leu
370 375 380
Asp Ser Leu Lys Ile Ser Val Asp Glu Ala Ser Asp Lys Asn Pro Arg
385 390 395 400

Glu Phe Ala Ile Ser Ser Met Pro Asp Phe Gly His Pro Asp Lys Leu
405 410 415
Leu Val Glu Gly Arg Glu Ile Pro Leu Val Asn Lys Glu Gln Thr Ile
420 425 430
Glu Leu Ala Asp Gly Arg Lys Thr Thr Ile Arg Thr Cys Cys Asp Phe
435 440 445
Leu Thr Tyr Val Lys Ile Gly Arg Met Gln Thr Glu Arg Pro Ala Ala
450 455 460

Lys Pro Lys Ala Gln Asp Glu Glu Arg Asp Glu Glu Asp Thr Gly Val
465 470 475 480
Asp Ser Val Glu Glu Gly Glu Asp Glu Ile Asp Asp Glu Glu Gly Thr
485 490 495
Glu Asp Ala Ala Val Lys Asp Glu Gly Ser Glu Glu Asp Glu Ala Val
500 505 510
Glu Gly Glu Asp Glu Ala Glu Glu Pro Glu Glu Glu Ser Pro Thr Glu
515 520 525

Glu Gly Gly Ser Gly Ser Asp Gly Ile Leu Pro Ala Pro Glu Ala Pro
530 535 540
Lys Gly Arg Asn Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu

545 550 555 560

Thr Asp Ile Pro Lys Thr Gly Glu Ala His Tyr Thr Gly Thr Trp Glu

565 570 575

Ala Arg Ile Gly Lys Pro Ile Gln Trp Asp Asn Gln Ala Asp Lys Glu

580 585 590

Ala Ala Lys Ala Val Phe Thr Val Asp Phe Gly Lys Lys Ser Ile Ser

595 600 605

Gly Thr Leu Thr Glu Glu Asn Gly Val Glu Pro Ala Phe His Ile Glu

610 615 620

Asn Gly Lys Ile Glu Gly Asn Gly Phe Tyr Ala Thr Ala Arg Thr Arg

625 630 635 640

Glu Asn Gly Ile Asn Leu Ser Gly Asn Gly Ser Thr Asp Pro Lys Thr

645 650 655

Phe Gln Ala Ser Asn Leu Arg Val Glu Gly Gly Phe Tyr Gly Pro Gln

660 665 670

Ala Glu Glu Leu Gly Gly Ile Ile Phe Asn Asn Asp Gly Lys Ser Leu

675 680 685

Gly Ile Thr Glu Gly Thr Glu Asn Lys Val Asp Val Glu Ala Glu Val

690 695 700

Asp Ala Glu Val Asp Val Gly Lys Gln Leu Glu Ser Glu Val Lys His

705 710 715 720

Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val Glu

725 730 735

Lys

<210> 1139

<211> 2226

<212> DNA

<213> N. lactamica LbpB

<400> 1139

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tccaaaccgt ccaaacctga ggacgttcct actccgcccc ctgccaaacc ctctatagaa 180

accacgccgg tcaatcaacc cgccgtcggt gcggcaatgc ggctgccaag gcggaatatt 240

gcttcctata aacaagacgg tacggaaatt cccgacaagc atcaggcgga ggagcatctg 300

ccgcttaaag agaaggatat cctgttttta gacggtacgc tgaaagaaca ggctgacaaa 360

cttaaaaaga aaatcaacga acggtattct gatgtgaggg ttatcacatc gaaaaaagaa 420

gaagaaaaat atcaatatca atttgtccgt gcgggctatg tgtttaccag ggcggaagga 480

aaggataatg aaaaagaaaa gacttctgat ggtaaggagt ttgttaaccg atttagttat 540

gacggttttg tatattattc cggagaacgt ccttcccaat ctttaccgag cgcgggaacg 600

gtgcaatatt ccggtaactg gcaatatatg accgatgcca aacgtcatcg gacaggtaag 660

gcggtttcca gtacggattt gggttatacc acatattatg gtaatgaaat tggggcaact 720

tcttatgagg ctagggatgc cgacgacagg gaaaagcatc ctgccgaata tacggttgat 780

tttgataaca aaaccctgaa tggcaagctg attaaaaatc agtatgtgca aaataaaagt 840

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aaccgcttta ccggcagtgc caaagttaac accgaggtga agaagagcca cgctgataaa 960

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aaggggggaag agcttgccgg acggtttatc agtaacgaca acagcgtatt cggcgtattc 1080

gcaggcaggc aaaaaacaga cgcatcaaac gcatcaggca caaatcctgc tatgccgtct 1140

gaaaaacaca ccaaaatctt ggattctcta aaaatttccg ttgacgaggc ggctgatgaa 1200

aaagcccgta cgtttgccat ttcctctatg cccgatcttg gtcatcccga caaacttctt 1260

gtcgaagggc gtgaaattcc tttggtaaac caagagaaaa ccatcaatct tgccgacggc 1320

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gccgaagacg aaatcggcga tgaagaagaa ggcacgggag atgaagccgt agaaggtgaa 1560

gacggcgaag aagacgaagg tgaagaagct gaagaacccg aagaagaatc gccggcagaa 1620

ggcggcggcg gttcagacgg catcctgccc gctccggaag cccctaaagg cagggacatc 1680

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cattatacgg gcacttggga agcgcgtatc agcaaaccca ttcaatggga taataaggcg 1800

gataaagcgg caaaagcaga gtttaatgtt gatttcggca agaaatcgat ttccggaacg 1860

ctgacggaga aaaacggtgt agaacctgct ttccgtattg aaaacggcgt gattgatggc 1920

aacggtttcc acgcaacagc acgcactcgg gataacggca tcaatctttc gggaaatggt 1980
tcgactaatc ctcaaagttt caaagccgac aatcttcttg taacgggcgg cttttacggc 2040
ccgcaggcgg aggaattggg cggtactatt ttcaataatg atgggaaatc tcttgatata 2100
actgaagata ctgaaaatga agctgaagct gaagctggtg ttgacgaaca gttagaacct 2160
gaagctaaac cccaattcgg cgtggtattc ggtgcgaaga aagataataa agaggtggaa 2220
aaatga 2226

<210> 1140
<211> 741
<212> PRT
<213> N. lactamica LbpB

<400> 1140

Met Cys Lys Leu Asn Tyr Gly Gly Ile Ala Leu Leu Pro Leu Met Leu
1 5 10 15
Ala Ala Cys Gly Gly Asn Phe Gly Val Gln Pro Val Ala Lys Pro Thr
20 25 30
Pro Ile Ala Gln Thr Pro Ser Asp Ser Lys Pro Ser Lys Pro Glu Asp
35 40 45
Val Pro Thr Pro Pro Pro Ala Lys Pro Ser Ile Glu Thr Thr Pro Val
50 55 60

Asn Gln Pro Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn Ile
65 70 75 80
Ala Ser Tyr Lys Gln Asp Gly Thr Glu Ile Pro Asp Lys His Gln Ala
85 90 95
Glu Glu His Leu Pro Leu Lys Glu Lys Asp Ile Leu Phe Leu Asp Gly
100 105 110
Thr Leu Lys Glu Gln Ala Asp Lys Leu Lys Lys Lys Ile Asn Glu Arg
115 120 125

Tyr Ser Asp Val Arg Val Ile Thr Ser Lys Lys Glu Glu Glu Lys Tyr
130 135 140
Gln Tyr Gln Phe Val Arg Ala Gly Tyr Val Phe Thr Arg Ala Glu Gly

145 150 155 160

Lys Asp Asn Glu Lys Glu Lys Thr Ser Asp Gly Lys Glu Phe Val Asn

165 170 175

Arg Phe Ser Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser

180 185 190

Gln Ser Leu Pro Ser Ala Gly Thr Val Gln Tyr Ser Gly Asn Trp Gln

195 200 205

Tyr Met Thr Asp Ala Lys Arg His Arg Thr Gly Lys Ala Val Ser Ser

210 215 220

Thr Asp Leu Gly Tyr Thr Thr Tyr Tyr Gly Asn Glu Ile Gly Ala Thr

225 230 235 240

Ser Tyr Glu Ala Arg Asp Ala Asp Asp Arg Glu Lys His Pro Ala Glu

245 250 255

Tyr Thr Val Asp Phe Asp Asn Lys Thr Leu Asn Gly Lys Leu Ile Lys

260 265 270

Asn Gln Tyr Val Gln Asn Lys Ser Asn Pro Asn Glu Pro Lys Lys Pro

275 280 285

Leu Thr Ile Tyr Asp Ile Thr Ala Lys Leu Asp Gly Asn Arg Phe Thr

290 295 300

Gly Ser Ala Lys Val Asn Thr Glu Val Lys Lys Ser His Ala Asp Lys

305 310 315 320

Glu Tyr Leu Phe Phe His Thr Asp Ala Asp Gln Arg Leu Glu Gly Gly

325 330 335

Phe Phe Gly Asp Lys Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn

340 345 350

Asp Asn Ser Val Phe Gly Val Phe Ala Gly Arg Gln Lys Thr Asp Ala

355 360 365

Ser Asn Ala Ser Gly Thr Asn Pro Ala Met Pro Ser Glu Lys His Thr

370 375 380

Lys Ile Leu Asp Ser Leu Lys Ile Ser Val Asp Glu Ala Ala Asp Glu

385 390 395 400

Lys Ala Arg Thr Phe Ala Ile Ser Ser Met Pro Asp Leu Gly His Pro
405 410 415
Asp Lys Leu Leu Val Glu Gly Arg Glu Ile Pro Leu Val Asn Gln Glu
420 425 430
Lys Thr Ile Asn Leu Ala Asp Gly Arg Lys Met Thr Val Arg Ala Cys
435 440 445

Cys Asp Phe Leu Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Asp Arg
450 455 460
Pro Ala Ser Lys Pro Lys Ala Glu Asp Lys Arg Glu Asp Glu Glu Ser
465 470 475 480
Ala Gly Val Asp Asn Gly Glu Glu Gly Thr Glu Asp Glu Ala Ala Glu
485 490 495
Gly Ser Glu Gly Ala Glu Asp Glu Ile Gly Asp Glu Glu Glu Gly Thr
500 505 510

Gly Asp Glu Ala Val Glu Gly Glu Asp Gly Glu Glu Asp Glu Gly Glu
515 520 525
Glu Ala Glu Glu Pro Glu Glu Glu Ser Pro Ala Glu Gly Gly Gly Gly
530 535 540
Ser Asp Gly Ile Leu Pro Ala Pro Glu Ala Pro Lys Gly Arg Asp Ile
545 550 555 560
Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Lys
565 570 575

Thr Gly Thr Ala His Tyr Thr Gly Thr Trp Glu Ala Arg Ile Ser Lys
580 585 590
Pro Ile Gln Trp Asp Asn Lys Ala Asp Lys Ala Ala Lys Ala Glu Phe
595 600 605
Asn Val Asp Phe Gly Lys Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys
610 615 620
Asn Gly Val Glu Pro Ala Phe Arg Ile Glu Asn Gly Val Ile Asp Gly
625 630 635 640

Asn Gly Phe His Ala Thr Ala Arg Thr Arg Asp Asn Gly Ile Asn Leu

645 650 655

Ser Gly Asn Gly Ser Thr Asn Pro Gln Ser Phe Lys Ala Asp Asn Leu

660 665 670

Leu Val Thr Gly Gly Phe Tyr Gly Pro Gln Ala Glu Glu Leu Gly Gly

675 680 685

Thr Ile Phe Asn Asn Asp Gly Lys Ser Leu Asp Ile Thr Glu Asp Thr

690 695 700

Glu Asn Glu Ala Glu Ala Glu Ala Gly Val Asp Glu Gln Leu Glu Pro

705 710 715 720

Glu Ala Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn

725 730 735

Lys Glu Val Glu Lys

740

<210> 1141

<211> 2190

<212> DNA

<213> N. gonorrhoeae LbpB

<400> 1141

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aagtctaagg acgttcccac ttccccccct gccgagcctt cggtagaaac cacgccggtc 180

aaccggcccg ccgtcggtgc ggcaatgcgg ttgttgaggc ggaatactgc ttttcatcgt 240

gaagatggca cggcaattcc cgatagcaaa caagcagaag aaaagctgtc gtttaaagaa 300

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attcataaac gtgattccga tgtagaaatt aggacgtcag aaaaggaaaa taaaaaatat 420

aattataaat ttgtggatgc cggttatgta tatactaaaa acggaaaaga tgaaatcgaa 480

cagaactcag gtggtaagcg gtttacccac cgttttggtt atgacggttt tgtatattat 540

tccggagaac gtccttccca atctttaccg agcgcgggaa cggtgcaata ttccggcaac 600

tggcaatata tgaccgatgc caaacgtcat cggacaggta aggcggttgc cagtgacgat 660

ttgggttata taacatttta tggtaacgat attggtgcaa cttcttatgc ggctaaggat 720

gccgacgaca gggaaaaaca tcctgccgaa tatacggttg atttcgacaa aaaaatccta 780

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gccaaagtta acaccgaggt gaagacgaga cacgctgata aagaatattt gtttttccat 960

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aaggatggga aatctcttgg tataactgaa gatattgaaa atgaagttga aaatgaagct 2100

gatgttggcg aacagttaga acctgaagtt aaaccccaat tcggcgtggt attcggtgcg 2160

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<210> 1142

<211> 729

<212> PRT

<213> N. gonorrhoeae LbpB

<400> 1142

Met Arg Lys Leu Asn Tyr Tyr Gly Ile Ala Leu Leu Pro Leu Met Leu

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Ala Ser Cys Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser Thr

20 25 30

Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr Ser

35 40 45

Pro Pro Ala Glu Pro Ser Val Glu Thr Thr Pro Val Asn Arg Pro Ala

50 55 60

Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Thr Ala Phe His Arg

65 70 75 80

Glu Asp Gly Thr Ala Ile Pro Asp Ser Lys Gln Ala Glu Glu Lys Leu

85 90 95

Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Gly Asn

100 105 110

Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asp Ser Asp Val

115 120 125

Glu Ile Arg Thr Ser Glu Lys Glu Asn Lys Lys Tyr Asn Tyr Lys Phe

130 135 140

Val Asp Ala Gly Tyr Val Tyr Thr Lys Asn Gly Lys Asp Glu Ile Glu

145 150 155 160

Gln Asn Ser Gly Gly Lys Arg Phe Thr His Arg Phe Gly Tyr Asp Gly

165 170 175

Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln Ser Leu Pro Ser Ala

180 185 190

Gly Thr Val Gln Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala Lys

195 200 205

Arg His Arg Thr Gly Lys Ala Val Ala Ser Asp Asp Leu Gly Tyr Ile

210 215 220

Thr Phe Tyr Gly Asn Asp Ile Gly Ala Thr Ser Tyr Ala Ala Lys Asp

225 230 235 240

Ala Asp Asp Arg Glu Lys His Pro Ala Glu Tyr Thr Val Asp Phe Asp

245 250 255

Lys Lys Ile Leu Lys Gly Glu Leu Ile Lys Asn Gln Tyr Val Gln Lys

260 265 270

Arg Asn Asp Pro Lys Glu Pro Lys Lys Pro Leu Thr Ile Tyr Asn Ile
275 280 285
Thr Ala Asp Leu Asn Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn
290 295 300
Thr Glu Val Lys Thr Arg His Ala Asp Lys Glu Tyr Leu Phe Phe His

305 310 315 320
Thr Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Asn Gly
325 330 335
Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Gly Val Phe Gly
340 345 350
Val Phe Ala Gly Lys Gln Lys Thr Asn Ala Ser Gly Thr Asn Pro Ala
355 360 365
Met Pro Phe Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile Ser

370 375 380
Val Asp Glu Ala Thr Asp Glu Asn Pro Arg Pro Phe Glu Val Ser Thr
385 390 395 400
Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly Arg Glu
405 410 415
Ile Pro Leu Val Ser Lys Glu Lys Thr Ile Asp Leu Ala Asp Gly Arg
420 425 430
Lys Met Thr Val Ser Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys Leu

435 440 445
Gly Arg Ile Lys Thr Glu Arg Pro Ala Val Lys Pro Lys Ala Gln Asp
450 455 460
Glu Glu Asp Ser Gly Ile Asn Asn Gly Glu Glu Ser Glu Asp Glu Glu
465 470 475 480
Ile Ala Glu Glu Ser Glu Asp Glu Val Ser Glu Asp Asp Asn Gly Glu
485 490 495
Asp Glu Asp Glu Ile Val Glu Glu Glu Ala Asp Glu Ala Glu Glu Ile

500 505 510
Glu Glu Glu Ala Glu Glu Glu Glu Pro Glu Glu Glu Ser Pro Glu Glu

515 520 525

Gly Asn Gly Val Ser Asp Gly Ile Pro Pro Ala Pro Glu Ala Leu Lys

530 535 540

Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Ala

545 550 555 560

Asp Ile Pro Lys Thr Gly Thr Ala His Tyr Thr Gly Thr Trp Glu Ala

565 570 575

Arg Ile Gly Glu Pro Ile Gln Trp Asp Asn Lys Ala Asp Lys Ala Ala

580 585 590

Lys Ala Glu Phe Asp Val Asp Phe Gly Asn Lys Ser Ile Ser Gly Thr

595 600 605

Leu Thr Glu Gln Asn Gly Val Glu Pro Ala Phe Arg Ile Glu Asn Gly

610 615 620

Val Ile Glu Gly Asn Gly Phe His Ala Thr Ala Arg Thr Arg Asp Asn

625 630 635 640

Gly Ile Asn Leu Ser Gly Asn Gly Ser Thr Asn Pro Gln Ser Phe Lys

645 650 655

Ala Asp Asn Leu Leu Val Thr Gly Gly Phe Tyr Gly Pro Gln Ala Ala

660 665 670

Glu Leu Gly Gly Thr Ile Phe Asn Lys Asp Gly Lys Ser Leu Gly Ile

675 680 685

Thr Glu Asp Ile Glu Asn Glu Val Glu Asn Glu Ala Asp Val Gly Glu

690 695 700

Gln Leu Glu Pro Glu Val Lys Pro Gln Phe Gly Val Val Phe Gly Ala

705 710 715 720

Lys Lys Asp Asn Lys Glu Val Glu Lys

725

<210> 1143

<211> 2070

<212> DNA

<213> N. cinerea LbpB

<400> 1143

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tccaaacctt ccaagcctga ggatattcct gctccggctc ctgccaaacc ttctatagaa 180

atcactccgg tcaatcagcc cgccgtcggt gcggcaatgc ggctgccaag gcggaatatg 240

gctttctata aacaagacgg tacggaaatt cctggcaagc atcaggcgga ggattatttg 300

ccgcttaaag aggaggatat cctgttttta gacggtgcgc cgcaagaaca ggccgacaaa 360

cttaaaaaga aaatcgacga acggtatcct aatgtaaaaa tctacacgtc cgattcaaaa 420

gatgatgcgt atcaatataa atatgtccgg gccggatatg tttatactaa agaaggaaaa 480

gacgaaatca aacagacccc aggcggtaag cggtttaccc accggtttgg ttatgacggt 540

tttgtatatt attccggaga acatccttcc caatctttac cgagtgcggg aacggtgaaa 600

tattccggta actggcaata tataactgat gccaaacgtc atcggacagg tcaggcggtt 660

gccagtgagg atttgggtta tatcacatat tatggtaacg atattggtgc aacttcttat 720

gcggctaggg atgccgacga cagggaaaaa catcctgccg aatatacggt agatttcggt 780

aacaaaaccc tgacgggcga cctgattaaa aaccaatatg tcaaacccca cgagaaaaaa 840

aagccgctga ccatttacaa cattactgca aaattggacg gaaaccgctt taccggcagt 900

gccaaggtca atcctgattt agcgaaaaac cctgccggta aggagcgttt gtttttccat 960

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gacaaactcc ttgtcgaagg acgtgaaatc tccttgctca aagatactca aaccatcgtt 1260

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tccaaaccat ttaaagccga gaaccttcat gtaacggggg gcttttacgg tcctcatgca 1980

tcggaattgg gcggcagctt tgccgaacct caacaaaaaa tcggtgtggt atttggtgcg 2040

aagaaagatg acaaggaggc aacacgatga 2070

<210> 1144

<211> 689

<212> PRT

<213> N. cinerea LbpB

<400> 1144

Met Cys Lys Leu Asn Tyr Tyr Gly Ile Ala Leu Leu Pro Leu Met Leu
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Ala Ser Cys Gly Gly Asn Phe Gly Val Gln Pro Val Ala Lys Ser Thr
20 25 30

Pro Thr Val Gln Thr Pro Ser Asp Ser Lys Pro Ser Lys Pro Glu Asp
35 40 45

Ile Pro Ala Pro Ala Pro Ala Lys Pro Ser Ile Glu Ile Thr Pro Val
50 55 60

Asn Gln Pro Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn Met
65 70 75 80

Ala Phe Tyr Lys Gln Asp Gly Thr Glu Ile Pro Gly Lys His Gln Ala
85 90 95

Glu Asp Tyr Leu Pro Leu Lys Glu Glu Asp Ile Leu Phe Leu Asp Gly
100 105 110

Ala Pro Gln Glu Gln Ala Asp Lys Leu Lys Lys Lys Ile Asp Glu Arg
115 120 125

Tyr Pro Asn Val Lys Ile Tyr Thr Ser Asp Ser Lys Asp Asp Ala Tyr
130 135 140

Gln Tyr Lys Tyr Val Arg Ala Gly Tyr Val Tyr Thr Lys Glu Gly Lys
145 150 155 160

Asp Glu Ile Lys Gln Thr Pro Gly Gly Lys Arg Phe Thr His Arg Phe

165 170 175

Gly Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser

180 185 190

Leu Pro Ser Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Ile

195 200 205

Thr Asp Ala Lys Arg His Arg Thr Gly Gln Ala Val Ala Ser Glu Asp

210 215 220

Leu Gly Tyr Ile Thr Tyr Tyr Gly Asn Asp Ile Gly Ala Thr Ser Tyr

225 230 235 240

Ala Ala Arg Asp Ala Asp Asp Arg Glu Lys His Pro Ala Glu Tyr Thr

245 250 255

Val Asp Phe Gly Asn Lys Thr Leu Thr Gly Asp Leu Ile Lys Asn Gln

260 265 270

Tyr Val Lys Pro His Glu Lys Lys Lys Pro Leu Thr Ile Tyr Asn Ile

275 280 285

Thr Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn

290 295 300

Pro Asp Leu Ala Lys Asn Pro Ala Gly Lys Glu Arg Leu Phe Phe His

305 310 315 320

Asp Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Asn Gly

325 330 335

Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly

340 345 350

Val Phe Ala Gly Lys Gln Asn Ser Ser Val Pro Ser Glu Ala His Thr

355 360 365

Lys Ile Leu Asp Ser Leu Lys Ile Ala Ala Asp Glu Ala Ala Asp Pro

370 375 380

Lys Ala Arg Pro Phe Ile Ala Glu Pro Met Pro Asp Phe Ala His Pro

385 390 395 400

Asp Lys Leu Leu Val Glu Gly Arg Glu Ile Ser Leu Leu Lys Asp Thr

405 410 415

Gln Thr Ile Val Leu Ala Asp Gly Arg Lys Thr Thr Ile Arg Thr Cys
420 425 430
Cys Asp Phe Leu Thr Tyr Val Lys Ile Gly Arg Met Gln Thr Asp Arg
435 440 445
Pro Val Ile Lys Pro Thr Pro Thr Glu Asp Glu Asp Ser Asp His Glu
450 455 460

Gly Ala Gly Pro Asp Asp Glu Asn Glu Gly Leu Glu Pro Glu Asp Gly
465 470 475 480
Glu Asp Gly Leu Glu Asn Asp Thr Asp Asp Gly His Ala Ser Ser Glu
485 490 495
Leu Pro Thr Glu Lys Asp Asn Gly Glu Ala Asn Thr Ala Gly Lys Asn
500 505 510
Glu Gly Asn Asn Ala Glu Ser Val Gly Thr Asp Gly Lys Pro Pro Val
515 520 525

Gln Pro Ala Ser Ala Tyr Arg Asn Ile Asp Leu Phe Ile Lys Gly Ile
530 535 540
Arg Thr Ser Glu Ala Asp Ile Pro Lys Ile Gly Asn Val His Tyr Arg
545 550 555 560
Gly Ser Trp Glu Ala Arg Ile Gly Ala Pro Ile Gln Trp Asp Asn His
565 570 575
Ala Asp Lys Ala Ala Lys Ala Glu Phe Asp Val Asn Phe Ala Asn Lys
580 585 590

Ser Leu Ser Gly Thr Leu Thr Glu Lys Asn Gly Val Glu Pro Ala Phe
595 600 605
Tyr Ile Glu Lys Gly Ile Ile Glu His Asn Gly Phe His Ala Val Ala
610 615 620
Arg Thr Arg Asp Thr Gly Ile Asp Leu Leu Gly Arg Gly Ala Thr Ser
625 630 635 640
Ser Lys Pro Phe Lys Ala Glu Asn Leu His Val Thr Gly Gly Phe Tyr
645 650 655

Gly Pro His Ala Ser Glu Leu Gly Gly Ser Phe Ala Glu Pro Gln Gln

660 665 670

Lys Ile Gly Val Val Phe Gly Ala Lys Lys Asp Asp Lys Glu Ala Thr

675 680 685

Arg

<210> 1145

<211> 2847

<212> DNA

<213> M. catarrhalis LbpB

<400> 1145

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accaataaca ccaacaatca gggcaacaac acggataaca gtaccagcac aactgaccca 360

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aacaaattcc ctgcattgtc tgatttgcac ttagacagtg aacgccatcg ttttgacccc 660

caaaagataa acaccattaa agtgtatggt tatggtaact taacaacacc ttccaacaat 720

aacactcaca tcaatcatca gcaagctgat aatgccaaag ccaaaaagcc caccgatgct 780

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ggagaaaacg ccagcagcca gctgcccagt gctggtaaat ttaactacac aggcaactgg 960

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tatctaaacg gctttcaata caagcacacg cctgccactt atcaggtgga ttttgacaca 1140

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aacattcaag acattgatgt taaggggcaa ttttttggta caaatggcga agagttggca 2760

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gtctttgggg ctgttaaaga taaataa 2847

<210> 1146

<211> 948

<212> PRT

<213> M. catarrhalis LbpB

<400> 1146

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Leu Val Val Asp Ala Trp Ala Asp Leu Ile Lys Arg Ser Ser Gln His
            20                  25                  30
Thr Lys Arg Asp Ile Thr Met Ser Thr Val Lys Thr Pro His Ile Phe
        35                  40                  45
Tyr Gln Lys Arg Thr Leu Ser Leu Ala Ile Ala Ser Ile Phe Ala Ala
    50                  55                  60
Leu Val Met Thr Gly Cys Arg Ser Asp Asp Ile Ser Val Asn Ala Pro
65                  70                  75                  80

Asn Val Thr Gln Leu Pro Gln Gly Thr Val Ser Pro Ile Pro Asn Thr
                85                  90                  95
Gly His Asp Asn Thr Asn Asn Thr Asn Asn Gln Gly Asn Asn Thr Asp
            100                 105                 110
Asn Ser Thr Ser Thr Thr Asp Pro Asn Gly Asp Asn Asn Gln Leu Thr
        115                 120                 125
Gln Ala Gln Lys Thr Ala Ala Ala Ala Gly Phe Phe Val Met Gly Lys
    130                 135                 140

Ile Arg Asp Thr Ser Pro Lys Asn Asp Pro Asp Tyr Gly Asp Asp Leu
145                 150                 155                 160
Lys Gln Gln Trp Leu Gly Lys Leu Tyr Val Gly Ile Asp Ala His Arg
                165                 170                 175
Pro Asp Gly Ile Gly Lys Gly Lys Asn Leu Arg Gln Pro Ile Thr Ala
            180                 185                 190
Asn Asp Ile Lys Pro Leu Tyr Phe Asn Lys Phe Pro Ala Leu Ser Asp
        195                 200                 205

Leu His Leu Asp Ser Glu Arg His Arg Phe Asp Pro Gln Lys Ile Asn
    210                 215                 220
Thr Ile Lys Val Tyr Gly Tyr Gly Asn Leu Thr Thr Pro Ser Asn Asn
225                 230                 235                 240
Asn Thr His Ile Asn His Gln Gln Ala Asp Asn Ala Lys Ala Lys Lys
```

245 250 255

Pro Thr Asp Ala Tyr Glu Asn Ile Arg Phe Gly Tyr Leu Glu Leu Gln

260 265 270

Gly Ser Ser Leu Thr Gln Lys Asn Ala Asp Asn Gln Asn Asp Gln Asp

275 280 285

Arg Ile Pro Lys Pro Met Pro Ile Leu Phe Tyr His Gly Glu Asn Ala

290 295 300

Ser Ser Gln Leu Pro Ser Ala Gly Lys Phe Asn Tyr Thr Gly Asn Trp

305 310 315 320

Leu Tyr Leu Ser Asp Val Lys Lys Arg Pro Ala Leu Ser Ala Ser Asp

325 330 335

Asp Arg Val Gly Val Tyr Leu Asn Ala Ser Gly Lys Ala Asn Glu Gly

340 345 350

Asp Val Val Ser Ala Ala His Ile Tyr Leu Asn Gly Phe Gln Tyr Lys

355 360 365

His Thr Pro Ala Thr Tyr Gln Val Asp Phe Asp Thr Asn Ser Leu Thr

370 375 380

Gly Lys Leu Ser Tyr Tyr Asp Asn Pro Asn Lys Lys Thr Ala Gln Gly

385 390 395 400

Glu Tyr Leu Lys Ser Gln Phe Asp Thr Ser Lys Lys Val Asn Glu Thr

405 410 415

Asp Val Tyr Gln Ile Asp Ala Lys Ile Asn Gly Asn Arg Phe Val Gly

420 425 430

Thr Ala Lys Ser Leu Val Asn Glu Asn Thr Lys Thr Ala Pro Phe Ile

435 440 445

Lys Glu Leu Phe Ser Lys Lys Ala Asn Pro Asn Asn Pro Asp Pro Asn

450 455 460

Ser Asp Thr Leu Glu Gly Gly Phe Tyr Gly Lys Ser Gly Asp Glu Leu

465 470 475 480

Ala Gly Lys Phe Leu Ser Asn Asp Asn Ala Thr Tyr Val Val Phe Gly

485 490 495

Gly Lys Arg Asp Lys Thr Ala Glu Pro Val Ala Thr Lys Thr Val Tyr
500 505 510
Phe Ser Ala Gly Phe Glu Lys Pro Ser Thr Ser Phe Val Asp Asn Glu
515 520 525

Thr Ile Gly Arg Ile Ile Asn Ser Lys Gly Leu Asn Asp Asn Ile Glu
530 535 540
Glu Asp Ala Ile Thr Pro Ser Asp Asn Ser Tyr Tyr Glu Tyr Asn Trp
545 550 555 560
Gly Lys Pro Glu Lys Gln Phe Thr Lys Lys Val Ser Ser Ser Thr Gln
565 570 575
Ala Val Pro Ala Tyr Phe Gly Gln His Asp Lys Phe Tyr Phe Asn Gly
580 585 590

Asn Tyr Tyr Asp Leu Ser Ala Ser Ser Val Asp Lys Leu Ala Pro Ala
595 600 605
Asp Ala Val Lys Ala Asn Gln Ser Ile Lys Glu Lys Tyr Pro Asn Ala
610 615 620
Thr Leu Asn Lys Asp Lys Val Thr Thr Ile Val Leu Gln Glu Ala Lys
625 630 635 640
Asp Asn Lys Pro Tyr Thr Ala Ile His Ala Lys Ser Tyr Asp His Ile
645 650 655

Ser Phe Gly Glu Val Leu Tyr Asn Asp Asn Lys Gly Asn Pro Thr Arg
660 665 670
Ser Tyr Phe Val Gln Gly Gly Gln Ala Asp Val Ser Thr Gln Leu Pro
675 680 685
Ser Ala Gly Lys Phe Thr Tyr Asn Gly Leu Trp Ala Gly Tyr Leu Ala
690 695 700
Gln Lys Lys Asp Lys Gly Tyr Ser Asn Lys Glu Glu Thr Ile Lys Ala
705 710 715 720

Lys Gly His Gln Asp Tyr Leu Leu Thr Glu Asp Phe Thr Pro Glu Asp
725 730 735
Asp Asp Asn Asp Leu Ile Ala Ser Asp Asp Ser Gln Asp Asp Asn Thr

740 745 750

His Gly Asp Asp Asp Leu Ile Ala Ser Asp Asp Ser Gln Asp Asp Asn

755 760 765

Thr His Gly Asp Asp Asp Leu Ile Ala Ser Asp Asp Ser Gln Asp Asp

770 775 780

Asp Ala Asp Gly Asp Asp Asp Ser Asp Asp Leu Gly Asp Gly Ala Asp

785 790 795 800

Asp Asp Ala Ala Gly Lys Val Tyr His Ala Gly Asn Ile Arg Pro Glu

805 810 815

Phe Glu Asn Lys Tyr Leu Pro Ile Asn Glu Pro Thr His Glu Lys Thr

820 825 830

Phe Ala Leu Asp Gly Lys Asn Lys Ala Lys Phe Asp Val Asp Phe Asp

835 840 845

Thr Asn Ser Leu Thr Gly Lys Leu Asn Asp Glu Arg Gly Asp Ile Val

850 855 860

Phe Asp Ile Lys Asn Gly Lys Ile Asp Gly Thr Gly Phe Thr Ala Lys

865 870 875 880

Ala Asp Val Pro Asn Tyr Arg Glu Glu Val Gly Asn Asn Gln Gly Gly

885 890 895

Gly Phe Leu Tyr Asn Ile Gln Asp Ile Asp Val Lys Gly Gln Phe Phe

900 905 910

Gly Thr Asn Gly Glu Glu Leu Ala Gly Gln Leu Gln Tyr Asp Lys Gly

915 920 925

Asp Gly Ile Asn Asp Thr Ala Glu Lys Ala Gly Ala Val Phe Gly Ala

930 935 940

Val Lys Asp Lys

945

<210> 1147

<211> 1803

<212> DNA

<213> N. gonorrhoeae TbpB

<400> 1147

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tgcgcgggcg gcggcagttt cgatttggac agtgtggaaa cgaaacagca caacccgcag 120

tccgaagcac cgaaatacca agacgaacag actgaaaaac cggcaaaacc cgatgaagcg 180

caggcggaaa acgaccgtcc ggcttacggt tttgcagtca aaataccgcg ccggttctgg 240

tacccgagaa ataaagaaga tcataaggca ttatcagaag cggattggga gaaattaggt 300

gcgggtgcgc cgaatgagtt tccccaaaag aatgaaatct cgaatatgac tgaaggaact 360

ctgaacgagt ctattcagcc gggtgaggac ggcaaaagcc gcgtggaagg atacacgaaa 420

ttcgagtatg tccgctcggg ctatatctac cgcaacggct tgccgatgga aagaatcgat 480

ggcagtgtgc gcaacggtcc gaaaggctac cttttctaca aaggcagtaa tccttcccaa 540

gctctgccga cgggcaaggc gatttacaaa ggtacttggg attatgtaac cgatgccaag 600

atgggacaaa agttttccca gttgggtggt tcgcaagcgg gggacaggta cggggctttg 660

tctgccgagg aagcggatgt gttgcgcaac aaaaacgagg cgaaggaagg taccgatttc 720

gggctgacca gcgagtttga ggtggatttc gctgccaaga ctatgaccgg caaactctac 780

cgcaataacc ggattaccca taacgaaacc gaaaatagag acaaacaaat taaacgttac 840

gacattcagg ctgacctgca cggcaaccgc ttcaaaggta aggcggtggc agcagataaa 900

ggcgcaacaa atggaagtca tccctttatt tccgattccg acagtttgga aggcggattt 960

tacggaccga aaggcgagga acttgccggt aaattcttga gcaacgacaa caaagttgca 1020

gcggtgtttg gtgcgaagca gaaagataag aaggaggggg aaaacacggc agagcttgca 1080

acggaaaccg tgatagatgc ataccgtatt accggagggg ggtttaagaa agagcaaata 1140

gacagttttg gagatgtgaa aaagctgctg gttgacggag tggagctttc actgctgccg 1200

tctgagggca ataaggcggc atttcagcac gggattgagc aaaacggcgt gaaggcaacg 1260

gtgtgttgtt ccaacttgga ttacatgagt tttgggaagc tgtcaaaaga aaataaagac 1320

gatatgttcc tgcaaggtgt ccgcactccg gtatccgatg tggcggcaag gacggaggca 1380

aacgccaaat atcgcggtac ttggtacgga tatattgcca acggcacaag ctggagcggc 1440

gaagcctcca atcaggaagg cggtaatagg gcagagtttg acgtggattt ttccactaaa 1500

aaaatcagtg gcacactgac ggcaaaagac cgtacgtctc ccacgtttat cattaccgcc 1560

gcgattcagg acaacggttt tgaaggtacg gcgaaaaccg gtgaaaacgg ctttgcatta 1620

gatccgaaaa ataccggaaa ttcccactat gcgcatattg aagccactgt atccggcggt 1680

ttctacggca aaaacgccat tgagatgggc ggttcattct catttccggg aaatgcaccg 1740

gagggaaaac aagaaaaagc atcggtggta ttcggtgcga aacgccaaca gcttgtgcaa 1800

taa 1803

<210> 1148

<211> 600

<212> PRT

<213> N. gonorrhoeae TbpB

<400> 1148

Met Lys Lys Ser Leu Ile Ala Gln Ala Ala Gly Ile Leu Pro Val Leu
1 5 10 15

Leu Leu Ser Ala Cys Ala Gly Gly Gly Ser Phe Asp Leu Asp Ser Val
20 25 30

Glu Thr Lys Gln His Asn Pro Gln Ser Glu Ala Pro Lys Tyr Gln Asp
35 40 45

Glu Gln Thr Glu Lys Pro Ala Lys Pro Asp Glu Ala Gln Ala Glu Asn
50 55 60

Asp Arg Pro Ala Tyr Gly Phe Ala Val Lys Ile Pro Arg Arg Phe Trp
65 70 75 80

Tyr Pro Arg Asn Lys Glu Asp His Lys Ala Leu Ser Glu Ala Asp Trp
85 90 95

Glu Lys Leu Gly Ala Gly Ala Pro Asn Glu Phe Pro Gln Lys Asn Glu
100 105 110

Ile Ser Asn Met Thr Glu Gly Thr Leu Asn Glu Ser Ile Gln Pro Gly
115 120 125

Glu Asp Gly Lys Ser Arg Val Glu Gly Tyr Thr Lys Phe Glu Tyr Val
130 135 140

Arg Ser Gly Tyr Ile Tyr Arg Asn Gly Leu Pro Met Glu Arg Ile Asp
145 150 155 160

Gly Ser Val Arg Asn Gly Pro Lys Gly Tyr Leu Phe Tyr Lys Gly Ser
165 170 175

Asn Pro Ser Gln Ala Leu Pro Thr Gly Lys Ala Ile Tyr Lys Gly Thr
180 185 190

Trp Asp Tyr Val Thr Asp Ala Lys Met Gly Gln Lys Phe Ser Gln Leu
195 200 205

Gly Gly Ser Gln Ala Gly Asp Arg Tyr Gly Ala Leu Ser Ala Glu Glu
210 215 220

Ala Asp Val Leu Arg Asn Lys Asn Glu Ala Lys Glu Gly Thr Asp Phe
225 230 235 240

Gly Leu Thr Ser Glu Phe Glu Val Asp Phe Ala Ala Lys Thr Met Thr
245 250 255

Gly Lys Leu Tyr Arg Asn Asn Arg Ile Thr His Asn Glu Thr Glu Asn
260 265 270

Arg Asp Lys Gln Ile Lys Arg Tyr Asp Ile Gln Ala Asp Leu His Gly
275 280 285

Asn Arg Phe Lys Gly Lys Ala Val Ala Ala Asp Lys Gly Ala Thr Asn
290 295 300

Gly Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe
305 310 315 320

Tyr Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp
325 330 335

Asn Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Glu
340 345 350

Gly Glu Asn Thr Ala Glu Leu Ala Thr Glu Thr Val Ile Asp Ala Tyr
355 360 365

Arg Ile Thr Gly Gly Gly Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly
370 375 380

Asp Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro
385 390 395 400

Ser Glu Gly Asn Lys Ala Ala Phe Gln His Gly Ile Glu Gln Asn Gly
405 410 415

Val Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly
420 425 430

Lys Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg

435 440 445

Thr Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr

450 455 460

Arg Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly

465 470 475 480

Glu Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp

485 490 495

Phe Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr

500 505 510

Ser Pro Thr Phe Ile Ile Thr Ala Ala Ile Gln Asp Asn Gly Phe Glu

515 520 525

Gly Thr Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Lys Asn

530 535 540

Thr Gly Asn Ser His Tyr Ala His Ile Glu Ala Thr Val Ser Gly Gly

545 550 555 560

Phe Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro

565 570 575

Gly Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly

580 585 590

Ala Lys Arg Gln Gln Leu Val Gln

595 600

<210> 1149

<211> 1800

<212> DNA

<213> N. meningitidis TbpB

<400> 1149

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tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 180

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 240

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 300

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 360

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 420

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 480

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 540

ccatcggaaa agataactta taaaggtact tgggattatg ttactgatgc tatggaaaaa 600

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 660

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 720

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 780

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 840

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 900

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 960

gggccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 1020

gtgtttggtg cgaagcagaa agataagaag gatggggaaa acgcggcagg gcctgcaacg 1080

gaaaccgtga tagatgcata ccgtattacc ggcgaggagt ttaagaaaga gcaaatagac 1140

agttttggag atgtgaaaaa gctgctggtt gacggagtgg agctttcact gctgccgtct 1200

gagggcaata aggcggcatt tcagcacgag attgagcaaa acggcgtgaa ggcaacggtg 1260

tgttgttcca acttggatta catgagtttt gggaagctgt caaaagaaaa taaagacgat 1320

atgttcctgc aaggtgtccg cactccagta tccgatgtgg cggcaaggac ggaggcaaac 1380

gccaaatatc gcggtacttg gtacggatat attgccaacg gcacaagctg gagcggcgaa 1440

gcctccaatc aggaaggtgg taatagggca gagtttgacg tggatttttc cactaaaaaa 1500

atcagtggca cactgacggc aaaagaccgt acgtctcctg cgtttactat tactgccatg 1560

attaaggaca acggtttttc aggtgtggcg aaaaccggtg aaaacggctt tgcgctggat 1620

ccgcaaaata ccggaaattc ccactatacg catattgaag ccactgtatc cggcggtttc 1680

tacggcaaaa acgccatcga gatgggcgga tcgttctcat ttccgggaaa tgcaccagag 1740

ggaaaacaag aaaaagcatc ggtggtattc ggtgcgaaac gccaacagct tgtgcaataa 1800

<210> 1150

<211> 599

<212> PRT

<213> N. meningitidis TbpB

<400> 1150

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe

1 5 10 15

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
20 25 30
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
35 40 45
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala

50 55 60
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn
65 70 75 80
Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys
85 90 95
Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu
100 105 110
Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp

115 120 125
Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser
130 135 140
Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile
145 150 155 160
Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro
165 170 175
Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp

180 185 190
Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser
195 200 205
Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly
210 215 220
Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly
225 230 235 240
Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly

245 250 255
Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys

260 265 270

Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn

275 280 285

Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly

290 295 300

Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr

305 310 315 320

Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn

325 330 335

Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly

340 345 350

Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg

355 360 365

Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp

370 375 380

Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser

385 390 395 400

Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val

405 410 415

Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys

420 425 430

Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr

435 440 445

Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg

450 455 460

Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu

465 470 475 480

Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe

485 490 495

Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser

500 505 510

Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly
515 520 525

Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr
530 535 540

Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
545 550 555 560

Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly

565 570 575

Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala
580 585 590

Lys Arg Gln Gln Leu Val Gln
595

<210> 1151

<211> 1800

<212> DNA

<213> N. polysaccharea TbpB

<400> 1151

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tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaagagc cagcctgaaa gccaacagga tgtatcggaa 180

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 240

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 300

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 360

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 420

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 480

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 540

ccatcggaaa agataattta taaaggtact tgggattatg ttactgatgc tatggaaaaa 600

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 660

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 720

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 780

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 840

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcagc agataaaggt 900

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 960

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gtgtttggtg cgaagcagaa agataagaag gaggggggaaa acgcggcagg gcctgcaacg 1080

gaaaccgtga tagatgcata ccgtattacc ggaggggagt ttaagaaaga gcaaatagac 1140

agttttggag atgtgaaaaa gctgctggtt gacggggtgg agctttcact gctgccgtct 1200

gagggcaata aggcggcatt tcagcacggg attgagcaaa gcggcgtgaa ggcaacggtg 1260

tgttgttcca acttggatta catgagtttt gggaagctgt caaaagaaaa taaagacgat 1320

atgttcctgc aaggtgtccg cactccagta tccgatgtgg cggcaaggac ggaggcaaac 1380

gccaaatatc gcggtacttg gtatggatat attgccaacg gcacaagctg gagcggcgaa 1440

gcctccaatc aggaaggcgg taatagggca gagtttgacg tggatttttc cactaaaaac 1500

atcagtggca cactgacggc aaaaaaccgt acgtctcctg cgtttactat tactgccacg 1560

attcagggca acggtttttc cggtacggcg aaaaccggta atgacggctt tgcgctggat 1620

ccgcaaaata ccggaaattc ccactatacg catattgaag ccactgtatc cggcggtttc 1680

tacggcaaaa acgccatcga gatgggcggt tcgttctcat ttccgggaaa tgcaccggag 1740

ggaaaacaag agaaagcatc ggtggtatta ggtgcgaaac gccaacagct tgtgcaataa 1800

<210> 1152

<211> 599

<212> PRT

<213> N. polysaccharea TbpB

<400> 1152

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
1 5 10 15

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
20 25 30

Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
35 40 45

Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala
50 55 60

Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn
65 70 75 80

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys

85 90 95

Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu

100 105 110

Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp

115 120 125

Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser

130 135 140

Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile

145 150 155 160

Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro

165 170 175

Ser Lys Glu Leu Pro Ser Glu Lys Ile Ile Tyr Lys Gly Thr Trp Asp

180 185 190

Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser

195 200 205

Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly

210 215 220

Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly

225 230 235 240

Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly

245 250 255

Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys

260 265 270

Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn

275 280 285

Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly

290 295 300

Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr

305 310 315 320

Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn

325 330 335

Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Glu Gly
340 345 350
Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg
355 360 365
Ile Thr Gly Gly Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp
370 375 380

Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser
385 390 395 400
Glu Gly Asn Lys Ala Ala Phe Gln His Gly Ile Glu Gln Ser Gly Val
405 410 415
Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys
420 425 430
Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr
435 440 445

Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg
450 455 460
Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu
465 470 475 480
Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe
485 490 495
Ser Thr Lys Asn Ile Ser Gly Thr Leu Thr Ala Lys Asn Arg Thr Ser
500 505 510

Pro Ala Phe Thr Ile Thr Ala Thr Ile Gln Gly Asn Gly Phe Ser Gly
515 520 525
Thr Ala Lys Thr Gly Asn Asp Gly Phe Ala Leu Asp Pro Gln Asn Thr
530 535 540
Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
545 550 555 560
Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly
565 570 575

Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Leu Gly Ala

580 585 590

Lys Arg Gln Gln Leu Val Gln

595

<210> 1153

<211> 1779

<212> DNA

<213> N. flavescens TbpB

<400> 1153

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caggcggcgg aaaacgaacg ttctgcttac ggttttgcag ccaaaatacc gcgtcggaac 240

tggtacaaaa ataaagaaga tcataaggca ttatcagaag cggattggga gaaattaggt 300

gcgggtgagc cgggtgagtt tcgccaaaag aatgagattt ttgcgatgga taagggtacg 360

ctgaacgaat ccatcacaac gggcgacggc aaaagccgtg tggaaggata cacggctttc 420

aagtatgtcg gctcgggcta tatctaccgc aacggtgcca ataaaatcga tctcaaaaac 480

gatatcgccc ttttcggtcc ggacggctac cttttctaca aaggcagtaa tccttcccaa 540

gctctgccga cgggcaaggc gatttataaa ggtacttggg attatgtaac cgatgccaag 600

ggaaaacaga agtttcccca gttgggtagt ccgccagcgg gggataggta cggggctttg 660

tctgccgagg aagcggatgt gttgcgcaat gaaagcgagg caccggaagg tcagaccgat 720

ttcgggctga ccagcgagtt taaggtggac ttcgccgcca agaccatgac cggcgcgctc 780

taccgcaata accggattac ccataacgaa accgaaaata aaaccaaaca aattaaacgg 840

tacgacattc aggctaacct gcacggcaac cgcttcaaag gtaaggcgtt ggccgcggat 900

aaagatactg ggaacggtca tcccttcgtt tctgattctg acagtctgga aggtggtttc 960

tacgggcctc agggcgacga gttgggcggt aagtttttgg caaaagataa gaaagtgctt 1020

gccgtattca gcgcgaaaca gaaagacggt gcagaaaaac cattggctga aacctttatg 1080

gacgcttacc gcatcggtgc ggattttgtg aaaaaacaga tagacagctt cggcaacgtg 1140

gccaaactgc tgattgacgg cgtggagctt tcactgctgc cgtctgaggg caataaggcg 1200

gcatttcaac acgggattga gcaaaacggc gtgaaggcaa cggtgtgttg ttccaacttg 1260

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acggcgaaag atcgcattga ccctgcattc accatcactg cccagattca gggcaacggt 1560

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gatccggtct atacgcacat tcaggcggat gtatccggtg gcttctacgg caaaaacgcc 1680

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gtggtatttg gtgcgaaacg ccaacagctt gtgcaataa 1779

<210> 1154

<211> 592

<212> PRT

<213> N. flavescens TbpB

<400> 1154

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Leu Leu Ser Ala Cys Ala Gly Gly Gly Ser Phe Asp Leu Asp Ser Val

20 25 30

Glu Thr Lys Pro His Asn Pro Gln Pro Glu Ala Pro Lys Tyr Gln Asp

35 40 45

Glu Gln Thr Glu Lys Pro Ala Lys Pro Asp Glu Ala Gln Ala Ala Glu

50 55 60

Asn Glu Arg Ser Ala Tyr Gly Phe Ala Ala Lys Ile Pro Arg Arg Asn

65 70 75 80

Trp Tyr Lys Asn Lys Glu Asp His Lys Ala Leu Ser Glu Ala Asp Trp

85 90 95

Glu Lys Leu Gly Ala Gly Glu Pro Gly Glu Phe Arg Gln Lys Asn Glu

100 105 110

Ile Phe Ala Met Asp Lys Gly Thr Leu Asn Glu Ser Ile Thr Thr Gly

115 120 125

Asp Gly Lys Ser Arg Val Glu Gly Tyr Thr Ala Phe Lys Tyr Val Gly

130 135 140

Ser Gly Tyr Ile Tyr Arg Asn Gly Ala Asn Lys Ile Asp Leu Lys Asn

145 150 155 160

Asp Ile Ala Leu Phe Gly Pro Asp Gly Tyr Leu Phe Tyr Lys Gly Ser
165 170 175
Asn Pro Ser Gln Ala Leu Pro Thr Gly Lys Ala Ile Tyr Lys Gly Thr
180 185 190
Trp Asp Tyr Val Thr Asp Ala Lys Gly Lys Gln Lys Phe Pro Gln Leu

195 200 205
Gly Ser Pro Pro Ala Gly Asp Arg Tyr Gly Ala Leu Ser Ala Glu Glu
210 215 220
Ala Asp Val Leu Arg Asn Glu Ser Glu Ala Pro Glu Gly Gln Thr Asp
225 230 235 240
Phe Gly Leu Thr Ser Glu Phe Lys Val Asp Phe Ala Ala Lys Thr Met
245 250 255
Thr Gly Ala Leu Tyr Arg Asn Asn Arg Ile Thr His Asn Glu Thr Glu

260 265 270
Asn Lys Thr Lys Gln Ile Lys Arg Tyr Asp Ile Gln Ala Asn Leu His
275 280 285
Gly Asn Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Asp Thr Gly
290 295 300
Asn Gly His Pro Phe Val Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe
305 310 315 320
Tyr Gly Pro Gln Gly Asp Glu Leu Gly Gly Lys Phe Leu Ala Lys Asp

325 330 335
Lys Lys Val Leu Ala Val Phe Ser Ala Lys Gln Lys Asp Gly Ala Glu
340 345 350
Lys Pro Leu Ala Glu Thr Phe Met Asp Ala Tyr Arg Ile Gly Ala Asp
355 360 365
Phe Val Lys Lys Gln Ile Asp Ser Phe Gly Asn Val Ala Lys Leu Leu
370 375 380
Ile Asp Gly Val Glu Leu Ser Leu Leu Pro Ser Glu Gly Asn Lys Ala

385 390 395 400
Ala Phe Gln His Gly Ile Glu Gln Asn Gly Val Lys Ala Thr Val Cys

405 410 415

Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys Leu Ser Lys Glu Asn

420 425 430

Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr Pro Val Ser Asp Val

435 440 445

Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg Gly Thr Trp Tyr Gly

450 455 460

Tyr Ile Val Asn Gly Thr Ser Trp Ser Gly Glu Ala Ser Asn Gln Glu

465 470 475 480

Ser Gly Asn Arg Ala Glu Phe Asp Val Asn Phe Ala Lys Lys Thr Leu

485 490 495

Asn Gly Met Leu Thr Ala Lys Asp Arg Ile Asp Pro Ala Phe Thr Ile

500 505 510

Thr Ala Gln Ile Gln Gly Asn Gly Phe Ser Gly Val Ala Lys Thr Gly

515 520 525

Glu Lys Gly Phe Ala Leu Asp Pro Lys Ser Thr Ile Asp Pro Val Tyr

530 535 540

Thr His Ile Gln Ala Asp Val Ser Gly Gly Phe Tyr Gly Lys Asn Ala

545 550 555 560

Ile Glu Met Gly Gly Ser Phe Ser Gly Asn Thr Leu Gly Gly Glu Asn

565 570 575

Gly Lys Ala Ala Val Val Phe Gly Ala Lys Arg Gln Gln Leu Val Gln

580 585 590

<210> 1155

<211> 1800

<212> DNA

<213> N. lactamica TbpB

<400> 1155

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tccaaaccta agtatgagga tgaaaagagc cagcctgaaa gccaacagga tgtatcggaa 180

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 240

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 300

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 360

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 420

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 480

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 540

ccatcggaaa agataactta taaaggtact tgggattatg ttactgatgc tatggaaaaa 600

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 660

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 720

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 780

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 840

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 900

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 960

ggaccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 1020

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atgttcctgc aaggtgtccg cactccagta tccgatgtgg cggcaaggac ggaggcaaac 1380

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attcagggca acggtttttc aggtgtagcg aaaaccggtg aaaacggctt tgcattagat 1620

ccgaaaaata ccatcgatcc gggctatacg cgcattcagg cggatgtatc cggcggcttc 1680

tacggcaaaa acgccatcga gatgggcggt tcgttctcat ttccgggaaa tacaccggag 1740

ggagaacaag aaaaagcatc ggtggtattc ggtgcgaaac gccaacagct tgtgcaataa 1800

<210> 1156

<211> 599

<212> PRT

<213> N. lactamica TbpB

<400> 1156

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
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Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
20 25 30
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
35 40 45
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala
50 55 60
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn
65 70 75 80

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys
85 90 95
Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu
100 105 110
Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp
115 120 125
Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser
130 135 140

Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile
145 150 155 160
Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro
165 170 175
Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp
180 185 190
Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser
195 200 205

Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly
210 215 220
Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly
225 230 235 240
Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly

245 250 255

Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys

260 265 270

Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn

275 280 285

Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly

290 295 300

Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr

305 310 315 320

Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn

325 330 335

Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Glu Gly

340 345 350

Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg

355 360 365

Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp

370 375 380

Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser

385 390 395 400

Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val

405 410 415

Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys

420 425 430

Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr

435 440 445

Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg

450 455 460

Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu

465 470 475 480

Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe

485 490 495

Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser
500 505 510

Pro Ala Phe Thr Ile Thr Ala Thr Ile Gln Gly Asn Gly Phe Ser Gly
515 520 525

Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Lys Asn Thr
530 535 540

Ile Asp Pro Gly Tyr Thr Arg Ile Gln Ala Asp Val Ser Gly Gly Phe
545 550 555 560

Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly
565 570 575

Asn Thr Pro Glu Gly Glu Gln Glu Lys Ala Ser Val Val Phe Gly Ala
580 585 590

Lys Arg Gln Gln Leu Val Gln
595

<210> 1157

<211> 1782

<212> DNA

<213> N. cinerea TbpB

<400> 1157

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tccgaagcac cgaaatacca agacgaacag actgaaaaac cggcaaaacc cagtgaagcg 180

caggcagcgg aaaacgaacg ttcggcttac ggttttgcag ccaaaatacc gcgtcggaat 240

atccatttca acgtgaagca ggggcatcag ccgctgtcgg atgcggattg ggtgaaattg 300

gcggcgggtg aaccggataa gtttccccaa aaggatgaca tttttgcgat ggataagggt 360

acgctgaacg aatccatcac aacgggcgac ggcaaaagcc gcgtggaagg atacacgaaa 420

tttaagtatg tccgctcggg ctatatctac cgcaacggtg ccaataagat cgatcccaaa 480

aacaatatcg ccctttcgg tccggacggc taccttttct acaaaggcag caatccttcc 540

caagctctgc cgacgggcaa ggcaatttac aaaggtactt gggattatgt aaccgatgcc 600

aaggaaaaac agaagtttcc ccagttgggt agtccgccag cgggggatag gtacggggct 660

ttgtctgcag aggaagcgga tgttttgcgc aatgaaagcg aggcaccgaa aggtcagacc 720

gatttcgggc tgaccagcga gtttgaggtg gatttcgccg ccaagactat gaccggcgcg 780

ctctaccgca ataaccggat tacccataac gaaaccgaaa ataaagccaa acaaattaaa 840

cgttacgaca ttcaggctaa cctgcacggt aaccgtttca aaggtaaggc gttggcagcg 900

gataaaaatg ctaatgagaa agaacatccc ttcgtttctg attctgatag tctggaaggt 960

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tttatggacg cttaccgcat cggtgcggat tttgtgaaaa aacagattga cagcttcggc 1140

aacgtggcca aactgctgat tgacggcgtg gagcttgcgc ttgtgccgtc cgaaggcact 1200

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gaaggcggta accgggcgga gtttaaagtt aattttgccg agaaaaccct caacggtatg 1500

ctgacggcga aagaccgcat tgcccccgta ttcaccatca ctgcccagat tcagggcaac 1560

ggtttttcag gtgtggcgaa aaccggtgaa aacggctttg cattagatcc gaaaaatacc 1620

atcgatccga tacggacgaa tatccgtgca gatgtgtccg gcggcttcta cggcaaaaac 1680

gccatcgaga tgggcggatc gttctccgga aatacattgg agggaggaag cggcaaggcg 1740

gcagtggtat tcggtacgaa acgccaacag cttgtccggt aa 1782

<210> 1158

<211> 593

<212> PRT

<213> N. cinerea TbpB

<400> 1158

Met Lys Lys Leu Leu Ile Ala Gln Ala Ala Gly Ile Leu Pro Val Leu
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Leu Leu Ser Ala Cys Ala Gly Gly Gly Ser Phe Asp Leu Asp Ser Val
20 25 30

Glu Thr Lys Gln Arg Asn Pro Gln Ser Glu Ala Pro Lys Tyr Gln Asp
35 40 45

Glu Gln Thr Glu Lys Pro Ala Lys Pro Ser Glu Ala Gln Ala Ala Glu
50 55 60

Asn Glu Arg Ser Ala Tyr Gly Phe Ala Ala Lys Ile Pro Arg Arg Asn

65 70 75 80

Ile His Phe Asn Val Lys Gln Gly His Gln Pro Leu Ser Asp Ala Asp
85 90 95
Trp Val Lys Leu Ala Ala Gly Glu Pro Asp Lys Phe Pro Gln Lys Asp
100 105 110
Asp Ile Phe Ala Met Asp Lys Gly Thr Leu Asn Glu Ser Ile Thr Thr
115 120 125
Gly Asp Gly Lys Ser Arg Val Glu Gly Tyr Thr Lys Phe Lys Tyr Val
130 135 140

Arg Ser Gly Tyr Ile Tyr Arg Asn Gly Ala Asn Lys Ile Asp Pro Lys
145 150 155 160
Asn Asn Ile Ala Leu Phe Gly Pro Asp Gly Tyr Leu Phe Tyr Lys Gly
165 170 175
Ser Asn Pro Ser Gln Ala Leu Pro Thr Gly Lys Ala Ile Tyr Lys Gly
180 185 190
Thr Trp Asp Tyr Val Thr Asp Ala Lys Glu Lys Gln Lys Phe Pro Gln
195 200 205

Leu Gly Ser Pro Pro Ala Gly Asp Arg Tyr Gly Ala Leu Ser Ala Glu
210 215 220
Glu Ala Asp Val Leu Arg Asn Glu Ser Glu Ala Pro Lys Gly Gln Thr
225 230 235 240
Asp Phe Gly Leu Thr Ser Glu Phe Glu Val Asp Phe Ala Ala Lys Thr
245 250 255
Met Thr Gly Ala Leu Tyr Arg Asn Asn Arg Ile Thr His Asn Glu Thr
260 265 270

Glu Asn Lys Ala Lys Gln Ile Lys Arg Tyr Asp Ile Gln Ala Asn Leu
275 280 285
His Gly Asn Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Asn Ala
290 295 300
Asn Glu Lys Glu His Pro Phe Val Ser Asp Ser Asp Ser Leu Glu Gly
305 310 315 320

Gly Phe Tyr Gly Pro Gln Gly Asp Glu Leu Gly Gly Lys Phe Leu Ala
325 330 335

Asn Asp Lys Lys Val Leu Ala Val Phe Ser Ala Lys Gln Lys Asp Asp
340 345 350
Ala Glu Lys Pro Leu Ala Glu Thr Phe Met Asp Ala Tyr Arg Ile Gly
355 360 365
Ala Asp Phe Val Lys Lys Gln Ile Asp Ser Phe Gly Asn Val Ala Lys
370 375 380
Leu Leu Ile Asp Gly Val Glu Leu Ala Leu Val Pro Ser Glu Gly Thr
385 390 395 400

Gln Thr Ala Phe Gln His Val Phe Glu Lys Asp Gly Val Lys Val Ser
405 410 415
Ala Cys Cys Ser Asn Leu Asp Tyr Leu His Phe Gly Val Leu Glu His
420 425 430
Gly Gly Ser His Asp Leu Phe Leu Gln Gly Ser Arg Thr Ala Val Ser
435 440 445
Glu Met Pro Thr Thr Ala Glu Pro Ala Val Tyr Arg Gly Thr Trp Ser
450 455 460

Gly Thr Ile Val Asn Gly Thr Ser Trp Ser Ala Glu Pro Ser Asp Lys
465 470 475 480
Glu Gly Gly Asn Arg Ala Glu Phe Lys Val Asn Phe Ala Glu Lys Thr
485 490 495
Leu Asn Gly Met Leu Thr Ala Lys Asp Arg Ile Ala Pro Val Phe Thr
500 505 510
Ile Thr Ala Gln Ile Gln Gly Asn Gly Phe Ser Gly Val Ala Lys Thr
515 520 525

Gly Glu Asn Gly Phe Ala Leu Asp Pro Lys Asn Thr Ile Asp Pro Ile
530 535 540
Arg Thr Asn Ile Arg Ala Asp Val Ser Gly Gly Phe Tyr Gly Lys Asn
545 550 555 560
Ala Ile Glu Met Gly Gly Ser Phe Ser Gly Asn Thr Leu Glu Gly Gly

565 570 575

Ser Gly Lys Ala Ala Val Val Phe Gly Thr Lys Arg Gln Gln Leu Val

580 585 590

Arg

<210> 1159

<211> 1812

<212> DNA

<213> H. parahaemolyticus TbpB

<400> 1159

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aaacaattta aagatgaaga gtctcaattg acacctgtgc caagtaagaa tctttctgca 180

ttgcaaagcc caacattagg taccgcaatg aaattaaaag cacataattt atttgatcgc 240

agtggaaagg agaatctttt ttcagaagaa gaatatgaaa cgttagactt caatatgata 300

aaagcaagag tcgcagcatc aacagctgat ggctctattg tggatagtaa tgatggatcc 360

agtccttatt ttactcggct tttgaaatat gttcgttcag gagtttatta caatgatagc 420

tggagagaaa gagatatacc taataaacgt tttttatctg gtttttatgg ctatgcattt 480

tattttggtg aaaacccatc aagagcgtta ccagtagagg gtaatgctca ttataaaggg 540

acttgggact ttattacgaa tgttaaaaat ggtagaactt atccattact tggaagtcag 600

gcaggcaata agagaagtgc tgtgccaaat gatattgatg atttgctaac gaataaaaat 660

gatgcggttg atcctaattc aactgatttt ggtttaagca gtgagtttga cgttaacttt 720

ggcaataaaa cattaactgg gcagttatat cgaaataaac gtcaaacgct tgcaaattcg 780

tcagctaaaa aagaaaaagt ttatgattta aacgcaacgc ttcacggtaa tcgttttatt 840

ggaaatgctg tcgctaccga taaaataagt caagattatc catttacttc tgatgcaaaa 900

gatgcgttag aaggaggatt ttatggccct catggtgagg agttaggtgg aaaatttttg 960

acagatgaca agcgagtctt cactgtattt agtgcaaaac gaaatgatga atcattaaca 1020

gccgaaacac agtttgatgc aaaacaaatt tccttttctg cagtaggaaa tgggaatgtt 1080

ggagacgatt ttaacataaa agataccact acatttggtg aggtaaatta tctagtggtt 1140

ggcaaccaac gtcttcctct tttagccagc gattcaacaa cttctgcctt tacaacaaca 1200

tcagaacacc acgtaaaaga gaacacagct gagaaaacga tagagacagt tgtttgctgc 1260

caaaatctga atagcgtaaa atttggtctt tactatgata aagataataa agaacgtaag 1320

cagtatcatc aattccttat agggcagaga agttcgacta aagaaattga ggctttaaaa 1380

ggaccagcat tttatcgtgg tacttgggat ggttatatca ctaatgggga aacctcttac 1440

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aataaaaccc tgactggcga attgaaaaaa gcaggtagcc ttaatactgt ttttgatatt 1560

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<210> 1160

<211> 603

<212> PRT

<213> H. parahaemolyticus TbpB

<400> 1160

Met Cys Phe Asn Lys Lys Trp Phe Phe Ile Thr Ser Pro Phe Leu Leu
1 5 10 15

Asn Ala Cys Ser Ser Gly Gly Gly Ser Phe Asp Val Asp Thr Val Ser
20 25 30

Lys Asp Ser Pro Thr Pro Ser Lys Lys Gln Phe Lys Asp Glu Glu Ser
35 40 45

Gln Leu Thr Pro Val Pro Ser Lys Asn Leu Ser Ala Leu Gln Ser Pro
50 55 60

Thr Leu Gly Thr Ala Met Lys Leu Lys Ala His Asn Leu Phe Asp Arg
65 70 75 80

Ser Gly Lys Glu Asn Leu Phe Ser Glu Glu Glu Tyr Glu Thr Leu Asp
85 90 95

Phe Asn Met Ile Lys Ala Arg Val Ala Ala Ser Thr Ala Asp Gly Ser
100 105 110

Ile Val Asp Ser Asn Asp Gly Ser Ser Pro Tyr Phe Thr Arg Leu Leu
115 120 125

Lys Tyr Val Arg Ser Gly Val Tyr Tyr Asn Asp Ser Trp Arg Glu Arg

130 135 140

Asp Ile Pro Asn Lys Arg Phe Leu Ser Gly Phe Tyr Gly Tyr Ala Phe
145 150 155 160
Tyr Phe Gly Glu Asn Pro Ser Arg Ala Leu Pro Val Glu Gly Asn Ala
165 170 175
His Tyr Lys Gly Thr Trp Asp Phe Ile Thr Asn Val Lys Asn Gly Arg
180 185 190
Thr Tyr Pro Leu Leu Gly Ser Gln Ala Gly Asn Lys Arg Ser Ala Val
195 200 205

Pro Asn Asp Ile Asp Asp Leu Leu Thr Asn Lys Asn Asp Ala Val Asp
210 215 220
Pro Asn Ser Thr Asp Phe Gly Leu Ser Ser Glu Phe Asp Val Asn Phe
225 230 235 240
Gly Asn Lys Thr Leu Thr Gly Gln Leu Tyr Arg Asn Lys Arg Gln Thr
245 250 255
Leu Ala Asn Ser Ser Ala Lys Lys Glu Lys Val Tyr Asp Leu Asn Ala
260 265 270

Thr Leu His Gly Asn Arg Phe Ile Gly Asn Ala Val Ala Thr Asp Lys
275 280 285
Ile Ser Gln Asp Tyr Pro Phe Thr Ser Asp Ala Lys Asp Ala Leu Glu
290 295 300
Gly Gly Phe Tyr Gly Pro His Gly Glu Glu Leu Gly Gly Lys Phe Leu
305 310 315 320
Thr Asp Asp Lys Arg Val Phe Thr Val Phe Ser Ala Lys Arg Asn Asp
325 330 335

Glu Ser Leu Thr Ala Glu Thr Gln Phe Asp Ala Lys Gln Ile Ser Phe
340 345 350
Ser Ala Val Gly Asn Gly Asn Val Gly Asp Asp Phe Asn Ile Lys Asp
355 360 365
Thr Thr Thr Phe Gly Glu Val Asn Tyr Leu Val Val Gly Asn Gln Arg
370 375 380

Leu Pro Leu Leu Ala Ser Asp Ser Thr Thr Ser Ala Phe Thr Thr Thr
385 390 395 400

Ser Glu His His Val Lys Glu Asn Thr Ala Glu Lys Thr Ile Glu Thr
405 410 415
Val Val Cys Cys Gln Asn Leu Asn Ser Val Lys Phe Gly Leu Tyr Tyr
420 425 430
Asp Lys Asp Asn Lys Glu Arg Lys Gln Tyr His Gln Phe Leu Ile Gly
435 440 445
Gln Arg Ser Ser Thr Lys Glu Ile Glu Ala Leu Lys Gly Pro Ala Phe
450 455 460

Tyr Arg Gly Thr Trp Asp Gly Tyr Ile Thr Asn Gly Glu Thr Ser Tyr
465 470 475 480
Thr Ala Ser Ala Thr Asn Lys Ser Thr Gly Asp Ile Ala Glu Phe Thr
485 490 495
Val Asn Phe Asp Asn Lys Thr Leu Thr Gly Glu Leu Lys Lys Ala Gly
500 505 510
Ser Leu Asn Thr Val Phe Asp Ile Asn Gly Lys Leu Asp Gly Asn Ser
515 520 525

Phe Ser Gly Met Ala Ser Thr Lys Gly Asp Gly Phe Ala Leu Asp Thr
530 535 540
Lys Asn Thr Leu Asp Ser Thr Lys Val Arg Ile Asn Thr Glu Val Lys
545 550 555 560
Gly Ala Phe Tyr Gly Ala Lys Gly Ser Glu Leu Gly Gly Ala Phe Ser
565 570 575
Ala Asn Thr Leu Asp Asp Ser Asn Lys Ala Lys Ala Ala Val Val Phe
580 585 590

Gly Ala Lys Arg Gln Val Glu Val Thr Ala Gln
595 600

<210> 1161
<211> 1779
<212> DNA

<213> A.pleuropneumoniae TbpB

<400> 1161

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gaaaaagcaa caacctctta tcaagatgag gaaacgaaga aaaagacaaa ggaagaatta 180

gataagttga tggagcctgc tttggggtat gaaactcaaa ttttacggcg aaataaggct 240

cctaaaacag aaacaggaga gaaaaggaat gagagagttg ttgagttatc cgaagataaa 300

attacgaaat tataccaaga gagtgtagaa ataatccctc atttagatga gctaaatgga 360

aaaacaacga gcaatgatgt ttatcattct cacgatagta aaaggcttga taagaataga 420

gatctcaaat atgttcgttc aggttatgtt tatgatgggt ctttcaatga aatacgacga 480

aatgactcag gattccatgt ttttaaacag ggtatagatg gctatgtcta ttaccttgga 540

gttactccat caaaagagtt accaaaagga aaagtcataa gttataaagg tacttgggat 600

tttgtaagta acatcaattt agatcgtgaa atagatggat tcgacacttc aggtgatggt 660

aaaaatgtat ctgcaacatc tattacagaa actgtcaatc gagatcataa agttggtgaa 720

aaactaggtg ataatgaagt taaaggggta gctcattcta gtgaatttgc agtagatttt 780

gataacaaaa aattgacagg tagtttatat cgtaatggtt atatcaacag aaataaagcg 840

caagaagtaa cgaaacgcta tagcattgaa gctgatattg caggcaaccg ttttagggga 900

aaagccaaag cagaaaaagc aggtgatccg atctttactg attcaaatta tcttgaaggg 960

ggattctatg gtcctaaagc tgaagaaatg gcagggaagt ttttcacaaa taataaatct 1020

ctctttgcag tatttgcagc taaaagtgaa aacggcgaga cgaccacaga acgaatcatt 1080

gatgcaacta aaattgattt aacccaattt aatgctaaag aactcaacaa ttttggtgat 1140

gcctctgttt taattattga tggacaaaaa atagatctag caggtgtcaa ttttaaaaat 1200

agtaaaacgg ttgaaatcaa cggcaaaaca atggtagccg tagcttgctg tagtaatctg 1260

gaatatatga aatttggtca attgtggcaa aaagagggca aacaagttaa agataatagt 1320

ttattcctac aaggtgaacg tactgcaacg gataaaatgc ccgcaggagg taactataag 1380

tatgttggaa cttgggatgc actcgtatct aaagggacga actggatagc ggaagcagat 1440

aataatcgag aatcgggcta tcgcactgaa tttgatgtta attttagtga taaaaaagta 1500

aacggtaagt tatttgataa aggcggtgta aatcctgtat ttaccgtaga tgcgacaatt 1560

aatggtaatg gctttatcgg cagtgcgaaa acctctgata gtggctttgc tttagatgca 1620

ggctctagcc aacacggaaa tgcggtattt agtgatataa aagtcaatgg tggcttctat 1680

ggtccaaccg ctggagaact tggcggacaa ttccatcata aatcagacaa tggcagtgtt 1740

ggcgctgtct ttggtgcaaa acgacaaata gaaaaataa 1779

<210> 1162

<211> 592

<212> PRT

<213> A. pleuropneumoniae TbpB

<400> 1162

Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1 5 10 15

Leu Val Ala Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Glu Asp Val
20 25 30

Arg Pro Asn Gln Thr Ala Lys Ala Glu Lys Ala Thr Thr Ser Tyr Gln
35 40 45

Asp Glu Glu Thr Lys Lys Lys Thr Lys Glu Glu Leu Asp Lys Leu Met
50 55 60

Glu Pro Ala Leu Gly Tyr Glu Thr Gln Ile Leu Arg Arg Asn Lys Ala
65 70 75 80

Pro Lys Thr Glu Thr Gly Glu Lys Arg Asn Glu Arg Val Val Glu Leu
85 90 95

Ser Glu Asp Lys Ile Thr Lys Leu Tyr Gln Glu Ser Val Glu Ile Ile
100 105 110

Pro His Leu Asp Glu Leu Asn Gly Lys Thr Thr Ser Asn Asp Val Tyr
115 120 125

His Ser His Asp Ser Lys Arg Leu Asp Lys Asn Arg Asp Leu Lys Tyr
130 135 140

Val Arg Ser Gly Tyr Val Tyr Asp Gly Ser Phe Asn Glu Ile Arg Arg
145 150 155 160

Asn Asp Ser Gly Phe His Val Phe Lys Gln Gly Ile Asp Gly Tyr Val
165 170 175

Tyr Tyr Leu Gly Val Thr Pro Ser Lys Glu Leu Pro Lys Gly Lys Val
180 185 190

Ile Ser Tyr Lys Gly Thr Trp Asp Phe Val Ser Asn Ile Asn Leu Asp

195 200 205

Arg Glu Ile Asp Gly Phe Asp Thr Ser Gly Asp Gly Lys Asn Val Ser
210 215 220
Ala Thr Ser Ile Thr Glu Thr Val Asn Arg Asp His Lys Val Gly Glu
225 230 235 240
Lys Leu Gly Asp Asn Glu Val Lys Gly Val Ala His Ser Ser Glu Phe
245 250 255
Ala Val Asp Phe Asp Asn Lys Lys Leu Thr Gly Ser Leu Tyr Arg Asn
260 265 270

Gly Tyr Ile Asn Arg Asn Lys Ala Gln Glu Val Thr Lys Arg Tyr Ser
275 280 285
Ile Glu Ala Asp Ile Ala Gly Asn Arg Phe Arg Gly Lys Ala Lys Ala
290 295 300
Glu Lys Ala Gly Asp Pro Ile Phe Thr Asp Ser Asn Tyr Leu Glu Gly
305 310 315 320
Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe Phe Thr
325 330 335

Asn Asn Lys Ser Leu Phe Ala Val Phe Ala Ala Lys Ser Glu Asn Gly
340 345 350
Glu Thr Thr Thr Glu Arg Ile Ile Asp Ala Thr Lys Ile Asp Leu Thr
355 360 365
Gln Phe Asn Ala Lys Glu Leu Asn Asn Phe Gly Asp Ala Ser Val Leu
370 375 380
Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Val Asn Phe Lys Asn
385 390 395 400

Ser Lys Thr Val Glu Ile Asn Gly Lys Thr Met Val Ala Val Ala Cys
405 410 415
Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Lys Glu
420 425 430
Gly Lys Gln Val Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu Arg Thr
435 440 445

Ala Thr Asp Lys Met Pro Ala Gly Gly Asn Tyr Lys Tyr Val Gly Thr
450 455 460

Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Ile Ala Glu Ala Asp
465 470 475 480
Asn Asn Arg Glu Ser Gly Tyr Arg Thr Glu Phe Asp Val Asn Phe Ser
485 490 495
Asp Lys Lys Val Asn Gly Lys Leu Phe Asp Lys Gly Gly Val Asn Pro
500 505 510
Val Phe Thr Val Asp Ala Thr Ile Asn Gly Asn Gly Phe Ile Gly Ser
515 520 525

Ala Lys Thr Ser Asp Ser Gly Phe Ala Leu Asp Ala Gly Ser Ser Gln
530 535 540
His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn Gly Gly Phe Tyr
545 550 555 560
Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His Lys Ser Asp
565 570 575
Asn Gly Ser Val Gly Ala Val Phe Gly Ala Lys Arg Gln Ile Glu Lys
580 585 590

<210> 1163
<211> 1752
<212> DNA
<213> M. haemolytica TbpB
<400> 1163
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cccaaaaagc caagtttaca agatgataat agtaacgcaa gacgtacagt aagcgcttct 180
gaaactgaag ctttattgca gccggggttt ggtttttcag ccaaaattcc gcgtcgtaat 240
ctctttccgc aggggaagga agatgtagcc cctattggtg atataaaaga gattactgga 300
gatctgacaa aaattccgta tgaagaagag gttaaagcgt acggtagtag tgctgatgga 360

tttagccata ctcatgatag aaatcataag ttgtatacta gagattttaa ttttgttcgt 420
tccggctatg ttctgcattc tggtgcaaaa cctgaaataa agcctaaaga aattttgaga 480

acaggtgcac atgggtatgt ttactattta ggtatagagc cggcaaaagc aatacctact 540

caaaaagcta cttataaagg atattgggat tttactaccg atgcgagaaa agggagagat 600

agtaaatatt tttctaattc cgcaggcatc aatattggcg ccacaccgga aaatagttac 660

gatattaatg ttgatgattc tgaaaaacca atggggcata caggagaatt tacggctgat 720

tttgctaata aaactttaac tggaacattg gttcgtaatg ggtatgttag tcgtagcaaa 780

gagcaaaaaa ttacaacaat ttacgatatt gatgcaaaaa ttaaaggtaa tcgcttttct 840

ggtaaagcaa acgcaaaaaa taccgatgat ccttattttg gtaaaagctc tacgacactt 900

gaaggtggat tttttggtgg gaaggctcaa gaacttgccg gtaaattctt agctgatgat 960

aagtcggtat ttgttgtttt tgctggcaaa cgagatgcta aaaaagatga tagtgaatct 1020

gcctttgatg ctttcaaaat taaacttaaa gatttaaata aatctgagat ggatactttc 1080

gggaatgcga cacatttgat tattaacaat aagcagattc cacttattgc ggaaggcaaa 1140

aaaagctttg ccgagatgaa atttgatgat ttggttaccc gtactattga tgataaaacg 1200

tatcgagttt cagtctgctg taataattta gattatgtca aatttgggac ttatagcgag 1260

ggaaataata gtgatactgc tcaccaatat ttagtaggag aacgtacagc tgtggcagat 1320

ttgccaacag ggacagtaaa atatcgaggt acttgggacg gggtaatgta cagtaaatct 1380

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gtagattttg tcaataaaaa aattaatggc aagctgattg ctaatgatgg tgttgaagaa 1500

cgcccaatgc tgacacttga aggcaatctg aaagggaatg gttttgcagg cacagccaaa 1560

acgggcaatt ctggttttaa tcttgatccg aaaagtacga atggtggcac ggtagtgcat 1620

ataaatactc aatttgaagg gggcttttat ggccctaagg cgacggaatt aggtggtatt 1680

gtacatagtg cagaaacgga taaagataga gtcagtatta cattcggcgg aaaacgtcaa 1740

atagaaaaat aa 1752

<210> 1164

<211> 583

<212> PRT

<213> M. haemolytica TbpB

<400> 1164

Met Phe Lys Leu Lys Ser Ser Phe Val Leu Leu Asn Ala Ala Leu Leu

1 5 10 15

Ala Ala Cys Ser Ser Asn Gly Gly Ser Phe Asp Val Gln Ser Ala Lys

20 25 30

Val Glu Ser Gln Thr Gln Thr Thr Pro Lys Lys Pro Ser Leu Gln Asp
35 40 45
Asp Asn Ser Asn Ala Arg Arg Thr Val Ser Ala Ser Glu Thr Glu Ala
50 55 60
Leu Leu Gln Pro Gly Phe Gly Phe Ser Ala Lys Ile Pro Arg Arg Asn
65 70 75 80
Leu Phe Pro Gln Gly Lys Glu Asp Val Ala Pro Ile Gly Asp Ile Lys

85 90 95
Glu Ile Thr Gly Asp Leu Thr Lys Ile Pro Tyr Glu Glu Glu Val Lys
100 105 110
Ala Tyr Gly Ser Ser Ala Asp Gly Phe Ser His Thr His Asp Arg Asn
115 120 125
His Lys Leu Tyr Thr Arg Asp Phe Asn Phe Val Arg Ser Gly Tyr Val
130 135 140
Leu His Ser Gly Ala Lys Pro Glu Ile Lys Pro Lys Glu Ile Leu Arg

145 150 155 160
Thr Gly Ala His Gly Tyr Val Tyr Tyr Leu Gly Ile Glu Pro Ala Lys
165 170 175
Ala Ile Pro Thr Gln Lys Ala Thr Tyr Lys Gly Tyr Trp Asp Phe Thr
180 185 190
Thr Asp Ala Arg Lys Gly Arg Asp Ser Lys Tyr Phe Ser Asn Ser Ala
195 200 205
Gly Ile Asn Ile Gly Ala Thr Pro Glu Asn Ser Tyr Asp Ile Asn Val

210 215 220
Asp Asp Ser Glu Lys Pro Met Gly His Thr Gly Glu Phe Thr Ala Asp
225 230 235 240
Phe Ala Asn Lys Thr Leu Thr Gly Thr Leu Val Arg Asn Gly Tyr Val
245 250 255
Ser Arg Ser Lys Glu Gln Lys Ile Thr Thr Ile Tyr Asp Ile Asp Ala
260 265 270
Lys Ile Lys Gly Asn Arg Phe Ser Gly Lys Ala Asn Ala Lys Asn Thr

275 280 285

Asp Asp Pro Tyr Phe Gly Lys Ser Ser Thr Thr Leu Glu Gly Gly Phe

290 295 300

Phe Gly Gly Lys Ala Gln Glu Leu Ala Gly Lys Phe Leu Ala Asp Asp

305 310 315 320

Lys Ser Val Phe Val Val Phe Ala Gly Lys Arg Asp Ala Lys Lys Asp

325 330 335

Asp Ser Glu Ser Ala Phe Asp Ala Phe Lys Ile Lys Leu Lys Asp Leu

340 345 350

Asn Lys Ser Glu Met Asp Thr Phe Gly Asn Ala Thr His Leu Ile Ile

355 360 365

Asn Asn Lys Gln Ile Pro Leu Ile Ala Glu Gly Lys Lys Ser Phe Ala

370 375 380

Glu Met Lys Phe Asp Asp Leu Val Thr Arg Thr Ile Asp Asp Lys Thr

385 390 395 400

Tyr Arg Val Ser Val Cys Cys Asn Asn Leu Asp Tyr Val Lys Phe Gly

405 410 415

Thr Tyr Ser Glu Gly Asn Asn Ser Asp Thr Ala His Gln Tyr Leu Val

420 425 430

Gly Glu Arg Thr Ala Val Ala Asp Leu Pro Thr Gly Thr Val Lys Tyr

435 440 445

Arg Gly Thr Trp Asp Gly Val Met Tyr Ser Lys Ser Gly Ser Ala Gly

450 455 460

Ala Glu Ser Pro Ser Asn Ser Glu Ser Gly Thr Arg Ser Leu Phe Asp

465 470 475 480

Val Asp Phe Val Asn Lys Lys Ile Asn Gly Lys Leu Ile Ala Asn Asp

485 490 495

Gly Val Glu Glu Arg Pro Met Leu Thr Leu Glu Gly Asn Leu Lys Gly

500 505 510

Asn Gly Phe Ala Gly Thr Ala Lys Thr Gly Asn Ser Gly Phe Asn Leu

515 520 525

Asp Pro Lys Ser Thr Asn Gly Gly Thr Val Val His Ile Asn Thr Gln

530 535 540

Phe Glu Gly Gly Phe Tyr Gly Pro Lys Ala Thr Glu Leu Gly Gly Ile

545 550 555 560

Val His Ser Ala Glu Thr Asp Lys Asp Arg Val Ser Ile Thr Phe Gly

565 570 575

Gly Lys Arg Gln Ile Glu Lys

580

<210> 1165

<211> 2085

<212> DNA

<213> M. catarrhalis TbpB

<400> 1165

atgaaacaca ttcctttaac cacactgtgt gtggcaatct ctgccgtctt attaaccgct 60

tgtggtggca gtggtggttc aaatccacct gctcctacgc ccattccaaa tgctagcggt 120

tcaggtaata ctggcaacac tggtaatgct ggcggtactg ataatacagc caatgcaggt 180

aatacaggcg gtgcaaactc tggtacaggc agtgccagca caccagaacc aaaatatcaa 240

gatgtgccaa ctgagaaaaa tgaaaaagat aaagtttcac ccattcaaga acctgccatg 300

ggttatgcaa tggaattaaa gcttcgtaac tatataagcg gacaggaaga acatgccaaa 360

atcagtacag atgatgttgt aaaacttgaa ggtggcttgg agcataagcc atttgacaac 420

tctatttggc aaaacatcaa aaatagcaaa gaagtacaaa gtgtttacaa ccaagagaag 480

caaaacattg aaaatcaaat caaaaaagaa aataaaggac ttgatgaagc ggcactaaaa 540

gctcgtattg aaaaagttct tgatgactat ctaacagaac ttgctaaacc catttatgaa 600

aaaaatatta attattcaca tgatgggcag aataaagcac gcactcgtga tttgacttat 660

gtgcgttctg gttatattta tcgctcaggt tattctaata tcgactttca aaagaaaata 720

gctaaaactg gttttgatgg tgctttattt tataaaggtg aacaaactgc taaacaattg 780

cctgtatctg aagttaagta taaaggcact tgggatttta tgaccgatgc caaaaatagg 840

caatcattta gcagttttgg aggacgagct ggtaatcaat atagtgcaat atcttcccat 900

gagtacccat ctttattaac tgatgagaaa aacaaaccaa ataattatac tggcgaatat 960

ggtcatagca gtgagtttac ggtagatttt agtaaaaaga gcctaaaagg tgagctgttt 1020

agtaacctac aagacagcca taaaaaaaca gtaaccaaaa ccaaacgcta tgatatcgat 1080

gccagtatcc acggcaaccg cttccgtggc agtgccaccg caatcgataa agcaaaagac 1140

agcgaaacca aacacccctt taccagtgat gccaacgata agctagaagg tggtttttat 1200

ggaccaaacg ccgaggagct ggcaggtaaa ttcctaaccg atgacaacaa actctttggt 1260

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tatgcacttg gtacatttaa caccaaagaa gcaaccacat tcaccccatt taccaaaaaa 1380

caactggata actttggcaa tgccaaaaag ttggtcttgg gttctaccgt cattgatttg 1440

gtgcctaccg atgccaccaa atatgtcaat aaatttcacc aaaaaaagcc agagtctgcc 1500

acaaacaaag cgggcgagac tttgatggtg aatgatgaag ttagcgtcaa aacctatggc 1560

aaaaactttg aatacctaaa atttggtgag ctcagtgtcg gcacaagcaa cagcgtcttt 1620

ttacaaggcg aacgcaccgc taccacaggc gataaagccg taccaaccac aggcgcagcc 1680

aaatatttgg ggaactgggt aggatacatc acaggaaagg acacaggagc gggctcatca 1740

aaaggcttta ccgatgccaa agatgttgct gattttgaca ttgactttga gaaaaaaaca 1800

gttaatggca aactgaccac ccaaggccgc caagaccctg tatttagcat cacaggtaac 1860

atctcaggta atggctggac aggcaaagcc agcaccgccg aagcggacgc agggggctac 1920

aagatagatt ctagcagtac aggcaaatcc atcgtcatca aagatgccga ggttactggg 1980

ggcttttatg gtccaaatgc aaacgagatg ggtgggtcat ttacacacaa cgctgatgac 2040

aaagtctctg tggtctttgg cgcaaaaaaa caagaagtta agtag 2085

<210> 1166

<211> 694

<212> PRT

<213> M. catarrhalis TbpB

<400> 1166

Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
1 5 10 15

Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
20 25 30

Thr Pro Ile Pro Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn Thr Gly
35 40 45

Asn Ala Gly Gly Thr Asp Asn Thr Ala Asn Ala Gly Asn Thr Gly Gly
50 55 60

Ala Asn Ser Gly Thr Gly Ser Ala Ser Thr Pro Glu Pro Lys Tyr Gln

65 70 75 80

Asp Val Pro Thr Glu Lys Asn Glu Lys Asp Lys Val Ser Pro Ile Gln
85 90 95

Glu Pro Ala Met Gly Tyr Ala Met Glu Leu Lys Leu Arg Asn Tyr Ile
100 105 110

Ser Gly Gln Glu Glu His Ala Lys Ile Ser Thr Asp Asp Val Val Lys
115 120 125

Leu Glu Gly Gly Leu Glu His Lys Pro Phe Asp Asn Ser Ile Trp Gln
130 135 140

Asn Ile Lys Asn Ser Lys Glu Val Gln Ser Val Tyr Asn Gln Glu Lys
145 150 155 160

Gln Asn Ile Glu Asn Gln Ile Lys Lys Glu Asn Lys Gly Leu Asp Glu
165 170 175

Ala Ala Leu Lys Ala Arg Ile Glu Lys Val Leu Asp Asp Tyr Leu Thr
180 185 190

Glu Leu Ala Lys Pro Ile Tyr Glu Lys Asn Ile Asn Tyr Ser His Asp
195 200 205

Gly Gln Asn Lys Ala Arg Thr Arg Asp Leu Thr Tyr Val Arg Ser Gly
210 215 220

Tyr Ile Tyr Arg Ser Gly Tyr Ser Asn Ile Asp Phe Gln Lys Lys Ile
225 230 235 240

Ala Lys Thr Gly Phe Asp Gly Ala Leu Phe Tyr Lys Gly Glu Gln Thr
245 250 255

Ala Lys Gln Leu Pro Val Ser Glu Val Lys Tyr Lys Gly Thr Trp Asp
260 265 270

Phe Met Thr Asp Ala Lys Asn Arg Gln Ser Phe Ser Ser Phe Gly Gly
275 280 285

Arg Ala Gly Asn Gln Tyr Ser Ala Ile Ser Ser His Glu Tyr Pro Ser
290 295 300

Leu Leu Thr Asp Glu Lys Asn Lys Pro Asn Asn Tyr Thr Gly Glu Tyr
305 310 315 320

Gly His Ser Ser Glu Phe Thr Val Asp Phe Ser Lys Lys Ser Leu Lys
325 330 335
Gly Glu Leu Phe Ser Asn Leu Gln Asp Ser His Lys Lys Thr Val Thr
340 345 350
Lys Thr Lys Arg Tyr Asp Ile Asp Ala Ser Ile His Gly Asn Arg Phe
355 360 365
Arg Gly Ser Ala Thr Ala Ile Asp Lys Ala Lys Asp Ser Glu Thr Lys
370 375 380

His Pro Phe Thr Ser Asp Ala Asn Asp Lys Leu Glu Gly Gly Phe Tyr
385 390 395 400
Gly Pro Asn Ala Glu Glu Leu Ala Gly Lys Phe Leu Thr Asp Asp Asn
405 410 415
Lys Leu Phe Gly Val Phe Gly Ala Lys Arg Glu Ser Lys Ala Gly Glu
420 425 430
Lys Thr Glu Ala Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe Asn Thr
435 440 445

Lys Glu Ala Thr Thr Phe Thr Pro Phe Thr Lys Lys Gln Leu Asp Asn
450 455 460
Phe Gly Asn Ala Lys Lys Leu Val Leu Gly Ser Thr Val Ile Asp Leu
465 470 475 480
Val Pro Thr Asp Ala Thr Lys Tyr Val Asn Lys Phe His Gln Lys Lys
485 490 495
Pro Glu Ser Ala Thr Asn Lys Ala Gly Glu Thr Leu Met Val Asn Asp
500 505 510

Glu Val Ser Val Lys Thr Tyr Gly Lys Asn Phe Glu Tyr Leu Lys Phe
515 520 525
Gly Glu Leu Ser Val Gly Thr Ser Asn Ser Val Phe Leu Gln Gly Glu
530 535 540
Arg Thr Ala Thr Thr Gly Asp Lys Ala Val Pro Thr Thr Gly Ala Ala
545 550 555 560
Lys Tyr Leu Gly Asn Trp Val Gly Tyr Ile Thr Gly Lys Asp Thr Gly

565 570 575

Ala Gly Ser Ser Lys Gly Phe Thr Asp Ala Lys Asp Val Ala Asp Phe
580 585 590
Asp Ile Asp Phe Glu Lys Lys Thr Val Asn Gly Lys Leu Thr Thr Gln
595 600 605
Gly Arg Gln Asp Pro Val Phe Ser Ile Thr Gly Asn Ile Ser Gly Asn
610 615 620
Gly Trp Thr Gly Lys Ala Ser Thr Ala Glu Ala Asp Ala Gly Gly Tyr
625 630 635 640

Lys Ile Asp Ser Ser Ser Thr Gly Lys Ser Ile Val Ile Lys Asp Ala
645 650 655
Glu Val Thr Gly Gly Phe Tyr Gly Pro Asn Ala Asn Glu Met Gly Gly
660 665 670
Ser Phe Thr His Asn Ala Asp Asp Lys Val Ser Val Val Phe Gly Ala
675 680 685
Lys Lys Gln Glu Val Lys
690

<210> 1167
<211> 1893
<212> DNA
<213> H. influenzae TbpB

<400> 1167
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caagacgata cttcaagttc aagaacaaaa tctaatttgg aaaagttgtc cattccttct 180
ttaggaggag ggatgaagtt agtggctcag aatctgagtg gtaataaaga acctagtttc 240
ttaaatgaaa atggctatat atcatatttt tcctcacctt ctacgattga agatgatgtt 300
aaaaatgtta aaacagaaaa taaaatacat acaaatccaa ttgggcttga acctaataga 360
gcattacaag accccaattt acaaaaatac gtttattctg gtttgtacta tattgagaat 420

tggaaagact tttccaaatt agcaacagaa aaaaaagcct atagtggcca ttatggttat 480
gcgttttatt atggtaataa aactgcaaca gacttgccag taagcggtgt agcaacgtat 540

aaaggaactt gggatttcat cactgcaact aaatatggcc aaaattattc tttgttcagt 600

aatgctagag gtcaagctta ttttcgacgt agtgctactc gaggagatat tgatttagaa 660

aataattcaa agaatggtga tataggctta ataagtgaat ttagtgcaga ttttgggact 720

aaaaaactga caggacaact gtcttacacc aaaagaaaaa ctgatattca acaatatgaa 780

aaggaaaaac tctatgatat agatgcccat atttatagta atagattcag gggtaaagtt 840

actcctacga aatccacatc ggatgaacat ccctttacca gcgagggaac attagaaggt 900

ggtttttatg gacctaatgc tgaagaacta gggggtaaat tcttagctag ggataaacga 960

gtttttgggg tatttagtgc caaagaaacg ccagaaacag aaaaggaaaa attatccaaa 1020

gaaaccttaa ttgatggcaa gctaattact ttctctacta aaacagccga tgcaacaacc 1080

agtacaacag ccagtacaac agccgatgta aaaaccgatg aaaaaaactt tacgacaaaa 1140

gatatatcaa gttttggtga agctgattac cttttaattg ataattaccc tgttcctctt 1200

ttccctgaag gggatactga tgacttcgta acgagtaaac atcacgatat tggaaataaa 1260

acctataaag tagaagcatg ttgcaagaat ctaagctatg taaaatttgg tatgtattat 1320

gaggataaag agaagaaaaa cacaaatcaa acaggacaat accaccaatt tttgttaggt 1380

ctccgtactc ccagttctca aattcctgta acgggaaacg tgaaatatct cggtagttgg 1440

tttggttata ttggtgatga caagacatct tactccacta caggaaataa acaacaagat 1500

aaaaatgctc ccgccgagtt tgatgtcaat tttgacaata aaacattaac aggcaaatta 1560

aaacgagccg actcacaaaa taccgtgttt aacattgagg caacctttaa aaatggtagt 1620

aatgccttcg aaggtaaagc aaccgcaaat gtagtgattg atcccaaaaa tacacaagcc 1680

acatctaaag tcaatttcac gacaacagta aacggggcat tttatggtcc gcacgctaca 1740

gaattaggcg gttatttcac ctataacgga aacaatccta cagctacaaa ttctgaaagt 1800

tcctcaaccg taccttcacc acccaattca ccaaatgcaa gagctgcagt tgtctttgga 1860

gctaaaagac aagtagaaaa aaccaacaag tag 1893

<210> 1168

<211> 630

<212> PRT

<213> H. influenzae TbpB

<400> 1168

Met Lys Ser Val Pro Leu Ile Thr Gly Gly Leu Ser Phe Leu Leu Ser

1 5 10 15

Ala Cys Ser Gly Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn

20 25 30

Pro Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Ser Arg

35 40 45

Thr Lys Ser Asn Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly

50 55 60

Met Lys Leu Val Ala Gln Asn Leu Ser Gly Asn Lys Glu Pro Ser Phe

65 70 75 80

Leu Asn Glu Asn Gly Tyr Ile Ser Tyr Phe Ser Ser Pro Ser Thr Ile

85 90 95

Glu Asp Asp Val Lys Asn Val Lys Thr Glu Asn Lys Ile His Thr Asn

100 105 110

Pro Ile Gly Leu Glu Pro Asn Arg Ala Leu Gln Asp Pro Asn Leu Gln

115 120 125

Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Glu Asn Trp Lys Asp Phe

130 135 140

Ser Lys Leu Ala Thr Glu Lys Lys Ala Tyr Ser Gly His Tyr Gly Tyr

145 150 155 160

Ala Phe Tyr Tyr Gly Asn Lys Thr Ala Thr Asp Leu Pro Val Ser Gly

165 170 175

Val Ala Thr Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Lys Tyr

180 185 190

Gly Gln Asn Tyr Ser Leu Phe Ser Asn Ala Arg Gly Gln Ala Tyr Phe

195 200 205

Arg Arg Ser Ala Thr Arg Gly Asp Ile Asp Leu Glu Asn Asn Ser Lys

210 215 220

Asn Gly Asp Ile Gly Leu Ile Ser Glu Phe Ser Ala Asp Phe Gly Thr

225 230 235 240

Lys Lys Leu Thr Gly Gln Leu Ser Tyr Thr Lys Arg Lys Thr Asp Ile

245 250 255

Gln Gln Tyr Glu Lys Glu Lys Leu Tyr Asp Ile Asp Ala His Ile Tyr

260 265 270

Ser Asn Arg Phe Arg Gly Lys Val Thr Pro Thr Lys Ser Thr Ser Asp
275 280 285
Glu His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly
290 295 300
Pro Asn Ala Glu Glu Leu Gly Gly Lys Phe Leu Ala Arg Asp Lys Arg
305 310 315 320
Val Phe Gly Val Phe Ser Ala Lys Glu Thr Pro Glu Thr Glu Lys Glu
325 330 335

Lys Leu Ser Lys Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr Phe Ser
340 345 350
Thr Lys Thr Ala Asp Ala Thr Thr Ser Thr Thr Ala Ser Thr Thr Ala
355 360 365
Asp Val Lys Thr Asp Glu Lys Asn Phe Thr Thr Lys Asp Ile Ser Ser
370 375 380
Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu
385 390 395 400

Phe Pro Glu Gly Asp Thr Asp Asp Phe Val Thr Ser Lys His His Asp
405 410 415
Ile Gly Asn Lys Thr Tyr Lys Val Glu Ala Cys Cys Lys Asn Leu Ser
420 425 430
Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Lys Glu Lys Lys Asn Thr
435 440 445
Asn Gln Thr Gly Gln Tyr His Gln Phe Leu Leu Gly Leu Arg Thr Pro
450 455 460

Ser Ser Gln Ile Pro Val Thr Gly Asn Val Lys Tyr Leu Gly Ser Trp
465 470 475 480
Phe Gly Tyr Ile Gly Asp Asp Lys Thr Ser Tyr Ser Thr Thr Gly Asn
485 490 495
Lys Gln Gln Asp Lys Asn Ala Pro Ala Glu Phe Asp Val Asn Phe Asp
500 505 510
Asn Lys Thr Leu Thr Gly Lys Leu Lys Arg Ala Asp Ser Gln Asn Thr

515 520 525

Val Phe Asn Ile Glu Ala Thr Phe Lys Asn Gly Ser Asn Ala Phe Glu
530 535 540
Gly Lys Ala Thr Ala Asn Val Val Ile Asp Pro Lys Asn Thr Gln Ala
545 550 555 560
Thr Ser Lys Val Asn Phe Thr Thr Thr Val Asn Gly Ala Phe Tyr Gly
565 570 575
Pro His Ala Thr Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Asn
580 585 590

Pro Thr Ala Thr Asn Ser Glu Ser Ser Ser Thr Val Pro Ser Pro Pro
595 600 605
Asn Ser Pro Asn Ala Arg Ala Ala Val Val Phe Gly Ala Lys Arg Gln
610 615 620
Val Glu Lys Thr Asn Lys
625 630

<210> 1169
<211> 180
<212> DNA
<213> N. meningitidis TbpB lipobox plus anchor peptide
<400> 1169
atgaacaatc cattggtaaa tcaggctgct atggtgctgc ctgtgttttt gttgagtgct 60
tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 120

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 180

<210> 1170
<211> 60
<212> PRT
<213> N. meningitidis TbpB lipobox plus anchor peptide
<400> 1170
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
1 5 10 15
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
20 25 30

Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu

35 40 45

Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu

50 55 60

<210> 1171

<211> 63

<212> DNA

<213> N. meningitidis TbpB signal sequence

<400> 1171

atgaacaatc cattggtaaa tcaggctgct atggtgctgc ctgtgttttt gttgagtgct 60

tgt 63

<210> 1172

<211> 21

<212> PRT

<213> N. meningitidis TbpB signal sequence

<400> 1172

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe

1 5 10 15

Leu Leu Ser Ala Cys

20

<210> 1173

<211> 12

<212> DNA

<213> N. meningitidis TbpB lipobox

<400> 1173

ttgagtgctt gt 12

<210> 1174

<211> 4

<212> PRT

<213> N. meningitidis TbpB lipobox

<400> 1174

Leu Ser Ala Cys

1

<210> 1175

<211> 117

<212> DNA

<213> N. meningitidis TbpB anchor peptide

<400> 1175

ctgggtggcg gcggcagttt cgatttggac agcgtggaaa ccgtgcaaga tatgcactcc 60

aaacctaagt atgaggatga aaaaagccag cctgaaagcc aacaggatgt atcggaa 117

<210> 1176

<211> 39

<212> PRT

<213> N. meningitidis TbpB anchor peptide

<400> 1176

Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Glu Thr Val Gln

1 5 10 15

Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu Lys Ser Gln Pro Glu

20 25 30

Ser Gln Gln Asp Val Ser Glu

35

<210> 1177

<211> 765

<212> DNA

<213> A. baumannii His-Slp

<400> 1177

atgggcagca gccatcatca tcatcatcac agcggaattg atggtatttc gagtaatgaa 60

agtaacatca aaatcggtgc tgctgccaat gcaagtcatc cgggtggtgt agcagcggtg 120

tcggttcaag ctgcgggtgc gccatataac gcttttacag gttttagttc gttaaaaggt 180

ttggctcagg cttttgctgc tcagggaacg agtaacacca atgtaacggt tggcagcaaa 240

acctttaata tttcacatat tccagtgtct gcaatgccac cttcacacag tgcattaggt 300

aattttaact ttggtcaggt gggcacacag gaagtctatt ttggtgaatg gtggaaagcg 360

ggcgacacgc cggcaagcgc gagccatacc gtttactacg cgggtgataa taccaatacc 420

actgttccaa ccgcgggtac tgcaacttat accgttgcag ggattaacgg ctctggaagc 480

aatctgttaa gtggtacgtt cacggcaaat tatggcgcgg gtacacttga aggaacactt 540

actggaactg gtacggctgt ttcatcatta agcctagatg gtgtggcatt taacccgggt 600

actgctgcgt ttgcaggttt ggcaacggct aacggtacgg ctggtatcga caactctggt 660

gtggtgcaag gtcaattctt tggtgcaaat gcttcggctt tagcgggtat tgcccagttt 720

gataacgtgt cttacaacac tgcatttggc ggtgctaaaa attaa 765

<210> 1178

<211> 254

<212> PRT

<213> A. baumannii His-Slp 2

<400> 1178

Met Gly Ser Ser His His His His His His Ser Gly Ile Asp Gly Ile
1 5 10 15

Ser Ser Asn Glu Ser Asn Ile Lys Ile Gly Ala Ala Ala Asn Ala Ser
20 25 30

His Pro Gly Gly Val Ala Ala Val Ser Val Gln Ala Ala Gly Ala Pro
35 40 45

Tyr Asn Ala Phe Thr Gly Phe Ser Ser Leu Lys Gly Leu Ala Gln Ala
50 55 60

Phe Ala Ala Gln Gly Thr Ser Asn Thr Asn Val Thr Val Gly Ser Lys
65 70 75 80

Thr Phe Asn Ile Ser His Ile Pro Val Ser Ala Met Pro Pro Ser His
85 90 95

Ser Ala Leu Gly Asn Phe Asn Phe Gly Gln Val Gly Thr Gln Glu Val
100 105 110

Tyr Phe Gly Glu Trp Trp Lys Ala Gly Asp Thr Pro Ala Ser Ala Ser
115 120 125

His Thr Val Tyr Tyr Ala Gly Asp Asn Thr Asn Thr Thr Val Pro Thr
130 135 140

Ala Gly Thr Ala Thr Tyr Thr Val Ala Gly Ile Asn Gly Ser Gly Ser
145 150 155 160

Asn Leu Leu Ser Gly Thr Phe Thr Ala Asn Tyr Gly Ala Gly Thr Leu
165 170 175

Glu Gly Thr Leu Thr Gly Thr Gly Thr Ala Val Ser Ser Leu Ser Leu
180 185 190
Asp Gly Val Ala Phe Asn Pro Gly Thr Ala Ala Phe Ala Gly Leu Ala
195 200 205
Thr Ala Asn Gly Thr Ala Gly Ile Asp Asn Ser Gly Val Val Gln Gly
210 215 220
Gln Phe Phe Gly Ala Asn Ala Ser Ala Leu Ala Gly Ile Ala Gln Phe
225 230 235 240

Asp Asn Val Ser Tyr Asn Thr Ala Phe Gly Gly Ala Lys Asn
245 250

<210> 1179
<211> 70
<212> DNA
<213> E. coli SLAM signal sequence
<400> 1179
atgaaatacc tgctgccgac cgctgctgct ggtctgctgc tcctcgctgc ccagccggcg 60
atggccatgg 70

<210> 1180
<211> 23
<212> PRT
<213> E. coli SLAM signal sequence
<400> 1180
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala

1 5 10 15
Ala Gln Pro Ala Met Ala Met
20

<210> 1181
<211> 1446
<212> DNA
<213> N. meningitidis SLAM with signal sequence
<400> 1181
atgaaatacc tgctgccgac cgctgctgct ggtctgctgc tcctcgctgc ccagccggcg 60
atggccatgg gcgaagaaac accgcgcgaa ccggatttga gaagccgtcc cgagttcagg 120

cttcatgaag cggaggtcaa accaatcgac agggagaagg taccggggca ggtgcgggaa 180

aaaggaaaag ttttgcagat tgacggagaa accctgctga aaaatcccga attgttgtcc 240

cgcgcgatgt attccgcagt ggtctcaaac aatattgccg gtatccgcgt tattttgccg 300

atttacctac aacaggcgca gcaggataag atgttggcac tttatgcaca agggattttg 360

gcgcaggcag acggtagggt gaaggaggcg atttcccatt accgggaatt gattgccgcc 420

caacccgacg cgcccgccgt ccgtatgcgt ttggcggcgg cattgtttga aaacaggcag 480

aacgaggcgg cggcagacca gttcgaccgc ctgaaggcgg aaaacctgcc gccgcagctg 540

atggagcagg tcgagctgta ccgcaaggca ttgcgcgaac gcgatgcgtg gaaggtaaat 600

ggcggcttca gcgtcacccg cgaacacaat atcaaccaag ccccgaaacg gcagcagtac 660

ggcaaatgga ctttcccgaa acaggtggac ggcacggcgg tcaattaccg gctcggcgcg 720

gagaaaaaat ggtcgctgaa aaacggctgg tacacgacgg ctggcggcga cgtgtccggc 780

agggtttatc cggggaataa gaaattcaac gatatgacgg caggcgtttc cggcggcatc 840

ggttttgccg accggcgcaa agatgccggg ctggcagtgt tccacgaacg ccgcacctac 900

ggcaacgacg cttattctta caccaacggc gcacgccttt atttcaaccg ttggcaaacc 960

ccgaaatggc aaacgttgtc ttcggcggag tgggggcgtt tgaagaatac gcgccgggcg 1020

cgttccgaca atacccattt gcaaatttcc aattcgctgg tgttttaccg gaatgcgcgc 1080

caatattgga tgggcggttt ggatttttac cgcgagcgca accccgccga ccggggcgac 1140

aatttcaacc gttacggcct gcgctttgcc tgggggcagg aatggggcgg cagcggcctg 1200

tcttcgctgt tgcgcctcgg cgcggcgaaa cggcattatg aaaaacccgg ctttttcagc 1260

ggttttaaag gggaaaggcg cagggataaa gaattgaaca catccttgag cctttggcac 1320

cgggcattgc atttcaaagg catcacgccg cgcctgacgt tgtcgcaccg cgaaacgcgg 1380

agtaacgatg tgttcaacga atacgagaaa aatcgggcgt ttgtcgagtt taataaaacg 1440

ttctga 1446

<210> 1182

<211> 481

<212> PRT

<213> N. meningitidis SLAM with signal sequence

<400> 1182

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala

1 5 10 15

Ala Gln Pro Ala Met Ala Met Gly Glu Glu Thr Pro Arg Glu Pro Asp

20 25 30

Leu Arg Ser Arg Pro Glu Phe Arg Leu His Glu Ala Glu Val Lys Pro

35 40 45

Ile Asp Arg Glu Lys Val Pro Gly Gln Val Arg Glu Lys Gly Lys Val

50 55 60

Leu Gln Ile Asp Gly Glu Thr Leu Leu Lys Asn Pro Glu Leu Leu Ser

65 70 75 80

Arg Ala Met Tyr Ser Ala Val Val Ser Asn Asn Ile Ala Gly Ile Arg

85 90 95

Val Ile Leu Pro Ile Tyr Leu Gln Gln Ala Gln Gln Asp Lys Met Leu

100 105 110

Ala Leu Tyr Ala Gln Gly Ile Leu Ala Gln Ala Asp Gly Arg Val Lys

115 120 125

Glu Ala Ile Ser His Tyr Arg Glu Leu Ile Ala Ala Gln Pro Asp Ala

130 135 140

Pro Ala Val Arg Met Arg Leu Ala Ala Ala Leu Phe Glu Asn Arg Gln

145 150 155 160

Asn Glu Ala Ala Ala Asp Gln Phe Asp Arg Leu Lys Ala Glu Asn Leu

165 170 175

Pro Pro Gln Leu Met Glu Gln Val Glu Leu Tyr Arg Lys Ala Leu Arg

180 185 190

Glu Arg Asp Ala Trp Lys Val Asn Gly Gly Phe Ser Val Thr Arg Glu

195 200 205

His Asn Ile Asn Gln Ala Pro Lys Arg Gln Gln Tyr Gly Lys Trp Thr

210 215 220

Phe Pro Lys Gln Val Asp Gly Thr Ala Val Asn Tyr Arg Leu Gly Ala

225 230 235 240

Glu Lys Lys Trp Ser Leu Lys Asn Gly Trp Tyr Thr Thr Ala Gly Gly

245 250 255

Asp Val Ser Gly Arg Val Tyr Pro Gly Asn Lys Lys Phe Asn Asp Met

260 265 270

Thr Ala Gly Val Ser Gly Gly Ile Gly Phe Ala Asp Arg Arg Lys Asp
275 280 285
Ala Gly Leu Ala Val Phe His Glu Arg Arg Thr Tyr Gly Asn Asp Ala
290 295 300
Tyr Ser Tyr Thr Asn Gly Ala Arg Leu Tyr Phe Asn Arg Trp Gln Thr

305 310 315 320
Pro Lys Trp Gln Thr Leu Ser Ser Ala Glu Trp Gly Arg Leu Lys Asn
325 330 335
Thr Arg Arg Ala Arg Ser Asp Asn Thr His Leu Gln Ile Ser Asn Ser
340 345 350
Leu Val Phe Tyr Arg Asn Ala Arg Gln Tyr Trp Met Gly Gly Leu Asp
355 360 365
Phe Tyr Arg Glu Arg Asn Pro Ala Asp Arg Gly Asp Asn Phe Asn Arg

370 375 380
Tyr Gly Leu Arg Phe Ala Trp Gly Gln Glu Trp Gly Gly Ser Gly Leu
385 390 395 400
Ser Ser Leu Leu Arg Leu Gly Ala Ala Lys Arg His Tyr Glu Lys Pro
405 410 415
Gly Phe Phe Ser Gly Phe Lys Gly Glu Arg Arg Arg Asp Lys Glu Leu
420 425 430
Asn Thr Ser Leu Ser Leu Trp His Arg Ala Leu His Phe Lys Gly Ile

435 440 445
Thr Pro Arg Leu Thr Leu Ser His Arg Glu Thr Arg Ser Asn Asp Val
450 455 460
Phe Asn Glu Tyr Glu Lys Asn Arg Ala Phe Val Glu Phe Asn Lys Thr
465 470 475 480
Phe

<210> 1183
<211> 1467
<212> DNA
<213> N. meningitidis B16B6 SLAM 1

<400> 1183

atggttattt tttatttttg tgggaagaca tttatgcctg cacgaaacag atggatgctg 60

ctgctgcctt tattggcaag cgcggcatat gccgaagaaa caccgcgcga accggatttg 120

agaagccgtc ccgagttcag gcttcatgaa gcggaggtca aaccaatcga cagggagaag 180

gtaccggggc aggtgcggga aaaaggaaaa gttttgcaga ttgacggaga aaccctgctg 240

aaaaatcccg aattgttgtc ccgcgcgatg tattccgcag tggtctcaaa caatattgcc 300

ggtatccgcg ttattttgcc gatttaccta caacaggcgc agcaggataa gatgttggca 360

ctttatgcac aagggatttt ggcgcaggca gacggtaggg tgaaggaggc gatttcccat 420

taccgggaat tgattgccgc ccaacccgac gcgcccgccg tccgtatgcg tttggcggcg 480

gcattgtttg aaaacaggca gaacgaggcg gcggcagacc agttcgaccg cctgaaggcg 540

gaaaacctgc cgccgcagct gatggagcag gtcgagctgt accgcaaggc attgcgcgaa 600

cgcgatgcgt ggaaggtaaa tggcggcttc agcgtcaccc gcgaacacaa tatcaaccaa 660

gccccgaaac ggcagcagta cggcaaatgg actttcccga aacaggtgga cggcacggcg 720

gtcaattacc ggctcggcgc ggagaaaaaa tggtcgctga aaaacggctg gtacacgacg 780

gctggcggcg acgtgtccgg cagggtttat ccggggaata agaaattcaa cgatatgacg 840

gcaggcgttt ccggcggcat cggttttgcc gaccggcgca aagatgccgg gctggcagtg 900

ttccacgaac gccgcaccta cggcaacgac gcttattctt acaccaacgg cgcacgcctt 960

tatttcaacc gttggcaaac cccgaaatgg caaacgttgt cttcggcgga gtgggggcgt 1020

ttgaagaata cgcgccgggc gcgttccgac aatacccatt tgcaaatttc caattcgctg 1080

gtgttttacc ggaatgcgcg ccaatattgg atgggcggtt tggattttta ccgcgagcgc 1140

aaccccgccg accggggcga caatttcaac cgttacggcc tgcgctttgc ctgggggcag 1200

gaatggggcg gcagcggcct gtcttcgctg ttgcgcctcg gcgcggcgaa acggcattat 1260

gaaaaacccg gctttttcag cggttttaaa ggggaaaggc gcagggataa agaattgaac 1320

acatccttga gcctttggca ccgggcattg catttcaaag gcatcacgcc gcgcctgacg 1380

ttgtcgcacc gcgaaacgcg gagtaacgat gtgttcaacg aatacgagaa aaatcgggcg 1440

tttgtcgagt ttaataaaac gttctga 1467

<210> 1184

<211> 488

<212> PRT

<213> N. meningitidis B16B6 SLAM 1

<400> 1184

Met Val Ile Phe Tyr Phe Cys Gly Lys Thr Phe Met Pro Ala Arg Asn
1 5 10 15
Arg Trp Met Leu Leu Leu Pro Leu Leu Ala Ser Ala Ala Tyr Ala Glu

20 25 30
Glu Thr Pro Arg Glu Pro Asp Leu Arg Ser Arg Pro Glu Phe Arg Leu
35 40 45
His Glu Ala Glu Val Lys Pro Ile Asp Arg Glu Lys Val Pro Gly Gln
50 55 60
Val Arg Glu Lys Gly Lys Val Leu Gln Ile Asp Gly Glu Thr Leu Leu
65 70 75 80
Lys Asn Pro Glu Leu Leu Ser Arg Ala Met Tyr Ser Ala Val Val Ser

85 90 95
Asn Asn Ile Ala Gly Ile Arg Val Ile Leu Pro Ile Tyr Leu Gln Gln
100 105 110
Ala Gln Gln Asp Lys Met Leu Ala Leu Tyr Ala Gln Gly Ile Leu Ala
115 120 125
Gln Ala Asp Gly Arg Val Lys Glu Ala Ile Ser His Tyr Arg Glu Leu
130 135 140
Ile Ala Ala Gln Pro Asp Ala Pro Ala Val Arg Met Arg Leu Ala Ala

145 150 155 160
Ala Leu Phe Glu Asn Arg Gln Asn Glu Ala Ala Ala Asp Gln Phe Asp
165 170 175
Arg Leu Lys Ala Glu Asn Leu Pro Pro Gln Leu Met Glu Gln Val Glu
180 185 190
Leu Tyr Arg Lys Ala Leu Arg Glu Arg Asp Ala Trp Lys Val Asn Gly
195 200 205
Gly Phe Ser Val Thr Arg Glu His Asn Ile Asn Gln Ala Pro Lys Arg

210 215 220
Gln Gln Tyr Gly Lys Trp Thr Phe Pro Lys Gln Val Asp Gly Thr Ala
225 230 235 240
Val Asn Tyr Arg Leu Gly Ala Glu Lys Lys Trp Ser Leu Lys Asn Gly

245 250 255

Trp Tyr Thr Thr Ala Gly Gly Asp Val Ser Gly Arg Val Tyr Pro Gly

260 265 270

Asn Lys Lys Phe Asn Asp Met Thr Ala Gly Val Ser Gly Gly Ile Gly

275 280 285

Phe Ala Asp Arg Arg Lys Asp Ala Gly Leu Ala Val Phe His Glu Arg

290 295 300

Arg Thr Tyr Gly Asn Asp Ala Tyr Ser Tyr Thr Asn Gly Ala Arg Leu

305 310 315 320

Tyr Phe Asn Arg Trp Gln Thr Pro Lys Trp Gln Thr Leu Ser Ser Ala

325 330 335

Glu Trp Gly Arg Leu Lys Asn Thr Arg Arg Ala Arg Ser Asp Asn Thr

340 345 350

His Leu Gln Ile Ser Asn Ser Leu Val Phe Tyr Arg Asn Ala Arg Gln

355 360 365

Tyr Trp Met Gly Gly Leu Asp Phe Tyr Arg Glu Arg Asn Pro Ala Asp

370 375 380

Arg Gly Asp Asn Phe Asn Arg Tyr Gly Leu Arg Phe Ala Trp Gly Gln

385 390 395 400

Glu Trp Gly Gly Ser Gly Leu Ser Ser Leu Leu Arg Leu Gly Ala Ala

405 410 415

Lys Arg His Tyr Glu Lys Pro Gly Phe Phe Ser Gly Phe Lys Gly Glu

420 425 430

Arg Arg Arg Asp Lys Glu Leu Asn Thr Ser Leu Ser Leu Trp His Arg

435 440 445

Ala Leu His Phe Lys Gly Ile Thr Pro Arg Leu Thr Leu Ser His Arg

450 455 460

Glu Thr Arg Ser Asn Asp Val Phe Asn Glu Tyr Glu Lys Asn Arg Ala

465 470 475 480

Phe Val Glu Phe Asn Lys Thr Phe

485