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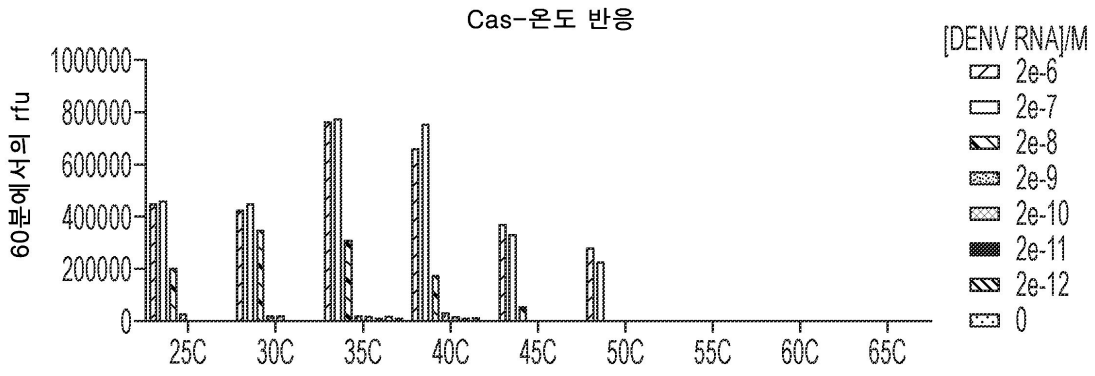
(54) 발명의 명칭 **개선된 검출 검정**

(57) 요 약

본 개시내용은 Cas 단백질 부수적 절단 활성을 이용하는 개선된 검출 (예를 들어, 진단) 검정을 제공한다.

대 표 도



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명 세 서

청구범위

청구항 1

검출 방법으로서,

적어도 60-65℃ 초과의 온도에서 열안정성인 부수적(collateral) 절단 활성을 갖는 Cas 단백질; 및

표적 서열에 상보적으로 선택되거나 조작된 가이드 RNA를 포함하는 CRISPR-Cas 복합체를,

상기 표적 서열의 핵산을 잠재적으로 포함하는 샘플과 접촉시키는 단계를 포함하는, 검출 방법.

청구항 2

제1항에 있어서, 상기 접촉시키는 단계는 상기 CRISRP-Cas 복합체와 샘플을 상기 Cas 단백질 부수적 활성에 의해 절단되기 쉬운 리포터와 접촉시키는 것을 포함하는, 방법.

청구항 3

제1항 또는 제2항에 있어서, 상기 접촉시키는 단계는 상기 온도 초과의 일정 기간 동안 인큐베이션하는 것을 포함하는, 방법.

청구항 4

제1항 내지 제3항 중 어느 한 항에 있어서, 상기 샘플에 존재하는 핵산을 증폭시키는 단계를 추가로 포함하는, 방법.

청구항 5

제4항에 있어서, 상기 증폭시키는 단계는 열안정성 핵산 중합효소를 이용하는, 방법.

청구항 6

제4항 또는 제5항에 있어서, 상기 증폭시키는 단계 및 접촉시키는 단계는 단일 용기에서 수행되는, 방법.

청구항 7

제1항에 있어서, 상기 Cas 단백질은 Cas12 단백질인, 방법.

청구항 8

제7항에 있어서, 상기 Cas 단백질은 서열번호 15의 것과 적어도 80% 동일한 아미노산 서열을 갖는, 방법.

청구항 9

제7항에 있어서, 상기 Cas 단백질은 서열번호 3-21, 33-47, 51-56, 68-178, 및 274-283 중 어느 하나와 적어도 80% 서열 동일성을 갖는 아미노산 서열을 갖는, 방법.

청구항 10

제1항에 있어서, 상기 Cas 단백질은 서열번호 1-283 중 어느 하나와 80% 서열 동일성을 갖는 아미노산 서열을 갖는, 방법.

청구항 11

부수적 절단 활성을 갖는 Cas 단백질을 이용하여 검출 검정을 수행하는 방법에서, 열안정성 부수적 절단 활성을 갖는 Cas 단백질을 이용하는 것을 포함하는, 개선.

청구항 12

제11항에 있어서, 상기 Cas 단백질은 Cas12 단백질인, 개선.

청구항 13

제12항에 있어서, 상기 Cas 단백질은 서열번호 15의 것과 적어도 80% 동일한 아미노산서열을 갖는, 개선.

청구항 14

제12항에 있어서, 상기 Cas 단백질은 서열번호 3-21, 33-47, 51-56, 68-178, 및 274-283 중 어느 하나와 적어도 80% 서열 동일성을 갖는 아미노산 서열을 갖는, 개선.

청구항 15

제11항에 있어서, 검출 검정을 수행하는 방법은 단일 반응 용기에서 수행되는, 개선.

청구항 16

제11항에 있어서, 상기 열안정성 부수적 절단 활성은 약 60℃의 온도 초과에서 열안정성인, 개선.

청구항 17

제11항에 있어서, 상기 열안정성 부수적 절단 활성은 약 65℃의 온도 초과에서 열안정성인, 개선.

청구항 18

제11항에 있어서, 상기 Cas 단백질은 서열번호 1-283 중 어느 하나와 적어도 80% 서열 동일성을 갖는 아미노산 서열을 갖는, 개선.

발명의 설명

기 술 분 야

[0001] 관련 출원에 대한 상호 참조

[0002] 본 출원은 2020년 1월 27일에 출원된 미국 가특허 출원 번호 제62/966,527호; 2020년 1월 29일에 출원된 제62/967,536호; 2020년 2월 4일에 출원된 제62/970,159호; 2020년 6월 12일에 출원된 제63/038,710호; 2021년 1월 19일에 출원된 제63/139,267호 각각의 우선권을 주장하며, 이들 각각의 전체 내용은 본원에 참조로 포함된다.

배 경 기 술

[0003] 다양한 클러스터링된 규칙적으로 간격을 띤 짧은 회문 반복부-CRISPR-연관 ("Cas") 단백질이 특정 관심 핵산을 검출하기 위한 검출 (예를 들어, 진단) 시스템에 유용한 부수적 절단 활성을 갖는 것으로 밝혀졌다. 예를 들어, Sashital *Genome Med* 2018:10, 32의 리뷰를 참조한다.

발명의 내용

[0004] 본 개시내용은 Cas-단백질 부수적 활성을 이용하는 개선된 검출 (예를 들어, 진단) 기술을 제공한다.

[0005] 무엇보다도, 본 개시내용은 특정 부수적 활성 검정에서 특정 Cas 효소의 사용과 관련된 문제의 근원을 확인한다. 예를 들어, 본 개시내용은 이러한 특정 검정이 일정 기간 동안 상승된 온도에서 인큐베이션을 수반하는 단계를 포함하고 다양한 Cas 효소가 그러한 조건 하에서 충분한 수준의 활성 (예를 들어, 부수적 활성)을 유지하기에 불충분하게 안정할 수 있음을 보여준다. 많은 구현예에서, 이러한 단계는 핵산 연장 및/또는 증폭 단계이거나 이를 포함할 수 있다.

[0006] 대안적으로 또는 추가적으로, 본 개시내용은 다양한 부수적 활성 검정의 특히 바람직한 구현예가 단일 반응 용기 (즉, 소위 "원 포트 (one pot)") 검정에서 수행될 수 있을 것이라는 통찰력을 제공한다. 본 개시내용은 그의 활성 (예를 들어, 부수적 절단 활성)이 임의의 모든 상승된 온도 단계(들) (예를 들어 하나 이상의 핵산 연장 및/또는 증폭 단계(들)이거나 이를 포함할 수 있음)를 통해 충분한 활성을 유지하기에 불충분하게 안정한 Cas 효소가 이러한 원-포트 검정에 유용하지 않을 수 있음을 인식한다. 본 개시내용은 또한 특정 Cas 단백질(들)

(예를 들어, Cas13 및 Cas12)이 관련 온도(들), 예를 들어 핵산 연장 및/또는 증폭 반응이 전형적으로 수행되는 온도 (예를 들어 약 60-65℃ 이상) 에서 불충분하게 안정함을 보여준다.

[0007] 본 개시내용은 다양한 Cas 단백질 (예를 들어, Cas9)의 열안정성 변이체가 이미 기술되어 있고/있거나 그렇지 않으면 공개적으로 이용 가능하게 된 인식을 포함한다 (예를 들어, Mougiakos 등 *Nat Commun.* 8:1647, 2017 참조). 당업자는 열안정성을 달성하기 위해 필요하고/하거나 충분할 수 있는 서열 변화 및/또는 요소를 평가하기 위하여 이러한 열안정성 변이체를 관련된 비-열안정성 상동체 (homolog) (예를 들어, 이종상동체 (ortholog))와 비교할 수 있고, 또한 다른 상동체 (예를 들어, 이종상동체)에서 이러한 서열 변화 및/또는 요소를 식별할 수 있고/있거나 이들을 그 안에 도입할 수 있다. 더 나아가, 당업자는 자연적으로 발생하는 열안정성 Cas 단백질의 잠재적인 공급원 (예를 들어, 열수구 (sea vent)에서와 같은 상승된 온도 조건에서 생존하거나 그렇지 않으면 호열성인 미생물에서)을 잘 알고 있다. 따라서, 본 개시내용을 읽는 당업자는 본원에 기술된 바와 같이 사용하기 위한 적절한 열안정성 Cas 단백질을 용이하게 식별하고/하거나 개발할 수 있다.

[0008] 일부 구현예에서, 유용한 열안정성 Cas 단백질은 Cas12 또는 Cas13 상동체 (예를 들어, 이종상동체)이다. 일부 구현예에서, 유용한 열안정성 Cas 단백질은 서열번호 1-283 중 어느 하나와 80%, 85%, 90%, 99% 또는 100% 서열 동일성을 갖는 아미노산 서열을 포함하는 Cas 효소이다.

[0009] 대안적으로 또는 추가적으로, 일부 구현예에서, 유용한 열안정성 Cas 단백질은 약 50℃ 이상의 온도; 일부 구현예에서, 약 55℃, 약 56℃, 약 57℃, 약 58℃, 약 59℃, 약 60℃, 약 61℃, 약 62℃, 약 63℃, 약 64℃, 약 65℃, 약 66℃, 약 67℃, 약 68℃, 약 69℃, 약 70℃, 약 71℃, 약 72℃, 약 73℃, 약 74℃, 약 75℃, 약 76℃, 약 77℃, 약 78℃, 약 79℃, 약 80℃, 약 81℃, 약 82℃, 약 83℃, 약 84℃, 약 85℃, 약 86℃, 약 87℃, 약 88℃, 약 89℃, 약 90℃, 약 91℃, 약 92℃, 약 93℃, 약 94℃, 약 95℃, 약 96℃, 약 97℃, 약 98℃, 약 99℃, 약 100℃, 또는 이들의 조합으로 이루어진 군으로부터 선택된 온도 이상에서 수행한다 (예를 들어, 그의 부수적 절단 활성이 충분히 기능한다). 많은 구현예에서, 유용한 열안정성 Cas 단백질은 60℃이상의 온도에서 수행한다 (예를 들어, 그의 부수적 절단 활성이 충분히 기능한다).

[0010] 일부 구현예에서, 유용한 열안정성 Cas 단백질은 핵산 연장 및/또는 증폭 반응(들)이 수행되는 온도 범위 내에서 수행하고 (예를 들어, 그의 부수적 절단 활성이 충분이 기능함); 당업자는 이러한 다양한 반응 및 이들이 수행되는 온도 범위에 대해 잘 알고 있으며, 일부 구현예에서 이러한 온도 범위는 약 60℃, 약 61℃, 약 62℃, 약 63℃, 약 64℃,65℃, 약 66℃, 약 67℃, 약 68℃, 약 69℃, 약 70℃, 약 71℃, 약 72℃, 약 73℃, 약 74℃, 약 75℃, 약 76℃, 약 77℃, 약 78℃, 약 79℃, 약 80℃, 약 81℃, 약 82℃, 약 83℃, 약 84℃, 약 85℃, 약 86℃, 약 87℃, 약 88℃, 약 89℃, 약 90℃, 약 91℃, 약 92℃, 약 93℃, 약 94℃, 약 95℃, 약 96℃, 약 97℃, 약 98℃, 약 99℃, 약 100℃, 또는 이들의 조합으로 이루어진 군으로부터 선택된 온도 이상일 수 있다. 일부 구현예에서, 온도 범위는 약 60℃ 내지 약 90℃일 수 있다. 일부 구현예에서, 온도 범위는 약 60℃ 내지 약 80℃일 수 있다. 일부 구현예에서, 온도 범위는 약 60℃ 내지 약 75℃일 수 있다. 일부 구현예에서, 온도 범위는 약 65℃ 내지 약 90℃일 수 있다. 일부 구현예에서, 온도 범위는 약 60℃ 내지 약 80℃일 수 있다. 일부 구현예에서, 온도 범위는 약 60℃ 내지 약 75℃일 수 있다.

[0011] 따라서, 본원에 제시된 바와 같이, 일부 구현예에서, 유용한 열안정성 Cas 단백질은 Cas12 또는 Cas13 상동체 (예를 들어, 이종상동체), 예를 들어 약 50℃이상의 온도, 및 일부 구현예에서 약 60℃ 이상의 온도, 예를 들어 약 60-65℃ 이내 및/또는 이상의 온도에서 열안정성인, 서열번호 1-283 중 어느 하나와 80%, 85%, 90%, 99% 또는 100% 서열 동일성을 갖는 아미노산 서열을 포함하는 Cas 효소이다. 본 개시내용을 읽는 당업자는 일부 구현예에서 그의 활성 (예를 들어, 그의 표적 결합 및 부수적 절단 활성)이 예를 들어 본원에 기술된 바와 같은 검정 (예를 들어, 일부 구현예에서, 원-포트 검정)에서 수행하기 위해 60-65℃ 범위 내의 온도에서 충분히 열안정적인 유용한 열안정성 Cas 단백질이 Cas12 (예를 들어, 적어도 90%, 95%, 99% 또는 그 이상의 아미노산 서열 동일성을 갖는 서열번호 3-21, 33-47, 51-56, 68-178, 및 274-283, 또는 이의 변이체) 또는 Cas13 (예를 들어, 적어도 90%, 95%, 99% 또는 그 이상의 아미노산 서열 동일성을 갖는 서열번호 1-2, 22-32, 48-50, 57-67, 179-273, 또는 이의 변이체)임을 특히 이해할 것이다. 예를 들어, 일부 구현예에서, 충분한 열안정성 활성은 본원에 기술된 바와 같은 적절한 참조 열안정성 Cas 단백질 (예를 들어, 서열번호 15)과 상당히 비슷한 (예를 들어, 약 25% 이내) 활성이다.

[0012] 일부 구현예에서, 본 개시내용은 적어도 60-65℃ 이상의 온도에서 열안정성인 부수적 절단 활성을 갖는 Cas 단백질; 및 표적 서열에 상보적으로 선택되거나 조작된 가이드 RNA를 포함하는 CRISPR-Cas 복합체를 상기 표적 서열의 핵산을 잠재적으로 포함하는 샘플과 접촉시키는 단계를 포함하는 검출 방법을 기술한다.

[0013] 일부 구현예에서, 상기 접촉시키는 단계는 상기 CRISRP-Cas 복합체 및 샘플을 상기 Cas 단백질 부수적 활성에 의해 절단되기 쉬운 리포터와 접촉시키는 것을 포함한다. 일부 구현예에서, 상기 접촉시키는 단계는 상기 온도 이상의 일정 기간 동안 인큐베이션하는 것을 포함한다. 일부 구현예에서, 검출 방법은 상기 샘플에 존재하는 핵산을 증폭시키는 단계를 추가로 포함한다. 일부 구현예에서, 상기 증폭시키는 단계는 열안정성 핵산 중합효소를 이용한다. 일부 구현예에서, 상기 증폭시키는 단계 및 접촉시키는 단계는 단일 용기에서 수행된다.

[0014] 일부 구현예에서, 상기 Cas 단백질은 Cas12 단백질이다. 일부 구현예에서, 상기 Cas 단백질은 서열번호 15의 것과 적어도 80% 동일한 아미노산 서열을 갖는다. 일부 구현예에서, 상기 Cas 단백질은 서열번호 3-21, 33-47, 51-56, 68-178, 및 274-283 중 어느 하나와 적어도 80% 서열 동일성을 갖는 아미노산 서열을 갖는다. 일부 구현예에서, 상기 Cas 단백질은 서열번호 1-283 중 어느 하나와 80% 서열 동일성을 갖는 아미노산 서열을 갖는다.

[0015] 일부 구현예에서, 부수적 절단 활성을 갖는 Cas 단백질을 이용하여 검출 검정을 수행하는 방법에서, 개선은 열안정성 부수적 절단 활성을 갖는 Cas 단백질을 이용하는 것을 포함한다. 일부 구현예에서, 상기 Cas 단백질은 Cas12 단백질이다. 일부 구현예에서, 상기 Cas 단백질은 서열번호 15의 것과 적어도 80% 동일한 아미노산 서열을 갖는다. 일부 구현예에서, 상기 Cas 단백질은 서열번호 3-21, 33-47, 51-56, 68-178, 및 274-283 중 어느 하나와 적어도 80% 서열 동일성을 갖는 아미노산 서열을 갖는다. 일부 구현예에서, 검출 검정을 수행하는 방법은 단일 반응 용기에서 실시된다. 일부 구현예에서, 상기 열안정성 부수적 절단 활성은 약 60℃의 온도 이상에서 열안정성이다. 일부 구현예에서, 상기 열안정성 부수적 절단 활성은 약 65℃의 온도 이상에서 열안정성이다. 일부 구현예에서, 상기 Cas 단백질은 서열번호 1-283 중 어느 하나와 적어도 80% 서열 동일성을 갖는 아미노산 서열을 갖는다.

도면의 간단한 설명

[0016] 도 1a 및 1b는 특정 Cas13 단백질(들)이 관련 온도(들), 예를 들어 핵산 연장 및/또는 증폭 반응이 전형적으로 수행되는 온도 (예를 들어, 약 60-65℃ 이상)에서 불충분하게 안정하다는 본 개시내용에 의해 제공된 통찰력을 보여준다.

도 2는 특정 Cas12 단백질(들)이 관련 온도(들), 예를 들어 핵산 연장 및/또는 증폭 반응이 전형적으로 수행되는 온도 (예를 들어, 약 60-65℃ 이상)에서 불충분하게 안정하다는 본 개시내용에 의해 제공된 통찰력을 보여준다.

도 3a 내지 3c는 TccCas13 부수적 활성의 열안정성을 확인하고 추가로 입증한다.

도 4는 열안정성 Cas 효소 후보 (예를 들어, Cas12 및 Cas 13 효소)의 발견 및 스크리닝을 위한 예시적인 방법을 나타낸다.

도 5는 엔드포인트 검정에 의한 Cas12a 후보 효소의 예시적인 평가를 나타낸다.

도 6는 동역학 검정에 의한 Cas12a 후보 효소의 예시적인 평가를 나타낸다.

도 7은 58℃에서 엔드포인트 및 동역학 검정에 의한 후보 효소의 예시적인 평가를 나타낸다.

도 8은 60℃ 엔드포인트 및 동역학 검정에 의한 후보 효소의 예시적인 평가를 나타낸다.

도 9는 62℃에서 엔드포인트 및 동역학 검정에 의한 후보 효소의 예시적인 평가를 나타낸다.

도 10은 정제되고 다양한 온도 (예를 들어, 대략 35℃ 내지 대략 65℃)에서 활성이 측정된 4개의 후보 효소의 예시적인 평가를 나타낸다.

도 11은 58℃ 및 70℃ 둘 다에서 주형이 없는 대조군과 비교하여 3개의 상이한 가이드 및 표적 세트를 사용한 효소 후보의 서브세트의 예시적인 특성 분석을 나타낸다.

도 12는 52℃ 및 58℃ 둘 다에서 다중 가이드/표적 쌍을 갖는 Cas12 후보 효소의 예시적인 특성 분석을 나타낸다.

도 13은 52℃에서 활성을 보여주는 Cas12a 효소 후보인 RS62에 대한 동역학 검정을 보여준다.

도 14는 37℃ 및 52℃ 둘 다에서 엔드포인트 검정에 의한 Cas13 후보 효소의 특성 분석을 나타낸다.

도 15는 예시적인 열안정성 Cas12a 효소인 RS9가 증폭을 위해 열안정성 무기 피로포스파타제 (Thermostable Inorganic Pyrophosphatase, TIPP)를 필요로 함을 나타낸다. ORF1ab 증폭의 실시간 검출은 TIPP의 유무에 따라

ORF1ab의 시작 농도 범위 (4.5 카피/μL 내지 4,500 카피/μL에 걸쳐 완료되었다.

도 16은 예시적인 열안정성 Cas12a 효소인 RS9가 그의 표적에 특이적이며 증폭을 위해 TIPP를 필요로 함을 입증한다. 증폭은 4,500 카피/μL ORF1ab 주형의 시작 농도와 ORF1ab에 특이적인 프라이머 및 가이드 또는 ORF1ab 가이드가 있는 비-표적화 프라이머로 실시되었다. 각 반응 조건 또한 TIPP 유무에 따라 실시되었다.

도 17은 예시적인 열안정성 Cas12a 효소인 RS9가 부수적 절단 활성을 나타냄을 입증한다.

도 18은 공지된 Cas12a인 LbaCas12a와 비교하여 RS9 부수적 절단 활성을 입증한다.

도 19는 예시적인 열안정성 Cas13a 효소인 TccCas13a의 특성 분석을 입증한다. TccCas13a 활성을 위한 최적 온도는 온도 범위에 걸친 Cas 반응을 사용하여 결정되었다. 온도 프로파일은 TccCas13a이 대략 62℃에서 가장 높은 활성을 보임을 시사한다.

도 20은 TccCas13a가 RNA에 의해 활성화될 수 있지만 가장 높은 농도의 ssDNA에서도 ssDNA에 의해 활성화될 수 없음을 입증한다.

도 21은 TccCas13a 활성화가 LwaCas13 ssDNA 활성화에 대해 관찰된 것과 유사한 RNA보다 더 높은 농도의 ssDNA를 필요로 함을 나타낸다. TccCas13a는 대조군과 비교하여 임의의 농도 (10 nM, 100 nM, 또는 1,000 nM)에서 ssDNA*에 의해 활성화되지 않았다.

도 22는 TccCas13a가 "UU" 부위와 비교하여 "NN" 부위에서 증가된 부수적 활성을 보이는 반면, LwaCas13a는 "UU" 부위와 비교하여 "NN" 부위의 부수적 활성에 대한 선호도를 보이지 않음을 입증한다.

도 23은 후보 열안정성 Cas 효소인 Pal1, Pal2 저 MW, Pal2 고 MW, 및 Pal3의 예시적인 특성 분석을 입증한다.

도 24는 56℃에서 예시적인 Pal1 및 Pal2 활성을 입증한다.

도 25 상이한 예시적인 가이드를 사용하여 37℃, 56℃, 및 70℃에서 Pal1의 예시적인 활성을 입증한다.

도 26은 대조군과 비교하여 56℃ 및 70℃에서 Pal1의 예시적인 활성을 입증한다. 이들 데이터는 Pal1의 활성이 표적 DNA에 특이적임을 시사한다.

도 27은 Pal1의 예시적인 온도 프로파일을 입증한다.

도 28은 상이한 예시적인 가이드를 사용하여 37℃, 56℃, 및 70℃에서 Pal2 고 MW의 예시적인 활성을 입증한다.

도 29는 대조군과 비교하여 56℃에서 Pal2 고 MW의 예시적인 활성을 입증한다. 이들 데이터는 Pal2 고 MW의 활성이 표적 DNA에 특이적임을 시사한다.

도 30은 Pal2 고 MW의 예시적인 온도 프로파일을 입증한다.

발명을 실시하기 위한 구체적인 내용

[0017] 부수적 활성 검정

[0018] 당업자는 Cas 단백질 부수적 활성을 사용하여 개발되었고 개발되고 있는 유용한 검출 (예를 들어, 진단) 검정이 급증하고 있음을 잘 알고 있다. 예를 들어, Sashital *Genome Med* 2018:10, 32를 참조한다. 또한, 당업자는 Cas 단백질 부수적 활성에 기초한 "CRISPR/Cas 바이오센싱 시스템의 상세한 분류"가 최근 공개적으로 이용 가능하게 되었다는 것을 잘 알고 있다. Li 등 *Trends Biotechnol.* 37:730, July 2019의 리뷰를 참조한다.

[0019] 특히 관심 있는 포맷은 "SHERLOCK" 및/또는 "HUDSON" 시스템 (예를 들어, Gootenberg 등, *Science* 356:438, 2017; Gootenberg 등, *Science* 360:339, 2018; Myhrvold 등, *Science* 360:444, 2018 참조; 또한 US10266887 참조)으로 참조되는 것을 포함한 Cas13-기반 (예를 들어, Cas13a- 또는 Cas13b-기반) 시스템 및 "HOLMES" 또는 "DETECTR" 시스템 (예를 들어, Cheng 등 CN patent filing CN107488710A; PCT/CN18/82769 및 US 16/631,157; Li 등 *Cell Disc.* 4:20, 2018; Chen 등 *Science* 360:436, 2018; Li, L. 등 bioRxiv Published online July 26, 2018. http://dx. doi.org/10.1101/362889; US10253365 참조)으로 참조되는 것을 포함한 Cas12-기반 (예를 들어, Cas12a- 또는 Cas12b-기반) 시스템을 포함한다. Cas13a 및 Cas13b 효소 둘 다; Cas12a 및 Cas12b 둘 다 유사하게 SHERLOCK 및/또는 HUDSON 시스템에서 사용되었다.

[0020] 당업계에 공지되어 있고 본원에 인용된 참고문헌에 기술된 바와 같이, Cas 단백질 부수적 절단 활성을 이용하는 전형적인 검출 검정은 부수적 활성을 갖는 Cas 단백질 및 관심 표적 서열에 상보적인 가이드 RNA를 포함한 적절

한 CRISPR-Cas 복합체를 표적 서열을 함유할 수 있는 샘플과 접촉시키는 것을 수반한다. 표적 서열을 인식하면, Cas 단백질의 부수적 활성이 활성화되어 관련이 없는 핵산 (효소에 따라 DNA 또는 RNA 또는 둘 다)을 절단한다. 관련 절단 가능한 핵산의 리포터가 제공되고, 활성화된 부수적 활성의 결과로서 그의 절단이 검출 가능하도록 (예를 들어, 형광이 검출 가능하게 되도록 소광제로부터 형광단을 분리하는 등) 적절하게 구성 (예를 들어, 표지) 된다.

[0021] 많은 검정에서, 표적 서열이 생성되고/되거나 증폭 (예를 들어, RNA에서 DNA로 복사 및/또는 예를 들어 프라이머 연장, DNA 복제 (예를 들어, 중합효소 연쇄 반응에 의한) 및/또는 전사에 의해 증폭) 된다. 예를 들어, 위에서 언급한 Li 리뷰 (Li 등 *Trends Biotechnol.* 37:730, July 2019)의 도 3 및 도 4를 참조한다.

[0022] 따라서, 많은 실시예에서, 부수적 활성 검정은 (1) 표적 복사 및/또는 증폭; (2) 표적 결합; 및 (3) 신호 방출 및/또는 검출 단계를 포함한다.

[0023] 전형적으로, 본원에 기술한 바와 같은 부수적 활성 검정은 *시험관내* 검정이다. 일부 구현예에서, 이들은 무세포 검정일 수 있다 (예를 들어, 무손상 세포, 또는 일부 구현예에서 세포 단편이 실질적으로 없을 수 있음).

[0024] 일부 구현예에서, 본원에 기술한 바와 같은 부수적 활성 검정은 생물학적 (예를 들어, 혈액, 타액, 눈물, 소변 등) 또는 환경적 (예를 들어, 토양, 물 등) 1차 샘플이거나 이로부터 제조된 샘플에 대해 수행된다.

[0025] 열안정성 Cas 효소

[0026] 본원에 기술된 바와 같이, 본 개시내용은 부수적 활성을 갖는 특정 Cas 단백질이 관련 온도 (예를 들어, 핵산 연장 및/또는 증폭이 수행되는 온도)에서 불충분하게 안정하다는 점에서, 상기 기술된 바와 같이 Cas 단백질 부수적 활성을 이용하는 특정 검출 (예를 들어, 진단 검정)과 관련된 문제의 근원을 확인한다. 추가적으로, 본 개시내용은 놀랍게도 일부 단백질의 경우 온도 상승 시 활성 손실이 비가역적일 수 있음을 추가로 입증한다. 이러한 현실은 열안정성 부수적 활성을 갖는 Cas 단백질이 본원에 기술된 검정에 사용하기에 특히 바람직하다는 본 개시내용에 의해 제공되는 통찰력의 중요성을 증가시킨다. 도 1 및 2는 이들 결과를 보여준다.

[0027] 따라서, 본 개시내용은 Cas 단백질 부수적 활성을 이용하는 개선된 검출 (예를 들어, 진단) 검정을 제공하며, 개선된 검정은 본원에 기술된 바와 같은 열안정성 Cas 단백질 (예를 들어, 그의 부수적 활성이 열안정성임)을 이용한다.

[0028] 일부 구현예에서, 핵산 검출 및 표적 결합 단계는 단일 용기에서 수행되고; 일부 구현예에서, 표적 결합 신호 방출 단계는 단일 용기에서 수행되고; 일부 구현예에서, (1) 표적 복사 및/또는 증폭; (2) 표적 결합; 및 (3) 신호 방출 및/또는 검출 단계의 단계는 단일 용기에서 수행되고; 일부 구현예에서 모든 단계는 단일 용기에서 수행되고 - 즉, 개선된 검정이 원-포트 검정인 경우 제공된다.

[0029] 일부 구현예에서, 본원에 기술된 바와 같은 개선된 부수적 활성 검정은 *시험관내* 검정이다. 일부 구현예에서, 이들은 무세포 검정일 수 있다 (예를 들어, 무손상 세포, 또는 일부 구현예에서 세포 단편이 실질적으로 없을 수 있음).

[0030] 일부 구현예에서, 본원에 기술된 바와 같은 개선된 부수적 활성 검정은 생물학적 (예를 들어, 혈액, 타액, 눈물, 소변 등) 또는 환경적 (예를 들어, 토양, 물 등) 1차 샘플이거나 이로부터 제조된 시료에 대해 수행된다.

[0031] 일부 구현예에서, 열안정성 부수적 절단 활성을 갖는 Cas 효소는 입증 가능한 부수적 절단 활성을 갖지 않거나 입증 가능한 부수적 절단 활성을 갖지만, 본원에 기술된 바와 같은 관련 온도 이상에서 이러한 활성을 잃는 Cas 효소의 상동체 (예를 들어, 이종상동체)이다.

[0032] 일부 구현예에서, 본원에 기술된 바와 같은 열안정성 부수적 절단 활성을 갖는 Cas 효소는 Cas12 (예를 들어, Cas12a 또는 Cas12b) 효소이다. 일부 구현예에서, 본원에 기술된 바와 같은 열안정성 부수적 절단 활성을 갖는 Cas 효소는 Cas13 (예를 들어, Cas13a 또는 Cas13b) 효소이다.

[0033] 일부 구현예에서, 본원에 기술된 바와 같은 열안정성 부수적 절단 활성을 갖는 Cas 효소는 서열번호 1-283 중 어느 하나와 80%, 85%, 90%, 99% 또는 100% 서열 동일성을 갖는 아미노산 서열을 포함하는 Cas 효소이다. 일부 구현예에서, 본원에 기술된 바와 같은 개선된 부수적 활성 검정은 서열번호 1-283 중 어느 하나와 80%, 85%, 90%, 99% 또는 100% 서열 동일성을 갖는 아미노산 서열을 포함하는 Cas 효소를 사용하여 수행된다.

[0034] 표적 핵산

[0035] 당업자는 본원에 제공된 기술이 예를 들어 감염원 (예를 들어, 바이러스, 미생물, 기생충 등)으로부터의 핵산, 특정 병리학적 상태 또는 병태 (예를 들어, 암 또는 염증성 또는 대사성 질환, 장애 또는 병태 등과 같은 질환, 장애 또는 병태의 존재 또는 상태)를 나타내는 핵산, 산전 핵산 등을 포함한 광범위한 핵산의 검출을 달성하기 위해 광범위하게 적용 가능하다는 것을 즉시 이해할 것이다.

[0036] 일부 구현예에서, 표적 핵산은 본원에 기술된 바와 같은 Cas 효소 및 cRNA를 포함하는 검정에 의해 검출된다. 일부 구현예에서, cRNA의 구조는 Cas/cRNA 복합체의 활성에 영향을 미칠 수 있다. 일부 구현예에서 Cas/cRNA 복합체의 구조는 Cas 부수적 활성의 열안정성에 기여한다.

[0037] 전형적으로, 제공된 기술은 샘플에서 하나 이상의 표적 핵산의 존재 및/또는 수준을 평가하기 위해 하나 이상의 샘플에 적용될 것이다. 일부 구현예에서, 샘플은 생물학적 샘플이고; 일부 구현예에서, 샘플은 환경적 샘플이다. 일부 구현예에서, 샘플은 미정제 샘플 (예를 들어, 1차 샘플 또는 최소한의 처리를 거친 샘플)이다.

[0038] 일부 구현예에서, 샘플은 처리될 것이고 (예를 들어, 핵산은 1차 샘플에서 부분적으로 또는 실질적으로 단리되거나 정제될 것임); 일부 구현예에서, 최소한의 처리만 수행될 것이다 (즉, 샘플은 미정제 샘플일 것이다).

[0039] **예시**

[0040] 실시예 1: LwaCas13a에 대한 온도 프로파일

[0041] LwaCas13a의 열안정성을 테스트하였다. 간단히 말해서, 표지된 RNA 표적을 Rnase 억제제; T7 RNA 중합효소, LwaCas13a, MgCl2 및 cRNA와 함께 인큐베이션하였다. 개별 샘플을 다양한 온도에서 인큐베이션하여 부수적 활성을 결정하였다.

[0042] 도 1a는 LwaCas13a 부수적 활성에 대한 온도 프로파일을 나타낸다. 보다시피, 45℃ 초과에서는 낮은 활성이 관찰되었고; 활성은 약 55℃에서 완전히 폐지되었다.

[0043] 또한, 도 1b는 더 높은 온도에서 LwaCas13a 손실의 가역성을 테스트한 결과를 나타낸다. LwaCas13a은 65℃ ("열 펄스")에서 5분 동안 인큐베이션된 반면, 대조군 ("열 펄스 없음")은 실온에서 인큐베이션되었다. 그런 다음 두 효소의 활성을37℃에서 테스트하였다. 열 펄스 군은 활성을 보이지 않았다. 이러한 현실은 열안정성 부수적 활성을 갖는 Cas 단백질이 본원에 기술된 바와 같은 검정에 사용하기에 특히 바람직하다는 본 개시내용에 의해 제공되는 통찰력의 중요성을 증가시킨다.

[0044] 실시예 2: AsCas12a 및 Lbacas12a에 대한 온도 프로파일

[0045] AsCas12a 및 Lbacas12a의 열안정성을 테스트하였다. 간단히 말해서, 표지된 RNA 표적을 Rnase 억제제; T7 RNA 중합효소, AsCas12a 또는 Lbacas12a, MgCl2 및 cRNA와 함께 인큐베이션하였다. 개별 샘플을 다양한 온도에서 인큐베이션하여 부수적 활성을 결정하였다.

[0046] 도 2는 AsCas12a 및 LbaCas12a에 대한 온도 프로파일을 나타낸다. 보다시피, 55℃ 보다 높은 온도에서 낮은 AsCas12a 활성이 관찰되었다. AsCas12a는 ~5분 동안 60℃에서 활성 상태를 유지한다. AsCas12a는 몇 분 동안 65℃에서 <10%의 활성을 갖는다. 또한, LbaCas12a 활성은 55℃보다 높은 온도에서 상당히 감소한다.

[0047] 실시예 3: 예시적인 열안정성 Cas 후보

[0048] 본 실시예는 본원에 기술된 바와 같은 개선된 부수적 활성 검정에 사용하기 위한 특정 열안정성 Cas13 후보를 기술한다.

[0049] 본 실시예에서, 약 62- 약 68℃의 온도 범위 내에서 부수적 활성 열안정성을 갖는 Cas13이 무엇보다도 LAMP 사전-증폭을 사용한 원-포트 검정에서 특히 바람직할 것으로 결정되었다.

[0050] 본 발명자들은 잠재적으로 열안정성인 Cas 후보에 대한 컴퓨터 검색을 수행하고 다음을 식별하였다:

[0051] · 2 Cas13a 후보:

[0052] TccCas13a (*써모클로스트리디움 카이니콜라* (*Thermoclostridium caenicola*))

[0053] TccCas13a로 사용하기 위한 예시적인 서열은 다음을 포함하지만, 이에 한정되지 않는다:

[0054] Agtgtctttgcaggaaagaacacagatcttgagggtcacaactcccatgtaggcggagactgcaacccctatagtgagtcgtattaatt tc (서열번호 284) (정방향 DR crRNA); 및

[0055] agtgtctttgcaggaaagaacacagatcttgagggttgcagtctccgcctacatgggagttgtgacccctatagtgagtcgtattaat ttc (서열번호 285) (역 상보체 DR crRNA);

[0056] ThpCas13a (*탈라쏘스피라 프로푼디마리스* (*Thalassospira profundimaris*))

[0057] ThpCas13a로 사용하기 위한 예시적인 서열은 다음을 포함하지만, 이에 한정되지 않는다:

[0058] Tctttgcaggaaagaacacagatcttgaggggtgtagttcccctcaatttggggatgaacgtcgacccctatagtgagtcgtattaat ttc (서열번호 286) (정방향 DR crRNA); 및

[0059] tctttgcaggaaagaacacagatcttgagggtcgacgttcatccccaaattgaggggaactacacccctatagtgagtcgtattaa tttc (서열번호 287) (역상보체 DR crRNA);

[0060] · 4 Cas12b 후보:

[0061] · AacCas12b (*알리시클로바실러스 애시도테레스트리스* (*Alicyclobacillus acidoterrestris*))

[0062] · AkCas12b (*알리시클로바실러스 카케가웬시스* (*Alicyclobacillus kakegawensis*))

[0063] · BhCas12b (*바실러스 히사시* (*Bacillus hisashii*))

[0064] · LsCas12b (*라세엘라 세디미니스* (*Laceyella sediminis*))

[0065] AacCas12b로 사용하기 위한 예시적인 서열은 다음을 포함하지만, 이에 한정되지 않는다:

[0066] ttgtgagcggataaacacaggtgccacttctcagatttgagaagctcaacgggctttgccacctggaaagtggccattggcacaccc gttgaaaaattctgtcctctagacccctatagtgagtcgtattaatttc (서열번호 288) (crRNA)

[0067] AkCas12b로 사용하기 위한 예시적인 서열은 다음을 포함하지만, 이에 한정되지 않는다:

[0068] Ttccggctcgtatgttgtgtggaattgtgagcggagtgccacttctcagaccgctcgccctatagtgagtcgtattaatttc (서열번호 289) (crRNA); 및

[0069] cgagcggtcatcttgaagccaacggggtgtttgctcttggaaagagcacattggcacttcccgttgtcctcgccgtcctatagacgac ccctatagtgagtcgtattaatttc (서열번호 290) (tracrRNA)

[0070] BhCas12b로 사용하기 위한 예시적인 서열은 다음을 포함하지만, 이에 한정되지 않는다:

[0071] aattgtgagcggataaacacaggtgctaatgcctcccctatagtgagtcgtattaatttc (서열번호 291) (crRNA); 및

[0072] gagacatcgtccagcaataggagtttctcacaccctgcagcacttatagctagacggttgtcctgaccaaaagacagaaccccctata gtgagtcgtattaatttc (서열번호 292) (tracrRNA)

[0073] LsCas12b로 사용하기 위한 예시적인 서열은 다음을 포함하지만, 이에 한정되지 않는다:

[0074] Atggtcatagctgtttcctgtgtttatccgctcagtgctaatcacatttaattcatctaccctatagtgagtcgtattaatttc (서열번호 293) (crRNA); 및

[0075] Gataaataatgtaatcctgtggttgaatggatttttttccatccttagcacacgcacagtattctttgccctttaggcaaaccctatagtg agtcgtattaatttc (서열번호 294) (tracrRNA).

[0076] 열안정성 부수적 활성을 갖는 Cas 단백질의 예시적인 서열은 표 1에 기술된 것들을 포함한다:

[0077] 표 1: 열안정성 부수적 활성을 갖는 Cas 단백질의 예시적인 서열

서열 번호	Cas 효소	추정 서열
1	TccCas13a (써모클로스트리디움 카이니콜라)	MKITKRKWGEHHPPLYFYRDEDSGRLLAQNDRKQDYTDTLFNDIAQDTFERSLRNRLLKT PEKGDKRFYSNEIVKLVEKLCQGADVAEIMKSMERNEKLRPKNEKEIKNLKKQLDGTLSEY GKRYTAPEGAMTLNDALFYLVEGNPLKQAMAKAELGKIREALIKEKENRINRVRYSIKNNKI PLRIQEDGGITPNNDRAAWLLGLMKPADPAKGITDCYPLLGELEEVFDFDKLSKTLHEKISR CQGRPRSIAMAVDEALKQYLRELWEKSPSRQQDLKYYFQAVQEYFKDNFPIRTKRMGAR LRQELLKDKTSLSRLLEPKHMANAVRRRLINQSTQMHILYGKLYAYCCGEDGRLLVNSETL QRIQVHEAVKKQAMTAVLWSISRLRYFYQFEDGDILSNKNPIKDFRDKFLRDTNKYTHED VEACKEKLQDFFPLKELQEKIKEDAKGLQETDNKQADTTDFKAIGHIVRDDRKLCNQLLAE CVSCIGELRHHIFHYKNVTLIQALKRIADKVKPEDLSVLRAIYLLDRRNLKKAFAKRISSMNL PLYYREDLLSRIFKKEGTAFFLYSAKIQMTPSFQRVYERGKNLRREFECERMKAEASNGQN GQDGDRLKWFRQLAAGDSADTHFNWAVEAYAESAADVENNVEFDTDVDAQRALRNLL LLIYRHHFLPEVQKDETLVTGKIHKVLERNRQLSEGQGPNQGKAHGYSVIEELYHEGMPLS DLMKQLQRRISETERESRELAQEKTDYAQRFILDIFAEAFNDFLEAHYGEEYLEIMSPRKDAE AAKKWVKESKTVDLKTSIDEKEPEGHLLVLYPVLRLLDERELGELQQQMIRYRTSLASWQG ESNFSEEIRIAGQIEELTELVKLTEPEPQFAEEVWGKRAKEAFEDFIEGNMKNYEAFYLQSDN NTPVYRRNMSRLLRSGLMGVYQKVLASHKQALKRDYLLWSEKHWNVKDENGADISSAE QAQCLLQRLHRKYAESPSRFTEEDCKLYEKVLRRLEDYNQAVKNLSFSSLYEICVLNLEILSR WVGFVQDWERDMYFLLLAWVRQGKLDGIKEEDVRDIFSEGNIIRNLVDTLKGENMNAFE SVVYFPENKGSKYLGVRNDVAHLDLMRKNGWRLEAGKTCSVMEDYINRLRFLLSYDQKRM NAVTKTLQQIFDRHKVKIRFTVEKGGMLKIEDVTADKIVHLKGSRLSGIEIPSHGERFIDTLK ALMVYPRG*
2	ThpCas13a (탈라쏘스피라 프로푼디마리스)	MRIIKPYGRSHVEGVATEQPRRKLRLNTRPDISRDIPGFAQSHDALIIAQWISAIDKIATKPK PDQKPTQRQMNLRTTLGDAAWQHLMAKNLLPAAKDPAIREKLHLIWQSKIAPWGASRP QEEKRGKPTPKGGWYERFCGALSPEAITQNVARQIAKDIYDHLYVAAKRKGREPVKQGES SNKPGKFKPDRKLSLIEERAESIAKNALRPGTHAPCPWGQDDQAIYEQAGDVATKIYDDA RDYLEDKKRRSGNRNTSSVQYLPRDLAVKILYAQYGRVFGPDTTIKAALDEQQSLFALHTA IKDCYHRLVNDARKRHILRILPRNMAALFRLVRAQYDNRDINALIRLGKVIHYHAGEQGKD EHHGIRDYWPSQQDIQNSRFWGSDGQADIKRHEAFSRIWRHIIALASRTLHDWADPDS QKFTGDDDDILMRAGAIESNVWDAGRYERKCDVLFGAQASLFCGAEDFEKATLKQAITGT GNLRNATFHFKGKARFENELQRLADDVPVDVQSAIAALWQKDAEGRTRQIAETLQAVLA GHFLSERQNRHILATLMAAMAQPGDVPLPRLRRVLARHDSICQRGRILPLPPCPDRAKLEE	

[0078]

		SPALTCQYTVLKMLYDGPFRAWLAQQNSTILNHYIDSTIARTNKAAQDMNGRKLAPAEK DLITARAADIPRLSVDEKMVDFLGRLTAATATEMRVQRGYQSDGEKAQKQAGYIGEFECD VIARAFSDFLGQSGFDFVLKLKADTPKPDAAQCDVAALIAPGDVPALTPQAWQQVLYFIL HLVPVDDASRLLHQTRKWQALEKKGKDKEVKKEKDKEVKKEDEKPDIADLQSVLMLYLD MHDAKFTGGAALHGIEKFAEFFVEKADFRAVFPPQSLQDQDRSIPRRGLREIVRFGHLPLL QHMSGTVKITHDNVVAWQTARTPDATGTSPIARRQKQREELHALAVERPARFRNADLH NYMHALVDVIKHRQLSAQVTLSDQVRLHRLMMGVLGRLVDYAGLWERDLYFVLLALLY HHGVTPDDVLKGQGKRKLADGQVVEALKPKNRKAAAPVGVFDDLDHYGIYQDDRQSIR NGLSHFNMLRGGTAPDLSHWVNQTRRLVAHDRKLKNAVAKSVIEMLAREGFDLDWTIE PDSGKHILRHGKIRTRQAQHFQKSRIRIEKKSAKPDKNDTVKIRENLHGDAMVERVARLFA ARAQKYRDITTEKRLDHLFLKPKG*
3	AacCas12b (알리시클로바실러스 애시도테레스트리스)	MAVKSIKVKLRLDDMPEIRAGLWKLHKEVNAGVRYYTEWLSLLRQENLYRRSPNGDGEQ ECDKTAEECKAELLERLRARQVENGHRGPAGSDDELLQLARQLYELLVPQAIGAKGDAQQ IARKFLSPLADKDAVGGLGIAKAGNKPRWVRMREAGEPGWEEEKEKAETRKSADRTADVL RALADFGLKPLMRVYTDSEMSSVEWKPLRKGQAVRTWDRDMFQQAIERMMSWESWN QRVGQEYAKLVEQKNRFEQKNFVGQEHLVHLVNQLQQDMKEASPGLESKEQTAHYVTG RALRGSDKVFEKWGKLAPDAPFDLYDAEIKNVQRRNTRRFGSHDLFAKLAEPEYQALWRE DASFLTRYAVYNSILRKLNHAKMFATFTLPDATAHPIWTRFDKLGGNLHQYTFLFNEFGER RHAIRFHKLLKVENGVARFVDDVTVPISMSEQLDNLLPRDPNEPIALYFRDYGAEQHFTGE FGGAKIQCRRDQLAHMHRRRGARDVYLNVSVRVQSQSEARGERRPPYAAVFRLVGDNH RAFVHFDKLSDYLAEHPDDGKLGSEGLLSGLRVMSVDLGLRTSASISVFRVARKDELKPNS KGRVPFFFPIKGNDNLVAVHERSQLLKLPGETESKDLRAIREERQRTLRQLRTQLAYLRLLVR CGSEDVGRRERSWAKLIEQPVDAANHMTPDWREAFENELQKLKSLHGICSDKEWMDAV YESVRRVWRHMGKQVRDWRKDVRSGERPKIRGYAKDVVGGNSIEQIEYLERQYKFLKSW SFFGKVSGQVIRAEKGSRFAITLREHIDHAKEDRLKKLADRIIMEALGYVYALDERGKGKWV AKYPPCQLILLEELSEYQFNNDRPPSENNQLMQWSHRGVFQELINQAQVHDLLVGTMYA AFSSRFDARTGAPGIRCRRVPARCTQEHNPEPFPWWLNKFVVEHTLDACPLRADDLIPTG EGEIFVSPFSAEEGDFHQIHADLNAAQNLQQRLWSDFDISQIRLRCDWGEVDGELVLIPRL TGKRTADSYSNKVFYTNTGVTYYERERGKKRRKVFAQEKLSEEEAELLVEADEAREKSVVL MRDPSGIINRGNWTRQKEFWSMVNQRIEGYLVKQIRSRVPLQDSACENTGDI
4	AkCas12b (알리시클로바실러스 카케가웬시스)	MAVKSIKVKLRLSECPDILAGMWQLHRATNAGVRYYTEWVSLMRQEILYSRGPDGGQQC YMTAEDCQRELLRRLRNRQLHNGRQDQPGTDADLLAISRRLYEILVLQSIGKRGDAQQIA SSFLSPLVDPNSKGGRGEAKSGRKPAWQKMRDQGDPRWVAAREKYEQRKAVDPSKEIL NSLDALGLRPLFAVFTETYRSGVDWKPLGKSQGVRTWDRDMFQQALERLMSWESWNR RVGEEYARLFQQKMKFEQEHFAEQSHLVKLARALEADMRAASQGFEAKRGTAHQITRRA LRGADRVFEIWKSIPEEALFSQYDEVIRQVQAEKRRDFGSHDLFAKLAEPKYQPLWRADET FLTRYALYNGVLRDLEKARQFATFTLPDACVNPIWTRFESSQGSNLHKYEFLFDHLGPGRH AVRFQRLLVVESEGAKERDSVVVPVAPSGQLDKLVLREEEKSSVALHLHDTARPDGFMAE WAGAKLQYERSTLARKARRDKQGMRSWRRQPSMLMSAAQMLEDAKQAGDVYLNISV RVKSPSEVRGQRRPPYAALFRIDDKQRRVTVNYNKLSAYLEEHPDKQIPGAPGLLSGLRV MSVDLGLRTSASISVFRVAKKEEVEALGDGRPPHYYPIHGTDDLVAVHERSHLIQMPGETE TKQLRKLREERQAVLRPLFAQLALLRLLVRCGAADERIRTRSWQRLTKQGREFTKRLTPSW REALELELTRLEAYCGRVPDDEWSRIVDRTVIALWRRMGKQVRDWRKQVKSGAKVKVKG

[0079]

		YQLDVVGGNSLAQIDYLEQQYKFLRRWSFFARASGLVVRADRESHFAVALRQHIENAKR DRLKKLADRILMEALGYVYEASGPREGQWTAQHPPCQLIILEELSAYRFSDDRPPSENSKL MAWGHRGILEELVNQAQVHDVLVGTVYAAFSSRFDARTGAPGVRCRRVPARFVGATVD DSLPLWLTEFLDKHRLDKNLLRPDDVIPTGEGEFLVSPCGEEAARVRQVHADINAAQNLQ RRLWQNFDITELRLRCDVKMGGEGTVLVPRVNNARAKQLFGKKVLVSQDGVTFFERSQT GGKPHSEKQTDLTDKELELIAEADEARAKSVVLFRDPSGHIGKGHWIRQREFWSLVKQRIE SHTAERIRVRGVGSSLD
5	BhCas12b (바실러스 히샤시)	MATRSFILKIEPNEEVKKGLWKTHEVLNHGIAYYMNILKLIRQEAIYEHHEQDPKNPKKVSK AEIQAELWDFVLKMQKCNSFTHEVDKDEVFNILRELYEELVPSSVEKKGEANQLSNKFLYP LVDPNSQSGKGTASSGRKPRWYNLKIAGDPSWEEEKKKWEEDKKKDPLAKILGKLAEYGLI PLFIPYTDSNEPIVKEIKWMEKSRNQSVRRLDKDMFIQALERFLSWESWNLKVKEEYEKVE KEYKTLEERIKEDIQALKALEQYEKERQEQLLRDTLNTNEYRLSKRGLRGWREIIQKWLKMD ENEPSEKYLEVFKDYQRKHPREAGDYSVYEFLSKKENHFIWRNHPEYPYLYATFCEIDKKKK DAKQQATFTLADPINHPLWVRFEERSGSNLNKYRILTEQLHTEKLKKKLTVQLDRLIYPTES GGWEEKGKVDIVLLPSRQFYNQIFLDIEEKGKHAFTYKDESIKFPLKGTLGGARVQFDRDHL RRYPHKVESGNVGRIYFNMTVNIEPTESPVSKSLKIHRDDFPKVVNFKPKELTEWIKDSKGK KLKSGIESLEIGLRVMSIDLGQRQAAAASIFEVVDQKPDIEGKLFFPIKGTELYAVHRASFNIK LPGETLVKSREVLRKAREDNLKLMNQKLNFLRNVLHFQQFEDITEREKRVTKWISRQENSD VPLVYQDELIQIRELMYKPYKDWVAFLKQLHKRLEVEIGKEVKHWRKSLSDGRKGLYGISLK NIDEIDRTRKFLLRWSLRPTEPGEVRRLEPGQRFAIDQLNHLNALKEDRLKKMANTIIMHAL GYCYDVRKKKWQAKNPACQIILFEDLSNYNPYEERSRFENSKLMKWSRREIPRQVALQGE IYGLQVGEVGAQFSSRFHAKTGSPGIRCSVVTKEKLQDNRFFKNLQREGRLTLDKIAVLKEG DLYPDKGGEKFISLSKDRKCVTTHADINAAQNLQKRFWTRTHGFYKVYCKAYQVDGQTV YIPESKDQKQKIIEEFGEGYFILKDGVYEWVNAGKLKIKKGSSKQSSSELVDSDILKDSFDLAS ELKGEKLMLYRDPSGNVFPSDKWMAAGVFFGKLERILISKLTNQYSISTIEDDSSKQSM
6	LsCas12b (라세엘라 세디미니스)	MSIRSFKLKIKTKSGVNAEELRRGLWRTHQLINDGIAYYMNWLVLLRQEDLFIRNEETNEIE KRSKEEIQGELLERVHKQQQRNQWSGEVDDQTLLQTLRHLYEEIVPSVIGKSGNASLKARF FLGPLVDPNNKTTKDVSKSGPTPKWKKMKDAGDPNWVQEYEKYMAERQTLVRLEEMGL IPLFPMYTDEVGDIHWLPQASGYTRTWDRDMFQQAIERLLSWESWNRRVRERRAQFEKK THDFASRFSESDVQWMNKLREYEAQQEKSLEENAFAPNEPYALTKKALRGWERVYHSW MRLDSAASEEAYWQEVATCQTAMRGEFGDPAIYQFLAQKENHDIWRGYPERVIDFAELN HLQRELRRAKEDATFTLPDSVDHPLWVRYEAPGGTNIHGYDLVQDTKRNLTLILDKFILPD ENGSWHEVKKVPFSLAKSKQFHRQVWLQEEQKQKKREVVFYDYSTNLPHLGTLAGAKLQ WDRNFLNKRTQQQIEETGEIGKVFFNISVDVRPAVEVKNGRLQNGLGKALTVLTHPDGTK IVTGWKAEQLEKWVGESGRVSSLGLDSLSEGLRVMSIDLGQRTSATVSVFEITKEAPDNPY KFFYQLEGTELFAVHQRSFLLALPGENPPQKIKQMREIRWKERNRIKQQVDQLSAILRLHK KVNEDERIQAIDKLLQKVASWQLNEEIATAWNQALSQLYSKAKENDLQWNQAIKNAHH QLEPVVGKQISLWRKDLSTGRQGIAGLSLWSIEELEATKKLLTRWSKRSREPGVVKRIERFET FAKQIQHHINQVKENRLKQLANLIVMTALGYKYDQEQKKWIEVYPACQVVLFENLRSYRF SYERSRRENKKLMEWSHRSIPKLVQMQGELFGLQVADVYAAYSSRYHGRTGAPGIRCHA LTEADLRNETNIIHELIEAGFIKEEHRPYLQQGDLVPWSGGELFATLQKPYDNPRILTLHADI NAAQNIQKRFWHPSMWFRVNCESVMEGEIVTYVPKNKTVHKKQGKTFRFVKVEGSDVY EWAKWSKNRNKNTFSSITERKPPSSMILFRDPSGTFFKEQEWVEQKTFWGKVQSMIQAY

[0080]

		MKKTIVQRMEE
7	Cas12	MFKKKLFDDEEFISLAQNQEESNALNAFKGFTTHFKDFQENRKNMYSEDKESTAIAYRIIHE NLPVFITNNIRFEKIINELDRSNIHSIEKELKEELANNKLKDIFNIEYFQNTLTQNDITRYNTIIG GKVKADGKKVQGLNEYINLFNQHNKDKKLPLLKPLYKQILSEENSASFIVPAFEKDNEVLQ SIFDFWNKCIIDAKGPISGKKYNLLSKIQSLLQNLDKLKNNQLEEMYFENENLSTISNDVYG QWNLIRDALGNFYNSIDAKKNKKDYYSWKEIQDALVYYKQTNDEYKDIDQKAFLIYFKEM KVNDGEENTNNNIINLINERYKRIEPLLKEDRDNRKDLHQDKGKVAIIKEFLDSLKLLQNTIK LLYVDDSLDNMNYDFYNQLTDYYETLRPLNTLYNRVRNYMTRKPFSEEKFVLTFNSPTLLD GWDLNKEEANLGVILRKDNKYYLGIMNKGDNKIFKKYDEEPGDDYYEKMVYKLLPGPNR MLRKVFFSNKNIEYYKPNQDIQNLYNKGEFKKGESLNKESLHKLIDFYKNSISKNGDWSVF NFKFKKTTAYDDISQFYKDVENQGYKLFFKTIKTSYIDQLVNEGKLYLFQIYNKDFSENKKRK DESNPNLHTIYFKNLFSEDNLKNVVYKLNGKAEVFYRKKSIEYPEEIRRKGHHYNELKDKFD YPIIKDKRYSEDKFLFHVPITLNFLAKSDEKVNEMVKNYIAATNEKIHIIGIDRGERNLLYLSLI DSNGNIVKQQSLNIIELPKYQKQIDYHAKLNEKEKQRLAARQNWDVIENIKELKEGYLSQV IHQIARLMVDYKAILVMEDLNFGFKRGRFKVEKQVYQKFEKMLIDKLSYLVFKEKNLCEPG GSLRAYQLSAPFKSFKALGKQSGMIFYVPAQYTSKIDPTTGFYNFLNIDVSNLARSKETFSKF DKIVYNKKEDYFEFYCKMINFESANQLTKKSQNKANAELKEFQWILCSTHHDRFKVERKN NQINYCKINVNEELKKLLNSKGINYEKSNDLKSEILNIDESKFFKELGYLLKILVSLRYNNGKK GSEEQDFILSPVKNASGKFFCTLDNNNTLPLDADANGAYNIALKGLMIVQRVKAGGKLDL SISKDDWINFLIMNKKLPK
8	Cas12	MSNQSVFKDFTNLYELSKTLRFELKPVGKTLRMLEDAKVFKTDELIQKKYEQTKPFINKLHQ EFVKESLEGRSLEGLESYQDILKEWQKDKKDKIAQKNLGIKEKELYKQVTQLFNAKAKEWSE PYAHLGLKKKDIGILFEEGVFKILKEKYNNDKDAKITNKVTGEIFFEDFWKGFVGYFQKFFET RKNFYKDDGTSTAIATRIVAQNLKRFCDNIGLFEKIKDQIDSSEVEQSFGISMEKVFSLDFYN QCLLQGGIDKYNEILGGKTLENGEKFKGINELINKYRQDNKGDKSSFLKILDKQILSEKESFID EIKNDKELEETLKNLHETAKVKTKIFGTLFEDFIGNNTKYDLAKIYISKEAFNTISHKWTGGTD LFAENLFNALKDEQILKSSAKKKDGSYVFPDFIEFLHIKTALENVPKDINFWKERYYVNKEGE NKEFFLGNGEIWQQFLQIFNFEFNELFQKEIIDNQTGKKMHIGYKVYKEEISKLLEDFKVDK DSTVIIKHFADSVLWIYQMAKYFALEKKRTWRDEYDLDTFYTDPKNGYLAFYENAYEEIVQI YNKLRNYLTKKPYSTEKWKLNFQNSTLASGWDKNKEADNFTVILRKDGKYFLGLMRKGA NKLFDKRYGSEFSQGLEKGKYEKMNYKYFPSPSKMIPKTSTQVHEVKKHFKNSSEPFFLEES SSLGKFIKQLKITKEVFDLNNFEYKKSYLSTLNGESPDESQRVKADSKKTGQVKLFQKEFLNL SQNELLYKKSLFAWVDFCKEYLDCFPSTGDGFLQFKKYIQDTEKYESIDQFYKDIERGGYKIS FQNISEEYISCKNQNSELYLFKIHNKDWNLKDGKPKTGMKNLHTMYFESLFSSENIAQNFP MKLNGQAEIFYRPKTDINKLEMKKDSKGKNVVDHKRYEEDKIFFHLPMTLNRGKSLFNFN VQLNNFLADNPEINIIGVDRGEKHLAYYSVINQNGEILDGGTLNVVKGGNGKDIDYHKKL EDKAEKREQARKDWQDVEGIKDLKKGYISQVVRKLADLAIEHNAIIVFEDLNMRFKQIRGG IEKSVYQQLEKALIEKLSFLVRKNEKNPEEAGYLLKAYQLSAPFETFQRIGKQTGIIFYTQASY TSKIDPLTGWRPNLYLKYSNAKKAKADISKFSEIEFINNRFEFTYDLQEFRSQKDKKKEYPKK TLWTLCSSVERYRWNRKLNDNKGGYEHYSDLTSDFKKLFKKYNIININEDILGQIENMDTD DRKNNARFFSGFMFFWNLICQIRNTNSDVISGESDNDFILSPVEPFFDSRKASQFGSDLPE NGDDNGAFNIARKGIMILKKISQYVEENENCDKLKWGDLYISHTDWDNFI
9	Cas12	MTNYTDFIGLYPVQKTLRFELRPQGKTAEKMRESGLLEQDREKAKNYIVMKALIDDYHRRF INELLEKASFDWQPLFEALNNVKVNKDDKSKKELEKEQLHMRKELIGLFEKDERFKYLFSEK

[0081]

		LFSELLNKEISERNDPDEMEAMRSFDRFSGYFIGFHENRRNIYSNEDKHNSLAYRVVAENF PKFADNCRKYSLIKENMQEAVVEFKKEIASVVDIDVDQMFDISYFNKVLTQKGIDDYNTM LGGVSEEGSVKIRGLNEFLNLYYQKVTDNKRIKMAPLYKQILCESKTKSFIPYMFENDEEVIS SINQYYDSVKYDILQRSVYLLSNYKEYDASKIFIDQKSISSISIVLFGSWETLGGLMQIYKADQ IGDPGLEKTRKKVDKWLSSSYFTLKEVFEAIGEQDPFRVYVEKLSLVLKNIEEFDKSCLLEGTH FSGDELLTQDIKGFLDLLMEVQHLMKPFNAKEDLDKDAAFYSEYNEIYEALSEIIPLYNKVR NYATKKKYSTYKIKMNFGNPTLAAGWDLNKERDNTAVILLRGNNYYLGIMNPKKKTKFEE LPSGEDNDCYRKMVYKLLPGPNKMLPKVFFSKKGIGTFNPSKEILEGYETGKHKLGDSFDID YCHSLIDFFKENIPKYGDWGTYEFKFSPTEEYSDISQFYKEVSEQGYKITFQNISRKAIDDLVN NGALFLYQIYNKDFSEHSKGKNNLHTMYWKAAFSEENLRNVVIKINGEAELFYRDKSDISK TEHSAGTILVNRTDRKDNPIPNSIYYELFKYKTGQIKSVSDEAKQYLDDLVTHEAKYPITKDR RYTEDRMFFHIPITLNFGSSGNTNINKAVIDHVLNSKDVHIIGIDRGERNLLYVSVIDRKGNI IKQRSLNVIDGIDYHEKLDQREKENISARKSWSNVEKIKDLKEGYLSYVIH
10	Cas12	MKDFYQFTNLYALSKTLRFSLIPTPATKQMLEDAKVFEKDETIQKKYEATKPYFDRLHREFAL EALQDQKLDFKNYLELYRKYKADKKASGKLLINIEKDLRKEVVKLFDKQGEKWAKQYPGLK NKNIGVLFKEAVFTVILKERYGNEKETQILDESSGQLVSIFDSWKGFIGYFKKFHETRKNFYK DDGTSTALATRIIDQNLKRFCDNILIFESTKEKVDFSEVEISFGKPLSEVFTLEFYNTCFLQNGI DFYTKILGGETLQNGEKVKGLNECINLHKQKTGEKLPFFKSLDKQILSEKDKFFIDEISNETQL LEVLKSFVASAESKTDTIKTLVDDFVKDQDKYDLNYIYFSNDGLNTITRKWTTETQVFEEAL YTALKAAKVVSSSAKKNEGGYSFPDFIPFAHLKTALESIKIDGTIWRDNFNAIENFEEKSIWA QFLAIYNFELSNLFETEIKNPEIGNCPTIGYNVYKQDFEELLKSFVYDPNAKVTIKNFADNVL SIYQMAKYFAVEKKRGWNTDYELDVFYTDPQNGYLQYYENAYEEIVQVYNKLRNYLTKKP YSEEKWKLNFDSGTPIKYTTRAIIFNNTTNERYYLGLLKKGVAKPREFEPINNNIISSGEFRRM IIQQLKFQTLAGKGYVRDFGVKYSEDKDGVKHLQQLIKKQYLSKYPCLKKIADGVYNDKKA FDADIKDVLLETYNLDFQPISEEFILNKNRLGEIYLFEIHNKDWNLKDGKNKSGSKNLHTMY FESLFVDKTTFKLNNEGAEVFYRPATNEGKLGTKKDRNGKIIINHKRYATDKILFHCPIGLNK DAGKSYTFNAKINNMLANNPDINIIGVDRGEKHLAYYSVITQKGKILDRGSLNKVEGGDK QEIDYAKKLEETAKNREQARKDWQAVEGIKDLKRGYISQVVRKLADLAIEHNAIIVFEDLN MRFKQIRGGIEKSVYQQLEKALIDKLSFLVMKGEADPEKAGHLLKAYQLVAPFESFQSMGK QTGIIFYTQANYTSKIDPITGWRPNLYLKYTSAEKAKADILKFSKIEFVNNRFELTYDIKNFVL DKKVVLSNKTKWTVCSSVERFRWNRRLESNQGNYEHYENLTENLSSLFKDFGFEIEQNIIR QVEQLATKGNEQFFRSFIFYVNLIFQIRNTDAKAKDQNKEDFILSPVEPFFDSRTPEKFGENL PENGDDNGAFNIARKGIIMLNKISAYKQEVGNVDKIIWKDLFISAAEWDNFTQE
11	Cas12	MDSYEQFTKLYPIQKTIRFELKPQGRTKEHFDNSNFLEKDRERDDNYKILKEVIDDYHREFID ECLSNIQLNWDDLKKFSEEYRRSKEKKNNRDSESEQKRMSTTSETRAINKKNLEAEQKRM RGEIVSAFKKDDRFKHLFSEKLFSILLKNQIYEKGTLEEIEAFDCFNKFSGYFKSFHENRKNMY SDEDKETAISYRIINENFPKLLDNFEKYQYVCREYPEQIREAESTLAEAGCYIKMDEIFSIDNF NNVMMQGGKESGISRYNLAIGGIVQGTGEKPKGLNEFLNLAYQNEPNGRKKIRMEPLYK QILSKEESFSYRLEAFTDDSQLLSAIRSFFDIVEKDKNGNIFDRAVNLMSSFSNYDTSKIYIRK AYLNQVSKEIFGYRGKSDSKPAKTADESLNKSGGWEKLGQMLRDYKADSIGDRNLEKTCK KVDKWLDSDEFTLSDILGAISLAGSNETFEAYVSEICVARRNIDKEKEKEKNINVEKISGDTES IQIIKALLDSVQEFFHLLSPFQLHPNTPHDWTFYAEFNDIYDKLSAITPLYNQARNHLTKKN LDTSKIKLNFNNPTLANGWDVNKEYENTAVILIRDGKYYLGIMNPKNKRKIKFDEGSGAGP FYQKMVYKLLPGPYRMLPKVFFAKKNIDYYNPSQEIREGYKAGKHKKGKEFDKGFCHKLID

[0082]

		FFKESIQKNENWKVFDFKFSPTESYDDISEFYQEVEKQGYRMYFVNIPSDTIDRYVEGGDM FLFQIYNKDFAKGAKGNKDMHTLYWNAVFSEENLQKGVMKLSGEAELFYRKKSDIKDPP HREGEILVNRTYIDRTHVSGVMGEQNTVKESRIPVPDEIHKNLFDYYNHGRELTKEEKEYC DKVGSFKAYYGIVKDRRYLENKMYFHVPLTLNFKAIGEKRINKMAIEKFLTDENACIIGIDRG ERNLLYYSIIDRNGKIIDQKSLNVIDGFDYHEKLSQRQTEREVARQSWNSIGKIKDLKEGYLA KAVHEISKMAIKYNAIVVLEDLHFGFKKGRLKVEKQIYQKFEEMLINKLNYLVFKDVSDSSD AGGVLNAYQLTAPLESFSKLGKQSGILFYVPAAFTSVIDPTTGFVDLFNSSSITSTQKKKEFL QRFESIVYSARDGGIFAFTFDYRNFSKIATDHRNMWTVYTHGERIRYVRDEKCYKTTDPTK RIKEALSGIEYDDGSDIRDKITQSGDNNLINTVYHSFMDTIKMRNKDGRIDYIISPVKNRNG EFFRSDYKHRDFPVDADANGAYHIALKGELLMRMIGKTYDSNSDKMPKLEHKDWFEFM QTRGDQ
12	Cas12	MKKEKEFKSFGDFTNLYEISKTLRFELKPVENTQTMLDEADVFGKDKVIKDKYTKTKPFIDKL HREFVDESLKDVSLSGLKKYSEVLENWKKNKKDKDIVKELKKEEERLRKEVVEFFDNTAKK WANEKYKELGLKKKDIGILFEESVFDLLKEKYGEEQDSFLKEEKGDFLKNEKGEKVSIFDEWK GFVGYFTKFQETRKNFYKNDGTETALATRIIDQNLKRFCDNIDDFKKIKNKIDFSEVEKNFN KTADVFSLDFYNQCLLQKGIDSYNEFIGGKTLENGKKLKGVNELVNEYRQKNKNEKVSFLK LLDKQILSEKEKLSFGIENDEQLLVVLNSFYETAEEKTKILRTLFGDFVEHNENYDLDKTYISK VAFNTISHKWTNETHKFEELLYGAMKEDKPIGLNYDKKEDSYKFPDFIALGYLKKCLNNLD CDTKFWKEKYYENNADKKDKDKGFLTGGQNAWDQFLQIFIFEFNQLFNSEAFDNKGKEI KIGYDNFRKDFEEIINQKDFKNDENLKIAIKNFADSVLWIYQMAKYFAIEKKRGWDDDFEL SEFYTNPSNGYSLFYDRAYEEIVQKYNDLRNYLTKKPYKEDKWKLNFENPTLANGFDKNKE SDNSTVILRKKRKYYLGLMKKGNNKIFEDRNKAEFIRNIESGAYEKMAYKYLPDVAKMIPKC STQLNEAKNHFRNSADDLEIKKSFSNPLKITKRIFDLNNIQYDKTNVSKKISGDNKGIKIFQK EYYKISGDFDVYKSALNDWIDFCKDFLSKYDSTKDFDFSILRKTKDYKSLDEFYVDVAKITYK ISFTPVSESYIDQKNKNGELYLFEIYNQDFAKGKMGAKNLHTLYFENVFSPENISKNFPIKLN GNAELFFRPKSIESKKEKRNFVREIVNKKRYSEDKIFFHCPITLNRETGSIYRFNNYVNNFLSE NNINIIGVDRGEKHLAYYSVIDKNGVKIGGGSFNEINKVDYAKKLEERAGEREQSRKDWQ VVEGIKDLKKGYISQVVRELADLAIKHNAIIVLEDLNMRFKQIRGGIEKSIYQQLEKALIDKLS FLVEKGEKDPNQAGHILKAYQLAAPFTSFKDMGKQTGIVFYTQASYTSKTCPNCGFRKNN NKFYFENNIGKAQDALKKLKTFEYDSENKCFGLSYCLSDFANKEEVEKNKNKKRNNAPYS DIEKKDCFELSTKDAVRYRWHDKNTERGKTFFEGESVYEEKEEKEIGQTKRGLVKEYDISKCL IGLFEKTGLDYKQNLLDKINSGKFDGTFYKNLFNYLNLLFEIRNSISGTEIDYISCPECQFHTD KSKTIKNGDDNGSYNIARKGMIILDKIKQFKKENGSLDKMGWGELFIDLEEWDKFAQKKN NNIIDK
13	Cas12	MKSFDSFTNLYSLSKTLKFEMRPVGNTQKMLDNAGVFEKDKLIQKKYGKTKPYFDRLHRE FIEEALTGVELIGLDENFRTLVDWQKDKKNNVAMKAYENSLQRLRTEIGKIFNLKAEDWVK NKYPILGLKNKNTDILFEEAVFGILKARYGEEKDTFIEVEEIDKTGKSKINQISIFDSWKGFTGY FKKFFETRKNFYKNDGTSTAIATRIIDQNLKRFIDNLSIVESVRQKVDLAETEKSFSISLSQFFS IDFYNKCLLQDGIDYYNKIIGGETLKNGEKLIGLNELINQYRQNNKDQKIPFFKLLDKQILSE KILFLDEIKNDTELIEALSQFAKTAEEKTKIVKKLFADFVENNSKYDLAQIYISQEAFNTISNK WTSETETFAKYLFEAMKSGKLAKYEKKDNSYKFPDFIALSQMKSALLSISLEGHFWKEKYYKI SKFQEKTNWEQFLAIFLYEFNSLFSDKINTKDGETKQVGYYLFAKDLHNLILSEQIDIPKDSK VTIKDFADSVLTIYQMAKYFAVEKKRAWLAEYELDSFYTQPDTGYLQFYDNAYEDIVQVYN KLRNYLTKKPYSEEKWKLNFENSTLANGWDKNKESDNSAVILQKGGKYYLGLITKGHNKIF

[0083]

		DDRFQEKFIVGIEGGKYEKIVYKFFPDQAKMFPKVCFSAKGLEFFRPSEEILRIYNNAEFKKGE TYSIDSMQKLIDFYKDCLTKYEGWACYTFRHLKPTEEYQNNIGEFFRDVAEDGYRIDFQGIS DQYIHEKNEKGELHLFEIHNKDWNLDKARDGKSKTTQKNLHTLYFESLFSNDNVVQNFPI KLNGQAEIFYRPKTEKDKLESKKDKKGNKVIDHKRYSENKIFFHVPLTLNRTKNDSYRFNA QINNFLANNKDINIIGVDRGEKHLVYYSVITQASDILESGSLNELNGVNYAEKLGKKAENRE QARRDWQDVQGIKDLKKGYISQVVRKLADLAIKHNAIIILEDLNMRFKQVRGGIEKSIYQQ LEKALIDKLSFLVDKGEKNPEQAGHLLKAYQLSAPFETFQKMGKQTGIIFYTQASYTSKSDP VTGWRPHLYLKYFSAKKAKDDIAKFTKIEFVNDRFELTYDIKDFQQAKEYPNKTVWKVCSN VERFRWDKNLNQNKGGYTHYTNITENIQELFTKYGIDITKDLLTQISTIDEKQNTSFFRDFIF YFNLICQIRNTDDSEIAKKNGKDDFILSPVEPFFDSRKDNGNKLPENGDDNGAYNIARKGI VILNKISQYSEKNENCEKMKWGDLYVSNIDWDNFVTQANARH
14	Cas12	MNTQKKEFNPKSFKDFTNLYSLNKTLRFSLTPNKKTAEILEFNKQKEVKCFSNDRKIAGAY QEIKKYLNKLHQEFIQEAMKFFAFSEEELKGFEKEYLNLLNFTDKDNFKKKNKIRNEYEQERK ILTIKIATYFSKFKSEKYQSFNLANITGKKVFSILEQKYKEDKKTLKIIHIFKYKPTKDEKKEGEAV NFSTYLTGFNENRKNFYKSEDKAGQFATRTIDNLAQFIKNKKLFEDKYQKNYSKIGILDEQI KIFNLDYFNNLFLQEGLDEYNGILGNNKGEENKSNEGINQKINIFKQKEKARLKKEKENFNK SDFPLFKELYKQIGSIRKENDVYVEIKTDKELVEELNNFPKNVENYLKDIQSFYKTFFEKLQNE EYELDKIYLPKSVGTYFSYIAFSDWNKLAFIYNKRYKNEKIKIVEGGDVNVQYRSLEVLKNRI DELKDEDNLNFNKFFIDKLKFNEAKKENNWQNFWFCIEYYINSQFIGGEKNILNKEKNEYEI LPFGSLKELKEKYFEAVKKYKEKMVDTESGLTDDEEKEIKETLKNYLDRIKEIERIAKYFDLKKS FEEIKQEDLDSNFYGEYQKVVDKTNELKIYQYYSEFRNYLTQNNSVEEKIKLNFNSGLLLDG WDLNKEKVKFSIIFQENGKYYLGIINKEKDKTILDKDKHPEIFTKNSDFRKMEYKLFPSPSKM LPKISFSETAKKGDEDVGWSEEIQKIKDEFAEFQEYKKKSKDNWKDEFNRGKLNKLIDYYK QVLEKHSEGYMNTYNFELKDSSKYKNLGEFNDDIARQNYKVKFVGIDKNYIDEKVANGEL FLFQIYNKDFSEDKKEGSTNNLETIYFKELFSKENLENPVFKLSGGAEMFFRNKIEKKKEKKKL DKDGKPMISKKGEKVVDKRRFSENKILFHLPIEINYGKGKMPNFNKKINEYISKNPENIKIIGI DRGEKHLLYYSIIDQNGNNIESMSLNAVDEFGNFVNPEKLEEYEIDNNGKKERRWKYIVN DKEIKVTNYQRKLDELEKERQKSRQSWQNINKIKNLKKGYISFVVKKIVDLAIENNAIIILEDL NFGFKSFRQKIEKNVYQQFEKALIDKLGFVVDKQKQNQRFAPQLSAPFESFQKIGKQTGIV YYVLANNTSKVCPSCQWIKNFYLKYEKKNTIFNLQKNQKLKVFFEQEKNRFREYQMSKEY ISVYSSDVDRQRYDKTKNQNKGGYLEYKNSNQKEIIDKDGVIQKQSITLQLKELFKENHIDLE KEILKQLDNKKEKNSGYTGVYNKFIYLFNLILQIRNAISFREKDYIQCPSCHFDTRKENYLKIN DGDGNGAYNIALRGLYLLKGKNGIINNLEKIKLIFSNNDYFQWAKKLKNKK
15	Cas12	MEEKMLKSYDYFTKLYSLQKTLRFELKPIGKTLEHIKNSGIIESDETLEEQYAIVKNIIDKLHRK HIDEALSLVDFTKHLDTLKTFQELYLKRGKTDKEKEELEKLSADLRKLIVSYLKGNVKEKTQH NLNPIKERFEILFGKELFTNEEFFLLAENEKEKKAIQAFKGFTTYFKGFQENRKNMYSEEGNS TSIAYRIINENLPLFIENIARFQKVMSTIEKTTIKKLEQNLKTELKKHNLPGIFTIEYFNNVLTQE GISRYNTIIGGKTTHEGVKIQGLNEIINLYNQQSKDVKLPILKPLHKQILSEEYSTSFKIKAFEN DNEVLKAIDTFWNEHIEKSIHPVTGNKFNILSKIENLCDQLQKYKDKDLEKLFIERKNLSTVS HQVYGQWNIIRDALRMHLEMNNKNIKEKDIDKYLDNDAFSWKEIKDSIKIYKEHVEDAKE LNENGIIKYFSAMSINEEDDEKEYSISLIKNINEKYNNVKSILQEDRTGKSDLHQDKEKVGIIK EFLDSLKQLQWFLRLLYVTVPLDEKDYEFYNELEVYYEALLPLNSLYNKVRNYMTRKPYSVE KFKLNFNSPTLLDGWDKNKETANLSIILRKNGKYYLGIMNKENNTIFEYYPGTKSNDYYEK MIYKLLPGPNKMLPKVFFSKKGLEYYNPPKEILNIYEKGEFKKDKSGNFKKESLHTLIDFYKEA

[0084]

		IAKNEDWEVFNFKFKNTKEYEDISQFYRDVEEQGYLITFEKVDANYVDKLVKEGKLYLFQIY NKDFSENKKSKGNPNLHTIYWKGLYDSENLKNVVYKLNGEAEVFYRKKSIDYPEEIYNHGH HKEELLGKFNYPIIKDRRYTQDKFLFHVPITMNFISKEEKRVNQLACEYLSATKEDVHIIGIDR GERHLLYLSLIDKEGNIKKQLSLNTIKNENYDKEIDYRVKLDEKEKKRDEARKNWDVIENIKE LKEGYMSQVIHIIAKMMVEEKAILIMEDLNIGFKRGRFKVEKQVYQKFEKMLIDKLNYLVFK NKNPLEPGGSLNAYQLTSKFDSFKKLGKQSGFIFYVPSAYTSKIDPTTGFYNFIQVDVPNLE KGKEFFSKFEKIIYNTKEDYFEFHCKYGKFVSEPKNKDNDRKTKESLTYYNAIKDTVWVVCS TNHERYKIVRNKAGYYESHPVDVTKNLKDIFSQANINYNEGKDIKPIIIESNNAKLLKSIAEQ LKLILAMRYNNGKHGDDEKDYILSPVKNKQGKFFCTLDGNQTLPINADANGAYNIALKGL LLIEKIKKQQGKIKDLYISNLEWFMFMMSR
16	Cas12	MNNYDEFTKLYPIQKTIRFELKPQGRTMEHLETFNFFEEDRDRAEKYKILKEAIDEYHKKFID EHLTNMSLDWNSLKQISEKYYKSREEKDKKVFLSEQKRMRQEIVSEFKKDDRFKDLFSKKLF SELLKEEIYKKGNHQEIDALKSFDKFSGYFIGLHENRKNMYSDGDEITAISNRIVNENFPKFL DNLQKYQEARKKYPEWIIKAESALVAHNIKMDEVFSLEYFNKVLNQEGIQRYNLALGGYVT KSGEKMMGLNDALNLAHQSEKSSKGRIHMTPLFKQILSEKESFSYIPDVFTEDSQLLPSIGG FFAQIENDKDGNIFDRALELISSYAEYDTERIYIRQADINRVSNVIFGEWGTLGGLMREYKA DSINDINLERTCKKVDKWLDSKEFALSDVLEAIKRTGNNDAFNEYISKMRTAREKIDAARKE MKFISEKISGDEESIHIIKTLLDSVQQFLHFFNLFKARQDIPLDGAFYAEFDEVHSKLFAIVPLY NKVRNYLTKNNLNTKKIKLNFKNPTLANGWDQNKVYDYASLIFLRDGNYYLGIINPKRKK NIKFEQGSGNGPFYRKMVYKQIPGPNKNLPRVFLTSTKGKKEYKPSKEIIEGYEADKHIRGD KFDLDFCHKLIDFFKESIEKHKDWSKFNFYFSPTESYGDISEFYLDVEKQGYRMHFENISAET IDEYVEKGDLFLFQIYNKDFVKAATGKKDMHTIYWNAAFSPENLQDVVVKLNGEAELFYR DKSDIKEIVHREGEILVNRTYNGRTPVPDKIHKKLTDYHNGRTKDLGEAKEYLDKVRYFKAH YDITKDRRYLNDKIYFHVPLTLNFKANGKKNLNKMVIEKFLSDEKAHIIGIDRGERNLLYYSII DRSGKIIDQQSLNVIDGFDYREKLNQREIEMKDARQSWNAIGKIKDLKEGYLSKAVHEITK MAIQYNAIVVMEELNYGFKRGRFKVEKQIYQKFENMLIDKMNYLVFKDAPDESPGGVLN AYQLTNPLESFAKLGKQTGILFYVPAAYTSKIDPTTGFVNLFNTSSKTNAQERKEFLQKFESI SYSAKDGGIFAFAFDYRKFGTSKTDHKNVWTAYTNGERMRYIKEKKRNELFDPSKEIKEALT SSGIKYDGGQNILPDILRSNNNGLIYTMYSSFIAAIQMRVYDGKEDYIISPIKNSKGEFFRTD PKRRELPIDADANGAYNIALRGELTMRAIAEKFDPDSEKMAKLELKHKDWFEFMQTRGD
17	Cas12	MASSHFISLDNSFSKFTNLYSLSKTLRFELVPTENTTVMLENNNVFKKDQIIQVKYEKTKPFI DRLHREFIKEALSNYAVSGLQEYFEILRAGGKKANLDSAKKQLRKHVVDQFNATASLWVS RHKDVGFKGEGIELLFKEAVFKLLKEKYGTDMNALIEDNHGKQISIFDSWKGFTGYFDKFQ QTRRNLYKDDGKEGRVATRIIDQNLTRFCDNIFVYEKIKDKVSFIDVEKSFGKTCSEVFIPDY YNTCLLQDGIDSYNEFIGGKPLENGEKVQGLNELINLYRQTTGDKVPYFKKLEKQILGEKDE VFIDEITDEDFVPRVLAFYRTVDAKYKLFLKLLDDFVTNQDVYELSQIYISKKGLQEKLYRWL TPSAREVYDEELFEVLKKAKKVNNKDKQKVSGYVPDFVEVLYIKQALENIDAKLIWSDRYYS DGENEGIIDKGFSSWKQFLVILNHEYRQLLSFEDHVIIDKELDFDKEVKQLTDTVEIVSQDK NARTVTYRGGYDVYKAKLAELGQSFEKDTCTKKVIKNFADSVLSMYHFAMMFAVWDDT YPLDVFYTNNEFGYLLYYEDAYKNIVQEYNKLRNYLTKKPYSTEKWKLNFENPTLAAGFDK NKESDNSTVILRQGDKYFLGVMKKGFNKIFDNSQISQTGNSPEAYFEKMVYKYTKDVVTG IPKSSTQVKEVQEHFRNSDEDFFLEECSSVGNFIVPLKITKEIFDLNNKVYAKEDISQAMYR WALNTDEEKNYVKSFQKSYLSLGGSPELYCKSVTLWIGFCLNFLKSYPSAAYFDYSQLRQA SDYESVDECYQELNNAGYTILFQNVSEKYVRVKNKNGELYLFQIKNKDWNEGSTGKKNLH

[0085]

		TLYFESLFSKENAKQGFPFKLSGNAELFFRPGSIEQTYERRNFPREIPLKRRYSKDGIFFHIPV QVNRTKVGSPNQFNKEVNDFLAGNPNINIIGVDRGEKHLVYYSVISQNGEKIDGGSFNEI NGQDYHDKLEKRAKEREQQRRDWETVEGIKDLKKGYISQVVKKLADLAIEHNAIIVMEDL NMRFKQIRGGIEKSVYQQLEKALIDKLSFLVNKGEVDPQKAGHLLKAYQLTAPIDAFKDM GKQTGIMFYTQAAYTSKIDPVTGWRPHLYLKYSSVEKAKDDISRFTKIAYKNDRFEFTYNIT DFRTQKEWPLKTEWTVCSCVERFRWNKKLANGKGDYEHYPNVTDDFKKLFDSVGINYLQ ENIKSQVVNLDENTNVEFFREFIKLFALVCQIRNTNSEEAGNLNDFILSPVEPFFDSRSAEDF GKGLPSNGDENGAYNIARKGMIILNTLSTFKNDHGSCEGLSWGDLYISDTQWDDFAQSF HG
18	Cas12	MDAKEFTGQYPLSKTLRFELRPIGRTWDNLEASGYLAEDRHRAECYPRAKELLDDNHRAFL NRVLPQIDMDWHPIAEAFCKVHKNPGNKELAQDYNLQLSKRRKEISAYLQDADGYKGLF AKPALDEAMKIAKENGNESDIEVLEAFNGFSVYFTGYHESRENIYSDEDMVSVAYRITEDN FPRFVSNALIFDKLNESHPDIISEVSGNLGVDDIGKYFDVSNYNNFLSQAGIDDYNHIIGGH TTEDGLIQAFNVVLNLRHQKDPGFEKIQFKQLYKQILSVRTSKSYIPKQFDNSKEMVDCICD YVSKIEKSETVERALKLVRNISSFDLRGIFVNKKNLRILSNKLIGDWDAIETALMHSSSSEND KKSVYDSAEAFTLDDIFSSVKKFSDASAEDIGNRAEDICRVISETAPFINDLRAVDLDSLNDD GYEAAVSKIRESLEPYMDLFHELEIFSVGDEFPKCAAFYSELEEVSEQLIEIIPLFNKARSFCTR KRYSTDKIKVNLKFPTLADGWDLNKERDNKAAILRKDGKYYLAILDMKKDLSSIRTSDEDES SFEKMEYKLLPSPVKMLPKIFVKSKAAKEKYGLTDRMLECYDKGMHKSGSAFDLGFCHELI DYYKRCIAEYPGWDVFDFKFRETSDYGSMKEFNEDVAGAGYYMSLRKIPCSEVYRLLDEKS IYLFQIYNKDYSENAHGNKNMHTMYWEGLFSPQNLESPVFKLSGGAELFFRKSSIPNDAK TVHPKGSVLVPRNDVNGRRIPDSIYRELTRYFNRGDCRISDEAKSYLDKVKTKKADHDIVK DRRFTVDKMMFHVPIAMNFKAISKPNLNKKVIDGIIDDQDLKIIGIDRGERNLIYVTMVDR KGNILYQDSLNILNGYDYRKALDVREYDNKEARRNWTKVEGIRKMKEGYLSLAVSKLADM IIENNAIIVMEDLNHGFKAGRSKIEKQVYQKFESMLINKLGYMVLKDKSIDQSGGALHGYQ LANHVTTLASVGKQCGVIFYIPAAFTSKIDPTTGFADLFALSNVKNVASMREFFSKMKSVIY DKAEGKFAFTFDYLDYNVKSECGRTLWTVYTVGERFTYSRVNREYVRKVPTDIIYDALQKA GISVEGDLRDRIAESDGDTLKSIFYAFKYALDMRVENREEDYIQSPVKNASGEFFCSKNAGK SLPQDSDANGAYNIALKGILQLRMLSEQYDPNAESIRLPLITNKAWLTFMQSGMKTWKN
19	Cas12	MVNKQNERGDFDDLTNLYEISKTLRFELVPVGETDRMLKEENVFKVDENIKRKYQQTKLFF DRIHREFAKEALSVEGILSELEEYLAIFIEWRKDKKIHEKTLNQKEKELRKQVVSAFNAMANK WIERYGDVNLKKKNVEFLFEEGIFRVLKERYGEEDGSTITASDTGEVFSIFDSWKGFTGYFAK FFETRKNFYKDDGTATAIATRIVDENLRRFCDNLIVAQRLTENIDFSEVENNFQIKIKEVLFM EFYNKCLLQDDIDFYNKVIGGETLKTGEKLKGINELVNLHRHKTGEKLPFLKTLDKQILGRKE QFLDEIESEEELLEKLKDFQNVATKKIKVIKSLFGDFVENNENYDLEKIYISKKAFNTISRKWT GETEQFEKLLFESMKSDKPAGLKYDKKENNYKFPDFIAVSYIKDALENFSGEQKFWKDRYYI ELELDNQVVWKQFLDIFYWEFSSLFKRSFVNKETGEISEVGCDIFEKKFINLIDDFEYNQKSKI LIKDFADSVLSVYQMANYFSLEKKRKWSTEFETDSKFYDDSEIGFRNCFYEDVFEGIVQVYN KLRNYLTKKPFSEEKWKLNFENPTLAAGWDKNKEKDNSTVILRKDEKYFLAIMKKGNNVIF DDRNKALFSQNLEHGKYEKVVYKFAKDVTLGIPKSTTQTKSVIAHFKNSDEDYQITNGSAV GDFLEPLVVTKRIFELNNKIYSKNNLGKVLYRSEVSKDKQKEYIKLFQKKYLVLGGNKNLYR DAVKEWIDFCKSFIKVYPSYKYFDFSLLKEAVEYNSVDEFYKELNSYGYAISFQDISCDYIEEK NKNGELYLFQIKNKDWNKGSTGMKNLHTLYFESLFSEENIKNNFVTKLNGGAEIFYRPKTS KEKLGRKKIVRNGQEVFVVNHKRYSEDKIFFHCSIALNRGKGKLLKFNARINDLLANNPDI

[0086]

		NVIGVDRGEKHLAYYSIIDQKCKILDSGTLNEVGAKVDYHEKLSNRAKKREDGRRDWGW GQIEDIKNLKKGYVSQVVHKLAELIIKYNAILVFEDLNMRFKQIRGGIEKSIYQQLEKALIDKL NFLVKKGEKDSKSAGHLLKAYQLAAPFETFDKMGKQTGVIFYTQASYTSKIDPITGWRPNL YLKHSNANDSQKKIAKFSRIEFINDRFEFEYDLKKFIEMKEVPENTKWTLCSCVQRYRWNR KLNANKGGYDSYNDLTKNFKALFESVGIDIKKNIKEQIVKMEIKGNEKFFKSFIFYWQLLCQI RNTDELKKGDDNDFILSPVEPFFDSRKKNGDDLPKNGDDNGAYNIARKGVIVLNKISEFSK QNGNCEKCGWKELYVSAKDWDDFVQAK
20	Cas12	MQNKQSFADFTNLYSLSKTLRFELKPIGQTQAMLDENKIFEVDENRKKAYDKTKPYFDRLH REFINESLSNAQLKGISEYFETFKQFRSNQNNKDLKELINKQQKFLRHQIVTLFDENGKHW ATTKYAHLKIKKKNLDILFDEQVFYILKERYGSEKETQLVDKETGAVTSIFDNWKGFTGYFTK FFETRKNFYKSDGTSTALATRIIDQNLNRFFDNLETFHKIKDKIDVKEVEIFFKLKADNVFSID FYNQCLLQNGIDKYNDFLGGQTLENGEKQKGINEIINKYRQDNKDQKLPFLKKLDKQILSE KDRFINEIESKEEFFQVLTEFYQSATVKVTIIKTLLNDFVHNTDKYKLEKIYLTKEAFNTIANK WTDETQIFEDNLDLVLKNKKITAKQDFIPLAYIKEALEVIEKDRKFFKDRYYNDPQIGFFPDQ SYWEQFLAILNFEFMTHFQRVAKDKITGKKIELGYFVFEKRIKELLDSDPSLNSQSKIIIKEFAD EVLHIFQMAKYFALEKKREWKGDYYQLDDQFYNHIDYGFKDQFYENAYEKIVQPYNKIRN YLTKKPYSDVKWKLNFGNPTLANGWDKNKEADNTAVILKKDGNYYLGVMKKGKNKIFS DQNKEKYKAYNSAYYEKLVYKLFPDPSKMFPKVCFSKKGLNFFQPSEEILRIYKNNEFKKGN TFSISSMQKLIAFYIDCLGLYEGWKHYEFKNIKDVRQYKENIGEFYADVAESGYKLWFEKISE EYITQKNQLGELFLFQIYNKDFAKKTTGRKNLHTIYFEELFSQTNIDNNFPFKLNGQAELFYR PKSLEKIEEKRNFKRSIVNKKRYTQNKIFFHVPITLNRTSENIGRFNVRVNNFLANNSNVNIV GVDRGEKNLAYYSIIKQNGEVLKSGSLNIINGVDYHALLTDRAQRREQERRNWQDVESIK DLKRGYISQVVHELVSLAIKYNAIIVMEDLNMRFKQIRGGIEKSTYQQLEKALIEKLNFLVNK EETDSNQAGNLLNAYQLTAPFKTFKDMGKQTGIIFYTQASYTSKIDPLTGWRPNIYLRYSN AKQAKADILMFTNIYFSEKKDRFEFTYDLEKIDDKRKDLPIKTEWTVCSNVERFSWEKSLNN NKGGYVHYPIQDSNGEESITSKLKKLFMDFGIDLTDIKTQIESLDTNKKDNANFFRKFIFYFQ LICQIRNTQVNKSDDGNDFIFSPVEPFFDSRFADKFRKNLPKNGDENGAYNIARKGLIILHK ISDYFVKEGSTDKISWKDLSISQTEWDNFTTDK
21	Cas12	MDKQKNKLQNFTNLYELSKTLRFELKPVGETQHLLEENKVFGIDGNIKKKYEATKPFFDRLH RKFVKEALVNIALGGLDNYLEVYKKFTNDRKDKENQKELEKQEKLLRKQIKIFFDSQANQW KEKYNKINFKKSGLNILFEESIFQLLKEIYGKEDDAFLKNDDNEFIFDKDGNKISIFDSWKGFT GYFKKFFETRKNFYKDDGTSTAIATRIIDQNLRRFCDNIFIYNKIKNKLDFSSLEKEQDVVLEE IFTTAYYMDCILQDDIDLYNGVLGGETLDDGTKIKGLNEIINKYRQDNKGDKIPFFKKLDKQI LSEKDRKFLDEIESEEELAELLKIFINNTEAKVKVFDELVNQLCVNDSDFELDKIYISKEAFNTI SHKWTNQTHEFERVLFEEMKPDKITGLDYKKAEDKYKFPDFIALKYIIKSLNTLDKDSEFWK SHYYKTEENQNAILSLEEKVGEQFLQIYKYELQRLHSRNVNVENKDGKMKEKEIGLDYSLTT VKELLKNFKLTDKSKIIIKDFADNVLQYYQLAKYFSVEKNREWNYTKLELADFYINPDFGYEI FYGNAYEEIIQIYNKLRNYLTKKPFSEEKWKLNFENPTLAGGWDKNKERGNATVILRKNEK YYLGIMAKGYNDIFTDKNKDKFDGEGYEKMVYKLFPGPNKMMPKVCFSKKGLDFFEPSEK IIDIYKDGKFKQGDTFSIDSMQQLIDFYKRALREYNGWKMYDFSKLKDTNDYTTNIGEFYN DVACAGYKVWFDNISEEYIQEKNENGELYLFEIHNKDWNLKDEKKKTGTKNLHTLYFESLF SDENALRDFVMKLSGEAELFFRPKTNADKLGYRKDKKGNKVVKNKRYSEDKMFLHLSINL NRGKGQAFWFNRNINNFLANNSDINVIGIDRGEKHLAYYSVISQQGEILDNGSLNEIAGV DYYAKLSKRAKEREGQRKDWQAVSDIKNLKKGYISQVVRKLADLAIEHNAIIVLEDLNMRF

[0087]

		KQIRGGIEKSIYQQLEKALIEKLNFLVNKKEIDSDKAGNLLRAYQLTAPFETFQKMGKQTGII FYTQASYTSKIDPLTGWRPNLYLKKGNAKINKEQIEKFSKIEFTNNRFEITYDLKNFGDKKKK YPQKTKWTLCSSVERWRWDRKLNNNKGGYIHYEDLTTEFKSLFEKFEIDIEGDILEQIKTIDE NDRNNARLFSGFIYLWGLLSQIRNTDGELDEKIKKLEREDKNEEISEKEKFDVDFILSPVEPFF DSRTPEKFGENLPKNGDDNGAYNIARKGIITLERIKKFYELSDKEREKLKYPDLFITNAEWDD FATKRDS
22	Cas13	MDNNTTLEKTELGLGITYNHDKVEDKHYFGGFFNLAQNNIDLVAQEFKKRLLVQGKDSIN IFSNYFSDQCSITNLERGIKVLSEYFPVIFYFDLDENNKSKSIRQHIILLLDTINNLRNVYTHYY HKKVIIDDALYPLLDTILLKVVLEIKKKKLKEDKTKQLLKKGLEKEMAILFNLMKKEQKEKKIK GWNIDKNIKGAVLNRAFSHLLYNDGISDYRKSKSNTEDENLKDTLSESGILFLLSFFLNKKE QEQLKANIKGYKGKIASIPDEEITLKNNSLRNMATHWTYSHLTYKGLKHRIKTDHEKETLLV NMVDYLSKVPNEIYQNLSEQNKSLFLEDINEYMRDNEENNDSSEASRVIHPVIRKRYENKF AYFAIRFLDEFAEFPTLRFMVNVGNYIHDNRKKDIGGTSLITNRTIKQQINVFGNLTEIHKKK NDYFEKEENKEKILEWELFPNPSYHFQKENIPIFIDLEKSKETNELAKEYAKEKKKIFGSSRKK QQNTAKKNREAIINLVFDKYKTSDRKTVTFEQPTALLSFNELNAFLYAFLVENKTGKELEKIII EKIANQYQILKNCSSTVDKTNDSIPKSIKKIAHPTTDSFYSEGKKIDIEKLERDIKIEIEKTNEKL ETIKENETSAKNYKRNERDIQKRKLYRKYVFFTNEIGIEATWITNDILRFLDNKENWKGYQH SELQKFISQYDNYKKEALGLLESEWNLESEAFFGQKLKRIFQSNFTFETFYKKYLDNRKDTLE TYLSAIENLKTMTDVPPKILKKSWAELFRFFDKKIYLLSTIETKINELITKPINLSRGVFDEKPTFI NGKSPNKENDQHLFANWFIHAKEQTIFQDFYNLALETPKEINNLKKQNYKLERSINNLKIE DIYIKQMVDFLYQKLFEQSFKGSLQDLYTSKEKREVEKSKAKNEQTPDESFIWKKQVEINAL NGRIIAKTKIKDIGKFKNLLTDNKITHLISYDNRIWNFSLDNDGDTTKKLYSLNTELESYERIR REKLLKQIQEFEQFLLKQETEYSAERKHPEKFEKDGNPNFKKYIIEGMLNKITPVNEIEELEILK SKEDVFKIDFNEIVKLNNESIKKGYLLIMIRNKFAHNQLIDKNLFTFSLQLYSKNENENFSEYL DKVCQKIIQEFIEKLK
23	Cas13	MNETDYLAKRLEYNYASIEDKHYFGGYFNLAQNNINDLSKAFKEKFGMKPKSCILDFFTQD KAIAEYQLGVEFLQKNLPVIRYLYLPTSHKRFENVPKNQLISEQRNYFKNSLKVLKNLIRDYR NFYTHHFHKPIPVFPETYKLLDDLFLAVANDVKKHRMKTDASKQLLKKGLIEELAQLEKLKL EDLKKLKREGKKVNLNDKEAITNAILNDSFSHLLPKENTISKYYSAVPTEDIDTENGVTISESG IIFLLGLFLTKKQSEDLRSRVKGFKAKLIVNPENPINKKNNSLKYMATHWVFGYLGFKGLKN RFTTTFTKDTLLAQIVDELSKVPDELYQVLPEELKNEFLEDMNEYLKEENSESLDKATVIHPVI RKRYENKFAYFALRFLDEFVDFPTLRFQLHLGNYVHDKREKPIEGTKYVTERIVKEKIKAFAKL SEAAQLKQKYFEEKENHQSIGLQLYPNPSYNFVGNNIPIHLNLNEHFFPKEVKIVAGRLKKR NSSYKSDHPEEYKVRTDNKIKPDAILQDLGKPEKLAPVAMLSLNELPALLHLVLTKKTPEEIEI IIAQKIAERYNVLTNYKAGDDISKGQITKNLLKAKQKKEVNLDKLQLAIEKEIAVTNDKLQTI ALHIKERNDPKQKRKYVFTNKEIGLQVTWLANDLKRFMPKGSRQNWRGQHHSQLQKSL AFYDIQPKEPLSLLEEVWDFKNEAYLWNNGIRRSFDKRDFISFYTSYLNNRKETFQRFKDQL NGIRSNKKILDKFIKQQHLWNLFHKRLYVIDTIEEQVEKLLVKPMQFPKGVFDHKPTYIKGK SIQENPECFADWYVAWNQHTDYQKFYSWDRDYKSAYLSGEQEKTEKRFIRVQGSKINKV KQQDVLLAKMASIIFNELYLPEDAEHLDLNLSDIYKTQTERKAEIEAALIQSHKTTGDNSANI IKSTSAWTLTVPYCSKNIYEPQVKLKELGKFKKFIASQKVQTLFEYKPQKIWNKTELEEVLELK ANSYEVIRRDYLLKSIQEFEKYMIKKLPTLIDTNEHPNFNKYLTTFLKSLELVSEEDAKWLISKK DFDTTPIDELKKQSKIMEKAFLLVMIRNKFSHNQLPRKIYYDEIYKNVPNAVSINFNELFLEY TNQTILEFK

[0088]

24	Cas13	MESIIGLGLSFNPYKTADKHYFGSFLNLVENNLNAVFAEFKERISYKAKDENISSLIEKHFIDN MSIVDYEKKISILNGYLPIIDFLDDELENNLNTRVKNFKKNFIILAEAIEKLRDYYTHFYHDPIT FEDNKEPLLELLDEVLLKTILDVKKKYLKTDKTKEILKDSLREEMDLLVIRKTDELREKKKTNPK IQHTDSSQIKNSIFNDAFQGLLYEDKGNNKKTQVSHRAKTRLNPKDIHKQEERDFEIPLSTS GLVFLMSLFLSKKEIEDFKSNIKGFKGKVVKDENHNSLKYMATHRVYSILAFKGLKYRIKTDT FSKETLMMQMIDELSKVPDCVYQNLSETKQKDFIEDWNEYFKDNEENTENLENSRVVHP VIRKRYEDKFNYFAIRFLDEFANFKTLKFQVFMGYYIHDQRTKTIGTTNITTERTVKEKINVFG KLSKMDNLKKHFFSQLSDDENTDWEFFPNPSYNFLTQADNSPANNIPIYLELKNQQIIKEK DAIKAEVNQTQNRNPNKPSKRDLLNKILKTYEDFHQGDPTAILSLNEIPALLHLFLVKPNN KTGQQIENIIRIKIEKQFKAINHPSKNNKGIPKSLFADTNVRVNAIKLKKDLEAELDMLNKKH IAFKENQKASSNYDKLLKEHQFTPKNKRPELRKYVFYKSEKGEEATWLANDIKRFMPKDFK TKWKGCQHSELQRKLAFYDRHTKQDIKELLSGCEFDHSLLDINAYFQKDNFEDFFSKYLEN RIETLEGVLKKLHDFKNEPTPLKGVFKNCFKFLKRQNYVTESPEIIKKRILAKPTFLPRGVFDER PTMKKGKNPLKDKNEFAEWFVEYLENKDYQKFYNAEEYRMRDADFKKNAVIKKQKLKDF YTLQMVNYLLKEVFGKDEMNLQLSELFQTRQERLKLQGIAKKQMNKETGDSSENTRNQT YIWNKDVPVSFFNGKVTIDKVKLKNIGKYKRYERDERVKTFIGYEVDEKWMMYLPHNWK DRYSVKPINVIDLQIQEYEEIRSHELLKEIQNLEQYIYDHTTDKNILLQDGNPNFKMYVLNGL LIGIKQVNIPDFIVLKQNTNFDKIDFTGIASCSELEKKTIILIAIRNKFAHNQLPNKMIYDLANE FLKIEKNETYANYYLKVLKKMISDLA
25	Cas13	MEDKTTGAGISYDHTLMEDKHFFGGFLNLAQNNIDALLKAFKERFNVRYQSKQFAEVCFS DKLPDQDYLDRTLFLETHLPFIKYIGGKEANNRGTFRKNITLFFESIEQLRNFYTHYYHKPILF PEELYENLDRIFVEVSKEVKTHKVKNDQTRHLLTKNLANELDIRYKKNVEKLKELKAQGKKV NIHDKEAIKNSVLNNAFNHLIYKKEEDVFATEAYKSKYNLEDPSKNGISLSQSGLLFLLSMFL NKKDIEALKSRVKGFKAKIIRDGEENISGLKFMATHWVFSSLSFKNVKHKLSTDFHKETLLIQ IVDELSKVPDEVYKTFDKQTQEEFIEDINEYMKVGNKDLSLEESTVIHPVIRKRYDNKFNYFA LRFLDEFAGFPTLRFQVHIGNYIHDRRIKNIDGTAFQTERSVKERIKVFGKLSQMSNLKAEY VSGLMDEPVDTGWEIFPNPSYNIIENNIPIYIEMGDHFNDEVLQSKMARKKQKPEELKDR NSAKASKESMIQTLQNDKGLMDVITVSPTAQLSLNELPAILYELLVKKTPAKTIEKKLVGKL NQRLKEIKNYNPEKPLPASQISKRLRLNREEGSINTKKIIALLQKELNYTQEKLDLLEKNRKEY GKKVDGKILRKYVFGLKEIGNLATDMAMDIKRFMPANVRKEWKGYQHSQLQQSLAFYDK RPEEAFNILQEVWDINREKSLWDTWILNAFQTSGNFERFFELYHEGRKKYIQQQLENIDRY TDNKKFLQKFINQQFPTNFLEKRLYTLESLEIEKLKILSKPFILPRGTFDEKPTFIMGEKVTENP ELFADWYTYGYQQHEFQKFYSWPRDYKDLLQNEQKRDPDFAENKKGLSDLKQLELLQLK QDIIIKKIKTQDLYLKLIMDALFIEVFGQEADISLNDLYLTQEERLEKEKLALKQHQRVEGDDS PNVIKDNFIWSKTMPYKHDKIYEPQVRLKDFGKFKHFLLDDKVAKILSYDLQETWNKNELE IQINTGQDSYEVIRREELLKEIQLLEKQILETFSHTLDEHPKEFEDEKGNPNFKMYMANGVIR KGSSTTAKDEADWLEHEKDFDNLSLEIFNSKSEITQLTFLIVLIRNKFGHNQLPIKQFYEIIQN EYSITGETISRLYLNFIIYAKARLKDLM
26	Cas13	MEEKLGKGVEYNPFKKEDKYYFGGYFNLAENNINEVFKEVKKRLGETNSSSNIELLNNVFR KEMSLVDYEKWVNAFADYFPIVNYLDRETIKKGEKVVEVPREKRIECFRDMFKGLINTISQL RHYYTHYHHEPIEIDDKILSFLDEVLFNTIITTKNKYLKTDKTKELIKDSLQEELDILCKLKVKYL ESKRKRFDRKDKGAIENAVYNDVFRRFIYKDEKGNESLKDIIRTKQIKVHQNSSYLELPISSS GIIFLLSLFLNKKEVESLKSNIRGYKGKSKSEETTPEKNGLLFMTTHRIYSVLAYKGLKKRIKTS VKGDKETLLMQMIDEVSKVPHCIYQNLDQTLQATFIEDWNEYFKDNEENEENLENSRVLH

[0089]

		PVIRKRYEDKFNYFAIRFLDEYAEFPSLRFQVNLGNYVHHKATKKFGNSEVTTERVIKDKITV FGRLSEVNKAKADFFKNETELDPAWELFPNPSYEFPKEKGNNDKDAGKIGIQVKLLNKDIE AVLNESKNTLNNKTRKSDKISKKEIINKIVQINDDTKYNNKNIIYQGNAIAYLSLNDIHSLLY ELLVIGTKGDKLERKVVEKIQQQVTEIRNKDTSAKILSKYKDSEESNTIDKKKLVIDLKYEYDK LQDLLKEHKNREEDYIQTKKKKKDSPKRKYILYHNEKGQVAVWLSNDIKRFMPQNFKEKW KGYQHSEFQKSLAYYETNKEMLKIILQDLDLEQFPFDIKSCFYKNTLEDFYNRYLSLRISYLEN VIDRVECFSNEPKAFKSVLKECFVFLKKQNYTNHSLDEQVKKILANPIFIERGFLDTKPTMIQ GVKFSENKGCFADWFVHYKEYEHYQKFYDTNLYPVESIEDKERQKLEATIKKQQKNDVFTL LMIKKIFNDLFNQDFEANLYEMYQSKEEREKNQLVAKETQNRNLNFIWNKPIAIDLFDGK VKIDEVKLKDVGSFRKYENDKRVQTFITYIPEIQWIPYLPNTWEGINLPVNVIERQIDRYEKV RSEELLKEVQAIEKYIYEQVNDKTELLQNGNQNFKNYLVNGLLKQIQGIDVSNFKFINQQK FETINVKDLDNEASALEQKVYVLINIRNQFSHNQFPKSAFYQFCQKILSIEEDELFADYYLRL FKLLRNELLD
27	Cas13	MNTRVTGMGVSYDHTKKEDKHFFGGFLNLAQDNITAVIKAFCIKFDKNPMSSVQFAESC FTDKDSDTDFQNKVRYVRTHLPVIGYLNYGGDRNTFRQKLSTLLKAVDSLRNFYTHYYHS PLALSTELFELLDTVFASVAVEVKQHKMKDDKTRQLLSKSLAEELDIRYKQQLERLKELKEQ GKNIDLRDEAGIRNGVLNAAFNHLIYKEGEIAKPTLSYSSFYYGADSAENGITISQSGLLFLLS MFLGKKEIEDLKSRIRGFKAKIVRDGEENISGLKFMATHWIFSYLSFKGMKQRLSTDFHEETL LIQIIDELSKVPDEVYHDFDTATREKFVEDINEYIREGNEDFSLGDSTIIHPVIRKRYENKFNYF AVRFLDEFIKFPSLRFQVHLGNFVHDRRIKDIHGTGFQTERVVKDRIKVFGKLSEISSLKTEYI EKELDLDSDTGWEIFPNPSYVFIDNNIPIYISTNKTFKNGSSEFIKLRRKEKPEEMKMRGEDK KEKRDIASMIGNAGSLNSKTPLAMLSLNEMPALLYEILVKKTTPEEIELIIKEKLDSHFENIKNY DPEKPLPASQISKRLRNNTTDKGKKVINPEKLIHLINKEIDATEAKFALLAKNRKELKEKFRGK PLRQTIFSNMELGREATWLADDIKRFMPDILRKNWKGYQHNQLQQSLAFFNSRPKEAFTI LQDGWDFADGSSPWNGWIINSFVKNRSFEYFYEAYFEGRKEYFSSLAENIKQHTSNHRNL RRFIDQQMPKGLFENRHYLLENLETEKNKILSKPLVFPRGLFDTKPTFIKGIKVDEQPELFAE WYQYGYSTEHVFQNFYGWERDYNDLLESELEKDNDFSKNSIHYSRTSQLELIKLKQDLKIK KIKIQDLFLKLIAGHIFENIFKYPASFSLDELYLTQEERLNKEQEALIQSQRKEGDHSDNIIKDN FIGSKTVTYESKQISEPNVKLKDIGKFNRFLLDDKVKTLLSYNEDKVWNKNDLDLELSIGENS YEVIRREKLFKKIQNFELQTLTDWPWNGTDHPEEFGTTDNKGVNHPNFKMYVVNGILRK HTDWFKEGEDNWLENLNETHFKNLSFQELETKSKSIQTAFLIIMIRNQFAHNQLPAVQFFE FIQKKYPEIQGSTTSELYLNFINLAVVELLELLEK
28	Cas13	METQILGNGISYDHTKTEDKHFFGGFLNTAQNNIDLLIKAYISKFESSPRKLNSVQFPDVCF KKNDSDADFQHKLQFIRKHLPVIQYLKYGGNREVLKEKFRLLLQAVDSLRNFYTHFYHKPI QLPNELLTLLDTIFGEIGNEVRQNKMKDDKTRHLLKKNLSEELDFRYQEQLERLRKLKSEGK KVDLRDTEAIRNGVLNAAFNHLIFKDAEDFKPTVSYSSYYYDSDTAENGISISQSGLLFLLS MFLGRREMEDLKSRVRGFKARIIKHEEQHVSGLKFMATHWVFSEFCFKGIKTRLNADYHEE TLLIQLIDELSKVPDELYRSFDVATRERFIEDINEYIRDGKEDKSLIESKIVHPVIRKRYESKFNY FAIRFLDEFVNFPTLRFQVHAGNYVVHDRRIKSIEGTGFKTERLVKDRIKVFGKLSTISSLKAEY LAKAVNITDDTGWELLPHPSYVFIDNNIPIHLTVDPSFKNGVKEYQEKRKLQKPEEMKNRQ GGDKMHKPAISSKIGKSKDINPESPVALLSMNEIPALLYEILVKKASPEEVEAKIRQKLTAVFE RIRDYDPKVPLPASQVSKRLRNNTDTLSYNKEKLVELANKEVEQTERKLALITKNRRECREK VKGKFKRQKVFKNAELGTEATWLANDIKRFMPEEQKKNWKGYQHSQLQQSLAFFESRPG EARSLLQAGWDFSDGSSFWNGWVMNSFARDNTFDGFYESYLNGRMKYFLRLADNIAQ

[0090]

		QSSTNKLISNFIKQQMPKGLFDRRLYMLEDLATEKNKILSKPLIFPRGIFDDKPTFKKGVQVS EEPEAFADWYSYGYDVKHKFQEFYAWDRDYEELLREELEKDTAFTKNSIHYSRESQIELLAK KQDLKVKKVRIQDLYLKLMAEFLFENVFGHELALPLDQFYLTQEERLKQEQEAIVQSQRPK GDDSPNIVKENFIWSKTIPFKSGRVFEPNVKLKDIGKFRNLLTDEKVDILLSYNNTEIGKQVIE NELIIGAGSYEFIRREQLFKEIQQMKRLSLRSVRGMGVPIRLNLK
29	Cas13	MENQTQKGKGIYYYYTKNEDKHYFGSFLNLANNNIEQIIEEFRIRLSLKDEKNIKEIINNYFT DKKSYTDWERGINILKEYLPVIDYLDLAITDKEFEKIDLKQKETAKRKYFRTNFSLLIDTIIDLR NFYTHYFHKPISINPDVAKFLDKNLLNVCLDIKKQKMKTDKTKQALKDGLDKELKKLIELKK AELKEKKIKTWNITENVEGAVYNDAFNHMVYKNNAGVTILKDYHKSILPDDKIDSELKLNF SISGLVFLLSMFLSKKEIEQFKSNLEGFKGKVIGENGEYEISKFNNSLKYMATHWIFSYLTFKG LKQRVKNTFDKETLLMQMIDELNKVPHEVYQTLSKEQQNEFLEDINEYVQDNEENKKSM ENSIVVHPVIRKRYDDKFNYFAIRFLDEFANFPTLKFFVTAGNFVHDKREKQIQGSMLTSDR MIKEKINVFGKLTEIAKYKSDYFSNENTLETSEWELFPNPSYLLIQNNIPVHIDLIHNTEEAKQ CQIAIDRIKCTTNPAKKRNTRKSKEEIIKIIYQKNKNIKYGDPTALLSSNELPALIYELLVNKKS GKELENIIVEKIVNQYKTIAGFEKGQNLSNSLITKKLKKSEPNEDKINAEKIILAINRELEITENK LNIIKNNRAEFRTGAKRKHIFYSKELGQEATWIAYDLKRFMPEASRKEWKGFHHSELQKFL AFYDRNKNDAKALLNMFWNFDNDQLIGNDLNSAFREFHFDKFYEKYLIKRDEILEGFKSFI SNFKDEPKLLKKGIKDIYRVFDKRYYIIKSTNAQKEQLLSKPICLPRGIFDNKPTYIEGVKVESN SALFADWYQYTYSDKHEFQSFYDMPRDYKEQFEKFELNNIKSIQNKKNLNKSDKFIYFRYK QDLKIKQIKSQDLFIKLMVDELFNVVFKNNIELNLKKLYQTSDERFKNQLIADVQKNREKG DTSDNKMNENFIWNMTIPLSLCNGQIEEPKVKLKDIGKFRKLETDDKVIQLLEYDKSKVWK KLEIEDELENMPNSYERIRREKLLKGIQEFEHFLLEKEKFDGINHPKHFEQDLNPNFKTYVIN GVLRKNSKLNYTEIDKLLDLEHISIKDIETSAKEIHLAYFLIHVRNKFGHNQLPKLEAFELMKK YYKKNNEETYAEYFHKVSSQIVNEFKNSLEKHS
30	Cas13	MEKTQTGLGIYYDHTKLQDKYFFGGFFNLAQNNIDNVIKTFILKFFPERKDKDVNAAQFLD ICFKDNDADSDFLKKTKFLRMHFPVIGFLASNNDKAGFKRKFSLLLKAISELRNFVTHYYHQ PIEFPSELFELLDDIFVETTSEIKKLKKKDDKTQQLLNKNLSEEYDIRYQQQIERLKELNAQGK KIPLNDETAIRNGVFNAAFNHLIYKDGGDLKPSRVYQSSYSEPDPAENGTSLSQSSILFLLS MFLERKETEDLKSRVKGFKAKFIKNGEEKISNLKLTATHWVFSYLCFKGIKQKLSTEFHEETLL IQIIDELSKVPDEVYSAFGAKTKQKFVEDINEYMKEGNADLSLEDSKVIHPVIRKRYENKFNY FAIRFLDEYLSSTSLKFQVHVGNYVHDRRIKNINGTDFQTERVVKDSIKVFGRLSKISNLKAD YIKEQLSLPNDSNGWEIFPNPSYVFIDNNVPIHIQTDEATKNGIKLFKDTRRKEQPEELQKR KGKLSKHNIVEIIFKETKGKDKPRVDEPLALLSLNEIPALLYQILEKGATPEDIELIIKNKLAERFE KIKNYDPETPAPASQISKRLRNNTTAKGQETLNAEKLSILIEREIEDTETKLDAIEEKRRKAKKE YRRNSPQKSIFSNSELGRIAAWLADDIKRFMPAELRKNWKGYQHSQLQQSLAYFEKRPQE AFLLLKEGWDTSDGSSYWNIWVINSFSETEDFEKFYENYLRKRAKYFSELAGNIKQHTHNA KFLRKFIKQQMPADLFPKRHYILKDLETEKNKVLSKPLVFSRGLFDSNPTFIKGVKVTENPEL FAEXXNGIATGTKRNIPSSISMAGKETIMSF
31	Cas13	MEQNKLGKGIDYNPFKTVDKHYFGGFFNLADNNIQEVFDEINIRYKNGNLKPKVAIERYTT ENTSLVEYEKFVAILTEYFPIVKEIDQKNKKDSNDKVIEKTRIERITDFRDAFILFIETIEKLRSYY THYQHDDITIDNQLFIHLDKILLNTVLETKKKYLKTDKTKELLKNSLQAELKELYHLKINQLEQ KKNEVDALIKEQKSKGKKTDKPFKYSKDRDQIINSIYNDAIRPFLYENANKVELSDKKKTAF NEKDASASERDFNLPISSSGIIFLLSCFLNRKEIEDLKANIKGYKGKVIKGETFDLEKNSIRFMA THRIYSVMCYKGLKNKIRTSESATKETLLMQMIDELSKIPDIVYKNISTDLQNTFTEDWNEY

[0091]

		YKDNIENNENLENSKVIHPVIRKRYEDKFNYFAIRFLDEFVDFPSLRFQVHLGNYIKHSMPK NIGSVTTTREIKNKIFVFGKLNEINQSKNDFFNKNKEEEQETNWEIFPNPNYHFPMENSDE LKNANKIGIYIDLKDKRKKDTLNEAIKKREKETSIYKKDLVHQIIDKNLDMHIGQPVAYLSM NDIHAIIFSILSQNVFTKDNKLNGGDIEKKIKDQINNQITEITEKDASIKILKNHSDNNSNYP NTHKLYDDISNEIEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNEIEVLDKLMQKHEKRVKEYINTQ EDKKYKPARKHILYNSEKGEIATWLANDIKRFFPKEFKENWKGHYHSEFQRNLAYYETNKK EVKTILNDLDYRKEIPFIDFSKNTLADFYFEYLKKRKIYHKNLWVEVNKLIKGENINKEKLFDN CFRIYKRKNYVSNVIDEKVNTILSNPIFIERGFIDEKPTIIPKMPLEGNEEHFAAWFVAFKSFK NNEFQNFYDTNKYPLETKDKTNSELKKIQTKTYNQKKNDWATWLIVQYIFKDIFSTDLQN VKLSELFQTREQRIQNQVKALDGERNQNFIWNRTIDLQLNEKIKIPNVKLKDIGNFRKYVN DSRVEAFLRYNDITQWMAYLPSNWQKEDESKPKPVNVIQLQLDDYEKIRREELLKEVQKL EKTIYNNTNVKTVLLQDGNPNFKNYVLNGLLEEIKGINISAFTVLHEKTNFDKIDFNVLENC SEIEQSATLIILIRNKFAHNQLPSSDCYQFCSKILTRDTEQTYANYYLKLFMILKDKL
32	Cas13	MEETTTMGKGVAYDHTLFKDKHYFAGYLNLAVNNIENVFKTVYKNRFDIKQHNLYKILDS LDGQISEPDYIERVSFLKQYFPVLHYLDLHPDNKRFTKEEDKVKARRRYLINNLRLLIETLSKL RDFYTHYYHKPLSIEQNTFSLIDNIFLNVVIDVKRQKKKNDHTRQLLKDSLKEEMDILYQKT KASLKEKQKENTRIKLDSETINNTIFNNSFSHLIYRRKKADNDILSASCKSEYKGEPTENGIN VSVDGLLFFLGIFLSRKESNDLRGRIKGFKGTVIKDLPDFPNEKNNSLKFMATHWVFTYLNI KPIKQKLNTNFSRETLLLQIVDELTKIPNEIYRNLCFKKQQEFVEDINEYIKEGDDIDTLNSST VIHPVIRKRYENKFNYFVLRYLDEFVSFNSLRFQIYLGNYVHHIQRKKLSGTEYETERVIKEKI NVFGKLSEVSNIKGDYFIQNNPDNEALGWEIYPNPSYNFTGNNIPIYFDINDQDKEKINEY KSIRNFSEKRILRKKNKKNKQEIFDLINNTLTTRVFTAEPTAILSLNELPALLYTILCENKTASEI ENLLRRTYLKRLNTIKNYQPGTLPQSKITKNLNKSTNQESLDVSKLIKAMKHEISISNEKLTLI KKNQNEVKDTSHRRKYVFNSKELGIEATWLANDLKRFMPKKVRENWKGYMHSQLQNSI AYYSQKPKEALSILSSVWNFNDDNYIWNEGIKKAFNEKEFEKFYCKYLASRNKTLEKLKENL DNLEYKTDKRKLDKFIKQQNLDCLFHIRTYTIDSTQEQINKLLAKPLVFPRGIFDSKPTFVKN ESVTEKPELFADWYTYTYKEHPLQEFYSFTKDYECNFKKEKLTVKEFVKNQEQLNPEEQLNL FKLKEDLSIKCIKNQDLFLKLVVDNIYNKIFEYNIDISLKNLYISRKERIAIGLKAKELNQINDSY IWGKTILYQDKQIRETKVQLKDINKIKRFLEEDKVKQILSYDINKQWEIEELKYELYIKPNSYEV IRREKLFKAIQEFESYILTINNFDGSNHPSILEYNSNPRFKHYVVNGLLLKKGLATNEEIEWLL AKGQKEFNTFDKSIVEKPEIIQKAFLLVLIRNKFAHSQLPIKEYYEMIRSYTKNIENLNTTEIIFQ FTTNTINELKR
33	cas12b	MATRSFILKIEPNEEVKKGLWKTHEVLNHGIAYYMNILKLIRQEAIYEHHEQDPKNPKKVSK AEIQAELWDFVLKMQKCNSFTHEVDKDVVFNILRELYEELVPSSVEKKGEANQLSNKFLYP LVDPNSQSGKGTASSGRKPRWYNLKIAGDPSWEEEKKKWEEDKKKDPLAKILGKLAEYGLI PLFIPFTDSNEPIVKEIKWMEKSRNQSVRRLDKDMFIQALERFLSWESWNLKVKEEYEKVEK EHKTLEERIKEDIQAFKSLEQYEKERQEQLLRDTLNTNEYRLSKRGLRGWREIIQKWLKMDE NEPSEKYLEVFKDYQRKHPREAGDYSVYEFLSKKENHFIWRNHPEYPYLYATFCEIDKKKKD AKQQATFTLADPINHPLWVRFEERSGSNLNKYRILTEQLHTEKLKKKLTVQLDRLIYPTESG GWEEKGKVDIVLLPSRQFYNQIFLDIEEKGKHAFTYKDESIKFPLKGTLGGARVQFDRDHLR RYPHKVESGNVGRIYFNMTVNIEPTESPVSKSLKIHRDDFPKFVNFKPKELTEWIKDSKGKK LKSGIESLEIGLRVMSIDLGQRQAAAASIFEVVDQKPDIEGKLFFPIKGTELYAVHRASFNIKL PGETLVKSREVLRKAREDNLKLMNQKLNFLRNVLHFQQFEDITEREKRVTKWISRQENSD

[0092]

		VPLVYQDELIQIRELMYKPYKDWVAFLKQLHKRLEVEIGKEVKHWRKSLSDGRKGLYGISLK NIDEIDRTRKFLLRWSLRPTEPGEVRRLEPGQRFAIDQLNHLNALKEDRLKKMANTIIMHAL GYCYDVRKKKWQAKNPACQIILFEDLSNYNPYEERSRFENSKLMKWSRREIPRQVALQGE IYGLQVGEVGAQFSSRFHAKTGSPGIRCSVVTKEKLQDNRFFKNLQREGRLTLDKIAVLKEG DLYPDKGGEKFISLSKDRKLVTTHADINAAQNLQKRFWTRTHGFYKVYCKAYQVDGQTV YIPESKDQKQKIIEEFGEGYFILKDGVYEWGNAGKLKIKKGSSKQSSSELVDSDILKDSFDLA SELKGEKLMLYRDPSGNVFPSDKWMAAGVFFGKLERILISKLTNQYSISTIEDDSSKQSM
34	cas12b	MATAVDTSTTRAYTLRLSGGNNWRELLWQTHVAVNRGAWVWGDWLLTLRGGLPASLA DGDAERRVVLALSWLSVESPASLAPQAHIVAYGSDARDERNRKVTERFRDILRRMGIKQQ QEQEWLDACLPALMASIREDAVWVDRSACFAEAQQCYRGLSSEWARKTLFDFLGGEDD YFKPSAKEGASSKAKDFVQKAGRWLSRHWGAGKKSDPRDISTRLGKLAGVDPKAIDGHT GRAALEDLLRTLGSRPAQNADAEKLYRQLKRAVGWKGRPSKGAVALKKIRDAERVPNDL WKEIASTLREEAAVQSSQTSDHAAVPDWRSHWPAEITGLPMPYRVDRDYIWEHGVMLD HALRRVSSAHTWIKRAEAERRRFQQDAAKMGSIPEEARNWLDAFRERRSSSSGATGDYLI RERAINGWDKVVQAWETLGPNSTRDQRIAAARDVQANLDEDEKFGDIQLFAGFGDEHV DDPERCLADDRATCVWRNSSGRADGRILKDYVAATVAEHNQRRFKVPAYRHPDPLRHP VFVDYGKSRWSINYSALTAAQQRRKTTQKLAQAKTDNTRAKLQQQLASTADLRSVTLGV WDGNRIVKISQRWRSKRFWRDLDLDHFGSHPSAAVSRADRLGRVAARQDPGAAVYVA KVFEQQDWNGRLQVPRRELNRLADVVYGKGADPDFGKLERLDPRARRLWERLSWFLTTS ATVQPQGPWLDYVAAGLPSGIQYTKSRAGYYLNYDANHGRKGRARLCLARLPGLRVLSL DLGHRYAAACAVWQTLTIEQMTNECRQAAHPAPSNDDLFIHLRHPTHKPQKSGRKKGR PVTKTTIYRRIGPDKLPDGTDHPAPWARLERQFLIKLQGEDRPARYASQKEIDEVNQFRNF VGLEPIVDRPRVDDLHSDAVRVARLGLRRLADAARIAFAMTAAKKPISGGHEVELTTAQRI EFLQDALLLWQSLAASRRYRYRDDWAEKLWQSWVVEKLGGPQPAEIADDLPRSQRAASLKT ARQSLRKVAEKLSDGQSPSAAELHRLWAERWQQRQTEWRRHLRWLRRLILPRRKDHQQ EDRPLQRVGGLSVKRIQTIRQLYQVLKAFRMRPEPSDLRKNIPAPGDRSLASFGRRILNHLE RLREQRIKQLASRVVEAALGAGRISKPPGRDRRRPQQPVDRPCHAVVIENLQHYKPEDSR LRRENRQLMDWQARNLRKYIVEGCELHGLLFVEVSPAYTSRQDSRTGAPGLRCEDVSRTA LQEAARRMHASHSRPSNSSPGGSQTQFEREVCRWINEFKRVEGSSSSLSARQAVLKAFLH HQASIPTSLSTILLPRRGGELFVSADPDSPLACGLQADLNAAANIGLKALTDPDWMGAW WFVLVDRASGQPVEEQVQGCPIWLSCGPLSNSNPATIDPSDSPTAARRSNGTGAKGRAR ANEYWWSSLSATTLPDHKAWQPTQDYWRDIEQRVVKRLLRLLDGSEWSED
35	cas12b	MNRIYQGRVSKIEIKDSEGNFRNVPVGSPDTCPLWRHHRIFQDAVNYYLVALGALAGTGS ENAFVGLGSKDRVIHDLYSRLFDSWERFPRDMHGASSLRDSLRRTLPGLSERASLQDAFD AILSGNEANARERVLSLLSLIQDLGGDIQKGSKRYFPFFCEPATKATFPRARVGLLKVEGKDF VPRLLWSSDLEIAPDQVVEQLKFEYFANPNESVQPIEGNEARVRLIEALDNPQLGIELPIEILS DLRKRVHLIETDIRIPRYFFGGAGAELRKFRLDLFLIAAYVTPDPSILRALRNSFKEPSASKSSK KKDETEEVENLLRSLGDDPLILARGERGFVFPSFTSLPTWVGANAQKPIWRDFDIAAFAEAL KSLNQFTAKTEEREEKLKKAEETLHYMLGISDAIPRSSDSETEEQAPSRPGKDPRWPLVAQL EKELGENLSEGTWQLSRSAMRGLRDIIGLWRKHPGASVVTLQKDVKTYQADEKHKREIGS VQLFLLLCEERYHALWQTETDDERGDESEENDDPARILSDAIEVHQIRREVERFREPIRLTPA EPVFSRRLFMFSDLTDKLAKVKFGETTEENSEVKSQFVEAAIALKEGENLKEARVRITFSAPR LHRDELLGGAESRWLQPITAALGFSNPAPSVKFDSAVALMPDHMDDGRIRHLLNFPVNF DSAWLHQSIGKADLWKSQFNGTKDKNLHLHWAGTARDTTRKNTWWENRTIIENGFTVL

[0093]

		SNDLGQRSAGAWALLKVTCSRPDTKHPVRSIGHDGTREWFATVLATGIHRLPGEDQRILK NGKWATEQSGKKGRNATFSEYEAACVLAKNLGCESVENWLGMSGEKSYPALNDQLVKI ANRRITRLGTYHRWSCFSPEKFEDPARRANVIGGQLAELSAYQDENVTVSADILKSGDFEG FRHRAGAAFEALRTELEVHLVNLANLTAPLRQKVWSWQKRPDSSGYGDLLMVDLDDCH PKIRGQRGLSMARLEQLEGLRRLFLRYNRSLDRSPGIPAKFGREDVGRTSGEPCQALLVKID RMKEQRVNQTAHLILAQALGVRLCPHRIEENERKSRDLHGEYEKIPGREPVDFIVIEDLSRY LSSQGRAPSENSRLMKWAHRAVRDKLKMLAEEPFGIPVVETVPAYSSRFHALNGQAGSR LHELHELEAYQQQSLINLAAKTDFQNRDRSKAAGELFEQFQALAKLNERRRAEGKKVPRTL YYPKSGGPLFLASRDGDTIHADVNAAINLGLRAIAAPACIDIHRRLRATKEKEVYRPRVGNA REKSAFSKDDIIQPSGAPSKKFASSSSPNFFYEPEDLKQANGEPLFDRAMFGEYSLVSGVSL WSMVNNAIYIRCVELNRTRLHGKDPDDQIPM
36	cas12b	MSITRSIKVKLIVPRDASLEARQLREGLWATHLFVNDGCHYYERLLLEFRQRDVCVGKDDA GKDVIVPAAEWADRLRARLGRNGMVPSHIEAALPIFRELYENMVPSALKAKSGTGQAGRS WHSKLVSPTSRGGEASAARIDVLRPLLPVSGDDPAFEPAARALIEEAGDELLTSTGRCPAW VTAYRKGPEGSAWVEKLRIQLREAVEAGDFDPPSDPQILAAGAVPAAPPLGAGIDALRPLL PLLGGDPAFEPAARALVEDIGDELFTSTGRPPTWVTAHPTWVRAHRKDAECLEAADDFK WVERLRQRLRDDAKAGKFEQPLHERLGALGALPVAKPIGAGRVVSRADLTVFERGAMELA IEHLIGWESAGHRARAQYVERKKRHDDLLQWIEAEAPDALLAVRAYEAARTIHLATLGELG AAPQYTLRLREIRPWRKLREWLLQNPDATIDERRRRLATMQTNDPRGYGGEALAWLAAP ERRALVEHPAGDVVTRIAVLNIRKSILDRSRLFPTCTLADPVEHPRFAKFGKPGDKNSAGYA LAVDGVRREAIIKILVPRQDGLLVPTDLRVPFAPSGQMRDLRASGLDISYERQDGRGRQAA KLQGGNLMFDRTHFARCGAPGPEALGSVWIKVALDLSSPAASLAMKTATPVRTYLSTAVR GRPESTKYEKAAPPEGFRVLSVHMGLRTAATASMLRFGAPEEGGHEVPVSGLAGETLVAF HERTVTMKLPGEDPDTRTEANRGVAKRELRGLGRGIGCLKAIRRASASATPEDRAEALVIIE THVGQGDRHGWAPAEAVGRLDPHGDPDDWKTACAALYAAVEADLGVAISSWRKAAR AGGATGMLGGKSLWAVDHLERSFRFLRSWDLRARPHDGDPRRPRPGYASKLLHHIDGV KDDRVKTTADRIVQAACGRAWIGGPTVKRGTQDVRLPGRWEQRGPRADLILLPDLTHFR FRSDRPRAENSRLMRWAHRQLAIYVRMQAEVEGILVADTGAAFTTRFDAWTGAPGVRC EPVTADHLRGIAKREDYWLARLLREGALKHLRIDPASLRVDDLVPMDHGKILVALDGVDLP GLRILDTDVNASQGLGRRYIEGHGLAYRLPGARVPRGEGEREAAVVHIKGKRLASAMGGT VVVLRASEGPGDITWTAEVYDRPQGARKALGLSLAAFNSIATAAVDDEGPAPENDDEALE EEAEEALGIATGERIVFFRDPSGAVAGGGWLEASAFWGIANRMVTDRLRELGRLG
37	cas12b	MSLNRIYQGRVAAVETGTALAKGNVEWMPAAGGDEVLWQHHELFQAAINYYLVALLAL ADKNNPVLGPLISQMDNPQSPYHVWGSFRRQGRQRTGLSQAVAPYITPGNNAPTLDEV FRSILAGNPTDRATLDAALMQLLKACDGAGAIQQEGRSYWPKFCDPDSTANFAGDPAM LRREQHRLLLPQVLHDPAITHDSPALGSFDTYSIATPDTRTPQLTGPKARARLEQAITLWRV RLPESAADFDRLASSLKKIPDDDSRLNLQGYVGSSAKGEVQARLFALLLFRHLERSSFTLGLL RSATPPPKNAETPPPAGVPLPAASAADPVRIARGKRSFVFRAFTSLPCWHGGDNIHPTWK SFDIAAFKYALTVINQIEEKTKERQKECAELETDFDYMHGRLAKIPVKYTTGEAEPPPILAND LRIPLLRELLQNIKVDTALTDGEAVSYGLQRRTIRGFRELRRIWRGHAPAGTVFSSELKEKLA GELRQFQTDNSTTIGSVQLFNELIQNPKYWPIWQAPDVETARQWADAGFADDPLAALV QEAELQEDIDALKAPVKLTPADPEYSRRQYDFNAVSKFGAGSRSANRHEPGQTERGHNTF TTEIAARNAADGNRWRATHVRIHYSAPRLLRDGLRRPDTDGNEALEAVPWLQPMMEAL APLPTLPQDLTGMPVFLMPDVTLSGERRILLNLPVTLEPAALVEQLGNAGRWQNQFFGSR

[0094]

		EDPFALRWPADGAVKTAKGKTHIPWHQDRDHFTVLGVDLGTRDAGALALLNVTAQKPA KPVHRIIGEADGRTWYASLADARMIRLPGEDARLFVRGKLVQEPYGERGRNASLLEWEDA RNIILRLGQNPDELLGADPRRHSYPEINDKLLVALRRAQARLARLQNRSWRLRDLAESDKA LDEIHAERAGEKPSPLPPLARDDAIKSTDEALLSQRDIIRRSFVQIANLILPLRGRRWEWRPH VEVPDCHILAQSDPGTDDTKRLVAGQRGISHERIEQIEELRRRCQSLNRALRHKPGERPVL GRPAKGEEIADPCPALLEKINRLRDQRVDQTAHAILAAALGVRLRAPSKDRAERRHRDIHG EYERFRAPADFVVIENLSRYLSSQDRARSENTRLMQWCHRQIVQKLRQLCETYGIPVLAVP AAYSSRFSSRDGSAGFRAVHLTPDHRHRMPWSRILARLKAHEEDGKRLEKTVLDEARAVR GLFDRLDRFNAGHVPGKPWRTLLAPLPGGPVFVPLGDATPMQADLNAAINIALRGIAAP DRHDIHHRLRAENKKRILSLRLGTQREKARWPGGAPAVTLSTPNNGASPEDSDALPERVS NLFVDIAGVANFERVTIEGVSQKFATGRGLWASVKQRAWNRVARLNETVTDNNRNEEE DDIPM
38	cas12b	MPTRTINLKLQISPKTDEGRKIRSALWTTHSEINKAVAEIEKLLLLCRGEKYYTTNSKDEEVEV PEPQVKTDALEMARAVQAKNGKAGTGSDEEVLSALRMLYEATVPSSVLDDKGKPLSGDA QSIGGSYAGPICDPETCRIKDVDRLFESGPFAETASKKFTQLPAWFNEVTKKNFNKDEPEKF VKVGKDKDEKFYEIDLRQADAWYESPEVKDIVSKNKAFNKDKWWKNKRDGVDTWAAEF VKKQFDLRKDVRVSIREELWDRLGLLPLGSLYFKKPVGNKWNRMAFRLAIAHLLSWESWN HQTLAEYTKYTKYKDGLIELAGASRSLEVRFEPLRQYQKERHEELSRTSFVDDDRPFTIGAR MIRAWGRVREAWRNKGDGIDERRQILADLQTELKGKFGDPHLFLWLAEAGRESLWRDE DVLTTFVEINIAQRDLERHRPYSLMTFADARLHPRWAMYEALGGTNLRNYELTPEGKVKIP LLICEKDKLSEKTFTIPLAPSGQLKSLEIKSLPKKKVKISYASAHQFYAGIPGGSEILFDRLFME NRASSALANGSCGPAWLKLTVDVESKAPPEWLDKKGRVQTPPTVHHFKTGLANKSKHTD KLEPSLRVLSVDLGLRTFASCSVFELVDEKPAKGLFFETDHPHLWAKHERSFKLTLPGEEAG DDPKVAQARREAMDEVYSLRRDMYRLKDILRLKIISAPNERREKLESKIAEMREKQDARAV VTSNFFERLSEKCDLNPPMWEHSCNEIHRDAEKAFSARIGEWRKRTRKRPGSWEEWRETR SVHGGKSYWMIEYLEAVRKLLIGWSTHGRDYGEINRQNKKRYGTVASKLLKHINKLKEDRT KAGTDLIIQAARGYIPLPGKGWMEKYRPCRVILFEDLARYRFKVDRPRRENSQLMKWGHR EIINEATLQGEIYGMVVETAGAGFSSRFHAKTGAPGVRCRYLKEDDFENGAPKEFLVRQMK NLMKGDRLEPGLLVPWDGGELFATVDNGKPIVIHADINAAQNLQRRFWTRFADAYRVN AVEENDNWVVTDTGVRVLGALEMAVHGEADRKPRTGFTLHGTLQSGAELKAEGKKTDIK DVEEDKDDSISSEIIELQDEKERKGRETFFRDPSGGILDPGKWYGSKRFWGRAKGAVTEALL DNQGANNALEEKPGNDELPF
39	cas12b	MATRSFILKIEPNEEVKKGLWKTHEVLNHGIAYYMNILKLIRQEAIYEHHEQDPKNPKKVSK AEIQAELWDFVLKMQKCNSFTHEVDKDEVFNILRELYEELVPSSVEKKGEANQLSNKFLYP LVDPNSQSGKGTASSGRKPRWYNLKIAGDPSWEEEKKKWEEDKKKDPLAKILGKLAEYGLI PLFIPYTDSNEPIVKEIKWMEKSRNQSVRRLDKDMFIQALERFLSWESWNLKVKEEYEKVE KEYKTLEERIKEDIQALKALEQYEKERQEQLLRDTLNTNEYRLSKRGLRGWREIIQKWLKMD ENEPSEKYLEVFKDYQRKHPREAGDYSVYEFLSKKENHFIWRNHPEYPYLYATFCEIDKKKK DAKQQATFTLADPINHPLWVRFEERSGSNLNKYRILTEQLHTEKLKKKLTVQLDRLIYPTES GGWEEKGKVDIVLLPSRQFYNQIFLDIEEKGKHAFTYKDESIKFPLKGTLGGARVQFDRDHL RRYPHKVESGNVGRIYFNMTVNIEPTESPVSKSLKIHRDDFPKVVNFKPKELTEWIKDSKGK KLKSGIESLEIGLRVMSIDLGQRQAAAASIFEVVDQKPDIEGKLFFPIKGTELYAVHRASFNIK LPGETLVKSREVLRKAREDNLKLMNQKLNFLRNVLHFQQFEDITEREKRVTKWISRQENSD VPLVYQDELIQIRELMYKPYKDWVAFLKQLHKRLEVEIGKEVKHWRKSLSDGRKGLYGISLK

[0095]

		NIDEIDRTRKFLLRWSLRPTEPGEVRRLEPGQRFAIDQLNHLNALKEDRLKKMANTIIMHAL GYCYDVRKKKWQAKNPACQIILFEDLSNYNPYEERSRFENSKLMKWSRREIPRQVALQGE IYGLQVGEVGAQFSSRFHAKTGSPGIRCSVVTKEKLQDNRFFKNLQREGRLTLDKIAVLKEG DLYPDKGGEKFISLSKDRKCVTTHADINAAQNLQKRFWTRTHGFYKVYCKAYQVDGQTV YIPESKDQKQKIIEEFGEGYFILKDGVYEWVNAGKLKIKKGSSKQSSSELVDSDILKDSFDLAS ELKGEKLMLYRDPSGNVFPSDKWMAAGVFFGKLERILISKLTNQYSISTIEDDSSKQSM
40	cas12b	MYRGFCTVTATSGGWQSTTFLAGAQMADTTTRAYTLKLQGDRLALWRNHVIFNNGVKA WGEWLLCLRGGLPASLADHRDSLDVSKGEISRTFKERTAAITPATIRQELKFKAATEKKVRE EVASRRKKVTETAVAKELLAARRSELRRILALSWLCPETPVQLVPQAAIVAAADDSDREQK VLDGFRQILKRKGVSDVAGWVQDCDATLRATIRSDAVWVDRTACFCSMPRAVRPSEVD AAKHLFRLFGSMSDYFATASASSGPAEPKDFANTCRDWVSSFWGGGEKSNKASILAALSA IAQIKPTRVVGKRGPAALAVIAGVLEQKPVDDSVEALARAIGWLSGRPSAARLAINAIAASP RVSQKLWDRLVLACEKDCGRQKSKLAFEGSASTIASALEPRLAGLTGMPYASTGRELIGEY ATMLAFAMRRVSQIHTKAKQAEAERRSFAPEQARLALVPSAARKWLEDYVEARTAASGA VDGYQLRKRALGGWADVVAAWSRCETSEDRIAAVRELQADWEKAGDVQLFEALAADD AICVWQSANGKTAASILTDYVRAAVADQNATRFKVPAYRHPDPLRSPTFVGFGNSQWSI AYSAQGEARERRKLLDRASGSAKDAERAREGLAREAVLQNVSLDLWAGDKMVPTQFRW QSRRLLSDLALHSVPAMKGAKVTRATRFGRARIAAGPVLLDGIADDTPWNGRLQAPRRQ LEDLARILDAKGLPFDDESKWPPKVRSRLKHLGWFLTHSAKLTPSGPWLDYVAGGLANG WKWAEGREGACLFREDNKDRKGRAKLILSRLPGLRLLSVDLGLRTSAAAAVWQVVSKRQ LTAAKDGAKSVSDTDLFCLVRTGDRTQVYRRIGLSAWARLERQFLIRLDGEKAAARPATTN EWESLQSFRAWLGCGIERRPEKLPPVDSLQQSAERLCRLGLRRLSDLARVAYLLTAKERPIM GGRTAPLDEEGTVQAAQDALSILHALGSSEDFSDARLQGIWRTAIGDTPPLAARLTKKQR QELREALRPAAEKLRGKAALGKELADLWKERSAAWAKHLRWLRDWVIPRFDKRKNGERV RSARGVGGLSLDRIATIRGVYQIMRAYASRAEPTNLRAGVERLEKAAAKKLRPEFGRRMLA KMERLRENRVKQIASRIVEAALGVGSEDRLHWERGRRRPTAAISDPRFAPCHAVVIENLEN YRPDEKRTRRENRGLMSWAARAVGKYLAEGCQLHGLYLRQVSPAYTSRQDSRTGCPGLR CNDVRAQELLNPEGWIGRLVARAAEAVKEGKATPRQRLLVTLAESARAGIAESAAVRIIAP GGQLFIAADPQSPASNGIHADMNAAANIGLVALLDPDWPAAWWRLPCKAATGYVDES KVGGSEAVPLGRAILEVGAEAGKVYVNAWSDPQDSAVSRREWTDTKRYWRDVEERVVEI LLASNRGGRRGKPGAVPF
41	cas12b	MATKSFEAKIVCKPDEKYTAEQKKQFLWFTHQVFNDGVRKVIPYVFKMKRGELGPEFQAI YYAITSSQDAIGKLEAVINPDWTSGKIGKSDPNKWKELLKYQELEKGFRQRLKEEGIKSTKKF RKELEDEKKLAKEIGQKDIWADAAAILRNKNLLLFNRDELLPNLPSEFRRKIYEMTIQLIHG HQELVANWEDEHAEWLIEKDKWEEEHPEYMNVRPIFEKFEKEQGKVKGSRIRWLAYLDFL SSKPELANWRGKAKETIPLTKEERAGFRKPGQHFAAFFNKNPELQELDRLHKEYQEKFART QSKRTPHPDGFKHRPTFTLPDAMRHPVWYSFKGATDPTKGSTYRNLDLENCTLDLKVLTA MEGEGRNPGGMIQYAFEPDERIKGFRYVGTTEKGKRAKGYIYYDPILEKERPAKIQGIKLVF RPPRPDGTAYLIFSCQIEDEKPKIKIWKDKEEESPGEITKRKKTEVYPPELITLAIDFGQRHLGA ITICKNNNGRPEPIRFIPAYPKRRKDRESKPVSAWLAKIPGLTFNAVGMHEKEISAGMSRRF QDPKSIRQAGEKEGRKSKGQHIPETETPWAHLREHIANMKEDHYKKAANLIIRTALQNGA QVILIENLRNYRPMLERTNLENRRRMQWAVRQTAKFLEDTARPLGLIVRQVSSAYTSRFCS SCGHPGARVSLPGQKNWEKFYAEKYGKERKMIAVAGGQFFCCPACKKIINADINASLNM HKVFYQNFIWPGKIDKKDTKNFIWQGKNYNWDQIADDVQSFLDQKAGIKKEDDIPY

[0096]

42	cas12b	MAYGSEAPDERNRKVTERFRIILSRMGINQQQEQEWLDACRPALTASIREDAVWIDRSAC FAEAQQHYPGLSSEWARETLFDFLGGENDYFALPDPEAAPSSEAKDFVQKAGGWLSRHW GAGKKSDSTAISTNLNRLAGVESKAIVGRCGCDALAVLLTTLGGWPAKNADSGTLYHQLK QAVGWKGRPSRAAKALEKVRDAPEVTDALWRQTADTLRQEAVAQSSRAAGGSGVPAW MPAWREDMEARLGMPYRGARDYIWEHSVMLDHALRRVSSAHTWIKRAEAKRRRFQQD ADKIGSIPAKAREWLDAFRERRFSASGALRGYLIRERAIDGWDRVVQAWASLGPNCTREQ RIAAARDVQANLDEDEKFGDIQLFAGVGDEDEGDPQPCLADDDAICVWRDLNGRADSN ILKDYVAATVAKHDQQRFKVPAYRHPDPLRHPVYVDYGNSRWSIEYSALKAAHQRRKTTE KLVQAKTDRARAKFQQKPADTPDLRGVTLGVWTGSSIEKVSLHWHGKRFWKDLDLDHF GRDPSATVSRADRLGRVAASQHPEAAVHVAKVFEQQDWNGRLQVPRHELQRLADLVY GKGGDPDFAKLGSLDERRTRRQWEHLSWFLTTSTTIQPRGPWLDYVAQGLPQGIQYKKG RNGYYLEYAANQGRKRRARLCLARLPGLRVLSLDLGDRYAAACAVWETLTREQITQECHQ AGHPGPSQDDLFIHLRHRTGKPQKSGRNKGKPVTKTTIYRRIGPDLLPDGTPHPAPWARL QRQFLIRLQGEDRPARFASQHEIDGSNRFREFLGLPPLADRPRVDDLHRDMVRLARLGLR RLADAARIAFAMTATKKPISGGREETLATEQRIEFLQDALVRWQALAASSRYRDDWARQA WQEWIVEKLGGPQPAEIADELPRSQQATRVETARRSLREVAAKLSNPQSSSATELHGLWA ARWQERQTKWRQYLRWLRRLILPRRKDYQQANRQVHRVGGLSVKRLQTIRQLYQVLKA FRMRPEPSDLRKNIPAPGDPSLASFGRRILHHRERLRQQRIKQLASRLVEAALGAGRISKRL GRDRRRPRQSVDAPCHAVVIENLERYKPEDSRLRRENRQLMNWQARNLRKYIVEGCELH GLLFVEVWPAYTSRQDTRTGAPGVRCEDVPRSVLEEATRRIRALGSAPSGSSRGRSETRFE REVCRWIHEFNRVVGSSSGLSPRQSVLKAFLDHQAAIPTWRSTVRLPRRGGELFVSADAN SPLANGLQADLNAAANIGLKALTDPDWMGAWWFVLVKRDSGQPVPQQVQGSPIWES CTRLSSPATVDSSDSPAGARRSKGRGARGRARATEYRWSPLSAMTMPDNKTWWPTRDY WPEIERQIADRLLREQIDPENRF
43	cas12c	MKKTSPLKRSALRTARRQIARGCLPIGNRDISTTRTRVLPLADSVADAVWNQARTAALTLR GFGSGSLFDLLLDLHASGLRLFSSNGEREGFLLKQKFDAGKFDRAAAKDVGEDMPKFTAA NLRAALVAIPRGGGPDTDAKALATRLARAVGVKATKLDKPPKLLKDMAKELAMAFPTWK ELSTANGEVGAVIDDVARMYGLRWPSLRRGWAFRLPEVTRELGSPTLAFDPDAPVIDETS ATARFAAIVARYLPECGGLTDSAAAKGVQARITTTNANGLSWLFGVGLRGMRDLPVDTV ADTLAIDVTRGRDALRALVNDIKALPRLGEFGDRVYVESRATLQGAVDSLIANYVGRLADL VASADALEHDQPRPPVLDDADWKPAIFDGMGFTPWEVEDMLDARPVEVARLRLALGVL AGTTPAVAGDFARALADVEAFGAWAARTEAVAALINARVKVLKAPESLRLRGVLGGGRW KAVVSIHPDEGEPAQVIPQLDTQLQALLDDGQRAFDVLVADYTPTFAAALEHARSDMRA SLADKGREAPSAESIDLLARRKLLDMVARVTRRGSPSLGHAFLAACAVQGLTRPGTATERS LRGHILSGEQALFVHPYARARSIVRLEHAGLLRLDLDALLTAMERDAEQRADVREQIVLRFT RQSLLLGGLPGRIRLAKVPWTQEAAAASGVRGAPWLKLHPDDAGTVARSEVIKAFTARFH LSANGLLYRLNRMRFLERYDIRCFIGDTLLFAPKAGAWTPPEQYRHGKYAHWLSHPDLPR TEGGAVDVVPAARWLTEASRRADEDGRASAVALLAQFPHEWVAACEFEGAPVYEGVFPC EGKIGGWMKRRGYRLAPPRHFAGELLAAFKDASVSPHGLTFEREMLREGTTVRELSRRVV AAYPIAVPTHPDAERPWSPLHLMGLDLGEAGLGVCLRHIGTGAETTLLLPVRKTRLLAHRE EHYRRKVQPRQAFRKGYGDAMELAVKAAIGEVCGIIDNLIVRYRAVPVFESAVAQARGSN KMIQRVFAGVVQHYTFVANNGAAQTVRQSHWFGAGRWSYTYGADLLPAARQMTEKQ LLKAKAEAVFRPAMGFPGVMASGYRTSLVCACCGEDVLDAVDAAAEGGQVALTTDAEG SGVLDLGGRSLRIKLEAPSPNPIVQKAARRKRRRTPWEALADRTWTLTHKTDRADLVATLR

[0097]

		RGLRRPPASVQGHATSGWEFHCAACGHIAQADVNAATNLVRRYDDRVRKMEQARAH WDDPSVRAKLASELAERAAARS
44	cas12c	MLTTKFKLELPAGCPLREDAATFDECRKLYDVVEGCGNGTLTGFLFSVILSGFRIFPDGKTAE IFANRSVYDEDEFRSALVEAVGAPLPRFTVKALIKRLQMEVRARGNKDNRFVAEVMMKEY RQTLCGKTLPKGVDESYVDRLFEEMARELTSRYRSWNELKGDLLGACKAVDAALRGFGDF PSLATMVTRAAARRLPKDSTIVFDPQSPCIDVQTIGVDAMPYAAVSTILSYPESVGEKRRDF VQNHLTTPSAAGLSWLFNRGLELFSEESVEELCRLFHVPEDQRTRIVQIQNAARATPRQSF FLKKGGAPLGYHDFRSAFAGRINSWTANYLNRLEELQGLLHDLTDELRLPDLVRNGEDFLA TTDCRREEVEILCRSFSRERDRAQTAVEHLIGADPLQVVSDVAAIEEYSRIVNRLCAIKEQIV NSLRQAEDDKASRWTALWSEVKDEFQPWEKLIRLPKLNGMSGGVPPAQDELETILARYS DVGRGASEHFDAVMEWAAKTGAEGDVLKKFAETEQQRADQRAPGKYDGRELALRLVLQ RVARVVRDRSDACAENVRQWFLKENVFAERKDFNKFFFNRLGNLYVSPFSNRRHAGYKL SDGLVERSGAVWRELLALVKEMRGAYASFSEAGETFLRLESLLMGMRIGALTKNIPAEVAA LRLDDETALESVSEGLKLQLQQAEVPPSVLAKAFNVYVSLLSGCLIALRRERFFLRTKFSFVG NTALVYVPKEKSWPMPSRYEASPSWTPIFENDVLVRLSTGEVEVAETFRRAVALWGRTTD PVLKKALRELFHQLPHDWCCQVSVRSSGDMTPAKRKEDDRDVLIVEKKGKYDSTIISKKIA ATALVRLVGPSTHKERLNRLLLDVGEVACDMTLLADQEILQKVEDDRVHLSPGKLQFSLSV PISTPAEQCEDEVKSERKSTHFRRIVAIDQGERGFAFAVFRLEDAGKKGAQPIAQGFVNIPSI RRLIARVHSYRKGKQSVQKFSQRFDSTMFTLRENVAGDVCGAIAGLMSRYRAFPVLERQV SNLASGGKQLELVYKMVNARFLDDRIPMHSLERTSWWCGTSDWVIPDLWVEVPESYAV KAKKDEILEKDGKFYRTLRITPGAGVNAKWTSRICSQCGGNAMELIEKAREEKVKTVTLDA NGEVTLFGRTLRLYKRPSEERSREARRRNERAPWTEPRADVRLSLDDFRRAVAENMRRQP KSLQSRDTSQSRYFCVFTDCRCHNKEQHADINAAVNIGRRFLESLLRE
45	cas12c	MRRQHHGGQNARDWRRKVAAAALRQKESVFTYKFGLSVNDGDFDFDAAARTYDITEGI ERGSLIGLVCAVHLSGFRLFSKVAETRQFLNRSRYPENEFAQALAAHTEIENPSVTVQSIESV FVTPPRKQDGVARLWSADELAKRLFQTWNNRSPREGERNHPELLLAQGIARAVTKAFSG WKELADNAVHALTCADNYLATLGNRFPKLSDLPPLTAGSTQTGTLAFDPESPFLNMTGNE DIWLHQVVAVCAGRLKRYMPEIDPSSRKFASRLTDSIVSSQNNGLSWLFGNGLRFLRQSSI AQIAETLSVSQNEHRRVEQLKEFADAIPVNPFFATDGYAEFRGSVGGKISSWVSNYWKRIC ELTVLHSQPPDITIPEGLLASENATLFSGQHTAAAGLVALSARLPSQVRDAGKALFVLSGDG VPRADDIATVEDVAGELAELTGQLAMLDNRIQQEIERAQDANDEGRVGSLASLRPNPTKE LKEPPKLNRISGGTADAAGELARLETSLNDLIRARREHFYRLAEWTGNTASLDPLPALAERE RKALTDRGMDPTLAEADEYALRRLLHRIAGMARRLSPNEAKRVRETMTPLFLKKREANLYF HNRAGALYRHPFSNSRHQPYSIDLNRARATDWLAWLEERAREMLGLLGSGAPANHEYLR DLLSIETFVFTTRLSGLPAQVPGYLAKPKSDLTNIPPLLAAQLDVDEVSRDVALRAFNLFNSA INGLSFRAFRDSFIVRTKFLRLGHDELFYVPKARAWKPPADYRSAKGKISKGLALPAVKRNE AGSILPRETTQGLSRAKFPEGSHALLSQAPHDWFVELDLRHDKMPQLAGLPVKMNADGL KGWRARRRPTFRLAGPPSFKTWLDRALTSTAVKLGDYTLILDQSFKQSLRVEDGEVRLSAE PAGIKAEIAVPVIDARPFPETEAEALFDNIIGIDLGERRIGYAVFSLPALLKSGNPTRVKPTVV GSVAIPAFRRLMAAVRRHRGSRQPNQKVSQTYSTALQQFRENVVGDVCNRIDTLCERYR AFPVLESSVANFETGANQLKLIYGTVLRRYTFSNVDAHKSARSAYWYSANRWQHPYLFVR EWNKAQRTFTGSAKPLAIYPGVTIHPAGTSQICHRCGRNALRALRNMPDRTIRVGKDGLI VLADSTIRLLERADYSDRELKTFKRRKQRPPLNMPVPEGARPRDQLERVLRRNMRQQPQS EMSPDTTQARFTCVYTDCGFEGHADENAAVNIGRRFLERIDIEASSRT

[0098]

46	cas12c	MTHAKKIPFPVLKRSTLRKARQRIAAGSITAGERPFNSTVTRVVPVKDPVSDQVWAVARE AAMTLRGFGQGSLFDMLIHLHADGFRLFPSGREREAFFLKDLFDPTEFDDGARRAFGDVM PGFTANSLREILGAPARKCGKVTSVEILLPRLSKGLGVKKSAAPPEVLSSLAAALCEAFPTWS LLTAVDGGVGKVIDDVLRTHGSRLPSLEKAWSTNLPEVPKGLGVPTLAFDDQAPAQSEQT PTGRFAGVVARYLAETFASNPEATAGDASKAVQAKVTTPNGNALSWLFAVGRRAMCSTT LDELAIGLNITSPRGRHALSSLKERMMALPALSVLGERAYPDSRATLQGTVDSLIANYVNRL FELSSSATSIAQTKLILPAAIQGDTAVFDGMPFSAEDVGALFEQLPSEIAKLEHAVKVLVGKE RTSTLGYQKAVDDVDEFGVWASSVDAVIGQINARLKTLERAQEPLGKLMGDGKLKRLVNI HEPEGPAVEIIPVLDQELQDVLTSCRTAFADLEARYPMTVAKAQRHAEAEVRNALELASRK EGGLSLASADVPALAKRKILEPIISIARRSSPAMATAVLTECLRQKLIVKGTGSERSLRGYVLS GEQVIYAHPLSRRRSIVRLDREGLQNFDALEFLDALQKDATQRTNVRESLIVEMARQSLLLS ALPDRIEIGAISWQTPSQNQHAPWANLRPVNGTVGRSETIKSFTAVFHSRISGLLYRLNRQ KFMEKYDLRCFIGSTLLFSPKNADWAPPPQYRHGRFSALLARSDFPWEGAEGTHANAVRL AKFLIDETRNATDLQQAIAAKALLAQLPHDWVVCCDFDGAPSYEGAFVSAGEVSAWAKR SGYLLTPPRHFAGAFLEGFKSTKISPHGLTFERMLERDGDSVIETGRRVTAAFPITQEVAPAA QPWKPRHLAGLDLGEAGLGVCLKNLDNGHEQTLLLKTRKTRLLAHSAEHYRRKDQPRQV FRKQYNQSSENAIKAAIGEVCGLIDNLIARYDAVPVFESQAAAARGSNRMVARVYAGVLQ RYTYVVGNGAADATRTSHWLGANRWSYSFGADVIPKVRDLSPEVLRSIKKPENVFRDALG FPGVLANAWRTSMICSVCGTDPIGALEEAIAANQISFVTDNEGEGSLDLGDGRKVTLRVEV PTSSALTKREASRRKRRAPWEAKVGTVWTLTRKSHRDDLLTTIRRSLRRPSSTFQGSTTKQ WEFHCPCCGQIQQADVNAASNLVRRYFVRASDNARARQHWADDSKRLAFIASMGPDR SAREEKVS
47	cas12d	MRKKLFKGYILHNKRLVYTGKAAIRSIKYPLVAPNKTALNNLSEKIIYDYEHLFGPLNVASYA RNSNRYSLVDFWIDSLRAGVIWQSKSTSLIDLISKLEGSKSPSEKIFEQIDFELKNKLDKEQFK DIILLNTGIRSSSNVRSLRGRFLKCFKEEFRDTEEVIACVDKWSKDLIVEGKSILVSKQFLYWE EEFGIKIFPHFKDNHDLPKLTFFVEPSLEFSPHLPLANCLERLKKFDISRESLLGLDNNFSAFS NYFNELFNLLSRGEIKKIVTAVLAVSKSWENEPELEKRLHFLSEKAKLLGYPKLTSSWADYR MIIGGKIKSWHSNYTEQLIKVREDLKKHQIALDKLQEDLKKVVDSSLREQIEAQREALLPLLD TMLKEKDFSDDLELYRFILSDFKSLLNGSYQRYIQTEEERKEDRDVTKKYKDLYSNLRNIPRF FGESKKEQFNKFINKSLPTIDVGLKILEDIRNALETVSVRKPPSITEEYVTKQLEKLSRKYKINA FNSNRFKQITEQVLRKYNNGELPKISEVFYRYPRESHVAIRILPVKISNPRKDISYLLDKYQISP DWKNSNPGEVVDLIEIYKLTLGWLLSCNKDFSMDFSSYDLKLFPEAASLIKNFGSCLSGYYL SKMIFNCITSEIKGMITLYTRDKFVVRYVTQMIGSNQKFPLLCLVGEKQTKNFSRNWGVLIE EKGDLGEEKNQEKCLIFKDKTDFAKAKEVEIFKNNIWRIRTSKYQIQFLNRLFKKTKEWDLM NLVLSEPSLVLEEEWGVSWDKDKLLPLLKKEKSCEERLYYSLPLNLVPATDYKEQSAEIEQR NTYLGLDVGEFGVAYAVVRIVRDRIELLSWGFLKDPALRKIRERVQDMKKKQVMAVFSSS STAVARVREMAIHSLRNQIHSIALAYKAKIIYEISISNFETGGNRMAKIYRSIKVSDVYRESGA DTLVSEMIWGKKNKQMGNHISSYATSYTCCNCARTPFELVIDNDKEYEKGGDEFIFNVGD EKKVRGFLQKSLLGKTIKGKEVLKSIKEYARPPIREVLLEGEDVEQLLKRRGNSYIYRCPFCGY KTDADIQAALNIACRGYISDNAKDAVKEGERKLDYILEVRKLWEKNGAVLRSAKFL
48	cas13a	MPIVKKFGRSQTSLSDRKIVLKMETAARNIPDFLLSDPEAVIGQWASAMDKIAKKPKGKDK PSSYQRKFRERLGKAIWADLTGPEGPLRDVPAAELEDLRKRWDRRVHPYPDGTKDGPKPA TPKGRLYTRFAGEVGYGKADAVAIARDIRIHLLETEFKTGGGTRDAGRAVRRASSIEKNVLK KARVPQRPKPPQEAAWSKEDEDRYFIPHDVARKIVLAAKAQEKEDHRVAWRTAAAVLFE

[0099]

		HFGRIFQQDGRALSFAEAEKQMPGLLALHRAVEGYYRQALKRHRKDRREHEARPGREKG TGRRKVSAILPKDKTALLALIGHQHQNREIAALIRLGRILHYEAGRRGNSDMVANINRNWP ADVSESHYWTSAGQIEIKRNEAFVRIWRSALSHANRTLGDWLSPDEVANDITMSWESKH EKSGKRKTGKLEENREEAEAHAPVIFGGSAERLGTGDDFQKTLEAICEVFSQLRHSSFHFRG LDGFKDALTKTVKTCDPGAVARLQDLHAEDQANREARLKEDLRGAHAELFLDEGRLAEIW ALLHPKSTEKTLPPLPRYSRVVTRAENTCNGLKLPKSVNRESMKVPAIHCRYILTRLLYQSGF RTWIAEAPAAQLNRWIETATERAQKATVGITKNEADRARMVGQIKVPEGQGIRRFLDDLA GLTATEFRVQAGYESDREAARDQAAFLENLNCDVMALAFDKYLSDHKLGWLAGIDAESR PSETPLSNVDELPSSGSLGTPERWEAALYAVCHLIPVSEVGRLLHQLRRWSNGQKATPDG GRLERLFELYLDMHDAKFDGSTPLRDHDDLAVIFETTGIRDRVLPSSLQHGEHERLPLRGLR EMLRFGNLRVLAPIFATAKVDQAMIGELEGLEARIGDAPSQVDRAQALRTEMHAALCKKR KLAHDDKKSVKDYLTSLQTVIRHRRLANHVRLTNHVRTNEILMSVMGRLADFSGIWERDL YFVTNALLYQAGLTPCDVFSKEPPKENRRSPLQEFENGQIVFALRKMQAQCDTHAGLVD QIKGETARLFHIAEGAPGNDPRIQNRNWFAHFNALKPKTGDRLDLTADMNRARDLMAY DRKLKNAVVSAIVTLLERENIVIAWTMKDHQLTDAVLAAKSIEHLKQNKIRENLRDERSLG YVAALFGGRVAEEAPDIMHDRTVFHLVGALTEEMEPAE
49	cas13a	MRIVRPYGESRTDLGGERGQTRVLVDNTAARARHEIPDFAQSHDALVIAQWISVLDRIAT KPQGTQGATRAQHAFRDRLGRAAWAQMCAADRISAAAQADPYVAALWRFKTHPYGD AKYRPRKGKDGKPLGEPKPQGRWYGRFAANAEPEQADVAAIAALMDHHLHVAELRIDPK RPEKRKGLIEARAKSIEGNVLVAEPRKRPVGSWSREAITRYFMRQDVAAEIFAAARDREQG LNDVPRGPVRLALAAKILHGHWTRLFHAPGTRTAYSIREAEEKEPELFALHMAVKDAYAKL LKRRTQPKTLKKGVKPPQQAPVTTVLPKNAGELLRLVQHRSRNRDLSALIRRGKLIHYTAF DIAAAAAEAESKTPDVPDADRLAYVLTHWPDDLSASRYLTSDGQSAIKRSEAFVRVWRHT IAMASLTLRDWASMNNDLGDVLGSANKVDQAIGRANFDPAWHDKKVRLLFGARAALF PSDDDGRKALLASVIRAGLALRNSSFHFTGRGGFLAALKKLGSEEVMVPSILAAAHALWRE DATARAGRLRAALTGAHAAHYFEEDQNASILTLLDEAPPKESLPIPRFRRVLGRAENTWKG KEALVLPPTANRRQLEDPARRCRYTILKALYERPFRSWLIARAPEEVNAWIDRAIERTTRAA KDMNAKRGEDDKRSVIAAKAESLPRLSGERGIGDFFFDLSSATASEMRVQRGYGHDGEA AKEQAGYIDDLLCDVVALAFDAWLRNPQANGRPLTFICDLKPETPLPAAPKCTLQEIGSAA EPVRPEDWQAALYLLLHLVPVGEAGRLLHQLAKWTVTSRLADDLLNANVTDDPSKAERT ADEEDLKRLVHTLIQHLDMHDAKFEGGDALTGCEPFAALFASRPGFARIFPAEADERLDRR VPKRGLREIMRFGHHGLVASFAEDTRITDKEVGDVLRLEIEERPDNVAALQARKEEAHERW VKAKEKRKTVDPKHLEDYVTALCGIARHRRLASRVTLTDQVQVHRLLMTVLGRLVDFSGM FERDLYFAMLGLLDEKGARPDEVFSGPIDEPKSRLALLANGRVLAALREQIPHSKDLAEELR KDLERLFGMDCSGIRLLEADERGDTCLRDIRNDLSHFNLLHDDSFALDLTTLVNRTRGLMS YDRKLKNAVSKSIKELLAREGLTLSWDMTDRHDLENARIGAKPAVHLGGRKLAFRGGDRR PEPVRENLHSPTHLEAVARLFGGKVVEEDDVTNLDLSSIDWAAEPHNSKETHRHRPAGPR KSPPKRRAYHAPR
50	cas13a	MRIIKPYGRTLVEHDGAGERKRVLTLRPDHDSKLDIEAFARDHDELVVAQWVSTIDKIAAK PGPRKGATEEQRAFRDRIGKAAWALLVRNALLPGLADADRADRLAKIWRRKIAPYGDLRP NERPASAKGRWYGAFAGEADVADVDAGEIAAKIHEHLYDAEYRISGDGRKPDGCIAARA RSIAVNVLRPADSSACGQPEWSDRDLQAYRVADVAKQIWDAALSRENGRDGAGTKRVT NSVAGGVLFEHWARIFPGPDGKALSIREAIEKEPGLFALHMAVKDCYARILKHHKKKAPGR RERENGDVSPIRKVLPRDMDELFARIISGRGNRDLNALVRLGKVIHYTASDPNADHPESITE

[0100]

		NWPGDLAGSHYWTSAGQAEIKRNEAFVRVWRHVVVLAARTLTDWGDPHGEIGSDILGK ANDATGAKFDEAAFNRKCALLFGKRASHFTAAPDLAFKKAVLKTAIKGMAALRHKSFHFA GRGGFVKALEGIGGLNEIDRFPDVTRALRTLLVEDIEDQSRQVRATMVGAHFGVYLSKGQ VEAIYRAVTGAEPGSLPLPRFSRVLRRAKGAWEAEDVLPPPVNRLDLEQRGRLCQYTGLKL LYERPFRRWLEGRSAAKLNGFIYRAVTRASDAARTLNTKESDDWRDIIVARAEKLGKVPDG GDIHGFFFELSAETASEMRVQQAYESDGERARQQAEYIEDLKCDVVGLAYRSFLETEGFDF LRTLDPEAAIAEAHRFDPAELPDPAVDTDAEDWEAVLYFLVHLVPVDEIGRLLHQMRKWD LLAHDRTAPVADGGQARLVDKVQRVFTLYLDLHDAKFEGGEALTGIEPFRKLFEESDGFDT IFPPQQGYEEDRRVPLRGLREIMRFGDLPPLLSIYGRRPATKSNIERYRRAEVADAGGRSEIA RLQARREELHAKWVEAKKEGLGPEDRRAYVEALAEIVRHRHLAAHVTLTNHVRLHRLMM AVLGRLADFSGLWERDLYFATLALLHRAGKTPREVFENEGIDLLRNGQIVYALRKLNGSSN ASALRSGLFPHFGSAFKRGDPIGGIRNAFAHFNMLRAAQPPNLTECINRARQLMKHDRKL KNAVSKSVIDLLAREGLNIAWAVHTRAGAHDLAEAVLSSRQAQHLGKLRLFPVSGDGRD GKGFFIMEDLHGADFVEMAAELFGGRVSDRWRGKGCVSELRLDSIDWSRQREQKKHGG GKKPTGRARKANRGHKNRHRRA
51	cas12f	MSARNIKVKIDTKGNPELRLGLWKTHQVTNEGVKYYTEWLIKLRQQDIYRQSREDASPRVI ISASDLKADLLCHARQLQKERLPRITGSDAEILGTLRQVYELIVPSSVGKSGDSKTLARKFLSP LTDPGSAGGRDQSASGRKPTWMKMKSEGNPRWEETFRKWKDRKDNDPTPLVLNQIAD YGLLPLIPLFTDVGENIFDPKSKSQFVRTWDRSMFQQAIERLMSWESWNQRVRREWEAL NQKHSAFYREQFTADPDAALYRVAQSLEEEMRKEHQGFASDAPEAFRIRRVALKGFDRLL ERWQKTLGKNGQSATLLDDIRRVQSDLGDKFGSAPLYQKLLDERWQRLWAVDPTFLQR YAAFNDLTQRLQRAKRVANLTLPDAVAHPIWSRYEGANASSGNRYHIHLPTKGQPGSVT FDRILWPDGNGGWYERKRVTVFLRPSHQVDRIHEAPTDSVVDNFPLVVEDQSARTILRAS WGGAKLEYDRNRLPRQLKKGVPDSIYLSLTLNLDTNKPSGLFHTQQNGRVWIRKDVLMQ YYNETPGDNVQFKPLYVMSVDLGIRSAAAVSIFSVQLKAGIEEHRLTYPVADCPGLVAVHE RSVLLTMPGERREQWDRRYEQQRQGLRELRTDMRGMNDLLRGAYMDGDRREEFLARLS KLEETSPELWGPVYRSLNDSKVASATEWERLVVYCHRQVEQSLSSRIQNLRSGRSAYRMS GGLSLDHVQDLERIRGIIASWTNHPRIPGSVVRWQQGRSHTVALGRHILELKRDRVKKVA NYLIMTTLGYAYDSKRARGEKWVRRYPACHLMVFEDLTRYRFRTDRPRSENRQLMRWTH QELIAVTGIQAEPHGISVGTMYAGFSSRFDAVTKAPGVRGATVRQILRTRGMVRLKEIAAD VGIDINTLRPHDVLPTGDGEYLLSVVRHGESYRLKQVHADINAAHNLQRRLWTQDEVFRV SCRLALNSGRVVAMPPPSYNKRYGKGFFEKGDNGVYIWKTGGKIKISDTLEEDMDIPEDT AELLRGNSVTLFRDPSGTIAGGNWLEAKEFWGRVNSLVNKGVRDKILGGIPVDNSSAHAE
52	cas12f	MPMIKITECVTWGTTCDGLWDARPHLEVRRSWSPPVQGGRTNRLDAPPASVTLNIHGR VEHPRDADALSVAPLRVRHMFERTTTKAAFLSPLDLRPTQATDLERFAGTTRWAFNWAN ALLEAHHQAYEGRRQQAARHLFGLGPEQLDELRVLANGTRDENGKKAKGDPVKRREYESI QKATKKAVSEENKALGAEMKLWDEHRSLVVHKGRPLLTPGDEPALDAPPLAHRLYARRVE LAGIQKTDPDYYAEQRKKEREAITPNVVAMKRDLMAKGAYFPSEYDLQYIWRTVRDLPKE EGGSPWWPECPTILFYDGINRARTAWKNWMDSASGARKGPPVGMPRFKSKYKAKDTFT ITNPNRSVIKFETYRRIAITGIGSMRLHRGAKLLARRIAAGQAEITSATISRSGTAWYVSVLCT VHTTARTAPSKAQRSRGAVGVDWGVRALATTSKPIALTPGKPASRTVPAEKYGAAMSQKI ARAQRQLARMPKGSSRRRKAARHVADLQHLVAQRRASSVHQLSKALAQSFEIVAIEGLN VRGMTKSAKGTVENPGKNIRQKAGLNRAILDATPGELKRQLEYKTKKYGSRLVELDTWYP SSKTCSRCGWVHPKLKLSMRTFRCQQCGLVEDRDFNAAVNIERQGITHIVKENEGTDDRE

[0101]

		EG
53	cas12f	MSTPMGWTAVNGGDATSPTTRVSSPPGEPRTGACPRAAAADATRAESSPRRTSSPARPG ERHARARTSRYPIPNTYVVDRPSAEGDRHGQSSLDCGPCPVRRSGALHQSSQAAHRRSM TGAKQKTPIRVVRFSIDHSALTPAQVVAFARHAGAARQTWNWALGRWMDWRNNTKFY VDYKVFKAAGMGPGLSTDDLIQVIERAVSIRQDDKWMDAAWDEARQIHGEWDQFQKA STLQSLYLAGAQEPFDPSRDDGINPYHWWVTEGDKSGLPKAERHNVNSGATYTAPLRAF EEAVGRFYKLPGKKGTPKFKSKHDDEQGFCIQRLTETGLSPWRAIEGGHRIKVPSIGSIRVV QSTKRLRQLIKRGGKTTSARFTRRGGKWFVSVSVAFDLSAPRVQRPARLSRRQRAGGSTG VDLGVNRLATLSSGDQFPNRRLLRKSMAEIKRLQRKFDRQHRAGSPECFNEDGTHKKRC RWGREDGPAMSRSAQTTKRQLRRIHDLTARRRAGVLHEITKDLATRFELIGVEDLNVAGM TAKSKPKPDPDRPGHFLPNRRAAKAGLNRAILDVGFYEFKRQLGYKTEWYGSTMQMVHR YAATSKTCSGCGWVKPKLTLAERTFNCTQCGLAMDRDHNAAVNIRALALEGAAPMERE QPAPVGAAEKRHRDPVSHRRRPKSLAPCESTRPVRDLSPPATQEETA
54	cas12f	MAQAEAPRRLRAYKFALDPTEAQLREFEQHAGSARWAYNHANAILSRYSDTLRNRWNA WIAQHHGLSREQLYALPDRERTAIQAAARAAVKAENAQLAAELRIIDDHRKRVTHKGKPS VEPGEQPAEDAPERAYQLWRERVELARLHAEDPQAYRAERKRILDEIRPLVNATKRKLIEQ GAYRPTAMDISTLWREIRDLPPDEGGSPWWPEVSIYAFTSGFAHAETAWKNYLESLAGRR AGRPVGKPRFKKKRRSRRSFTLYGSVKLVTYRRIQVPSIGSVRLHGSAKRLHRALERRGGIIK SITISQGGHRWYASVLVDELDITPGRETQRGPSRRQRDRGAVGVDLGVHHLVALSDPNEK TLDNPRHLRKARKRLLKAQRAMSRRRGPDKRTGQEPSRRWVKARNRVARLHHELAVRR AGHLHEITKRLATSYELVAIEDLNVAGMTRSARGTIDQPGRGVRAKAGLNRSILDTSPAEFR RQLQYKASWYGATVAVIDRWAPTSRTCSSCGAVKAKLSLAERTFFCEHCGMELDRDINA ARNILAFAQSAYPGEGKALNACGGSVSPGSQSVVQAGADEAGRPARKPRRSSRGSDPPA TPTTRA
55	cas12a	MTSSSPTQRAYTLRLKSAAQGDKSWAEKLWDTHEIVNKGARAFGDWLLTLRGGISHKLE NLNDKETGEEGKKRRRILLALSWLSVESKDFAPEKYIVEKDGEDKHRTKEALEAILKSRNLED EEVESWVNDCKDSLTSSIRDDAVWVNRSRAFDDAVRKIGDSLTREEIWDVLGRFFGKKEA YLAPRTIDEKNGKTKKEEPKDLARKAGGWLSKRFGKGKGTDFSKLSKVYSEIVKWAEEPRK SEPRTLANLASALKEDSLQGILNLIKNSGSKSGTRNFLEEIGEGEVSKENLAILKAKAEGNRN YCKKEIGGKGRREWSDRILKSIEETLDGKFTYLQEKGPARHWEFAVMLDHAARRISAGHT WIKLAEARRRNFEEDSQKINEVPENARQWLETYREDRSKSSGAIEGYLISKRAVTEWETVV KAWKNCKTEEDRIAAAGALQDNLGIDQFGDINLFRALASEDVRCVWQVDGKPDANILLN YVAATKAEFDKRRFKVPAYRHPDPLLHPVFCDYGNSRWEIRFDVHEVNRTGKKAKQNKK TIETADVHGLKMDLWTGSKIENVSLRWQSKLLEKDLAVKQLDGKEDGKKEVSRASRLGRA AVGAGWETPVSASSVFAQKHWNGRLQASRKELSRIARRVKTRGWDEKANSMKKNLKW FITFSPKLKLQGPWISYVDNSEDKRPFTFTSKGEPILDEVFSIENKNRKGRARLILSRLPGLRV LSMDLGHRHAAACAVWETLSSRQLEDACAEGGYDKPAPDAMYHHIKSNRGKRVIYRRIG ADELSDDSIHPTPWARLERQFLIKLQGEERKARMATADEIWEVHELERALGRKTPLVDRLT KSGWGSDSGTPRQRQLLGELNQWGWEPDEAQENSEDDEITSRESLLVDKLMSRTVDTV RKGLRRHGNRARIANFLVAREKTVPGGQMDTLNNEGRKEIIADALAFWYELANGGEWKD TEALDWWKIHIEPELSVEELPDIAGTGIAPKERKRKKKELKEKLKPVAERLLTSGAKKLSDQW CERWKQDDKEWQKTLRWLRDWILPRGVRGKSELIRNVGGLSLDRLTTIQSLYQAQKAYFT RITPKGIQMDKDKPLTAVMNFGGHILNDLENMREQRVKQLASRIVEAALGVGRVKIPKKS KDPKRHYERVDAPCHAVVIENLTNYRPEETRTRRENRQLMTWCSGKVKKYLSESCSLHGL

[0102]

		FLWEVPPSYTSRQDSRTGSPGIRCEEVSVEKFFKTPFRQREVARAEEKDSKNKASAYEQYLI DLKERWKSRGEETALLRIPRKGGEIFVSANSNSPASKGLQADLNAAANIGLKAITDPDWSG SWWYVPCSSKDFVPIKDKIGGSRAFENITTPMPNPDDAKEATGKKRSGKKEIINLWRNPA CSPLERDEWERTAKYWNMVEYHVIKRLKRQMG
56	cas12a	MKNFQDFTNLYELSKTLRFELKPIWGTKKLIEEKNILKLDKKKRENYEKVKPYFNKIHQEFINF ALRNPNFDFSQFEEKYLNWLKDKKNKDLLKEKESIDKIFLEKIWKLFENSVKDFLKENGFESI VKSEDQNLKFFRRKEIFEVLQEKYGSELETQMVNKDWEIKSIFNGWEKWLWYFDKFFNTR DNFYKTDWTSTAIATRIIKDNLKIFLENTIIFEKVKNKKIDFSEVEKNFSVSIDTFFEINNFNNC FLQDWIDFYNKVIWGETLENWEKLKWLNEIINKYRQDTGEKIPYFKKLQKQILSEKDWVFI DKIEDDGGFYEVLKNFYKNAAEKEWFLKNIFENFYTISDKNLEKIYFNKIAFNTISHKFWSAL EFERILYEEMKKEKADWIKFEKKENKYKFPDFIQIIFIKRSLENYDSENLFWKERYYKSEENVD WFLEKNNNNIWEQFCKILNFEFLNILKRRIIDEAWEEYEVWFEISKNILWEKLENFELNQEN KWIIKDFADYSLALYSFWKYFAVEKWRNWDLNIDISDDFYGWEDWYIEKFYNTGYDEIVK PYNLMRNYISKKPWEDSKKWKINFETSSLLSWWDKNLESNWSYIFQKWNKYYIWIINWS KPAKEVLEKLYSWNGEKIKRFIYDFQKPDNKNTPRMFIRSKKDSFSPAVGKYNLPVEDILEIY DNWLFKTENKDNSNYKESLSKLIDYFKLGFSKHESFKHFNFVWKDSKEYENIADFYRDVEK SCYQITSEFLDFEELKKLTFKKHLYLFQIYNKDFELDESLQKNWYNFRDEWQKNIHTKYFEA LFLEENILRKSWAVFKLSWGWEVFFRKESIKAEKEKRKNIEVTKNRRYTEEKYFLHFPIQVNF KNEISWNFNQEINKFLANNPDINVIWIDRWEKHLAYFSVINQKWEILESWSFNKIENYNK NWEKLLFPEREIKEIHKDWSLIDLELVETWRKVDYVDYKLLLEYKERKRLLQRQSWKEVEQI KDLKKWYISALVRKIADLIIKHNAIVIFEDLNFRFKQIRGWIEKSIYQQLEKALIDKLNFLVNK NEINLEKAGSILKAYQLTVPVDSLKEIWKQTWVIFYTEAAYTSKIDPIKWWRPNLYLKKQNA EINKENILKFDNIIFNSKENRFEFTYDLKKFFWKDSKFPAKTVNTVCSCVERFKWNRNLNN NKWGYIHYENLTDWKLANKEQKEDEFSNFKELFEKYFIDINWNILEQIKNLDTKNNEKFFS SFIDLFTLVCQIRNTNQNAKWDENDFILSPVEPFFDSRKSQNFWKSLPKNWDENWAFNI ARKGLIILNRISENPEKPDLLIFNADWDNFARNI
57	cas13b	MTEQNEKPYNGTYYTLEDKHFWAAFFNLARHNAYITLAHIDRQLAYSKADITNDEDILFFK GQWKNLDNDLERKARLRSLILKHFSFLEGAAYGKKLFESQSSGNKSSKKKELTKKEKEELQA NALSLDNLKSILFDFLQKLKDFRNYYSHYRHPESSELPLFDGNMLQRLYNVFDVSVQRVKR DHEHNDKVDPHRHFNHLVRKGKKDKYGNNDNPFFKHHFVDREEKVTEAGLLFFVSLFLE KRDAIWMQKKIRGFKGGTEAYQQMTNEVFCRSRISLPKLKLESLRTDDWMLLDMLNELV RCPKSLYDRLREEDRARFRVPVDILSDEDDTDGTEEDPFKNTLVRHQDRFPYFALRYFDLKK VFTSLRFHIDLGTYHFAIYKKNIGEQPEDRHLTRNLYGFGRIQDFAEEHRPEEWKRLVRDLD YFETGDKPYITQTTPHYHIEKGKIGLRFVPEGQLLWPSPEVGATRTGRSKYAQDKRFTAEAF LSVHELMPMMFYYFLLREKYSEEASAEKVQGRIKRVIEDVYAVYDAFARDEINTRDELDACL ADKGIRRGHLPRQMIAILSQEHKDMEEKVRKKLQEMIADTDHRLDMLDRQTDRKIRIGRK NAGLPKSGVIADWLVRDMMRFQPVAKDTSGKPLNNSKANSTEYRMLQRALALFGGEKE RLTPYFRQMNLTGGNNPHPFLHETRWESHTNILSFYRSYLKARKAFLQSIGRSDREENHRF LLLKEPKTDRQTLVAGWKSEFHLPRGIFTEAVRDCLIEMGYDEVGSYKEVGFMAKAVPLYF ERACKDRVQPFYDYPFNVGNSLKPKKGRFLSKEKRAEEWESGKERFRDLEAWSHSAARRI EDAFVGIEYASWENKKKIEQLLQDLSLWETFESKLKVKADKINIAKLKKEILEAKEHPYHDFK SWQKFERELRLVKNQDIITWMMCRDLMEENKVEGLDTGTLYLKDIRTDVQEQGSLNVLN HVKPMRLPVVVYRADSRGHVHKEEAPLATVYIEERDTKLLKQGNFKSFVKDRRLNGLFSFV DTGALAMEQYPISKLRVEYELAKYQTARVCAFEQTLELEESLLTRYPHLPDESFREMLESWS

[0103]

		DPLLDKWPDLQREVRLLIAVRNAFSHNQYPMYDETIFSSIRKYDPSSLDAIEERMGLNIAH RLSEEVKLAKEMVERIIQA
58	cas13b	MESIKNSQKSTGKTLQKDPPYFGLYLNMALLNVRKVENHIRKWLGDVALLPEKSGFHSLLT TDNLSSAKWTRFYYKSRKFLPFLEMFDSDKKSYENRRETTECLDTIDRQKISSLLKEVYGKLQ DIRNAFSHYHIDDQSVKHTALIISSEMHRFIENAYSFALQKTRARFTGVFVETDFLQAEEKG DNKKFFAIGGNEGIKLKDNALIFLICLFLDREEAFKFLSRATGFKSTKEKGFLAVRETFCALCC RQPHERLLSVNPREALLMDMLNELNRCPDILFEMLDEKDQKSFLPLLGEEEQAHILENSLN DELCEAIDDPFEMIASLSKRVRYKNRFPYLMLRYIEEKNLLPFIRFRIDLGCLELASYPKKMGE ENNYERSVTDHAMAFGRLTDFHNEDAVLQQITKGITDEVRFSLYAPRYAIYNNKIGFVRTG GSDKISFPTLKKKGGEGHCVAYTLQNTKSFGFISIYDLRKILLLSFLDKDKAKNIVSGLLEQCE KHWKDLSENLFDAIRTELQKEFPVPLIRYTLPRSKGGKLVSSKLADKQEKYESEFERRKEKLT EILSEKDFDLSQIPRRMIDEWLNVLPTSREKKLKGYVETLKLDCRERLRVFEKREKGEHPVPP RIGEMATDLAKDIIRMVIDQGVKQRITSAYYSEIQRCLAQYAGDDNRRHLDSIIRELRLKDT KNGHPFLGKVLRPGLGHTEKLYQRYFEEKKEWLEATFYPAASPKRVPRFVNPPTGKQKELP LIIRNLMKERPEWRDWKQRKNSHPIDLPSQLFENEICRLLKDKIGKEPSGKLKWNEMFKLY WDKEFPNGMQRFVRCKRRVEVFDKVVEYEYSEEGGNYKKYYEALIDEVVRQKISSSKEKSK LQVEDLTLSVRRVFKRAINEKEYQLRLLCEDDRLLFMAVRDLYDWKEAQLDLDKIDNMLG EPVSVSQVIQLEGGQPDAVIKAECKLKDVSKLMRYCYDGRVKGLMPYFANHEATQEQVE MELRHYEDHRRRVFNWVFALEKSVLKNEKLRRFYEESQGGCEHRRCIDALRKASLVSEEEY EFLVHIRNKSAHNQFPDLEIGKLPPNVTSGFCECIWSKYKAIICRIIPFIDPERRFFGKLLEQK
59	cas13b	MESIKNSQKSTGKTLQKDPPYFGLYLNMALLNVRKVENHIRKWLGDVALLPEKSGFHSLLT TDNLSSAKWTRFYYKSRKFLPFLEMFDSDKKSYENRRETAECLDTIDRQKISSLLKEVYGKL QDIRNAFSHYHIDDQSVKHTALIISSEMHRFIENAYSFALQKTRARFTGVFVETDFLQAEEK GDNKKFFAIGGNEGIKLKDNALIFLICLFLDREEAFKFLSRATGFKSTKEKGFLAVRETFCALC CRQPHERLLSVNPREALLMDMLNELNRCPDILFEMLDEKDQKSFLPLLGEEEQAHILENSL NDELCEAIDDPFEMIASLSKRVRYKNRFPYLMLRYIEEKNLLPFIRFRIDLGCLELASYPKKMG EENNYERSVTDHAMAFGRLTDFHNEDAVLQQITKGITDEVRFSLYAPRYAIYNNKIGFVRT SGSDKISFPTLKKKGGEGHCVAYTLQNTKSFGFISIYDLRKILLLSFLDKDKAKNIVSGLLEQC EKHWKDLSENLFDAIRTELQKEFPVPLIRYTLPRSKGGKLVSSKLADKQEKYESEFERRKEKL TEILSEKDFDLSQIPRRMIDEWLNVLPTSREKKLKGYVETLKLDCRERLRVFEKREKGEHPLP PRIGEMATDLAKDIIRMVIDQGVKQRITSAYYSEIQRCLAQYAGDDNRRHLDSIIRELRLKD TKNGHPFLGKVLRPGLGHTEKLYQRYFEEKKEWLEATFYPAASPKRVPRFVNPPTGKQKEL PLIIRNLMKERPEWRDWKQRKNSHPIDLPSQLFENEICRLLKDKIGKEPSGKLKWNEMFKL YWDKEFPNGMQRFYRCKRRVEVFDKVVEYEYSEEGGNYKKYYEALIDEVVRQKISSSKEKS KLQVEDLTLSVRRVFKRAINEKEYQLRLLCEDDRLLFMAVRDLYDWKEAQLDLDKIDNML GEPVSVSQVIQLEGGQPDAVIKAECKLKDVSKLMRYCYDGRVKGLMPYFANHEATQEQV EMELRHYEDHRRRVFNWVFALEKSVLKNEKLRRFYEESQGGCEHRRCIDALRKASLVSEEE YEFLVHIRNKSAHNQFPDLEIGKLPPNVTSGFCECIWSKYKAIICRIIPFIDPERRFFGKLLEQK
60	cas13b	MDTPNFSERIPVSLQSHPYYFAHYLNMARHNAYVILEYVNRELIKPGKNLDEDNLIQSTVL KDGYFDRKPDELSHRNRLLVQHFPFLREAENEGARTCNPVSYKLKTALAALNQWRNNAS HYPLNQNHEKDFDLQPFFSFAIEACKKRMREVFQPDDFYLLETNEKQFYTLHNENGFTEK GLYCFICFFLEKKYAFQFLAGIKGFKNTTDNKFRATLETFTEHCCRLPKPKLDSSDIKLDMLG ELSRCPAPLFDLLDIEERKKFIREPEEVKPDESGDREEVQQVLMKRYDDRFPYFALRYFEEKN LLKGISFHIHIGRWIKSEHTKKIMGAERDRRLLKDIRTFGELKEFSPEHAPDYWLRDGITPDD

[0104]

		VDQFSPQYRIVGNRIGIKLNYNGHNRWSVPDKEINVKPDAIISTYEFLNLFLYEHLYQKKLT GLSPAEFIQDYLDRFNNFLSEFKAGHIRPVGDFSLEKRRGQGDEPDLTARRKSLQKELDRFV LKGKDLPDKIREYLLGYKQKSEKKQAKWILGGMIKETVYWRNKAEQSPEKMRSGDMAQQ LARDIIFLTPPHTVKEHKQKLNSLEYDVLQYALAYFSSNREKLYSFFKEHQLTVKGDRAHPFL YKIRLDECQGILDFFIVYMQQKEKWLGWLDRNLKSPRLNEEEFFNTYSYFIKTDTKRAIEMD YESCPNYLPRGIFNEPIAKALQKAGVKIKDEDNASYALSVYSNGKTQPFYNKERYYNKGIFR MEELPEKLQPKELLGKIQWTIKSSGKDTEEFRSLQNLKNRILNTEKEIRYVQSTDRALWIMV ADLFPETFELRPDDLECIGHDLSDDLLSRPYQMKEKVYNYTITDYLPIKRYGEFRRFLKDRRL ENLLTYFEEGVPLHREALVAELEAYDLQRKNLLEIIYRFEKLVFDRHRHELTFSGEGENQYVN HWDYLDFVARKYGLSAEVKELNSERFTELRNKMLHNQIPYQLWIKEAIAAREENTVCGRI MGMIGEIYERMTTEIEKQMQV
61	cas13b	MFDNEQKNLEKEPYWGVFLNQARLNAYIALRDISERLEENAADEDSLSEWPVLKYLDNDT DAVKSRRIFDLVEKHFSMLKIIYGGEKEGDLVKRSKEYKIILKCLFRALNFYRNKFCHMYSGN RARKYNEKELIKYLEDCFDASVRKIKELRRLDEKDVLHLRRKIAEGKDANKRVIDNPQFRYPF KNEKGELNEKGLYFLASIFLDKKEAHEFLKKQEYFKNDSEPKYRATLESFYHYRIKLPRPVIES DVDKNGLALDMLNELKKCPKELFDLLSKEQQEKFRVVDSEDADEEGNEILMRRYSDRFPY LALRYCDENQVFERIRFQIDLGRYYFKFYPKETIDGKTQQRSLDKRLKIFGRIKDVKSKVEQE WSGIIKSPDTIEENPNEPYKLKTTPRYNIVDNQIGFVITGDKNLPDVKRPDGRIELEKPDGW LSIYELPGMLFHGLKYGFDKTERMIKIYIEKQRKICKEICEKGTITPDDGESMPEALKGGAKAA KRNYSEKKLERMLQDTEQRIRAIQTTQKRMDEPGNKPGKKKFFDIRAGKLADFLARDIMA LQRFDPAKHGKDKLTAINFQVLQATLAFYGAKKDVIEDMFKGIGLLEGDNPHPFLNQIDP AQYNSIAGFYQAYLQKKRSYLEDYRKEEEYDEQFLRPKRQRYAQEKREIKTVARQLLDNPV NVPKNFFKKEIEEFVFSQDPSLKKSKMNTAYMIQALFEKHYGRQQPFYSYNRTYPVVSKAI EYGKKGKNKKIAKVLMAIEPKLNYMEIKKIVNEMPDGQYEPENLKRNLYEGYKDYEKDERII RRCKVQDVVSFMMVEETLKDQLDFNGNVLTLEKITPWEASPFKKPVLCHTIISIPFNTKGG HTDKDYVDFIKNNFEGSYDCEPNKIILKYKVTSKDTKLKDIGKYRMYSHDRRLPGLLIWKYR PNDQNGNEIKFTEIEQEIKAFERRRIEIAQCLYTLEKKVIDSWFTQDELGEEHIPFNKVIDVIK AKMPNFEDKCNVLLKIRNAINHNQFPVYEQAIQTAPGKEIAGKMLRITESYIEQIMAKIDP DFGRTEDAESSR
62	cas13b	MDTPNFSERIPVSLQSHPYYFAHYLNMARHNAYVILEYVNRELIKPGKNLDEDNLIQSTVL KDGYFDRKPDELSHRNRLLVQHFPFLREAENEGARTCNPVSYKLKTALAALNQWRNNAS HYPLNQNHEKDFDLQPFFSFAIEACKKRMREVFQPDDFYLLETNEKQFYTLHNENGFTEK GLYCFICFFLEKKYAFQFLAGIKGFKNTTDNKFRATLETFTEHCCRLPKPKLDSSDIKLDMLG ELSRCPAPLFDLLDIEERKKFIREPEEVKPDESGDREEVQQVLMKRYDDRFPYFALRYFEEKN LLKGISFHIHIGRWIKSEHTKKIMGAERDRRLLKDIRTFGELKEFSPEHAPDYWLRDGITPDD VDQFSXPQYRIVGNRIGIKLNYNGHNRWSVPDKEINVKPDAIISTYEFLNLFLYEHLYQKKL TGLSPAEFIQDYLDRFNNFLSEFKAGHIRPVGDFSLEKRRGQGDEPDLTARRKSLQKELDRF VLKGKDLPDKIREYLLGYKQKSEKKQAKWILGGMIKETVYWRNKAEQSPEKMRSGDMAQ QLARDIIFLTPPHTVKEHKQKLNSLEYDVLQYALAYFSSNREKLYSFFKEHQLTVKGDRAHP FLYKIRLDECQGILDFFIVYMQQKEKWLGWLDRNLKSPRLNEEEFFNTYSYFIKTDTKRAIE MDYESCPNYLPRGIFNEPIAKAVQKAGVKIKDEDNASYALSVYSNGKTQPFYNKERYYNK GIFRMEELPEKLQPKELLGKIQWTIKSSGKDTEEFRSLQNLKNRILNTEKEIRYVQSTDRALW IMVADLFPETFELRPDDLECIGHDLSDDLLSRPYQMKEKVYNYTITDYLPIKRYGEFRRFLKD RRLENLLTYFEEGVPLHREALVAELEAYDLQRKNLLEIIYRFEKLVFDRHRHELTFSGEGENQ

[0105]

		YVNHWDYLDFVARKYGLSAEVKELNSERFTELRNKMLHNQIPYQLWIKEAIAAREENTVC GRIMGMIGEIYERMTTEIEKQMQV
63	cas13b	MKTLGALSSHNYNNKKYYFSGLLNTAQYNFNLALQEVNDRLGKKGKNPGKTMIKNIFDQ KDSFSTQERAMYYLEEFFPWIFLVMKQSGINIPTEEQETKLHKEEIQLIQEHLISLYELLDDLR NEQTHYMHDPVIIPEEVSKMLDALLLQILKNTRKKCKDDEYRTFIVKKYQEEFQKEIKVQVK DRFGKEKEKIVTGEVKENYVINRCFRKWIQKEGEEETLRYSTVQEEQGKYVWSSSGFVFFLS LFLRRKELEDVMNHVPYFKDSRKLLFYLTRKTFSSYCFRDLRKSLRSDYSNDSLLMQMIEEL YKCPGELYEVLLKEQKQEFIEDINEYYKDNPEFEGSANEAQVIHPVIRKRYQDKFPYFALRFI DEYFNFPTLRFQLVLGEYVTDRRTKELQGTALFTDRVISQRISYVGKLSEAEMNKKREGYTE TGWKEYPNPYYKIENNRIPLYIEFSKNEELIFKEKKFKYNTLAKWENREIDKRTGEFNQVNK QRRITQLEEFKIDNPKKMKTPNVFLSIYELPALLHALLIEKKTEAEIEDIIKAKIKKQLTEIAEGR RNLSGLPKGIKKMRNCNSDFEKKKLISDIDNEIKKGEKILEEVQQWLNPVINKKGTGKQEN NKPFFSNTYRGKYATWLAYDIKRFTGKDHIQNWKGYQFSELQTLLSLYTLRKEELKNFLEK DLQLTSHPFLKEALKAVNLEDFMGAYLRGRQFFLEKAKKQIGIKGVKKSIFQYFEERKYKIYS SNLDYWEELWKHPVNLDRGLFDERGTVYNKNKELNDLQNRAAWFSFAETNPKQQFYHF PRIYSDEDITKPVTDRYGKTKEKLILFKLSPQKGFMEQIPSDLKKKYQEDKGKVEHPEVQKEK KYEEKKHPGINAFIKNAYKNEQKIRRISRNDIFLYEMVKYMLNKISPATEFSSLDKVWLTRIE REKQATEAREQSFKEKGDTSENKIRQDYLLSFPITLTLFNDIIKEKVKIKDIGRFRKLEKDERV QTMISYYTSGLWKNDQPSLTIKELEAELESYHKIRLQEIFKEVHKLEKEIYEFTPEEDKSKLLAR ESFPKFKYYISFYFIPKEDQEVFNEIQFDKYKNLEQIPGRKPEYDPYYLLIFIRNKFAHNQLPAE PIYKTALTFLPNNFNTLAEYYHKLFILLNNKNYNN
64	cas13b	MNILPAAPEKEKIAYSTATAPWFFGAFLNQARHNLFLTVNDLAIRLGEKVIDYDDQLLNSN VVRMLVNEKASPLQLEILMKYLDRHLPFLIPMQVALKGHQGDASDNPVIGSPADYGAILS KLIVCLNAARNHFSHYHSTSGWSGYNEVIEWMEHVFTRNIETVVKRFTLTEEEVQHLKKPV DKSPKGTIPPYYFSFCKGDIWTDTGLAFFICLFLTREEAYLFLKKLRGFKRGEERFHKATLEAF CVGSLKVPRERLESNNSPQSAFLDMCNELVRCPKSLFDLLEPEKQELFRRDPEPEDAEDNG IEEEEDQPQALLVRKENRFSYFALRYLDIAKAFPRLRFGVDLGTYFFSVYPKTFAGIEETRQLS KRLIGYGKLEEFAREKRPEHIAALFRSKEEANAAPTEPFIRETAPHYHLDGNNVYLYMSGDG EAQWPAVELEEVTGKSYPRKLVKKSTLLPFAVLTVNELPALLFYHLLHKEKGAGDAAERVIIN HMERVKRFFKALQDDKVDQVAGQPIRKPDVDADESLHMEYDRRWKLLKKKLSEYQLRAS YIPEKIINYLLNIEAVDLGDKAMAQLKNLQRQAQDDIAAIERRMEHLMKKGADGRKTLKV GNLAQQLAEDMLQMQPVQIGTDGEPVPASKANNLAFRLLQSHLAYFAENRHNLPAVFE ACGLIGASNKHPFLDNINIESCKGVVDFFILNFRNKLDFLDRCLQEGEWHRYHFISAAKLKS GAKVTIKKYLNEAFESKGRNHIPFTLPPSLFLDASLDWLAKFGDGKAKKVLAENEYVNSVFL IRRLFADGGLQPFYAWKREYRLFEKKAGKAVFLDEAGRMRKADKIGIEVERHREFLARPVK KGKQYDIKKAAAEQFLRSYRFYLQEEKYIRLLAAQDMLLFRCICDLLTYHVGDIGLEELAEAK AGTFSLANITPEKTETAKSLLNYRPAGGVVLDRHFYATDEKGAFVKQEGKLVPGGQVRIFD NTLKIKNAGNFRKLLKDRRMNNLFFYFKQHADEPVVLHRMVLENELRAYDRMRLKVLPVI AEFEKKLYQHCTDVEKERLVVNGSMHHRCYLDVYREKYQPDWGWEAAGNLLRIRNAFV HNQFPLMEGDGFKLEVAHWKKINADFVPSEQGSSLGYGIIDRLGQLAVEGYEGLIKNIHV
65	cas13b	MGEEEQAHILENSLNDELCEAIDDPFEMIASLSKRARYKDRFPYLMLRYIEEKNLLPFIRFRID LGCLELASYPKKMGEENNYERSVTDHAMAFGRLTDFHNEDEVLQQITKGITDEVRFSLYAP RYAIYNNKIGFVWTSRSKKKSFPTLKKKEGEGHRVAYTLQNEESFGFISIYDLRKILLLSFLDE GKNIVSGLFKQSKANWENLSENLFDAIRTELQKEFPVPLIRYTLPRSKGGKFVDPKLADKQE

[0106]

		KYESEFERRKEKLSEILSEKGFDLSQIPRRMIDEWLNVLPTSKEKKLKGYVETLKLDCRERLRV FEKREKGEHPVPPRIGEMATDLAKDIIRMVIDQGMKQRITSAYYSEIQRCLAQYAGDDNR RHLDSIIRELGLKDRKKGHPFLGKVLRPDLDHTEKLYQRYFKEKKEWLEATFYPAANPKRVP RFVNPPAEKQKELPLIIHNLMKERPEWRDWKQRKNSHPIDLPSQLFENEICRLLKDKIGKES SGKLKWNEMFKLYWDKEFPNGMQRFYRCKRRVEVFDKVVEYEYSEEGGNYKKYYEALIN EVVRQKISSSKENSKLQVEDLTLSVRRAFKRAINEKEYQLRLVCEDDRLLFMAVRDLYDWK EVQLDLNKIDNMLGEPVSVSQVIQLENGQPDAVIKAECKLKDVSKLMRYCYDGRVKGLM PYFANHEATQEQVEVELRHYEDHRRRVFDWVFALEKSVLKNEKLRRLVEKSQEGCEHRRCI DALRKATLVSEEEYKFLVHIRNKSAHNQFPDLEFGKLTPNVTSGFCECIWSKYKAIICRIIPFI DPERRFFGKLLEQK
66	cas13b	MRIPKLIEEHKSVFGAYSTMALSNVETVLNHIAERAGLDGYERDRGPGVEDYWEHPVMQ CLCRKDKPRSIPSDVLLDVRNRLFRSFPFLKIMAENQRDYRNAKGKVECVEINESDIFVVLN NSFRVLKAYRDTCTHYLIENRIWEDNSPMLMYNECPLAAMVNQYYTAALRVTKERYGYET RDLTFIQKRRFKQEPEKEASGNVKKKAVPDLAFFLSLVALNGDGRKWLHLSGWGVVLLICL FLEKKYVNVFLSKLPNPGNYPPSSKERRIIRRSMGVCSVVLPKERIHSETGDLSVALDMLNE LKRCPRELFDTLSPGDQERFRTISSDHNEVLQMRSKDRFAQLVLQYIDHNRLFENLRFHVN MGKLRYLFNPKKYCIDGQTRVRVLEHPLNGFGRLQEMEEKRLQENGPFARSGIKVRCFDE VRRDDANESNYPYIVDTYTHYVLENDMVEMFFCPEGSGMKMPEVTSREGKWYVDKKVP HCRMRMSVLELPAMLFHLLLCGAKNTEVHIGKVCDNYCHLFSDMAQGNLTEENILSYGIK KEDIPQKVWDCVRGVHMGKDSRAYREKEIRERYEDVTRRLERLEADRKAVLGGENKIGKR GFVQIVPGRLAAYLATDICRLQPSLRKGDGYGTDRLTGLNFRLLQSSIATYNCGESDILYGR FRDVFCSAGLIGGDNPHPFLDKVLPEAYSVCCPRNTIEFYERYLEEYQRYLKPLVIKLEKGKV PSLSFVNEGQRRWARRDDAYYHELGNLYLSQAIELPRQMFDDEIKDKLREMPEMRDVDF DHANVTFLIGEYLKRVRHDESQEFYSWPRHYKYVDMLKCILNPKNGSLQAVYIQMGEREG LWQERSELEEKYAKIRLRDLGRKGLDKDEANERIKTGLGNRKKEYQKAEKVIRRYKVQDALL FMLAKNTLFNSVEVDDERFKLKDIMPDGEKGILSEVVPMDFCFRSGNSATRKLMGTIHSD NTKIKNYGDFFALANDKRMVTLLPLVGEQCLVKEEVKEEFDKYDDCRPEMISMVFDFEQW AYSAYPELKELVSNEAIKGRLFSNLLQELLGRGELTYEEKYALVGIRNAFLHNSYPKDGGVVK VRTLPDIAKSLKDVFKEYIRLE
67	cas13b	MKMFYKSVLTAFFTAVDSLRNKYTHYSHKDLNIREIKIECTLGGKDYCIGLLNALDCIYDSA VNLLKLRFMAGEDEVAHLRRCKAVNKKVVVRTEKDGFYYRLSDNGGVTEKGVIFIASMFL NRKYGFLFLKQLEGFKRSDEKRYRLTLEAFLAFSNIKPVDRLKSDKLDRASLGLDMLNELTKI PKELSETLSVDCLYKYLASDGEDDLRSRIRYQDRFVPLALEFISQSDEFKDFRFYTYVGNYVY KGYIKRLIDGTDKERYLSDRLCGFYKSVNDASSDAIAQKYGVEIKDSNEPDYMLPDSFRPH VLRATPHFVINTNNIGIKICGNDCLPIVNGKGVESPEPDYWLSIYELPAMLFYAYLREKNGK RFKDYKSIRELIEGVEKKADEKNDRDKGALMARHIDKEIIWTQTKLDEVKRLEEKKVAAYGK KGRVVLKAGRMADLLAHDMVRLQPATKGSDKITGANFQALQVSLAYFKRDILADVFSRA MLTTGNHRHPFLYRIDVSHCSSLRDFYVAYLGERRKYFEDVAKKIAKNKLNTPCHILRRLQR EGSGEEAGKDVKPKFLPRGIFTDSIKNCLEQSKLNIYIRNARNDVKPAINAAYLILMYYKEIEK GEFQGFYGEKRRYDILEEGKPLDLAERKKALASIKPAKIDVSEANMPMSKEEHLMRKRYHA VCNNESAIRMYQVQDILLLLMAKDIFKKALSEGVMSKKIGLENLNGIFDAPVNFVKNFDNI KLTATGIKIKDYGKVCRLGTDFKFNSLIKAFHKVYSKSVEMDYSDYLKEEEEFEKYRLNMVKL CREVERGITEDLHLSLDGKSHLSFNDDVIKPYNDKYNVFNGGDLTFFINARNMFMHGDYK YECVKYVVSEHFKGSLNDVSFAKETYGHFCNLLESMRKKTGLRIDI

[0107]

68	cas12g	MLPTRYKPARTLVRPLGRLPHEPRKEFVEKCRRVRMHFEQFNIDVADLCQWLMSLRPNTR IGDAQSTVFWDFFLNPSILTVEADEKERDRWRLAAFDELLQIRFGHDPNAPPWSEEFRSAI RHVAQRPKSATAQRLFDRLRSLTAPHRLVLLKSAAEWIIARYQRGMENWQRQFAEWQRE KEEWEAAHPNLTPEVRDAFTRVFKNLFENPDGDGKIGVRRKNPRICSWERLKLNKDNCVY AGQKGHGPLCWEFSKFVKAQKNAGTIKTFFVDVANKYLHVRRNLSKPGVKLKKSPRQEA FKRLYNQKGMEKARNWFTDAWSGYLTALNLNEKTILDHGCLKHCGAIGAEFEKSLCQFN PHTHLCVQYRNALESLEPAIRELEGDYREWRRLFLAPPRKPSFRYPSSRRLPMPKIFGEHFH QIDFDQSILRLRLEDMAEGEWIEFGFKPWPKDYRPGKDEVRVTSVHVNFHGNRMRAGFH FEAPAKPSRFACTQDELDDLRSKQFPRQSQDRQLLEVARRRLLESFDGMLESDLRILAVDL GEKGAAAAVYQGHGHEADVAIPIVKIDRLYDHVPDVLDVESARVPPPKFDDSRDPRGVRK EHVGRHLGQLQRGAQTLAQHRQQDESAPAALRRHDFRSLTRHIRWMIRDWTRHNAAQ ITAAAETHRCHLIVFESLRGFKPRGYDQMDFAQKARLAFFAYGRVRRKVVEKAVERGLRVV TVPYGFTSQICSECGHRQRNKGRLRKNKYQRRFVCECGEPKKSANKTAAPDRSATVSPCT CRLQLGSDVNAARVLARVFWDEIVLPTREEMREPAVDSAPPSK
69	cas12g	MCLCTLSGRTRQEEEIIGSTQYTEARSLVRRIRRPRGESRRQFKSNVLLLRRHFEQFNVDAS EICQWLMGIRPGGRHADESTGPFWEFFLDPGRFLRETGRGPEDADERIDAYRRIAFDVVA GIEDESRMSDPSIPRQIVESLHAVSMATRTESARRLFERLAGLEPSHRQILLKAAAEWIVSRY WRSVQGWPDRYKHWSDEKEEWEKAHPRLTESLREEFTGIFRDLGIRRKKPRVCPWERLEK GMDNCMYAGERIKVGYSRQSHSQLCAKYERFSYKQRQRTKSGKNFKSYFVKNAELYLKL RRKNRSLIKKDVMKLFRKKVPQALWFEKAWDEYLKALGVDEATLTKDGKLPHCTQFADD KECLFNRHTELCLQYRERLLRLPHLQELEQLYREWRDKYLSGPRRPSLRYPSKRTLPMPKVF GRGYFCADFTNSLLDLRLEGMGEGDFVRFGFAPWPADYDAQPSDATVTSVHIHFVGTRA RAGFRFQAPHKTSRFASSQDEIDDLRSRKFPRAAQDGEFLDAARKLLLESFTGDAEREMKL LAVDLGDRGAGAAVFEGRCFKEAMPLKIIKTDTLIDKPPPVTKTPRKGKPGKRESKRARGLD KYHVARHLDTWRKGARKIAERRAKGEADPVKLGAHDMRSLSLHVRWMIRDWVRLNAS QIIKTAESHKTDLIVLESLRGFSAPGYHKLDDEKKRTLAFFAYGRIRRKLTEKAVERGMRVVV APYLRSSQVCAECGREQIDRNKLMKDKRKRRFICEYSDCTWQCDSDQNAACVLGRVFW GEIELPSERKKD
70	cas12g	MHPSRYKTARTLVRRLCRLPGEDRSAFRSKVGLLRGHFEQFNVDVSELCQWLMSLRKRN KVPENPATFGALGDFLLQPGLPGEETDEKEADRLRLAVFDAVAGFRMLEDRLAASIPASLS DAIRDEAVFLAGVRAAGKPSGLARVLARLEACAPAQRLVLLKSAAEWIVARFLRGTENWM RQRAEWEKEKAAWEAAHPHLTPEVRAQFNKIFESLHDPENSGKPGVSRKNPRICPWDRL KQNLDNCCYGEKGHSALCWRYQDFLKQRMGENRRDKKNFSATAMDLAQICREWKIQH SRNALNNPRVLDRLFAEHERRKQDKTKKESRSPKPRQGGYKANPKADYLRSFKAHWKAY LEHMKLNDTTVLERGCLPHCLSIKKNGKESTCKWNKHTELCLEYKRSLAPLPDSVLELEPEY REWRRLYLHGPGRPHFRYPSAGELPLPKVFGEGFHQVDLDRSIVRLRLEGAAEGEWLEFGF IPWPRGYQPSRREVLITSVQVHFVGTRPRAGFRFDVSHRTSRFGCSQDELDELRSRRYPRQ AQDKEFLAAARAQLIQTFEGGEGAARQQMRVMSVDLGEGGACASIYEGRTHQKDESLKV IKIDRRYDQHPEVLEKDVGAAKPQKFEKSDPRGVRKEHVARHLNRIAAGASAIAEHRRKER SDAECSVGELQEHDFRSLKRHIAWMIRDWVRLNAAQIIDVAKQHCCDLIVFESQRGFRLP GYDELDRGKKQRFAILAFGRIRRKVVEKAVEHGMRVVTVPYFASSQVCSACKRVQENRGS WRENKKKRVFACEFCKLKLNSDANASRVLARVFWGEIELPEPTRAHLPSKA
71	cas12g	MPVSRYSESRTLVRPLARLPHEERQDVTPKVARLRRHFERFNVDVAELCQWLMGLRNQF GPKESPASFGPLGDFLIEPALDNIDADETERDRWRLAVFDAVAGFRPIRGLGDHPVPDTLR

[0108]

		LAMQQAASLSPTPTTARLLERLRPLSPAHRLVLLKSAAEWIVARYQRGMENWVIQHAAW HKEKEAWEREHPALTPAVRERFTALYKQLSDSKPTDRPVSRRKNPRICEWERLRQNIDNC CYAGEKGHGPLCRKYANFVKARKAVDGKFNDLLFWDTATSFIALCRKFNVTRARNALQS QLDALFAEDQRRKAERDQAKGRQPRPLHPQAAARAKSDFLRIFKDGWNAYLSAMGLND STAIEKGRLPHCQKIGGTFENSKCEWNPHTDLCHQYRRLAGQLDDATLALEKDYREWRRL YLAGPRKPSFQYPSSRDLPMPKIFGAGFFELDMDRSILRLRLDDMVEGEWLEFGFKPWPRE YTPSRAQVARPGRITSVHVNFIGSRCRVGFRFEAPHAGSRFGCSQDEIDQLRRDHPRERD DQPFLEAARKRLVETFAGDARRDLRLLAVDVGEKGCCAAVYQGTRYVADALLPIIKINQLY TEPPTELKPDSHNRPAPDRRPFNDEKDPRDPRGVRKEHVARHLKRMADKAPEVAAYRLA QREKAAPSPSASPPPVTLGVHDFRRLKRHVTWMIRDWARHNAARIVAEAQRHGCDLIVF ESHRGRRPPGYHEVGDDAERRKLDNATFAFGRIRRKVTEKAVERGLRVVTVPYHCSSKVC SRCGRLQENDGLLRRNKKERKFICEQCKFETNSDGNAARVLARVFWGEIMLPSPEERKK REGSGGRSPTPANPGGLVDAPPSRRNLR

[0109]

[0110]

72	Cas12	MEDYSGFVNIYSIQKTLRFELKPVGKTLEHIEKKGFLKKDKIRAEDYKAVKKIIDKYHRAYIEEVFD SVLHQKKKKDKTRFSTQFIKEIKEFSELYYKTEKNIPDKERLEALSEKLRKMLVGAFKGEFSEEVAE KYKNLFSKELIRNEIEKFCETDEERKQVSNFKSFTTYFTGFHSNRQNIYSDEKKSTAIGYRIIHQN LPKFLDNLKIIESIQRRFKDFPWSDLKKNLKKIDKNIKLTEYFSIDGFVNVLNQKGIDAYNTILGG KSEESGEKIQGLNEYINLYRQKNNIDRKNLPNVKILFKQILGDRETKSFIPEAFPDDQSVLNSITE FAKYLKLDKKKKSIIAELKKFLSSFNRYELDGIYLANDNSLASISTFLFDDWSFIKKSVSFKYDESV GDPKKKIKSPLKYEKEKEKWLKQKYYTISFLNDAIESYSKSQDEKRVKIRLEAYFAEFKSKDDAKK QFDLLERIEEAYAIVEPLLGAEYPRDRNLKADKKEVGKIKDFLDSIKSLQFFLKPLLSAEIFDEKDL GFYNQLEGYYEEIDSIGHLYNKVRNYLTGKIYSKEKFKLNFENSTLLKGWDENREVANLCVIFRE DQKYYLGVMDKENNTILSDIPKVKPNELFYEKMVYKLIPTPHMQLPRIIFSSDNLSIYNPSKSIL KIREAKSFKEGKNFKLKDCHKFIDFYKESISKNEDWSRFDFKFSKTSSYENISEFYREVERQGYN LDFKKVSKFYIDSLVEDGKLYLFQIYNKDFSIFSKGKPNLHTIYFRSLFSKENLKDVCLKLNGEAE MFFRKKSINYDEKKKREGHHPELFEKLKYPILKDKRYSEDKFQFHLPISLNFKSKERLNFNLKVN EFLKRNKDINIIGIDRGERNLLYLVMINQKGEILKQTLLDSMQSGKGRPEINYKEKLQEKEIERDK ARKSWGTVENIKELKEGYLSIVIHQISKLMVENNAIVVLEDLNIGFKRGRQKVERQVYQKFEK MLIDKLNFLVFKENKPTEPGGVLKAYQLTDEFQSFEKLSKQTGFLFYVPSWNTSKIDPRTGFIDF LHPAYENIEKAKQWINKFDSIRFNSKMDWFEFTADTRKFSENLMLGKNRVWVICTTNVERYF TSKTANSSIQYNSIQITEKLKELFVDIPFSNGQDLKPEILRKNDAVFFKSLLFYIKTTLSLRQNNG KKGEEEKDFILSPVVDSKGRFFNSLEASDDEPKDADANGAYHIALKGLMNLLVLNETKEENLS RPKWKIKNKDWLEFVWERNR
73	Cas12	MKKFTNLYSLSKTLRFELIPQGKTLENIQKSGILEQDNSRAEKYEKIKKIIDDYHKFFIEKSFTGKKI DDYFLNQYFELFKIKDKDEEQKKDFKSIQENLRKNIISFFDKNKLKRLFEKEIIKEDLPNFVKEEED KKLISEFDKFTTYFVGFHENRKSMYSEEEKSTSIAYRTINENLPKFINNIFVFEKISKTPISENFRELY KDLEEYLNVNDIQDIFKLNYFSNVITQKQIDVYNLVIGGKTLENGTKIKGLNEYINLYNQNQTDK KNKLPLLTVLFKQILCDRDTISFLPEQFENDIDVLDNIKNTYSNMEKSIKDIKDLLSNLKDFDLSKI YITNDIALTDISQQVFNNYSIIINAIKENIKKENPKKKTENEEKYGERIDKIFKSNNSFSIKYINDCIK EKNIEIYFMDFGKKENNKKVKNLFDELQNNYSMVKDLLEYKKIQSLIQDEKSIELIKNFLDSIKNI QHFLKPLYVKDNDIVKDISFYRDFEELYLNIDKITPLYNKVRNYVTQKPYSVKKIKLNFENSTLLA GWDLNKERDNTCAILRKDDLYYLAIMDVNNRNVFNEKGIDGIGYEKMEYKLLPGANKMLPKV

		FFSKSRIKDFNPSEQIIRNYEKETHKKGSNFSLKDCHKLIDFFKSSINKHEDWKNFNFKFSNTDK YEDLSGFYREVEQQGYKITFRNISKEYVDKLVEEGKIYLFQIYNKDFSKYSKGTPNMHTLYWKAL FDEDNLKNVVYKLNGQAEIFYRKGSIEKENIVIHKANNAIENKNMDNKKKQSKFEYDIIKDRRY TVDKFQFHVPITLNFKAIGNERINEQVNQYIKDNNIKHIIGIDRGERHLLFLSLIDLKGNIIKQFSL NEIVNEYNGNSYKTNYHMLLEKREEERDKARKSWKTIENIKELKEGYISQVIHKITQLMIEYNAI VVLEDLNFGFMRGRQKVEKQVYQKFEKMLIDKLNYLVDKKKDKNEAGGLLKAHQLTNKFESF QKMGKQNGFLFYIPAWNTSKLDPITGFVNLFDTHYTNVDNAKKFFENFEDIRFNEKKNYFEFIV NDYTKFNTKAEGTKLNWTICSNEDRIKTFRSSSKNNQWVSETVNLTDSLIELFKKYDIDYKLELK EQIISKSEKNFFETLLYLFKLTLQMRNSITGTETDYLISPVADKTGNFFDSRKGIENLPNNADANG AYNIARKGLWVIEQIKKAKDLKKVKLAISNKEWLQFVQGK
74	Cas12	MAKNTIFSQFTGLYPVSKTLRFELKPMGKTLEKIKETGVIENDKKRHNDYFDAKKIIDKYHKYFID AALSKFPRIDWSPLKEAIERSLDRSDASKKKLEKTQTEFRKKIAKALTTHDHYKELTASTPKDLFLK VFPDHFGKQPAIDTFDGFSSYFTGFQENRQNIYSDEAISTAIPYRLVHDNFPKFLSNIEVYKTLKD NAPSVLSDAENELRDFLNGKSLANIFELNAYNEVLTQSGIDFFNQVIGGISDEGGEKKTRGINEF SNLYRQQHPEFAQKRLATKMIPLYKQILSDRETKSFILESYSNDSQVQNSVKEFFESQILNWDIA GRRVNVLNELTSLVKRISEFDLGNIYVNQEELSNISLKLFDNWNSINGLLFKHAENRIGSAEKSA NKKKIDAWMKNKEFSIATLNLAIAESNSEEISRVKIESYWNNFEAKVQSILCGDNRRNLDEFISA TFNENNALREDSKIIEKLKAFLDALIEIMHSIKPLISDAENRDLSFYNELIPLYDQLSLVVPLYNKIR NYATQKLTESEKFKLNFDNPTLADGWDQNKEEANTAILLLKNGLYYLGIMNAKNKPKIKDFKTS ESEDCYDKMVYKLLPGPNKMLPKVFFSEKGLATFKPPKDILDGYNAGKHKKGDLFDIGFCHQLI DFFKESIAKHPDWKKFDFNFSDTSSYEDISGFYKEVTDQGYKITFSKIPTSQIDEWVKEGKLFLFQ IYNKDFAPGAKGSPNLHTLYWKSVFSPENLKDVVVKLNGEAELFYRPSSVKKPYSHKVGEKLVN RIGKDGLPLPESVFGELFRYFNGKLEGELSDEAKRYLDVAVVKDVKHEIVKDRRYTQDKFEFHVP LTLNFKADSKNEYMNERVRHFLKDNPDVNIIGIDRGERHLLYMTLINQKGEILKQKSFNVVESV NYQAKLVQREKERDAARRSWSSVGKIKDLKEGFLSQVIHEITTTMIENNAIVVLEDLNFGFKRG RFCVERQVYQKFEKMLIDKLNYLVFKNKPEGDVGGVLKGYQLAEKFDSFQKLGKQSGFLFYIPA AYTSKIDPTTGFANLFNMTELTSAEKKKEFLSHFEDITYDGKNDRFLFSFDYKNFKCFQTDYIKK WTVYSQGKRIVYDKESKSAKEISPVEIIKAALAKQNIALTDQLDVLSAINSVEASPKSASFFGDIC YAFEKTLQMRNSIPNTDEDYLASPVMNKRGEFYDSRSCDDALPQNADANGAYHIALKGLYLIK NVFDAGGKELKISHEDWFKFAQSRNC
75	Cas12	MSKGKIWENFINQYSVSKTLRFELKPVGKTLENINAKGLIEEDEQRAEDYKKAKKIIDEYHKYFIE GALGSCSLDLNILNEFLQLYNKAQKTDADKKEYEKIQTTLRKNIAESFGKNADKKTKEQYENLFK KELLRNDLPDWVEDEEDAKIIERFKTFTTYFTGFHENRKNIYDNEEKSTAIGYRIVHENLPKFIDN MNAFEKISKALDLSEIDRDFQSELGEIKAEEFFTIEFFNQCLNQFGIDRYNTLLGGISEGENIKKKQ GLNERINLYNQQLKGERKKERLPKLKVLYKQILSDSSSHSFSIDEFENDNELLESLEIFYKNELIGF NHSGVDSNIFDLVKDLLLKIDESEQSSIYLKNDKGLTEISQRIFGDWNIIKSALEEYYDEHYPPKK DTFNKKELDERSRWLKENHSIGVIEKALANYENEIVREHLKQNSAPIVSYFKSLEVDGENLIDKIY SAYGNISDLLNSSYPDEKKLVSDRTSKDKIKVFLDSLMSLLHFLKPLDVKDLGNKDSAFYGDYDF IVEQLSKLVRLYNKTRNYLTRKPYSIEKIKLNFENSTLLAGWDVNKERDNNCVIFKRQDGDRELF YLGIMDKSHNKIFTKIEEAKSDDVYQKMNYKLLPGPNKMLPKVFFSKKSIDFYAPGEELLKNYK

[0111]

		NGTHKKGENFNLQHCHELIDFFKRSINKHEDWSQFNFKFSDTSEYEDTSFFFKEVSQQGYSITF KNIDRETIEKFVDEGKLYLFQIYNKDFSPKSKGRPNLHTLYWKMLFDERNLANTVYQLNGEAEV FYRKKSISEKDRVVHRADEPIGLKNSENSAQKSLFPYDIVKDRRFTVDKFQFHVPITLNFKSEGN ERLNISVNKFLKDNPDVNIIGLDRGERHLIYLTLINQKGEILHQESLNEVMGVNYQQKLHRVEK DRTEERRNWDRIENIKELKSGYLSQVVHKISQLMVEYNAIVVMEDLNFGFKRGRIKVEKQVYQ KFEKTLIDKLNYLVFKDREPEEPAGVLNALQLTNKFESFKKLGKQCGFLFYVTSDYTSKIDPATGFV NLLYPKYESVEKSQNFFRKFDNICFNSGAGYFEFDFDYSNFTDRADGTRTRWKVCTVGNERFG YNPKTKASETVNVTESLKELLLQHEIAFENGESLVESISKNTTKYFHKSLLNFLRLTLTLRHSKTGT DIDYILSPVANEEGVFFDSRNASDKMPKDADANGAYNVALKGLMVLERINAAEDLSQFKFKD MSIKNKDWLKFVQDRQG
76	Cas12	MKNLANFTNLYSLQKTLRFELKPIGKTLDWIIKKDLLKQDEILAEDYKIVKKIIDRYHKDFIDLAFE SAYLQKKSSDSFTAIMEASIQSYSELYFIKEKSDRDKKAMEEISGIMRKEIVECFTGKYSEVVKKKF GNLFKKELIKEDLLNFCEPDELPIIQKFADFTTYFTGFHENRENMYSNEEKATAIANRLIRENLPRY LDNLRIIRSIQGRYKDFGWKDLESNLKRIDKNLQYSDFLTENGFVYTFSQKGIDRYNLILGGQSV ESGEKIQGLNELINLYRQKNQLDRRQLPNLKELYKQILSDRTRHSFVPEKFSSDKALLRSLLDFHK EVIQNKNLFEEKQVSLLQAIRETLTDLKSFDLDRIYLTNDTSLTQISNFVFGDWSKVKTILAIYFDE NIANPKDRQRQSNSYLKAKENWLKKNYYSIHELNEAISVYGKHSDEELPNTKIEDYFSGLQTKD ETKKPIDVLDAIVSKYADLESLLTKEYPEDKNLKSDKGSIEKIKNYLDSIKLLQNFLKPLKPKKVQD EKDLGFYNDLELYLESLESANSLYNKVRNYLTGKEYSDEKIKLNFKNSTLLDGWDENKETSNLSV IFRDTNNYYLGILDKQNNRIFESIPEIQSGEETIQKMVYKLLPGANNMLPKVFFSEKGLLKFNPSD EITSLYSEGRFKKGDKFSINSLHTLIDFYKKSLAVHEDWSVFNFKFDETSHYEDISQFYRQVESQG YKITFKPISKKYIDTLVEDGKLYLFQIYNKDFSQNKKGGGKPNLHTIYFKSLFEKENLKDVIVKLNG QAEVFFRKKSIHYDENITRYGHHSELLKGRFSYPILKDKRFTEDKFQFHFPITLNFKSGEIKQFNA RVNSYLKHNKDVKIIGIDRGERHLLYLSLIDQDGKILRQESLNLIKNDQNFKAINYQEKLHKKEIE RDQARKSWGSIENIKELKEGYLSQVVHTISKLMVEHNAIVVLEDLNFGFKRGRQKVERQVYQK FEKMLIEKLNFLVFKDKEMDEPGGILKAYQLTDNFVSFEKMGKQTGFVFYVPAWNTSKIDPKTG FVNFLHLNYENVNQAKELIGKFDQIRYNQDRDWFEFQVTTDQFFTKENAPDTRTWIICSTPTK RFYSKRTVNGSVSTIEIDVNQKLKELFNDCNYQDGEDLVDRILEKDSKDFFSKLIAYLRILTSLRQ NNGEQGFEERDFILSPVVGSDGKFFNSLDASSQEPKDADANGAYHIALKGLMNLHVINETDD ESLGKPSWKISNKDWLNFVWQRPSLKA
77	Cas12	MNLIENETKSEEIKSKLDSIMEIMHWTKMFIIEEEIEKDVNFYNEIEEIYDELQPLVTIYNRIRNYVT QKPYSEEKIKLNFGIPTLANGWSKTKEYDNNAIIMIRDGKYYLGIFNAKNKPDKKIMEGHQSEE NGDYKKMIYRLLPGPNKMLPKVFMSKTGIAEYKPSQYILECYEQNKHIKSDKNFDIKFCRDLIDF FKTSINRHPEWSKFNFKFSETSEYEDISTFYREVEKQGYKIEWTYISEKEIKELDENGQLYLFQIYN KDFSEKSKGKENLHTMYLKNLFSEENLKNIVLKLNGEAEVFFRKSSIKKPIIHKKGSVLVNKTYNE NGERKSIPEEQYTEIYKYLNSIGTNELSEKSKKLMEEGKVEYYKANYDIVKDYRYSVDKFFIHLPM TINFKAAGFSPINNIALKSIALKEDMHIIGIDRGERNLIYVSVIDTKGNIVEQRNFNIVNGIDYKEK LKQKELDRDNARKNWKEIGKIKDLKEGYLSLVVHEIAKLVVKYNAIITMEDLNQGFKRGRFKVE RQVYQKFETMLINKLNYLVDKDLAVDQEGGLLRGYQLTYIPESLKVLGRQCGYIFYVPVAYTSKI DPTTGFVAIFNYKGMTDKDFVTSFDSIKYDDERGLFAFEFDYENFVTHKVEMARNKWTVYTYG

[0112]

		ERIKRKFKNGLWDTAEKVDLTYQMRSILEKYEIEYNKGQDILEQIEELDEKAQNGICKEIKYLVKDI VQMRNSLPDNAVEDYDAIISPVINNNGEFFDSTRGDEDKPLDADANGAYCIALKGLYEVMQIK KNWNEETEFPRKELKIRHQDWFDFIQNKRYL
78	Cas12	MENRYQVLQGLTAAQKKAAAAAKKRSSFSIVELNAATRSRVPDEKYVPVQNYFSAMGKVCSQ GEPKRENFVTRICAAYQELEEYIPSIRKSLLQEKRATELIKNYLDAVNDLLRFIKPLLGRGNETDKD ANFYGEFSFLTDCLFAIVPLYNEVRNYLTQKPYSTEKFKLNFRGSTLLNGWDKNKERDNLGVILR KEGKYFLAIMNKKHNTLFTEGKLQQHTGGECYQKMEYKLIPGSKMLPKVFFSKKGISTFQPSEE LLLNYRIGTYKKGEKFNLEHLHKLIDFYKHSIAVHEDWSKFDFHFSDTSSYRDISGFYKEVEQQG YKLTFRNVSVSYINRLVEEGKLYLFQIYNKDFSEYSKGTPNLHTLYWKMLFDPENLKDVVYKLSG EAEVFFRKKSLDVSHPTHPKNEPIEKKNINNKGEKSLFSYDLIKDRRFTVDKFQFHVPITMNFKG EQGDRVNQMVQSYVRNNKGLNVIGIDRGERNLLYLVVINEHGEILEQFSLNEIRNAYNGKEHK IDYHTLLEERSKKRQDARQSWQTIEGIKDLKTGYLSQVIHVITQLMVKYNAIVVLEDLNFGFKSS RQKFEQSVYQQFERKLIDKLNFLVNKKAAPNEVGGLLNAYQLTAPLGNSRKMGKQNGFLFYVP AWHTSKIDPRTGFVNLLDTRYENVAKAKEFFAKFASITYNPEKKWFEFAFDYKAFGNRADGSRT KWTICSYGERIETFRNPENNNQWDTKSVPLTERLTELFSKYGIDYTTNLKEQILNQTDKAFFVEL LGALRLTLQLRNSRKSTGEDFLFSPVADENGCFFDSREANDNEPKDADANGAYHIALKGLWVL DTIRNTEEGKNPKLAITNKEWLSFAQAKPFAHE
79	Cas12	MSDSYDELTKAQKEKQEKRKHVALTEVVAALEKYTIALDNGHEHKNAVNTFKNYFQNYFFHFD TDKKKTAKTLDCQIKDEYNGLKGILNTPWDKNKKLQQDKKLVQQIKSFLDSIQELLWFIKPLVLT DNTLEKDERFYGEFMPLYDEISNIIKLYNKIRNYLTKKPYSIEKYKLNFENGSLLSGWDVNKEKDN TSVLLCKDNQYYLAIMHIDHNKVFELDELIKHAGKGYQKINYKLLPGANKMLPKVFFSGKNISY YDPSKEILKIRNYGTHTKNGDPQPGFSKRDFSVDDCRKMIDFFKNSIAKHEDWKNFDFKFQPT KNYNSIDEFYREVEEQGYKITYSNVSEDYIDSLVEYGKIYLFHIYNKDFSDKRDESKKHTDNMHT LYWKALFDAKNLKDVVYKLNGEAEIFYRKKSIDIKKPTHEKGKPIDNKNPNARKKTSVFKYDLIK DKRFTVDKFFFHVPITLNFKSKSGYLSNDDVNAAIKKNNDIKIIGLDRGERNLIYLSLINSKGEIAY QESLNVVSTDKGFDVNYHKLLDDKEGNRDEARKNWDKIENIKELKAGYLSQVIHKIAKLMIDN NAIVVMEDLNFGFKRGRFKVEKQIYQKFEKMLIDKLNYLVFKNVHPEQAGGLYKAYQLTAQFES FKKLGKQSGFLFYIPAWNTSKIDPTAGFVDFLKPRYESVTQAKSFLQRFDKINYNKTKDYFEFAF DYKNFTDKANDTKTDWVVCTYGTERYYYDVRTKTTQKIDITAELKKLLEKSEINYLNGKDIKELII AVDSKEFHSALLKYLAIVLALRYSDSQSGRDFILSPVANEQGHFFNSDKTDDTLPKDADANGA YHIALKGLWAINQIRKTKNGDKLKLTISNKDWLNFVQKKEYRKGV
80	Cas12	MQTLFENFTNQYPVSKTLRFELIPQGKTKDFIEQKGLLKKDEDRAEKYKKVKNIIDEYHKDFIEKS LNGLKLDGLEKYKTLYLKQEKDDKDKKAFDKEKENLRKQIANAFRNNEKFKTLFAKELIKNDLM SFACEEDKKNVKEFEAFTTYFTGFHQNRANMYVADEKRTAIASRLIHENLPKFIDNIKIFEKMKK EAPELLSPFNQTLKDMKDVIKGTTLEEIFSLDYFNKTLTQSGIDIYNSVIGGRTPEEGKTKIKGLNE YINTDFNQKQTDKKKRQPKFKQLYKQILSDRQSLSFIAEAFKNDAEILEAIEKFYVNELLHFSNEG KSTNVLDAIKNAVSNLESFNLTKMYFRSGTSLTDVSRKVFGEWSIINRALDNYYATTYPIKPREK

[0113]

		SEKYEERKEKWLKQDFNVRLIQTAIDEYDNETVKGKNSGKVIADYFAKFCDDKETDLIQKVNEG YIAVKDLLNTPYPENEKIGSNKDQVKQIKAFMDSIMDIMHFVRPLSLKDTDKEKDETFYSLFTPL YDHLTQTIALYNKVRNYLTQKPYSTEKIKLNFENSTLLGGWDLNKETDNTAIILRKDNLYYLGIM DKRHNRIFRNVPKADKKDFCYEKMVYKLLPGANKMLPKVFFSQSRIQEFTPSAKLLENYANET HKKGDNFNLNHCHKLIDFFKDSINKHEDWKNFDFRFSATSTYADLSGFYHEVEHQGYKISFQS IADSFIDDLVNEGKLYLFQIYNKDFSPFSKGKPNLHTLYWKMLFDENNLKDVVYKLNGEAEVFY RKKSIAEKNTTIHKANESIINKNPDNPKATSTFNYDIVKDKRYTIDKFQFHIPITMNFKAEGIFNM NQRVNQFLKANPDINIIGIDRGERHLLYYALINQKGKILKQDTLNVIANEKQKVDYHNLLDKKE GDRATARQEWGVIETIKELKEGYLSQVIHKLTDLMIENNAIIVMEDLNFGFKRGRQKVEKQVYQ KFEKMLIDKLNYLVDKNKKANELGGLLNAFQLANKFESFQKMGKQNGFIFYVPAWNTSKTDP ATGFIDFLKPRYENLNQAKDFFEKFDSIRLNSKADYFEFAFNFKNFTEKADGGRTKWTVCTTNE DRYAWNRALNNNRGSQEKYDITAELKSLFDGKVDYKSGKDLKQQIASQESADFFKALMKNLS ITLSLRHNNGEKGDNEQDYILSPVADSKGRFFDSRKADDDMPKNADANGAYHIALKGLWCLE QISKTDDLKKVKLAISNKEWLEFVQTLKG
81	Cas12	MQLTDNLSDKYKEAAPLLNENYSNEKGLKNDDKSISLIKNFLDAIKEIEKFIKPLSETNITGEKND LFYSQFTPLLDNISRIDILYDKVRNYVTQKPFSTDKIKLNFGNSQLLNGWDRNKEKDCGAVVLC KDEKYYLAIIDKSNNSILENIDFQDCDESDCYEKIIYKLLPGPNKMLPKVFFSEKCKKLLSPSDEIL KIRKNGTFKKGDKFSLDDCHKLIDFYKESFKKYPNWLIYNFKFKKTNEYNDIREFYNDVASQGY NISKMKIPTSFIDKLVDEGKIYLFQLYNKDFSPHSKGTPNLHTLYFKMLFDERNLEDVVYKLNGE AEMFYRPASIKYDKPTHPKNTPIKNKNTLNDKKTSAFPYDLIKDKRYTKWQFSLHFPITMNFKA PDRAMINDDVRNLLKSCNNNFIIGIDRGERNLLYVSVIDSNGTIIYQHSLNIIGNKFKGKTYKTN YREKLATREKDRTEQRRNWKAIESIKELKEGYISQAVHVICQLVVKYDAIIVMEKLTEGFKRGRTK FEKQVYQKFEKMLIDKLNYYVDKKLDPDEEGGLLHAYQLTNKLESFDKLGTQSGFIFYVRPDFTS KIDPVTGFVNLLYPRYENIDKAKDMISRFDEIRYNAGEDFFEFDIDYDKFPKTASDYRKKWTICT NGERIEAFRNPANNNEWSYRTIILAEKFKELFDNNSINYRDSDDLKAEILSQTKGKFFEDFFKLLR LTLQMRNSNPETGEDRILSPVKDKNGNFYDSSKYDEKSKLPCDADANGAYNIARKGLWIVEQF KKADNVSTVEPVIHNDKWLKFVQENDMTNN
82	Cas12	MLPNEKERNEFKNSNAKQYIREISNIITDTETAHLEYDEHISLIESEEKADEMKKRLDMYMNMY HWAKAFIVDEVLDRDEMFYSDIDDIYNILENIVPLYNRVRNYVTQKPYNSKKIKLNFQSPTLAN GWSQSKEFDNNAIILIRDNKYYLAIFNAKNKPDKKIIQGNSDKKNDNDYKKMVYNLLPGANK MLPKVFLSKKGIETFKPSDYIISGYNAHKHIKTSENFDISFCRDLIDYFKNSIEKHAEWRKYEFKFS ATDSYNDISEFYREVEMQGYRIDWTYISEADINKLDEEGKIYLFQIYNKDFAENSTGKENLHTM YFKNIFSEENLKDIIIKLNGQAELFYRRASVKNPVKHKKDSVLVNKTYKNQLDNGDVVRIPIPDD IYNEIYKMYNGYIKENDLSEAAKEYLDKVEVRTAQKDIVKDYRYTVDKYFIHTPITINYKVTARN NVNDMAVKYIAQNDDIHVIGIDRGERNLIYISVIDSHGNIVKQKSYNILNNYDYKKKLVEKEKT REYARKNWKSIGNIKELKEGYISGVVHEIAMLMVEYNAIIAMEDLNYGFKRGRFKVERQVYQKF ESMLINKLNYFASKGKSVDEPGGLLKGYQLTYVPDNIKNLGKQCGVIFYVPAAFTSKIDPSTGFIS AFNFKSISTNASRKQFFMQFDEIRYCAEKDMFSFGFDYNNFDTYNITMSKTQWTVYTNGERL QSEFNNARRTGKTKSINLTETIKLLLEDNEINYADGHDVRIDMEKMDEDKNSEFFAQLLSLYKLT VQMRNSYTEAEEQEKGISYDKIISPVINDEGEFFDSDNYKESDDKECKMPKDADANGAYCIALK

[0114]

		GLYEVLKIKSEWTEDGFDRNCLKLPHAEWLDFIQNKRYE
83	Cas12	MSNLYSNLHNLYPVQKTLRFELKPQGKTKENMEKAGILKADEHRAEVYGKVKKYCDEYHKTFI DRCLSNIELNEIDKYYELYSINNRDDKQKEELDQLETGLRKQISDAFKKSAEYKGLFQKDMITSYL VTMYKENQEKMQDIGEFNRFTTYFTGYNKNRENMYSEEDKSTAISYRLINENLPTFIDNIKIYKK IVSLMPENIEKIYKDLEEYIQVNSVDEIFNISYYNDVLTQRGIECYNILISGRTKNDGDKIKGLNEYI NEFNQTHNEKIPKLQELYKQILSDAESASFKVDIIENDKELLNLIEVYYANILPTLNKIEDLFTRISN YNLELILVNNDGSLSTLSNMVFNEWSYIKGIISQKYDAEYSGKEKYGTEKYAQKKQEYLKKQKIY SLKFLNDCIGNNAICEYLKNYIIQNKNIETIKEDYNEVQNIKAEDDTKELIKDEKSIEKIKKFLDDV KSLQEFVKLVIPKDRTVEKDAKFYSELTPYYEKIKEIIPLYNKVRNYVTQKPYSTEKIKLNFECPTLL NGWDANKEEANLGVILLKEGKYYLGIMNPYCKKIFEVYEKDSNEQNNYKKMEYKLLPGPNKM LPKVFFSNSRIEEFNPSKELQEKYNKGYHKKGKDFDINFCHELIDFYKQSLNKHEDWKKFNFKFK DTSEYNDISEFYREVEEQGYKIEYTEYSEKYINELVDRGELYLFQIYNKDFSEYSKGKENLHTLYWK AVFDPDNIMNPVYKLNGNAEIFYRKKSLEMKVTHPANQPIANKNISTIEAGRSTSTFKYDLIKD KRYTMDKFQFHVPITVNFKSERLFNINQIVNKYLKYNDDIHVIGIDRGERNLLYVCVIDKNEKIV YQKSLNEIVSEYNNNRYTTDYHGLLDRKEKEREIAREDWKNIENIKELKEGYMSQIIHILVELMK KYNAIIVIEDLNKGFKNSRIKVEKQVYQKFEKMFIDKLNYLVFKDEDKMDEGGVLNAYQLTNKF ESFTKLGKQSGILYYIPAWCTSKIDPTTGFINRFYLKYENFDKSKEFVNRIDDIRYNEKENLFEFDID YSKFTDRLNDTKNKWTLCSYGERILTQKNANGEWFDRRIQLSIEFKNLFEKYVINLNNIKDSILK LDKDNIEFYKGNGENLGFIQLFKLMVQMRNSLTGKEEDNLISPVKNQHGKFFNTSERVEGLPID ADANGAYNIARKGFMLVEQMKNVEDEKLNKIKYNITEKEWLNYVQNRGMWWKRQYLYHI
84	Cas12	MAKNTIFSQFTGLYPVSKTLRFELKPMGKTLEKIKETGVIENDKKRHNDYFDAKKIIDKYHKYFID AALSKFPRIDWSPLKEAIERSLDRSDASKKKLEKTQTEFRKKIAKALTTHDHYKELTASTPKDLFLK VFPDHFGKQPAIDTFDGFSSYFTGFQENRQNIYSDEAISTAIPYRLVHDNFPKFLSNIEVYKTLKD NAPSVLSDAENELRDFLNGKSLANIFELNAYNEVLTQSGIDFFNQVIGGISDEGGEKKTRGINEF SNLYRQQHPEFAQKRLATKMIPLYKQILSDRETKSFILESYSNDSQVQNSVKEFFESQILNWDIA GRRVNVLNELTSLVKRISEFDLGNIYVNQEELSNISLKLFDNWNSINGLLFKHAENRIGSAEKSA NKKKIDAWMKNKEFSIATLNLAIAESNSEEISRVKIESYWNNFEAKVQSILCGDNRRNLDEFISA TFNENNALREDSKIIEKLKAFLDALIEIMHSIKPLISDAENRDLSFYNELIPLYDQLSLVVPLYNKIR NYATQKLTESEKFKLNFDNPTLADGWDQNKEEANTAILLLKNGLYYLGIMNAKNKPKIKDFKTS ESEDCYDKMVYKLLPGPNKMLPKVFFSEKGLATFKPPKDILDGYNAGKHKKGDLFDIGFCHQLI DFFKESIAKHPDWKKFDFNFSDTSSYEDISGFYKEVTDQGYKITFSKIPTSQIDEWVKEGKLFLFQ IYNKDFAPGAKGSPNLHTLYWKSVFSPENLKDVVVKLNGEAELFYRPSSVKKPYSHKVGEKLVN RIGKDGLPLPESVFGELFRYFNGKLEGELSDEAKRYLDVAVVKDVKHEIVKDRRYTQDKFEFHVP LTLNFKADSKNEYMNERVRHFLKDNPDVNIIGIDRGERHLLYMTLINQKGEILKQKSFNVVESV NYQAKLVQREKERDAARRSWSSVGKIKDLKEGFLSQVIHEITTTMIENNAIVVLEDLNFGFKRG RFCVERQVYQKFEKMLIDKLNYLVFKNKPEGDVGGVLKGYQLAEKFDSFQKLGKQSGFLFYIPA AYTSKIDPTTGFANLFNMTELTSAEKKKEFLSHFEDITYDGKNDRFLFSFDYKNFKCFQTDYIKK WTVYSQGKRIVYDKESKSAKEISPVEIIKAALAKQNIALTDQLDVLSAINSVEASPKSASFFGDIC YAFEKTLQMRNSIPNTDEDYLASPVMNKRGEFYDSRSCDDALPQNADANGAYHIALKGLYLIK

[0115]

		NVFDAGGKELKISHEDWFKFAQSRNC
85	Cas12	MYKDKTDKTKIIDSDLIKFINIAESTQLDSMSQDEAKELVKEFWGFTTYFVGFYDNRKNMYTAE EKSTGIAYRLVNENLPKFIDNMEAFKKAIARPEIQANMEELYSDFSEYLNVESVQEMFQLDYYN MLLTQKQIDVYNAIIGGKTDDEHDVKIKGINEYINLYNQQHKDDKLPKLKALFKQILSDRNAIS WLPEEFNGDQEVLNAIKDCYERLSENVLGDKVLKSLLGSLSDYSLDGIFIRNDLQLTDISQKMF GNWCVIQNAIMQNIKHVAPARKHKESEEDYEKRIAGIFKKVDSFSISFINDCLNEADPNNAYFV ENYFATFGAVNTPTMQRENLFALVQNAYTEVAALLHSDYPTAKHLAQDKVNVAKIKALLDAIK SLQHFVKPLLGKGDESDKDERFYGELASLWAELDTVTPLYNMIRNYMTRKPYSQKKIKLNFENP QLLGGWDANKEKDYATIILRRDGLYYLAIMNKESKKLLGKAMPSDGECYEKMVYKLLPGANK MLPKVFFAKSRMEDFKPSKELVEKYNNGTHKKGKNFNIQDCHNLIDYFKQSISKHEDWGKFGF NFSDTSTYEDLSGFYREVEQQGYKLSFARVSVSYISQLVEEGKMYLFQIYNKDFSEYSKGTPNM HTLYWKALFDERNLADVVYKLNGQAEMFYRKKSIENTHPTHPANHPILNKNKDNKKKESLFD YDLIKDRRYTVDKFMFHVPITMNFKSSGSENINQDVKAYLRHADDMHIIGIDRGERHLLYLVVI DLQGNIKEQYSLNEIVNEYNGNTYHTNYHDLLDVCEEERLKARQSWQTIENIKELKEGYLSQVI HKITQLMVKYHAIVVLEDLNMGFMRGRQKVEKQVYQKFEKMLIDKLNYLVDKKADASVSGGL LNAYQLTSKFDSFQKLGKQSGFLFYIPAWNTSKIDPVTGFVNLLDTRYQNVEKAKVFFSKFDAIR YNKDKDWFEFNLDYDKFGKKAEGTRTKWALCTRGMRIDTFRNKEKNSQWDNQEVDLTAEM KSLLEHYYIDIHGNLKDAISAQTDKAFFTGLLHILKLTLQMRNSITGTETDYLVSPVADENGIFYDS RSCGDELPENADANGAYNIARKGLMMIEQIKDAKDLDNLKFDISNKSWLNFAQQKPYKNE
86	Cas12	MNEADPNNAYFVENYFATFGAVNTPTMQRENLFALVLNAYTEVASLLHSYYPAEKNLAQDKA NVAKIKALLDAIKSLQHFVKPLLGKGDESDKDERFYGELASLWAELETVTPLYNMIRNYMTRKP YSQKKIKLNFENPQLLGGWDANKEKDYATIILRRNGLYYLAIMDKDSRKLLGKAMPSDGECYEK MVYKLLPGANKMLPKVFFAKSRMEDFKPSKELVEKYNNGTHKKGKNFNIQDCHNLIDYFKQSI SKHEDWGKFGFNFSDTSTYEDLSGFYREVEQQGYKLSFARVSVSYISQLVEEGKMYLFQIYNKD FSEYSKGTPNMHTLYWKALFDERNLADVVYKLNGQAEMFYRKKSIENTHPTHPATHPILNKNK DNKKKESLFEYDLIKDRRYTVDKFMFHVPITMNFKSVGSENINQGVKEYLHHADDMHIIGIDR GERHLLYLVVIDLQGNIKEQYSLNEIVNEYNGNTYHTNYHDLLDAREDERLKARQSWQTIENIK ELKEGYLSQVIHKITQLMVKYHAIVVLEDLNMGFMRGRQKVEKQVYQKFEKMLIDKLNYLVDK KADASVSGGLLNAYQLTSKFDSFQKLGKQSGFLFYIPAWNTSKIDPVTGFVNLLDARYQNVEKA KAFFSKFDAIRYNKDKDWFEFNLDYDKFGKKAEGTRTKWTLCTRGMRIDTFRNKEKNSQWD NQEVDLTAELKSLLEHYYIDIHGNLKEAISTQTDKAFFTGLLHILKLTLQMRNSITGTETDYLVSPV ADENGIFYDSRTCGDELPENADANGAYNIARKGLMMIEQIKNAEDLGNLKFDISNKAWLNFA QQKPYKNG
87	Cas12	MDNNNLHAVDGYFATLGAVNTPTMQRENLFALIQNAYTDISDLLDTPYPENKNLAQDKTNV AKVKALLDAIKSLQHFVKPLLGMGDESDKDERFYGELASLWTELDTVTPLYNMIRNYMTRKPY SEKKIKLNFENPQLLGGWDANKEKDYATIILRRNGMYYLAIMDKDSKKLLGKTMPSDGECYEK MVYKLLPGANKMLPKVFFAKSRINDFKPSKKIVENYNNGTHKKGKNFNINDCHDLIDYFKQSI

[0116]

		DKHEDWSKFGFNFSDTSTYEDLSGFYREVEQQGYKLSFTNISVSFIDKLVDEGKMYLFQIYNKD FSDYSKGTPNMHTLYWKALFDERNLADVVYKLNGEAEMFYRKKSINNTHPTHHANHPIQNK NKDNKKKESVFEYDLVKDRRYTEDKFLFHVPITMNFNSVGAENINQQVRKYLQQADDTHIIGI DRGERHLLYLVVIDMQGNIKEQFSLNEIVNEYNGNTYRTNYHDLLDVRADKRLKASQSWQTIE NIKELKEGYLSQAIHKITQLMVKYHAVVVLEDLNKGFMRGRQKVEKQVYQKFEKMLIDKLNYL VDKHKDANETGGLLHALQLTSEFKNFKKSEYQNGFLFYIPAWNTSKIDPVTGFVNRFDTRYTNA VEAQKFFRKFDEIRYNEEKDWFEFEFDYDKFTQKAHGTRTRWTLCTHGKRLRSFRNPAKQYN WDSEVVALTDEFKRILGEAGIDIHENLKDAISNLEGKRRKYLEPLMQFMKLLLQLRNSRKNPEE DYILSPVADENGVFYDSRSCGDKLPENADANGAYNIARKGLMLIRQIKEAKELGKVKYDISNKA WLNFAQQKPYKNE
88	Cas12	MQKKAFEENQQNLRSIIAKKLTEDKAYANLFGKNLLESYKDKTDKTKIIDSDLIKFINTAESTQLD SMSQDEAKEIVKEFWGFTTYFVGFFDNRKNMYTAEEKSTGIAYRLINENLPKFIDNMEAFKKAI ARPEIQADMEELYSNFSEYLNVESIQEMFLLDYYNMLLTQKQIDVYNAIIGGKTDDEHDVKIKGI NEYINLYNQQHKDDKLPKLKALFKQILSDRNAISWLPEEFNSDQEVLNAIKDCYERLSENVLGD KVLKSMLGSLADYSLDGIFIRNDLQLTDISQKMFGNWSVIQNAIMQNIKHVAPARKHKESEEE YENRIAGIFKKADSFSISYIDACLNETDPNNAYFVENYFATLGAVDTPTMQRENLFALVQNAYTE ITALLHSDYPTEKNLAQDKANVAKIKALLDAIKSLQHFVKPLLGKGDESDKDERFYGELASLWAE LDTMTPLYNMIRNYMTRKPYSQKKIKLNFENPQLLGGWDANKEKDYATIILRRNGLYYLAIMN KDSKKLLGKAMPSDGECYEKMVYKLLPGANKMLPKVFFAKSRMEDFKPSKELVEKYNNGTHK KGKNFNIQDCHNLIDYFKQSIDKHEDWSKFGFKFSDTSTYEDLSGFYREVEQQGYKLSFARVSV SYINQLVEEGKMYLFQIYNKDFSEYSKGTPNMHTLYWKALFDERNLADVVYKLNGQAEMFYR KKSIENTHPTHPANHPILNKNKDNKKKESLFEYDLIKDRRYTVDKFMFHVPITMNFKSVGSENI NQDVKAYLRHADDMHIIGIDRGERHLLYLVVIDLQGNIKEQFSLNEIVNDYNGNTYHTNYHDL LDVREDERLKARQSWQTIENIKELKEGYLSQVIHKITQLMVKYHAIVVLEDLNMGFMRGRQKV EKQVYQKFEKMLIEKLNYLVDKKADASVSGGLLNAYQLTSKFDSFQKLRKQSGFLFYIPAWNTS KIDPITGFVNLLDTRYQNVEKAKAFFSKFDAIRYNKDKEWFEFDLDYDKFGRKAEGTRTKWTLC TRGMRIDTFRNKEKNSQWDNQEIDLTAEMKSLLEHYYIDIQGNLKEAICTQTDKAFFTGLLHILK LTLQMRNSITGTQTDYLVSPVADENGIFYDSRSCGDSLPENADANGAYNIARKGLMLIEKIKNA EDLDTIKFDISNKAWLNFAQQKPYKNG
89	Cas12	MLENEQEAEKIKNKLDDIMNIYHWIKIFLVDEEIEKDMDFYSEIEDIYEELSPLVSLYNRVRNYVT QKPYSQEKMKLNFGSPTLADGWSKSKEFSNNAIIMLKDGKYYIGIFNIRNKPNKEVIEGRNNRI NDSDYKKMVYRLLPGANKMLPKVMFSKKGIEYYNPSQYILSGYNSKKHIKSNENFDINFCHDL IDFFKESINKNEEWKNFDFKFSDTESYNDISEFYREVEQQGYKIEWVYISEQDIEQLEKNGQLYIF QIYNKDFAKKSIGNKNLHTMYLENLFSEENLKDVVLKLNGEAEIFFRKSSIKKPIVHKAGSILVNK CIEDETGNKVSFPDDIYNEIYQYMNGMTDVLSERAQNYYEKVKHSVSKQDIVKDYRYTVDKYF IHLPITINFKASSFMPINDIALKYIAKRDDIHIIGIDRGERNLIYVSVIDLQGNIVYQKNYNVVNGY DYKAKLRETEIQRDNARKNWKEIGKIKQLKEGYLSLVVHEIAQLIVKYNAIVVMEDLNMGFKRG RFKVERQVYQKFENMLINKLNYLVDKNKKVDEDGGLLRGYQLTYVPGQKEHVGKQCGFIFYVP AAYTSKIDPTTGFVSIFNNKVNAKEFVTKFDSIKYNKNMKMFELKFDYNNFETYNITLAKSKWT IYTNGIRLKREYNNGRWNKITEVDLTKEMANTLKKYDIEFENNEEILKSISQLDEKNQRNICNEI

[0117]

		KEIIKLIVQLRNSMPDNGSKDNEYDKIISPVLNENNYFYDSSEVCDNSAPENADANGAYCIAM KGLYQVIQIKENWSQDSNPKNILGIKHYEWFDFMQNKRYL
90	Cas12	MAKNTIFTQFTGLYPVSKTLRFELKPMGKTLEKIKETGVIENDKKRHNDYFDAKKIIDKYHKYFID AALSKFSRIDWNPLKEAIEGSLDRSDASKKKLEKTQTEFRKKIAKALTTHDHYKELTASTPKDLFL KVFPDHFGKQPAIDTFDGFSSYFTGFQENRQNIYSDEAISTAIPYRLVHDNFPKFLSNIEVYKTLK DNAPSVLSDAENELKDFLNGKPLANIFELNAYNDVLTQSGIDFFNQVIGGISGEGGEKKTRGIN EFSNLYRQQHPEFAQKRLATKMIPLYKQILSDRETKSFILESYSTDSQVQESVKEFFESQILNCDIA GRKVNVLNELTSLIKRIAEFDLGSIYINQEELSNISLELFKSWNTINAVLFKNAENRIGSAEKAAN KKKIDAWMKSNEFSIATLNLAIAESDSEEISRVKIESYWNDFEAKVQSILCGDNRRNLDEFLSAT FNENNALREDSEIIGKLKAFLDALIEIMHSIKPLISDAENRDLSFYNELMPLYDQLSLVVPLYNKIR NYATQKLTESEKFKLNFDNPTLADGWDQNKEDANTAILLLKNGLYYLGIMNAKNKPKIKDFKT SESEDCYDKMVYKLLPGPNKMLPKVFFSEKGLATFKPPKDILDGYNAGKHKKGDLFDIGFCHQ LIDFFKESIAKHPDWKKFDFKFSDTSSYEDISGFYKEVTDQGYKITFSKIPTSQIDEWVNEGKLFLF QIYNKDFAPGAKGSPNLHTLYWKSVFSPENLKDVVVKLNGEAELFYRPSSVKKPYSHKVGEKLV NRIGKDGLPLPESVFGELFRYFNGKLDGELSDEAKRYLDVAVVKDVKHEIVKDRRYTQDKFEFH VPLTLNFKADSKNEYMNERVRHFLKDNPDVNIIGIDRGERHLLYMTLINQKGEILKQKSFNIVES VNYQAKLVQREKERDAARKSWSSVGKIKDLKEGFLSQVIHEITTTMIENNAIVVLEDLNFGFKR GRFCVERQVYQKFEKMLIDKLNYLVFKNKPEGDVGGVLKGYQLAEKFDSFQKLGKQSGFLFYIP AAYTSKIDPTTGFANLFNMTELTSAEKKKDFLSHFDDITYDGKNDRFLFGFDYKNFKCFQTDFIK KWTVYTQGKRIVYDKESKSAKEIFPVEIIKAALAKQNIALTDQLDVLSAINSVEASPKSASFFGNI CYAFEKTLQMRNSIPNTDEDYLVSPVMNKRGEFYDSRSCDDALPQNADANGAYHIALKGLYLI KNVFDAGGKDLKISHEDWFKFAQSRNC
91	Cas12	MRPVLQLTDTEDKLSQNKPAVGKIKALLDAFKDLQHFIKPLLGSGEENEKDELFYGAFQLIWDEL DTVTPLYNKVRNWLTRKPYSTEKIKLNFDNAQLLGGWDVNKEPDCTGVLLRKDGFYYLGIMN KKSNRIFDADVTPADGICYEKIDYKLLPGANKMLPKVFFSKSRIDEFAPSEAILSSYKRGTHKKGA DFSLSDCHRLIDFFKASINKHEDWSKFGFQFSDTKTYEDISGFYREVEQQGYMLSSHQVSEAYI NQMVEEGKLFLFRIWNKDFSEYSKGTPNMHTLYWRMLFDERNLADVVYKLNGQAEVFYRKA SIKAENQIMHPAHHPIENKNTLNEKRSSTFDYDLVKDRRYTVDKFQFHVPITINFKAIGQTNVN PIVHETIRRGGFTHVIGIDRGERHLLYLSLIDLKGHIVKQMTLNEIINEYNGLAHKTNYYDLLVKRE GERTTARRSWDTIENIKELKEGYLSQVIHIISKMMVEYNAIVVLEDLNMGFMRGRQKIERQVYE KFEKMLIDKLNCYIDKQADSQSEGGLLHPIQLANKFESFRKLGKQSGCLFYIPAWNTSKIDPVTG FVNLFDTRYETREKAKLFFSHFQRICFNAEKDWFEFSFDYNDFTTKAEGTRTQWTLCSYGTRIR NFRNPLQNHQWDDEEIVLTEAFKALFDKYDIDIHANLKEAINAQTDAQFFKDLMGLMKLLLQ MRNSKTNSEVDYLLSPVADEHGRFFDSRAGAGSLPDNADANGAYNIARKGLWVIRKIQETPE GEKLSLAITNKEWLEFAQTKPYLND
92	Cas12	MNLNTYFSQFTGLYPVSKTLRFELKPMGKTLEKIKETGIIENDKKRHNDYFDAKKIIDKYHKYFID AALSKFPCIDWNPLKEAIERSLDRSDASKKKLEKTQTEFRKKIAKALTTHGHYKELTASTPKDLFL

[0118]

		KVFPDHFGKQPAIDTFDGFSSYFTGFQENRQNIYSDEAISTAIPYRLVHDNFPKFLSNIEVYNILK DNAPSVLSDAENELKDFLNGKPLANIFELNAYNDVLTQSGIDFFNQVIGGFSGEGGEKKTRGIN EFSNLYRQQHPEFAQKRLATKMIPLYKQILSDRETKSFILESYSTDSQVQESVKEFFESQILNCDIA GRKVNVLKELSSLIKRITEFDLGSIYVNQEELSSISLELFKSWNTINAILFKNAENRIGSAEKAANK KKIDAWMKSNEFSIATLNLAIAESDSEEISRVKIESYWNNFEAKVQSILCGDNRRNLDEFISATF NENNALREDSKVIEKLKAFLDALIEIMHSIKPLISDAENRDLSFYNELMPLYDQLSLVVPLYNKIR NYATQKLTESEKFKLNFDNPTLADGWDQNKEEANTAILLLKNGLYYLGIMNAKNKPKIKDFKTS ESEDCYDKMVYKLLPGPNKMLPKVFFSEKGLATFKPPKDILDGYNAGKHKKGDLFDIGFCHQLI DFFKESIAKHPDWKKFDFKFSDTSSYEDISGFYKEVTDQGYKITFSKIPTPQIDEWVNEGKLFLFQ IYNKDFAPGAKGSPNLHTLYWKSVFSPENLKDVVVKLNGEAELFYRPSSVKKPYSHKVGEKLVN RIGKDGLPLPESVFGELFRYFNGKLDGELSDEAKRYLDVAVVKDVKHEIVKDRRYTQDKFEFHV PLTLNFKADSKNEYMNERVRHFLKDNPDVNIIGIDRGERHLLYMTLINQKGEILKQKSFNIVESV NYQAKLVQREKERDTARRSWSSVGKIKDLKEGFLSQVIHEITTTMIENNAIVVLEDLNFGFKRG RFCVERQVYQKFEKMLIDKLNYLVFKNKPEGDVGGVLKGYQLAEKFDSFQKLGKQSGFLFYIPA AYTSKIDPTTGFANLFNMTELTSAEKKKEFLSHFEDITYDGKNDRFLFSFDYKKFKCFQTDYIKKW TVYSQGKRIVYDKESKSAKAISPVEIIKAALAKQNIALTDQLDVLSAINSVEASRETASFFGDICYA FEKTLQMRNSIPNTDEDYLVSPVMNKKGEFYDSRSCGDSLPKNADANGAYHIALKGLYLIKNV FDAGGKDLKISHEDWFKFAQSRNR
93	Cas12	MQTLFENFTNQYPVSKTLRFELIPQGKTKDFIEQKGLLKKDEDRAEKYKKVKNIIDEYHKDFIEKS LNGLKLDGLEEYKTLYLKQEKDDKDKKAFDKEKENLRKQIANAFRNNEKFKTLFAKELIKNDLM SFACEEDKKNVKEFEAFTTYFTGFHQNRANMYVADEKRTAIASRLIHENLPKFIDNIKIFEKMKK EAPELLSPFNQTLKDMKDVIKGTTLEEIFSLDYFNKTLTQSGIDIYNSVIGGRTPEEGKTKIKGLNE YINTDFNQKQTDKKKRQPKFKQLYKQILSDRQSLSFIAEAFKNDTEILEAIEKFYVNELLHFSNEG KSTNVLDAIKNAVSNLESFNLTKIYFRSGTSLTDVSRKVFGEWSIINRALDNYYATTYPIKPREKSE KYEERKEKWLKQDFNVSLIQTAIDEYDNETVKGKNSGKVIVDYFAKFCDDKETDLIQKVNEGYI AVKDLLNTPYPENEKLGSNKDQVKQIKAFMDSIMDIMHFVRPLSLKDTDKEKDETFYSLFTPLY DHLTQTIALYNKVRNYLTQKPYSTEKIKLNFENSTLLGGWDLNKETDNTAIILRKENLYYLGIMDK RHNRIFRNVPKADKKDSCYEKMVYKLLPGANKMLPKVFFSQSRIQEFTPSAKLLENYENETHK KGDNFNLNHCHQLIDFFKDSINKHEDWKNFDFRFSATSTYADLSGFYHEVEHQGYKISFQSIA DSFIDDLVNEGKLYLFQIYNKDFSPFSKGKPNLHTLYWKMLFDENNLKDVVYKLNGEAEVFYRK KSIAEKNTTIHKANESIINKNPDNPKATSTFNYDIVKDKRYTIDKFQFHVPITMNFKAEGIFNMN QRVNQFLKANPDINIIGIDRGERHLLYYTLINQKGKILKQDTLNVIANEKQKVDYHNLLDKKEG DRATARQEWGVIETIKELKEGYLSQVIHKLTDLMIENNAIIVMEDLNFGFKRGRQKVEKQVYQK FEKMLIDKLNYLVDKNKKANELGGLLNAFQLANKFESFQKMGKQNGFIFYVPAWNTSKTDPA TGFIDFLKPRYENLKQAKDFFEKFDSIRLNSKADYFEFAFDFKNFTGKADGGRTKWTVCTTNED RYAWNRALNNNRGSQEKYDITAELKSLFDGKVDYKSGKDLKQQIASQELADFFRTLMKYLSVT LSLRHNNGEKGETEQDYILSPVADSMGKFFDSRKAGDDMPKNADANGAYHIALKGLWCLEQI SKTDDLKKVKLAISNKEWLEFMQTLKG
94	Cas12	MIDNTKEKKEGSVFDGFTRKYQLSKTLRFELRPILNTPKMLDDEQVIKNDETRRKKYEAVKPWF DQLHREFIEDALKSFKFKNLAIYQDTFQTWQKDRKSKQKKDTLVKIEVGLREEIVRRFEEVANIW

[0119]

		VRSEQYKLLGIKKEGLGMLFEAGVFRLLKERFKNEKDTTVDGNNIFDEWTRWTGYFKKFFETRK NFVKSDDTSTAIAYRVINQNLRRFCENIQIFEKISEKIEFSEVEKSFDISCAGIFSLAYYNACLLQGG IDTYNKIIGGEVDEKDKKIPGINELINKYRQDNSGEKIPFLKQLDKQIHSAKEAFIESIETNKELVGK LKTFYENAEVKIQSFRNLIADIVTDYSGYDIDKIYLTKEAVSHNASRWFASFESFERDLFAVVAEK QNKLVYELLRTHKNDSKISDKDGKFSFPDFIKCSHIKRALEKQEGRIWKGEYYEDIVDFEKIKDVF TQFLCVFKFELEQQFFRKTTSAQTGEQTKIGYEIFVTKINELITRENPVIDLEEKIAIKNFADATLLIY QIAKYFAVEKRRGWLDNYDLDDRFYKSSDIGYLNFYRDAFEQIVRPYNLFRNYLTKKPYNTNK WVLSFENPTLADGWDKNKEKTNAAVILRKDGRYYLGIIKEDCKSLFADRYSKEMSEGIESGSFQ KMAYKFFPEASKMIPKCSTQTKNVKEHFRKSSSDYNLFHEKDYKISVAITKNIYELNNVFYRKDN IEESFVPKNDFEKKLGVKKFQRQYLEISRDNNGYKQALAQWIEFCIRFLKAYKSTTIFDYSRLREA KEYESLDAFYQDINALTYNISFVPISEQYIKEKNDNGELFLFEIYNKDWSLGPMDKNRKRTKNLH TLYFEQLFSKENEQENFLFQLNGEAELFFRPKTEEKRLGYKVWDAGEKKWVKAKEKEDGAVIDR KRYAKDIILFHCPITLNRVSESKTKREMDVEIREVLSSTPGVHIIGVDRGEKHLAYYSVIDQNGKII ETDTLNSIGKDGRGKPVEYASKLEKRAQEREASRRDWEEVEAIKDLKKGYISQVIRNLADLIIKH NAIIVFEDLNMRFKQIRGGIEKSAYQQLERALIDKLSFLVKKGEEDPKQTGHILRAYQLAAPVIAF KDMGKQTGLIFYTQAGYTSKTCPECGYRRNIKCLFENIEQAKTLIENLESINYNKKEDVFQISYSL EKLSSKDQKKEKKVSNELYAKTLKKDIFILTTKNALRYKWYDRYSEKAKVAKRGIDEYKGEVNESE TKKGVVKEFNLTEYLKGLLKTYEIDYEHGGIREQILSVARGREFYKDFLYALFLLTETRHSISGRNTD YIQCPECEFDSRKGFKDIKEFNGDANGAYNIARKGIMILEKIKQFKKDNDGNLEKMGWGDLSIS IEEWDKFTQKE
95	Cas12	MKNFQDFTNLYELSKTLRFELKPIGGTKKLIEEKNILKLDKKKRENYEKVKPYFNKIHQEFINFALR NPNFDFSQFEEKYLNWLKDKKNKDLLKEKESIDKIFLEKIGKLFENSVKDFLKENGFESIVKEEDQ NLKFFRRKEIFEVLQEKYGSELETQMVNKDGEIKSIFNGWEKWLGYFDKFFNTRDNFYKTDGTS TAIATRIIKDNLKIFLENIVAFGKIKNKKIDFSEVEKNFSVSIDTFFEINNFNNCFLQDGIDFYNKVI GGETLENGEKLKGLNEIINKYRQDTGEKIPYFKKLQKQILSEKDGVFIDKIEDDGGFYEVLKNFYK NAAEKEGFLKNIFENFYTISDKNLEKIYFNKIAFNTISHKFGSALEFERILYEEMKKEKADGIKFEKK ENKYKFPDFIQIIFIKRSLENYDSENLFWKERYYKSEENVDGFLEKNNNNLWGQFCKILNFEFLN ILKRRIIDEAGEEYEVGFEISKNILGEKLENFELNQENKGIIKDFADYSLALYSFGKYFAVEKGRNW DLNIDISDDFYGGEDGYIEKFYNTGYDEIVKPYNLMRNYISKKPWEDNKKWKINFETSSLLSGW DKNLESNGSYIFQKGNKYYLGIINGSKPAKEILEKLYSGDGEKIKRFIYDFQKPDNKNTPRMFIRS KKDSFSPAVEKYNLPINDILEIYDNGLFKTENKGNPNYKESLRKLIDYFKLGFSRHESFKHFNFVW KDSKSYENIADFYRDVEKSCYKIDFEFLNFEELKKLTFEKHLYLFQIYNKDFELDESLQEKGYNFKG EGQKNIHTKYFEALFLEENISRKSGAVFKLSGGGEVFFRKKSIKAKKEKRNSVEVIKNKRYTECKY FLHFPIQVNFKEEISGNFNQEINKFLANNPDINVIGIDRGEKHLAYFSVINQKGEILESGSFNKIE NYNKNGEKLLFPEREIKEIHKDGSLIDLELVETGRKVDYVDYKLLLEYKERKRLLQRQSWKEVEQI KDLKKGYISALVRKIADLIIKHNAIVIFEDLNFRFKQIRGGIEKSIYQQLEKALIDKLNFLVNKNEINL EKAGSILKAYQLTVPVDSLKEIGKQTGVIFYTEAAYTSKIDPITGWRPNLYLKKNNSKINKENILKF DNIVFNSKENRFEFTYDLKKFFGKDSKFPAKTVNTVCSCVERFKWNRNLNNNKGGYIHYENLT DGKLANKEQKEDEFSNFKELFEKYFIDINGNILEQIKNLDTKNNEKFFSSFIDLFTLVCQIRNTNQ NAKGDENDFILSPVEPFFDSRKSQNFGKSLPKNGDENGAFNIARKGLIILNRISENPEKPDLLIF NADWDNFARNI

[0120]

96	Cas12	MSNNFQEFTQKYALSKTLRFELKPVGKTKEILEKEMPMYQIINADKNIKAKYIQTKPFFDQLHRD FIKEAFENVELSGLSDFFENWKIYKQDKKANEKIYKKSAENLRKEVVSFLNAKGKDWAEKYHSS GLKKADIEILFEEGIFKVLEIRYGTDTNSFITNATTGEITSIFQGWKGFTGYFLKFWNTRENYYKTD GTSTAIATRIVDQNLPGYLENLEIFEKMKGKIDFESVRGDFSDFEKIGTVEYYSTCLLQEGIDGYNR IIGGYTYENGEKIKGINEIINLYRQTHKDEKVPFLKTLDKQIGSEKIAFMETIDTPEEFRKIFEEFVLK SSEKVVLLKQCLNHLFENELTDGVFLSKESLNTISHKWIDIGNMKLFHESLFTILKKEGAKYDSKE DEYKFPDFIRISDIKTALVKITTESFFWKNRYLYEKDENPTGFLTSDNSLWEGFIQIFSHEFSSLFER TEKDEEGKDIQWGYDISLLNIQKLLENNEYNPNDEKNKIIIKSFADDILRIYQMGKYFALEKKRQ WNPDNLEIGEFYSHPEIGYDKFYFDSYKIIVQGYNDIRNYLTKNPWSEEKWKLNFENPTLANG WDKNKETDNSCIFLKRDNKFFLALMSRGNNQVFDERNIQKFAQNIEQGKYEKMVYKYMKDV ALGIPKATTQLNAVQEHFFQSDKDYIITKGGSSIGEFIKPLRVTKRIFELNNRIYPKDNLGISFLRN QVNKKEQKNYIKIFQKEFITLGGDEVVYKKAVHDWIDFCKEYTKSYPSCAYFDYSGLKDTKEYSS IDEFYNDLDSFGYQISWQDISSSYIDELVESGKLYLFEIYNQDFSNGKTGAKNLHTLYFEHIFSKE NQEVNFPLKLNGQAELFFRPKSIEAKGENRKFNREIIAKKRYTEDKIFFHVPLTLNRTEGDIYGFN TEINNFLAHNPDINIIGIDRGEKHLAYYSVIDQKGNIIESDSLNTVNEINYGEKLTDTAEKRKQAR QDWQAVEGIKNLKKGYISAVVHKLTDLIIKYNAIVIFEDLNMRFKQIRGGIEKSVYQQLEKALIEK LNYLVEKGEINPEKAGHLLNAYQLTAPFETFKDMGKQTGIVFYTQAAYTSKIDPVTGWRPHLYLK YSSAEQVKKEIAKFSNIIWNNTEKRFDFMYDIRNFSTQKEYPKNNIWTVCSSVERYRWDKTLN QNKGDYVHYKSITPEFEKLFSDFQIDGTKNILEQINRMETKGNEKFFKSFIFFFGLICQIRNTNKA DSDENKQDFILSPVVPFFDSRDSENTKNGLPRNGDENGAYNIARKGLIILQKINEFSDENGNC DKLGWKELSISQVDWDNYIKT
97	Cas12	MEYDEHISLIESEEKADEMKKRLDMYMNMYHWAKAFIVDEVLDRDEMFYSDIDDIYNILENIV PLYNRVRNYVTQKPYTSKKIKLNFQSPTLANGWSQSKEFDNNAIILIRDNKYYLAIFNAKNKPD KKIIQGNSDKKNDNDYKKMVYNLLPGANKMLPKVFLSKKGIETFKPSDYIISGYNAHKHIKTGE NFDISFCRDLIDYFKNSIEKHAEWRKYEFKFSATDSYNDISEFYREVEMQGYRIDWTYISEADIN KLDEEGKIYLFQIYNKDFAENSTGKENLHTMYFKNIFSEENLKNIVIKLNGQAELFYRKASVKNP VKHKKDSVLVNKTYKNQLDNGDVVRIPIPDDIYNEIYKMYNGYIKESDLSGAAKEYLDKVEVRT AQKEIVKDYRYTVDKYFIHTPITINYKVTARNNVNDMAVKYIAQNDDIHVIGIDRGERNLIYISVI DSHGNIVKQKSYNILNNYDYKKKLVEKEKTREYARKNWKSIGNIKELKEGYISGVVHEIAMLMV EYNAIIAMEDLNYGFKRGRFKVERQVYQKFESMLINKLNYFASKGKSVDEPGGLLKGYQLTYVP DNIKNLGKQCGVIFYVPAAFTSKIDPSTGFISAFNFKSISTNASRKQFFMQFDEIRYCAEKDMFSF GFDYNNFDTYNITMGKTQWTVYTNGERLQSEFNNARRTGKTKSINLTETIKLLLKDNEINYAD GHDVRIDMEKMDEDKNSEFFAQLLSLYKLTVQMRNSYTEAEEQEKGISYDKIISPVINDEGEFF DSDNYKESDDKECKMPKDADANGAYCIALKGLYEVLKIKSEWTEDGFDRNCLKLPHAEWLDFI QNKRYE
98	Cas12	MFGNWGVIQNAVMQNIKRVAPARKHKESEEDYEKRIAGIFKKADSFSISYINDCLNEADPNNA YFVENYFATFGAVNTPTMQRENLFALVQNAYTEITALLHSDYPTEKNLAQDKANVAKIKALLDA IKSLQHFVKPLLGKGDESDKDERFYGELASLWAELDTMTPLYNMIRNYMTRKPYSQKKIKLNFE

[0121]

		NPQLLGGWDANKEKDYATIILRRNGLYYLAIMNKDSKKLLGKAMPSDGECYEKMVYKLLPGA NKMLPKVFFAKSRMEDFKPSKELVEKYNNGTHKKGKNFNIQDCHNLIDYFKQSIDKHEDWSK FGFKFSDTSTYEDLSGFYREVEQQGYKLSFARVSVSYINQLVEEGKMYLFQIYNKDFSEYSKGTP NMHTLYWKALFDERNLADVVYKLNGQAEMFYRKKSIENTHPTHPANHPILNKNKDNNKKES LFEYDLIKDRRYTVDKFMFHVPITMNFKSSGSENINQDVKAYLCHADDMHIIGIDRGERHLLYL VVIDLQGNIKEQFSLNEIVNDYNGNTYHTNYHDLLDVREDERLKARQSWQTIENIKELKEGYLS QVIHKITQLMVKYHAIVVLEDLNMGFMRGRQKVEKQVYQKFEKMLIEKLNYLVDKKADASVS GGLLNAYQLTSKFDSFQKLGKQSGFLFYIPAWNTSKIDPVTGFVNLLDTRYQNVEKAKSFFSKFD AIRYNKDKEWFEFNLDYDKFGKKAEGTRTKWTLCTRGMRIDTFRNKEKNSQWDNQEVDLTA EMKSLLEHYYIDIHSNLKDAISAQTDKAFFTGLLHILKLTLQMRNSITGTETDYLVSPVVDENGIF YDSRSCGDELPENADANGAYNIARKGLMMIEQIKDAKDLDNLKFDISNKAWLNFAQQKPYK NG
99	Cas12	MSNLYSNLHNLYQVQKTLRFELKPQGKTKENMEKVGILKADEHRAEIYSKVKKYCDEYHKLFID KSLSNIELNGIDRYYELYSINNRDDKQKEELDQLEASLRKQISDAFKKSAEYKGLFQKDIITSYLVT MYKENQEKMQDIGEFNRFTTYFTGYNKNRENMYSEEDKSTAISYRLINENLPTFIDNIKIYKKIV SLMPEDIEKIYKDLEEYIQVDSIDEIFNISYYNDVLTQRGIECYNILISGRTKNDGDKIKGLNEYINE FNQTHNEKIPKLQELYKQILSDAESASFKIDVIKNDKELMNLIEVYYANILPILNKIEDLFTRISNYN LELILVNNDGTLSTLSNMVFNEWSYIKGAISEKYDEEYSGKEKYGTEKYAQKKQEYLKKQKIYSLK FLNDCIGNNAICEYLKNYIIQNKNIETIKEDYNEVQNIKVEDDTKELIKDEKSIEKIKKFLDDVKSL QEFVKLVIPKDRTVEKDAKFYSELTPYYEKIKEIIPLYNKVRNYVTQKPYSTEKIKLNFECPTLLKGW DANKEEANLGVILLKEGKYYLGIINPYCKKIFEVDEKDSNEQNNYKKMEYKLLPGPNKMLPKVF FSNSRIEEFNPSKELQEKYNKGYHKKGKDFDINFCHELIDFYKQSVNKHEDWKKFNFKFKDTSE YNDISEFYREVEKQGYKIEYTEYSEKYINELVDRGELYLFQIYNKDFSEYSKGKENLHTLYWKAVF DPDNIMNPVYKLNGNAEVFYRKKSLEMKVTHPANQPIANKNISTIEAGRSTSTFKYDLIKDKRY TMDKFQFHVPITMNFKSERLFNINQIVNKYLKYNDDIHVIGIDRGERNLLYVCVIDKNEKIVYQ KSLNEIVSEYNNNRYTTDYHGLLDRKEKEREIAREDWKNIENIKELKEGYMSQVIHILVELMKKY NAIIVIEDLNKGFKNSRIKVEKQVYQKFEKMFIDKLNYLVFKDEDKMNEGGVLNAYQLTNKFES FTKLGKQSGILYYIPAWCTSKIDPTTGFINRFYLKYENFDKSKEFVNRIDDIRYNEKENLFEFDIDY SKFTDRLNDTKNKWTLCSYGERILTQKNANGEWLDRRIQLSIEFKKLFEKYGINLNNIKDSILKL DKDNLEFYKGNGESLGFIQLFKLMVQMRNSLTGKEEDNLISPVKNQHGKFFNTSEKIEGLPIDA DANGAYNIARKGFMLVEQMKNVEDEKLNKIKYNITEKEWLNYVQNRGM
100	Cas12	MARIFEDFKRLYPLSKTLRFEAKPIGATLDNIVKSGLLDEDEHRAESYVKVKKLIDEYHKVFIDRVL DNGCLPLKNEGHNNSLTEYYDSYVSKSQNEDAKKAFEENQQNLRSIIAKKLTEDKAYANLFGK NLIESYKDKTDKTKIIDSDLIQFINTAESTQLNSMSQDEAKELVKEFWGFTTYFVGFFDNCKNM YTAEEKSTGIAYRLINENLPKFIDNMEAFKKAIARPEIQANMEELYSNFSEYLNVESIQEMFLLDY YNMLLTQKQIDVYNAIIGGKTDDEHDVKIKGINEYINLYNQQHKDDKLPKLKALFKQILSDRNA LSWLPEEFNSDQEVLNAIKDCYERLSENVLGDKVLKSLLGSLADYSLDGIFIRNDLQLTDISQKM FGNWGVIQNAIMQNIKRVAPARKHKESEEDYEKRIAGIFKKADSFSISYINDCLNEADPNNAYF VENYFATFGAVNTPTMQRENLFALVQNAYTEVASLLHSYYPAEKKLAQDKANVAKIKALLDAIK SLQHFVKPLLGKGDESDKDERFYGELASLWAELDTVTPLYNMIRNYITRKPYSQKKIKLNFENP

[0122]

		QLLGGWDANKEKDYATIILRRNGLYYLAIMDKDSRKLLGKAMPSDGECYEKMVYKLLPGANK MLPKVFFAKSRMDDFKPSKELIEKYNNGTHKKGKNFDIQDCHNLIDYFKQSIDKHEDWSKFGF NFSDTSTYEDLSGFYREVEQQGYKLSFARVSVSYINQLVEEGKMYLFQIYNKDFSEYSKGTPNM HTLYWKALFDERNLADVVYKLNGQAEMFYRKKSIENTHPTHPANHPILNKNKDNKKKESLFEY DLIKDRRYTVDKFMFHVPITMNFKSVGSENINQGVKEYLHHADDMHIIGIDRGERHLLYLVVID LQGNIKEQYSLNEIVNEYNGNTYHTNYHDLLDAREDERLKARQSWQTIENIKELKEGYLSQVIH KITQLMVKYHAIVVLEDLNMGFMRGRQKVEKQVYQKFEKMLIDKLNYLVDKKADASVSGGLL NAYQLTSKFDSFQKLGKQSGFLFYIPAWNTSKIDPVTGFVNLLDARYQNVEKAKAFFSKFDAIRY KRIRTGLSLISTMTSLVKKQKVQGLSGFYAPEECVLILSEIKKKTHNGIIRKLT
101	Cas12	MISLNYFQNQYAVAKTLCLELRPIEKTMEYIISSGILKEDEHRNESYKLVKKIIDDYHKAYIELSLSR FELKITSCSKNDALEDFYCQYLANSQEEKDKNIFKKTQDNLRKQIAKHLTQGEAYKRIDKKELIQ EDLLEFVAADPDAANKKILINEFRDFTTYFTGFYENRKNMYSEEAQSTAIAYRIIHENLPKFIDNM GTFKQLMQSSITDILPQIFDNFKKDLEVSSIQEIFDLNYFNKVLTQKQIDIYNAIIGGKSLNENSRI QGLNEYINLYNQQHKENKLPLLKLLFKQILSDRNSLSWLPEAFETDKQVLHAVRKCYANLKESV LHEAGLVQLLSSLPSYDSTRIYIRNDQALTTISQKLFGDWGIIPHAIKERLKKDISAKRKETEEAYLE RIEKAFKQADSYTIAYINDSLKEIGVDKKNIEDYFIHLGAICTEGQEQENILQRIASAYSQAQPLLE EKVPVHKNLMQDKDSVELIKSLLDELKNLQHFIKPLLGKGSESDKDERFYGEFVGLWNELDQIT TLYNKVRNYVTRKPYSIEKFKINFQNATLLKGWDRNKERDNTSIILRKNGLYYLAIMRKEYNKVF EKYPAGTEENCYEKMEYKLLPGANKMLPKVFFSKSRINEFNPSPQLLQNYQMGTHKKGDQFK KEDCHALIDFFKTSIEKHEDWKNFNFQFSPTSVYEDMSGFYREVEQQGYKLVFRSIDAEYIDKLV EEGKIFLFQIYNKDFSPFSKGTPNLHTLYWKMLFDERNLNNVVYKLNGEAEIFFRKKSITYTHPT HPAEIPIKNKNVQNKKKESVFQYDLIKNHRFTIDSFQFHVPITMNFKNAGLSNLNEQVYTYLRE NKDAHIIGIDRGERHLLYLVVIDRYGRIVKQFSLNEIVNEYHGNTYTTNYHDLLDKREEARQQA RQSWQSIENIKELKEGYLSQVVHKIANLMVEYHAIVVLEDLNIGFMRGRQKVEKQVYQKFEKM LIDKLNYLVDKKKAPEADGGLLKAFQLTNQFESFQKLGKQSGFLFYVPAWNTSKIDPCTGFTNL LDTRYENIAKAQKFFRTFDAIRYNAVKDYFELELDYDKFHKRAEGTQTKWTLCTYGTRIKTFRNP ENNNQWDNVEINLTEEFKKLFKQFGINLSGDLQQAICAQTEKSFFESLLRLLKLTLQMRNSITGT DVDYLLSPVQNAEGYFYDSRKGDKSLPANADANGAYNIARKGLWVIQQIKQTPQGQKAKLSI SNKEWLKFAQEKPYLKD
102	Cas12	MKTFENFTNLYSLPRTLRFELKPLYKTKELIDSKQELFPKDKRIDEIYQNIIKPCLNELHSDFIEKSM ENKDFQNIPDNILKIYSNEKNIDDFKNIEKDLIKQINWFLKSNKTFFAENYSDLLGKNSIDIIIKVF WEKIYKKDDSWKIFLYNDLLWKSYEELINIYFKWFSTYLSNFNKNRENLYDKKNEAKVWSVSG RTIWENFPRFLQNCINFRDKLEKLNLSIEQKDIFITNNFWKCISQKQIDYYNKIIWQINSKTNEFN QKNGLKWNKKLPKLLLLHKQILWKSENENILNFINNIIQTDFELEQEIKIINKDIFQRIDFIKKSIVS NIEDFELEKIFIKKNRLKDISSLLMDNYSVLEKLLPEFNEEWKIIKENELVNLSKIKKSFENIDLKDLK NIFKKEYFDESKDWFKLFLNWIYNHFSDLENNIKHTHKLVQDKLISWNFSENIQKSEKNINLRD EIFVSSKWLLKAYLDSILALDRFVHMFDYWEQKDFDSNFYNNIEEYSINFSPFKTYNAVRNYLTK KNYSTDKIKLNFDYPDFLGSNSLWKYAFIYKDSKWFYYLWVLDHSNSQSKYKPQILKNNTEFY QLEYKQIKFNTLAWKWYIRDFWVKYSEDENCIINLKTLIKKQYLERYPVLKEIVDFQTDDKKIFDA KVKTILEQAYSINFVNIDKNYILEENNNWNLHFFQIYNKDFSENKKINSMENLHTMYFKALFEK

[0123]

		ENFNWWACFKLNSQWAEIFFREKSINEKKVKDLKTRNENAIEKKRYTENKVFLHLPITLNFINK WYSKYSFWYINDSVKKYIKENKISIIWIDRWEKNLIYFSMINENLEIIELKSLNSLILKVSDLEEKEV NYFEKLSKKEWNRNKERKDWDEIETIKELKEWYISQIVDNLVKLIVKHNAIVVMEDLNSGFKR WRQKIEKQIYQKFELALAKKLNFTVDKNKKHDELWWIYKAYQLTPQIENFQDIYSQTWIIFYTQ AAYTSVTCPNCSFRKNIYQKYENESKFKEFFKKYILEIKFEDNCFIIKYKIDEKIDKKKNKLKKLEFQ VNTKNQIRLKFEKSLKWKWWETKEFNITEKFKEIFEKHKLDLWNLKEELLAWNWEIQLYKDFM FYFNLLLQLRNSKENDNWWYISCPSCWFHSGNWFQWFSYNWDANWAYNIARKWRIILDKI KKDEKNLWITNVEWDNYYQK
103	Cas12	MAVRSVKLKLLVPRDGSAESVRKRKALWATHQFVNDAAAAYAELLLEMRQEDVCRGTDDHG KDVIEPAAHWQAKLRARLAAKQLPPVAVAEALPLLKAFYGSRLIKSFVANDKGVAGTGNATDL NTWLSGLVDPASVAGEKTELRKQLLAELPLCEAADADFEGAARKMLAKSDAREALLEGPGTGV GWPAAYNANPTDSVWLDMLHKAAAKARLELADTTVSELKKLGVFPLLQAASSNRVFGSGVL NPFERMAAAQAAAALLPWETKRHEMRKRRDKFADQLNQWDTEFGASHATALAAIRAFEAEE SERARRESLGNEGTGYRIGGRELRDAWTLLRDWLKGHSTATAAAREDKVRELQAKQGRSFGSH RLLSWLAKPAQQWLADHSAGDVVTRIAVRNARQRKLDTARTLPIWTGADAVKHPRFANFDP PNNTNQPGFDLRAGTQKGRLTLRLSLLTERADGLLLAQDHDFQLVPSRQMAEIVLHKDGKER ALSWQSQDGIGRQVGDVGGSALLFSRDHAECLLERKQITRLERGAWPAALPVWFKLSLDIGAE HKALLKQRFKWGVWLNSALVTRNAKDAKGVPPPVGTRVLAVDLGLRSAATVSVWQVVDAAT PVVAGKWRVPLSDTLSAVHERSAMLALPGEHVDAGVLAARRAANEKLAGLLAATSHLSTVFK LGRAEQGDRRRELLERLGEGDDRRARAAVATTAAERDGLRAVLGATQDAWAGAVAAVWRRL ETDLAGAIAAYRKQQREDVQLRREARHGPGASQLPKQAAAERLLGGKSAWQIEYKERVRKLLT RWIMRQRPGDTAVRRLARKDLGKYCGGLLDHLTALKEDRAKTTADLIVQAARGRVRAHKDAH GRQQDRELWLAKYAPCDLIVMEDLGRYRFATDRPPSENRQLMQWTHREVFRLVQMQAEVE GIQVLETGAEFSSKFDARTWAPGVRCEPITKLWVERYRNGEMPWLADKADEWRREGIELAQL VPGQLLPTGSGEQFVAVSATGGLRVRHADLNAAQCIALRALTGHGTAFRLTARRLGDVFVSAK GLGKRPQGALWREFGSALPPAVVVLRPAGEVRYALRPFASARDAAAALGLQLGALRNVDATD AESDAEDGDLAELLAGADPDRATFFRDPSGDVHGGAWVQAKVFWAEVRRHVRLGLQAQGL LPAAARSSEPRQMQLPLAGALPGDDIPL
104	Cas12	MLDKFASLYPVTKTLRFRLLPQGRTEENMQVAKVLENDLERSEAAAVVKGLIKKYHLQFISDTLS GSTLSWQALTETLDKFKADHTATAELDSALAAYRCKLAELFTKSPKYKVMATPVSIIKEILKTETD PENIAALNKLNGYTYIIFDYVSTRMLTYSADAKATSLAYRLVDENYLRFYQDISAAAEISAVLEEA GFDNAEVEAFIRTDYNTCLTSEGIASFNAAAGSINQFVNVLLQQNPVLQSEPALRRHLQPLYK MLLDEAESKIIKFEDYGQLRDAVENFRRNFQDLPQSLIDIFAGRYDYSKIYVGYKYLNEASSQIA GGYNWKLLENALEDFYSKPYLVNGKLPVKYKTVVNKKMNQLAYSFTELQEALDAGDSGSSITD LFGKYAELHAAYAAADGNVFYKEYDRKSIASLKNYLDAVNAIARFIKIFAAPEVYVKDEGFYGIV DGAADKLRDFDLLYNMVRNYITKKPYKKSKVALTFNSSSFGRGWDENKIYDELTTIFTYNGKYY LGVINKNDKPDLAAAVSKDEGGYKRMVYKTFDIVKQLPRLSFTKAVKAHFAESDEDFIFDGPKF AKPLRVPKEIYLQSFTDNGDKLADSAKKYTKAYLDMSGDYKGYYEAIIKRIDYTKEFLSAYKSTSI YDLAFLKPAGKAAGSLCWTRHI

[0124]

105	Cas12	MKTFENFTNLYSLPRTLRFELKPLYKTKELIDSKQELFPKDKRIDEIYQNIIKPCLNELHSDFIEKSM ENKDFQNIPDNILKIYSNEKNIDDFKNIEKDLIKQINWFLKSNKTFFAENYSDLLGKNSIDIIIKVF WEKIYKKDDSWKIFLYNDLLWKSYEELINIYFKWFSTYLSNFNKNRENLYDKKNEAKVWSVSG RTIWENFPRFLQNCINFRDKLEKLNLSIEQKDIFITNNFWKCISQKQIDYYNKIIWQINSKTNEFN QKNGLKWNKKLPKLLLLHKQILWKSENENILNFINNIIQTDFELEQEIKIINKDIFQRIDFIKKSIVS NIEDFELEKIFIKKNRLKDISSLLMDNYSVLEKLLPEFNEEWKIIKENELVNLSKIKKSFENIDLKDLK NIFKKEYFDESKDWFKLFLNWIYNHFSDLENNIKHTHKLVQDKLISWNFSENIQKSEKNINLRD EIFVSSKWLLKAYLDSILALDRFVHMFDYWEQKDFDSNFYNNIEEYSINFSPFKTYNAVRNYLTK KNYSTDKIKLNFDYPDFLGSNSLWKYAFIYKDSKWFYYLWVLDHSNSQSKYKPQILKNNTEFY QLEYKQIKFNTLAWKWYIRDFWVKYSEDENCIINLKTLIKKQYLERYPVLKEIVDFQTDDKKIFDA KVKTILEQAYSINFVNIDKNYILEENNNWNLHFFQIYNKDFSENKKINSMENLHTMYFKALFEK ENFNWWACFKLNSQWAEIFFREKSINEKKVKDLKTRNENAIEKKRYTENKVFLHLPITLNFINK WYSKYSFWYINDSVKKYIKENKISIIWIDRWEKNLIYFSMINENLEIIELKSLNSLILKVSDLEEKEV NYFEKLSKKEWNRNKERKDWDEIETIKELKEWYISQIVDNLVKLIVKHNAIVVMEDLNSGFKR WRQKIEKQIYQKFELALAKKLNFTVDKNKKHDELWWIYKAYQLTPQIENFQDIYSQTWIIFYTQ AAYTSVTCPNCSFRKNIYQKYENESKFKEFFKKYILEIKFEDNCFIIKYKIDEKIDKKKNKLKKLEFQ VNTKNQIRLKFEKSLKWKWWETKEFNITEKFKEIFEKHKLDLWNLKEELLAWNWEIQLYKDFM FYFNLLLQLRNSKENDNWWYISCPSCWFHSGNWFQWFSYNWDANWAYNIARKWRIILDKI KKDEKNLWITNVEWDNYYQK
106	Cas12	MSFLVPHLPTVVSHRLGGYSSAMDQTPTRLTPAVKNTAAATPKPEVPLTQRAYTLRLRGANDG DQSWREAVWATHEAVNMGAKVFGDWLLTLRGGLDRELADAKVKAGNNNPDRNPTPEERR GRRVLLALSWLSVESAPKKGDAYEKFVIASGKKDSQSIRDEKVVRALREILAKRGVANQDLEG WIVDCEPSLSAAIRDDAVWVNRSAAFDAAQCRVGTSLTREEIWDLLKPFFGSCESYLASLTTDE DSDTEAAATDDKAKDLVQKAGQWLSSRFGTGKGADFAAMSKVYSETAFWAGRASPFRSGAE ALRLIAESLKSFCPKSFDADGILGLISGPGYKSATRNIIKAWSKRAGPVTADDLANLSAVAAEDA NKCSANTGSKGHRPWSDAILCEVENACGFTYLQPDGPALHSEFAVMLDHAARRVSIGHSWIK RAEAERDRFTKDALRIKEVPDPIRVCLDRFCADRAGTSGAIDGYRIRKRAVSAWKEVITRWGQA ACKTAEDRVIAVRETQADPDIDKFGDIQLFEALAVDDAECVWRVNGEVTPQPLIDYAAATDAE AKQKRFKVPAYRHPDPLSHPVFCDFGNSRWKIRFAAHDAVTKLANARTSLDRREADLAKAKE RLDKATAPEEQTEGKESLEEAERHLRDARDRVAWLSSMHAFSMRLWGAGRVGDGQRLFWSC KRLTDDMALRQNSGQAPTIAVTRADRLGRAAAGADTADSVDILGVFTEEHWNGRLQAPRAQ LDVIAAHVAKNQWDAKAKKMRDRIRWLVSFSAKLQPVGPWIEYSATFPEAALAKPFVSRKGEY AVRHVSNDDRAGLGKLVLSRLPGLRVLSVDLGHRYAAACAVWETVSIAQTNAACDAAGHELP TESDLFLQLSTTDLTGKNRTTIYRRIGADMITDPKTGEKTPHPAPWARLERQFLVKLPGEDIPARK ASPAEFDAIRRLEEAFGRTRTADDPLLVRVDELLAATVDSARLALRRHGDAARIAYAFKPSAEKLT PGGGREVMSPEARKAMILDALLLWHGLWHGDRWADVWASQQWDAYIKPELGMDLPPWS ETSGEPRCQYRSKVEGLLKRVAESLAARDGAGLHLLWAEQWRTRNAKWLGNTGHLRTLRSLL LPRGLTTSTPAAWNVGGLSLTRIATLKSLYQLHKAYHMRPEPEDPRKNVPAKGEEELRDFGRGM LDVMERLREQRVKQLASRLAEAALGIGRMKASEGKRDRKRPRAQIDQPCHAVVIENLKNYRP EETRTRRENRQLMSWSSSKVKKYLSEACQLNGLHLREVQASYTSRQDSRTGAPGIRCADVPV

[0125]

		QDFFTKPWWRRQVSIAVGRVNQGRGDARERFLADLDAKWSAAEKSERITAPPLRIPVNGGEL FVSADLHSPAALGLQADLNAAANIGLKALLDPDWPGKWWFVPASLDADGWRVPAAKSCAG AEWVKNWKVGQLGDSYAPNGKPLQPTDDEGVKKAEDGVKLAKASLDDAEQALKAAKKTKR KAEIDVASARAQEAKKNVDDMKKALVAAKKGASAKEIINLWRDPVGVDPADFASGEPWRAYT VYKQRVEYHVINDVLRGRAGPRSDRP
107	Cas12	MSITRSIKVKLIVPRDASLEARQLREGLWATHLFVNDGCHYYERLLLEFRQRDVCVGKDDAGK DVIVPAAEWADRLRARLGRNGMVPSHIEAALPIFRELYENMVPSALKAKSGTGQAGRSWHSK LVSPTSRGGEASAARIDVLRPLLPVSGDDPAFEPAARALIEEAGDELLTSTGRCPAWVTAYRKGPE GSAWVEKLRIQLREAVEAGDFDPPSDPQILAAGAVPAAPPLGAGIDALRPLLPLLGGDPAFEPA ARALVEDIGDELFTSTGRPPTWVTAHPTWVRAHRKDAECLEAADDFKWVERLRQRLRDDAK AGKFEQPLHERLGALGALPVAKPIGAGRVVSRADLTVFERGAMELAIEHLIGWESAGHRARAQ YVERKKRHDDLLQWIEAEAPDALLAVRAYEAARTIHLATLGELGAAPQYTLRLREIRPWRKLRE WLLQNPDATIDERRRRLATMQTNDPRGYGGEALAWLAAPERRALVEHPAGDVVTRIAVLNIR KSILDRSRLFPTCTLADPVEHPRFAKFGKPGDKNSAGYALAVDGVRREAIIKILVPRQDGLLVPT DLRVPFAPSGQMRDLRASGLDISYERQDGRGRQAAKLQGGNLMFDRTHFARCGAPGPEALG SVWIKVALDLSSPAASLAMKTATPVRTYLSTAVRGRPESTKYEKAAPPEGFRVLSVHMGLRTAAT ASMLRFGAPEEGGHEVPVSGLAGETLVAFHERTVTMKLPGEDPDTRTEANRGVAKRELRGLGR GIGCLKAIRRASASATPEDRAEALVIIETHVGQGDRHGWAPAEAVGRLDPHGDPDDWKTACA ALYAAVEADLGVAISSWRKAARAGGATGMLGGKSLWAVDHLERSFRFLRSWDLRARPHDGD PRRPRPGYASKLLHHIDGVKDDRVKTTADRIVQAACGRAWIGGPTVKRGTQDVRLPGRWEQR GPRADLILLPDLTHFRFRSDRPRAENSRLMRWAHRQLAIYVRMQAEVEGILVADTGAAFTTRF DAWTGAPGVRCEPVTADHLRGIAKREDYWLARLLREGALKHLRIDPASLRVDDLVPMDHGKIL VALDGVDLPGLRILDTDVNASQGLGRRYIEGHGLAYRLPGARVPRGEGEREAAVVHIKGKRLAS AMGGTVVVLRASEGPGDITWTAEVYDRPQGARKALGLSLAAFNSIATAAVDDEGPAPENDDE ALEEEAEEALGIATGERIVFFRDPSGAVAGGGWLEASAFWGIANRMVTDRLRELGRLG
108	Cas12	MATAVDTSTTRAYTLRLSGGNNWRELLWQTHVAVNRGAWVWGDWLLTLRGGLPASLADGD AERRVVLALSWLSVESPASLAPQAHIVAYGSDARDERNRKVTERFRDILRRMGIKQQQEQEWL DACLPALMASIREDAVWVDRSACFAEAQQCYRGLSSEWARKTLFDFLGGEDDYFKPSAKEGA SSKAKDFVQKAGRWLSRHWGAGKKSDPRDISTRLGKLAGVDPKAIDGHTGRAALEDLLRTLG SRPAQNADAEKLYRQLKRAVGWKGRPSKGAVALKKIRDAERVPNDLWKEIASTLREEAAVQSS QTSDHAAVPDWRSHWPAEITGLPMPYRVDRDYIWEHGVMLDHALRRVSSAHTWIKRAEAE RRRFQQDAAKMGSIPEEARNWLDAFRERRSSSSGATGDYLIRERAINGWDKVVQAWETLGP NSTRDQRIAAARDVQANLDEDEKFGDIQLFAGFGDEHVDDPERCLADDRATCVWRNSSGRA DGRILKDYVAATVAEHNQRRFKVPAYRHPDPLRHPVFVDYGKSRWSINYSALTAAQQRRKTT QKLAQAKTDNTRAKLQQQLASTADLRSVTLGVWDGNRIVKISQRWRSKRFWRDLDLDHFGS HPSAAVSRADRLGRVAARQDPGAAVYVAKVFEQQDWNGRLQVPRRELNRLADVVYGKGAD PDFGKLERLDPRARRLWERLSWFLTTSATVQPQGPWLDYVAAGLPSGIQYTKSRAGYYLNYD ANHGRKGRARLCLARLPGLRVLSLDLGHRYAAACAVWQTLTIEQMTNECRQAAHPAPSNDD LFIHLRHPTHKPQKSGRKKGRPVTKTTIYRRIGPDKLPDGTDHPAPWARLERQFLIKLQGEDRP ARYASQKEIDEVNQFRNFVGLEPIVDRPRVDDLHSDAVRVARLGLRRLADAARIAFAMTAAKK

[0126]

		PISGGHEVELTTAQRIEFLQDALLLWQSLAASRRYRDDWAEKLWQSWVVEKLGGPQPAEIAD DLPRSQRAASLKTARQSLRKVAEKLSDGQSPSAAELHRLWAERWQQRQTEWRRHLRWLRRLI LPRRKDHQQEDRPLQRVGGLSVKRIQTIRQLYQVLKAFRMRPEPSDLRKNIPAPGDRSLASFG RRILNHLERLREQRIKQLASRVVEAALGAGRISKPPGRDRRRPQQPVDRPCHAVVIENLQHYK PEDSRLRRENRQLMDWQARNLRKYIVEGCELHGLLFVEVSPAYTSRQDSRTGAPGLRCEDVSR TALQEAARRMHASHSRPSNSSPGGSQTQFEREVCRWINEFKRVEGSSSSLSARQAVLKAFLHH QASIPTSLSTILLPRRGGELFVSADPDSPLACGLQADLNAAANIGLKALTDPDWMGAWWFVL VDRASGQPVEEQVQGCPIWLSCGPLSNSNPATIDPSDSPTAARRSNGTGAKGRARANEYWW SSLSATTLPDHKAWQPTQDYWRDIEQRVVKRLLRLLDGSEWSED
109	Cas12	MLDKFASLYPVTKTLRFRLLPQGRTEENMQVAKVLENDLERSEAAAVVKGLIKKYHLQFISDTLS GSTLSWQALTETLDKFKADHTATAELDSALAAYRCKLAELFTKSPKYKVMATPVSIIKEILKTETD PENIAALNKLNGYTYIIFDYVSTRMLTYSADAKATSLAYRLVDENYLRFYQDISAAAEISAVLEEA GFDNAEVEAFIRTDYNTCLTSEGIASFNAAAGSINQFVNVLLQQNPVLQSEPALRRHLQPLYK MLLDEAESKIIKFEDYGQLRDAVENFRRNFQDLPQSLIDIFAGRYDYSKIYVGYKYLNEASSQIA GGYNWKLLENALEDFYSKPYLVNGKLPVKYKTVVNKKMNQLAYSFTELQEALDAGDSGSSITD LFGKYAELHAAYAAADGNVFYKEYDRKSIASLKNYLDAVNAIARFIKIFAAPEVYVKDEGFYGIV DGAADKLRDFDLLYNMVRNYITKKPYKKSKVALTFNSSSFGRGWDENKIYDELTTIFTYNGKYY LGVINKNDKPDLAAAVSKDEGGYKRMVYKTFDIVKQLPRLSFTKAVKAHFAESDEDFIFDGPKF AKPLRVPKEIYLQSFTDNGDKLADSAKKYTKAYLDMSGDYKGYYEAIIKRIDYTKEFLSAYKSTSI YDLAFLKPAGKAAGSLCWTRHI
110	Cas12	MCIRDRDLAVAALNRGDAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGQLNAIRNFLASDGYGAHDLVPVNYNGSNDRGAEVQ VGNQKNWTVTSSAPVVVQYNNADTTLTVQGHTDRLIVTGSGNDTITLKDSGDDKVLLGDGN NTVVAGSGADTIVGGAGNDVLIGTNGGYGTELLGGAGNDVLRNAGSHGIYMDGGAGNDTF YGGTGPDTMEGGDGNDLMYANGRGSSIDGGAGNDTIYGGPGGDTLTGGDGNDLLRSDSAF GTKGSGNLLVGGAGNDTLWAGAGYDTLKAGSGSDTLISGTGSSQMIGGSSGNTTFEVAYHTG NDTITGSGSGNTVYLDGRDFSDATISNHSGVTTVSFSDGQVLKISGVQDIVFSDHDYKV
111	Cas12	MSITRSIKVKLIVPRDASLEARQLREGLWATHLFVNDGCHYYERLLLEFRQRDVCVGKDDAGK DVIVPAAEWADRLRARLGRNGMVPSHIEAALPIFRELYENMVPSALKAKSGTGQAGRSWHSK LVSPTSRGGEASAARIDVLRPLLPVSGDDPAFEPAARALIEEAGDELLTSTGRCPAWVTAYRKGPE GSAWVEKLRIQLREAVEAGDFDPPSDPQILAAGAVPAAPPLGAGIDALRPLLPLLGGDPAFEPA ARALVEDIGDELFTSTGRPPTWVTAHPTWVRAHRKDAECLEAADDFKWVERLRQRLRDDAK AGKFEQPLHERLGALGALPVAKPIGAGRVVSRADLTVFERGAMELAIEHLIGWESAGHRARAQ

[0127]

		YVERKKRHDDLLQWIEAEAPDALLAVRAYEAARTIHLATLGELGAAPQYTLRLREIRPWRKLRE WLLQNPDATIDERRRRLATMQTNDPRGYGGEALAWLAAPERRALVEHPAGDVVTRIAVLNIR KSILDRSRLFPTCTLADPVEHPRFAKFGKPGDKNSAGYALAVDGVRREAIIKILVPRQDGLLVPT DLRVPFAPSGQMRDLRASGLDISYERQDGRGRQAAKLQGGNLMFDRTHFARCGAPGPEALG SVWIKVALDLSSPAASLAMKTATPVRTYLSTAVRGRPESTKYEKAAPPEGFRVLSVHMGLRTAAT ASMLRFGAPEEGGHEVPVSGLAGETLVAFHERTVTMKLPGEDPDTRTEANRGVAKRELRGLGR GIGCLKAIRRASASATPEDRAEALVIIETHVGQGDRHGWAPAEAVGRLDPHGDPDDWKTACA ALYAAVEADLGVAISSWRKAARAGGATGMLGGKSLWAVDHLERSFRFLRSWDLRARPHDGD PRRPRPGYASKLLHHIDGVKDDRVKTTADRIVQAACGRAWIGGPTVKRGTQDVRLPGRWEQR GPRADLILLPDLTHFRFRSDRPRAENSRLMRWAHRQLAIYVRMQAEVEGILVADTGAAFTTRF DAWTGAPGVRCEPVTADHLRGIAKREDYWLARLLREGALKHLRIDPASLRVDDLVPMDHGKIL VALDGVDLPGLRILDTDVNASQGLGRRYIEGHGLAYRLPGARVPRGEGEREAAVVHIKGKRLAS AMGGTVVVLRASEGPGDITWTAEVYDRPQGARKALGLSLAAFNSIATAAVDDEGPAPENDDE ALEEEAEEALGIATGERIVFFRDPSGAVAGGGWLEASAFWGIANRMVTDRLRELGRLG
112	Cas12	MAQASSTPAVSPRPRPRYREERTLVRKLLPRPGQSKQEFRENVKKLRKAFLQFNADVSGVCQW AIQFRPRYGKPAEPTETFWKFFLEPETSLPPNDSRSPEFRRLQAFEAAAGINGAAALDDPAFTNE LRDSILAVASRPKTKEAQRLFSRLKDYQPAHRMILAKVAAEWIESRYRRAHQNWERNYEEWKK EKQEWEQNHPELTPEIREAFNQIFQQLEVKEKRVRICPAARLLQNKDNCQYAGKNKHSVLCN QFNEFKKNHLQGKAIKFFYKDAEKYLRCGLQSLKPNVQGPFREDWNKYLRYMNLKEETLRGK NGGRLPHCKNLGQECEFNPHTALCKQYQQQLSSRPDLVQHDELYRKWRREYWREPRKPVFR YPSVKRHSIAKIFGENYFQADFKNSVVGLRLDSMPAGQYLEFAFAPWPRNYRPQPGETEISSVH LHFVGTRPRIGFRFRVPHKRSRFDCTQEELDELRSRTFPRKAQDQKFLEAARKRLLETFPGNAE QELRLLAVDLGTDSARAAFFIGKTFQQAFPLKIVKIEKLYEQWPNQKQAGDRRDASSKQPRPGL SRDHVGRHLQKMRAQASEIAQKRQELTGTPAPETTTDQAAKKATLQPFDLRGLTVHTARMIR DWARLNARQIIQLAEENQVDLIVLESLRGFRPPGYENLDQEKKRRVAFFAHGRIRRKVTEKAVE RGMRVVTVPYLASSKVCAECRKKQKDNKQWEKNKKRGLFKCEGCGSQAQVDENAARVLGR VFWGEIELPTAIP
113	Cas12	MNIIMENFEKFVNLYELSKTLRFELIPFSQTKVELEKDWIIEKDREIEEKYHIIKEKLDTLHIKFVWQ ALEWVDLSLLEEYAELYFACKKDTKNKKLKSKFEKLEKKIRQEITSFFDAEWNKWKEKYGFLKKW WTSFLTEKEILDVLIDIFPENKDDFEIFKWFFTYFSNFNESRKNFYKDEWKAGQIATRAIDENLTT FLENIIKYKNFKKENPDFFTENEEKVFELDFYNFCLTQKWIDNYNEIIWAKSLEEWKNTQGVNQ RINLLKQKNEKSNKKNLSYPKFDILYKQILSEKSENDFIPNIENTEELFTVIQKSIKENDKKITEIDKL FKKFFLEENNIDIWKVYISKQAVNTISSKYFENWSSLWWYLWENSKKKYFSLWEIKEALEDIKEK NIFKGEYYNNKIAFENKSNFENFLAIFYYEFQTNLSLLNWNQNNLESLQEKEFKKEEKQVDIIKK YFDSVMDLYAMSKYFFVDLKQAKNFPKDIEFYNDFDLYFSDYEPWKVYNLVRNFLTKKEVKTD KFKLNFSNSQFLTGWDKDKEKERFWVILRKNEKYFLAILKKNNNKIFENYRENNPTDFYEKMEY KQLNNVYRQIPRLGFPLQKKLDSLKWKELEEYLEKYKNNFWYNKEIAFIKEEFDIFQKNKEKWE KFDREKLKKLIDYYKKVVLEKYSDLYDLKKLENTDYDELVNFYDDVEKSMYSLHFTKIETEFLENL EKNWEIYLFQIYNKDFSDYKKENTKENIHTKYFKHLFSEENLENLKIKLSGWAEIFFRDKTHNLK QKLDKNWKKMFYWENKDKKVLEHRRYAKDSYGFHISITLWANNWDMYKFNQFFNKNFTPK

[0128]

		HIIGIDRWEKHLAYYSVIDLEGNLVETDTLNIVNGINYLEKLENIEKSRMQERKSWWEIENIKNLK DGYISAVVSKLTELIEKYQAIIVFEDLNLGFKRWREKIERQVYQKLELALAKKLNYLTFKNKKDCEI WGVLNGIQLVPRVKDYQDIANYKQSGIIFYTNPAYTSTTCPECGWRKTLKFPSKITKTSILEFFKEI QMSFYWEKFSFTYENILWKSETLFSNVKRTQWNNKSRKIEHKENITQELKSVFEKYNINLWENI SEKLQQTDMLLEDLKVLFYNFKLINNIRNSDSKLEEDIISCPCCLFNSENWFKGAYFNGDANGA YNTARKGIIMLENIKVNPERSNLFVRNEEWDEFLREEF
114	Cas12	MSKLFENMTNLYSLNKTLRFELKPVGNTRELIESKDFFKNDEEKAENYQFMKEKMDKIHRNYI QKSLETIKMLPILDQTEQKRLKKEDIKNELKSLRSFISAAFVSVKDLLSNKIIEWLISEASIEEKEKIK KFDKFFGYFKTYVQNRGNLYKAEDKAGQIAFRLIDENLPRFFKAKQIIEEIIKKTPDFVVKERNEK QEETEKKITEYLSIFYLNSYCHYLSQSGIDLFNEIVGHINLSINLYKQKTGVKFSLIPLLYKLPLAPRK QISRLPKQIENPEELELIVKSVLDRIDQKINPFINNILQTVLEENSVYDLNWIYISIKTTEQWWSIG LSGRNSLRELGYNQSKNWEEPVLKAEKNKFPFISLGEIKSFLDAKQLAWDDIKSVFWEGKSQSL MNWSWSNIFFHLIGKEISSLIEKYLHSRKNYQISQSKENQKHVLDNSLSLWRLLGWFVLMHKK THLTPEIKESFFYDWENGLDAIVFDENSDPIHTIYDKVRNCLTKKPYSNKDKIKVNFDCPYLLWG WDQNYDAFGWLIFHDWKKYFLWLIKGSWLNMEEKNKLYEWINPMNSITKIIYDYQKPDFKN VPRLFIRSKWDTFAPMVREYWLPVNDILYLYDNELYKPDKKNPWKHKSYLRRLIDYFKLWLSKH KSFKHYIFKRKESDQYENLAEFYSDVEFSCYAIKKEKVNFDQVKALCESERLYLFEIYNKDYNQFS KWKNKNLHTQYFEALFEERDNNLFMLSGGWSIFWRESNWKIVEKIRSYSPKYNIEIIDKRRYTK NKLMIHIPIVLNFCRNQEWRVNDMIKSLIQSQSNNFTILGIDRWEKHLLYYSLIRQDWTIIKTGS RNTITNKIKIVDYHKKLDDREKKRDEAQANWEQQEQIKDLKKWYISQVINEISKMIIEHNAIIVL EDLNGWFKRWRQKVEKSIYQQFELALAKKLNHLVFKNRWDTESWGTMKAYQLTPLVAQFQD LSFQTWVVFYTPAWYTSTTCPCCGWRKNIYFKYENEKQAKIELEKLNIVRENNYFSITYTAEWW NKKWKITWSVLNKTDRILTTKWQTRLQYDRASKNTKEYDITTDFNSVFTAKFLDYKIRLENAGS KQCRNLINSINLLLKIRNAKSGTDIDTIQCPACEFHSQWWFQWNEFNWDANWAYNIARKGK VIIDKIVKGEKNTTVSQIEFDNEIQK
115	Cas12	PAYRHPDPLLHPVFCDFGCSRWQICFDVRKNVRTTSPRRLCLTLFTGSGMELVPFSWQSKRLA RDLALEQRHRNPEASEVTRADRLGRAAAGVSAGGAVSIKNIFNEENWNGRLQAPRSQLAAIA ARVDKHGWDAKALRMLDRLRWLITFSPRLEPTGPWIEYALRIPDDAAAKPFLSRKNGFAVLHR SNDDRKGLAKLILSRLPGLRVLSVDLGHRYAAACAVWETLSADQVREACQAAGHDGPTECDL YLHLKKDGRTVIYRRIGADTLSDGTPHPAPWARLDRQFLIKLQGEEHKAREASNAEIWAVHQM EAALGRSVPLIDRLVASGWGQRTEGQRARLEALKQLGWRPVAEKLDSDDEPGVMEESPAIKPS LSIDELMSSAVRTMRLALKRHGDRARIAHYLITDEKTKPGNVKEQLDENGRIELLQDALVLWH DLFSSKGWQDNKAKELWYVHIATLPEYKAFQSSGEGHAGPERRGKPEEDREKLGVVAQALAP NVTLREALHNAWKKRWEEDDARWKALLRWCKDWILPRGEAANSPAIRKVGGLSLIRLATLTEF RRKVQVGFFARLRPDGKKAETGEKFGRKTLDALEELREQRVKQLASRIAEAALGIGKEHVFPTAK EPQKKCWCGSVHRKKDPKRPRERVHSPCHAVVIENLTHYRPEETRTRRENRQLMSWSSGKVK KYLAEACQLNGLHLREVNAAYTSRQDSRTGAPGIRCQDVPVKEFMRSPFWREQVAQAKKKQ AEGKGDARERFLCDLDEQWKNRSEDEWKKAGPVRVPLRGGEIFVSADGTSPTAKGLHADLNA AANIGLCALTDPDWPGRWWYVPCDPASFKPIMDKVEGSAAVQPDQALRQPAQAQRGDAA RDRKKRGKVGGRSREVVNLWRDVSSRPISPNDSWQEFTPYWNDVQARVVNILRQSAGLTRG

[0129]

		QGEP
116	Cas12	MPLRSINIKMRLKRAAEGRALRQSLWLTHSVVNCAVAEIERVLLLCRGRGYWTGDDEPVSAET VQQQALAFARETQARNGQPGIGGDAEILAALRGLYEAIVPSVNRDEQGRPLEGNAQAAGGFA GPMMDAESEGFQSVFDKILEPLPSWVAKMTGGTRGWEQESVQWLKSPESERLQHASGSPPA WVRRLRTGEPWQEAFVQDQENKRKEVKGVPSLIQRLKKELGLLPLMRPPITLQFEDKRSGLTP WDRLTLRLAVAHLLSWESWNHRAADEHGRVTERLARLETEAAPLASLIEGLREYEKIRHEELKR VAQANDENPFRIGARGVRGWDRVREAWLGATDDTKEGRFTSVAALQTKLGGRFGDPDLFRW LAEEGREHLWGEHDPLPILARLNALSRLLRRKKDHAIYTAPDARLHPRWTAYEAPGGGNLRNY SFEISGNDLALRLPLLRRVESGLEEDSQRAEIALAPSGQFQSASWKGDGKPNRHLTYYSAHEQF SAELGGAEILYRRRHLENRKVKELEQGDIGPVWLKLVLDVQPNAPEGWFTPRGRVVTPPTVHH FNTALVNRSKHAPDLVPGLRVLAVDLGVRTFAACSVFELVQGEPGNGMAFLADQERDLWAR HERSFLLPLPGEAVDSQLLAARRAAYNQLGLLRRDLGRLKGILRLSVKETAENRCGSLEELLASLE DEWNRGNAPAIDVAALLSAKGCLEMPQPAWEAAIAGTYQAAERELGNRVRDWRRTTRPRTT GEDDRRQRRGYSGGKSAWAVEYLDQVRRLLQGWSLHGRSYAQIRRLDREKMGTFAAGLLDH INALKQDRVKTGSDLIVQAARGYLPTGKKGWIKQYEPCRLILFEDLARYRFRTDRPRRENARLM RWNHRQILTETELQAEIFGLLIGTTGAGFSSRFHARSGAPGCRTRLLTAEDLRSPTLAKQLELLAE TQGIDPKCFRPGMQIPWDSGADFVTLDSEGKLVQIHADVNAAQNLQRRFWTRFRDAYRISAV EIKQDGRTSWYPDREGVRLRGALSTIVGGDGYARLVAADDDDGFVLEKVTRPHWRRAAGAQ AESGDDVGLDEVALEMAEAMDTDLERGEGRLVFFRDPSGSVIRADRWYQAKAFWGQVRSRV TRALGLRRPGASS
117	Cas12	MLDKFASLYPVTKTLRFRLLPQGRTEENMQVAKVLENDLERSEAAAVVKGLIKKYHLQFISDTLS GSTLSWQALTETLDKFKADHTATAELDSALAAYRCKLAELFTKSPKYKVMATPVSIIKEILKTETD PENIAALNKLNGYTYIIFDYVSTRMLTYSADAKATSLAYRLVDENYLRFYQDISAAAEISAVLEEA GFDNAEVEAFIRTDYNTCLTSEGIASFNAAAGSINQFVNVLLQQNPVLQSEPALRRHLQPLYK MLLDEAESKIIKFEDYGQLRDAVENFRRNFQDLPQSLIDIFAGRYDYSKIYVGYKYLNEASSQIA GGYNWKLLENALEDFYSKPYLVNGKLPVKYKTVVNKKMNQLAYSFTELQEALDAGDSGSSITD LFGKYAELHAAYAAADGNVFYKEYDRKSIASLKNYLDAVNAIARFIKIFAAPEVYVKDEGFYGIV DGAADKLRDFDLLYNMVRNYITKKPYKKSKVALTFNSSSFGRGWDENKIYDELTTIFTYNGKYY LGVINKNDKPDLAAAVSKDEGGYKRMVYKTFDIVKQLPRLSFTKAVKAHFAESDEDFIFDGPKF AKPLRVPKEIYLQSFTDNGDKLADSAKKYTKAYLDMSGDYKGYYEAIIKRIDYTKEFLSAYKSTSI YDLAFLKPAGKAAGSLCWTRHI
118	Cas12	MSRSIFSPFTNLYPIQKTLRRELKPLNENFQHDPALSALRNSEIPQRDEQREKDYQAIKPLLDEF HNQFITESLHSLEPQDRSDFILFYQTYQKKKKNKAEISEKELKSLDEEFESRTKALRNAIGTSFSVT AELRKSNPDYVSEKGKPFLTQKSYKILTEAGVLWLLEKKYTSDPEKLALIRRFGNFFTYFTGFNQN RENYYATDEKSTAVAYRAINENLLTFANNCELFEKLSVLSLSELEKKTFNPDSYSEYLTQSGIVFYN EMLANIRSKANLYTQEHKAKLPQPKLLYKQIWSPRGDTIPFDLIASEAEFQETLHTMIRETDQRI PEFNKLLEQIFEEKVDLSQIFFSKTSLNIISNRYFSSWHTLLEKGVELKLFKFKKNDEESFKLPAYLSL

[0130]

		AELKELLESAPFQMAEKADADEEKHHQASLFKLQRENLHLEKSHSNWELLLKSMKSDFESFWT WEGEFWSYTLAKKALQSLSALESTNQEHKNLIKMLLDNALYAYRMLKWFKVDTSKLGFVPEGE FYPSLDQLLQDYPLPKWYDMIRNYLTRKTYSQAKLKLNFDCSTLLNGRDKNKEIQNLSVILRKD GKFYLAIMKKDQNKFFENSALYEGNLGTMEKMDYKLLPWANKMLPKCLMPGSDKKKYGASD QVLELYAKGSFKKSEKSFNLADLHTLIDFYKLALPKYEDWKVFNFQFQATENYQDISQFYREVE QQGYLLNWRKVNEKLIKQGIKDWSLFLFQISSKDFEGKSKTPDLQTLYWQQLFEFSTNVKLNG EAEIFFRPWSMKKEKKKLKVDNYDVFKHKRYTEDKILFHVPITLWFGNNEVSPSAPSKFNQKLN QELIIPHFDDLHVIGVDRWEKHLAFYSVVSVKTGKIVKQGTLNLLNGTDYEAKLSQKAENRLHA RQNRDTIEKIADLKNGYISQVVNKLVELVLEYNAVIVFEDLNAGFKRGRQKIEQSVYQKLELALA KKLNFIVKKEKAVGEPWSVTSAYQLAPQINTFWDIKWKQRGIMLYTRANYTSVTDPLTGWRK QYYFKKGSSEEMKAQFFKSFKNLTRDAGQEAYIFDDGTWLLYSNVERRRGKRGDHRERTQIKY DPSLELDTLFSKYQIEKSDSLFDQLKNRELPQTFWTSFFRIIDLIMQIRNTDDEGRDIILSPIGNPQ ERFDSRKRYNQLPRDEKGGIIEESAFEYPTSWDANGAYNIARKGVMMLERIKENPEKPDLLIRD AEWDKKITRK
119	Cas12	MKNFQDFTNLYELSKTLRFELKPIWGTKKLIEEKNILKLDKKKRENYEKVKPYFNKIHQEFINFAL RNPNFDFSQFEEKYLNWLKDKKNKDLLKEKESIDKIFLEKIWKLFENSVKDFLKENGFESIVKSE DQNLKFFRRKEIFEVLQEKYGSELETQMVNKDWEIKSIFNGWEKWLWYFDKFFNTRDNFYKT DWTSTAIATRIIKDNLKIFLENTIIFEKVKNKKIDFSEVEKNFSVSIDTFFEINNFNNCFLQDWIDFY NKVIWGETLENWEKLKWLNEIINKYRQDTGEKIPYFKKLQKQILSEKDWVFIDKIEDDGGFYEVL KNFYKNAAEKEWFLKNIFENFYTISDKNLEKIYFNKIAFNTISHKFWSALEFERILYEEMKKEKAD WIKFEKKENKYKFPDFIQIIFIKRSLENYDSENLFWKERYYKSEENVDWFLEKNNNNIWEQFCKI LNFEFLNILKRRIIDEAWEEYEVWFEISKNILWEKLENFELNQENKWIIKDFADYSLALYSFWKYF AVEKWRNWDLNIDISDDFYGWEDWYIEKFYNTGYDEIVKPYNLMRNYISKKPWEDSKKWKI NFETSSLLSWWDKNLESNWSYIFQKWNKYYIWIINWSKPAKEVLEKLYSWNGEKIKRFIYDFQ KPDNKNTPRMFIRSKKDSFSPAVGKYNLPVEDILEIYDNWLFKTENKDNSNYKESLSKLIDYFKL GFSKHESFKHFNFVWKDSKEYENIADFYRDVEKSCYQITSEFLDFEELKKLTFKKHLYLFQIYNKD FELDESLQKNWYNFRDEWQKNIHTKYFEALFLEENILRKSWAVFKLSWGWEVFFRKESIKAEKE KRKNIEVTKNRRYTEEKYFLHFPIQVNFKNEISWNFNQEINKFLANNPDINVIWIDRWEKHLAY FSVINQKWEILESWSFNKIENYNKNWEKLLFPEREIKEIHKDWSLIDLELVETWRKVDYVDYKLL LEYKERKRLLQRQSWKEVEQIKDLKKWYISALVRKIADLIIKHNAIVIFEDLNFRFKQIRGWIEKSI YQQLEKALIDKLNFLVNKNEINLEKAGSILKAYQLTVPVDSLKEIWKQTWVIFYTEAAYTSKIDPIK WWRPNLYLKKQNAEINKENILKFDNIIFNSKENRFEFTYDLKKFFWKDSKFPAKTVNTVCSCVE RFKWNRNLNNNKWGYIHYENLTDWKLANKEQKEDEFSNFKELFEKYFIDINWNILEQIKNLDT KNNEKFFSSFIDLFTLVCQIRNTNQNAKWDENDFILSPVEPFFDSRKSQNFWKSLPKNWDEN WAFNIARKGLIILNRISENPEKPDLLIFNADWDNFARNI
120	Cas12	RPGASAALSLTPLKTLFSENFSSFMCGNWQIINDSLKTYYNENIKSKGKAKEEKVKKAIKAIEYKS LADINQLVERYNNDELNRKAEEYISAINEKIKDLDVNEIEYDEKINLIENETKSEEIKSKLDSIMEI MHWTKMFIIEEEIEKDVNFYNEIEEIYDELQPLVTIYNRIRNYVTQKPYSEEKIKLNFGIPTLANG WSKTKEYDNNAIIMIRDGKYYLGIFNAKNKPDKKIMEGHQSEENGDYKKMIYRLLPGPNKML PKVFMSKTGIAEYKPSQYILECYEQNKHIKSDKNFDIKFCRDLIDFFKTSINRHPEWSKFNFKFSE

[0131]

		TSEYEDISTFYREVEKQGYKIEWTYISEKEIKELDENGQLYLFQIYNKDFSEKSKGKENLHTMYLK NLFSEENLKNIVLKLNGEAEVFFRKSSIKKPIIHKKGSVLVNKTYNENGERKSIPEEQYTEIYKYLN SIGTNELSEKSKKLMEEGKVEYYKANYDIVKDYRYSVDKFFIHLPMTINFKAAGFSPINNIALKNI ALKDDMHIIGIDRGERNLIYVSVIDTKGNIVEQRNFNIVNGIDYKEKLKQKELDRDNARKNWKE IGKIKDLKEGYLSLVVHEIAKLVVKYNAIITMEDLNQGFKRGRFKVERQVYQKFETMLINKLNYL VDKDLAVDQEGGLLRGYQLTYIPESLKVLGRQCGYIFYVPAAYTSKIDPTTGFVAIFNYKGMTDK DFVTSFDSIKYDDERGLFAFEFDYENFVTHKVEMARNKWTVYTYGERIKRKFKNGSWDTAEKV DLTYQMRSILEKYEIEYNKGQDILEQIEELDEKAQNGICKEIKYLVKDIVQMRNSLPDNAAEDYD AIISPVINNNGEFFDSTRGDEDKPLDADANGAYCIALKGLYEVMQIKKNWNEETEFPRKELKIR HQDWLDFIQNKRYL
121	Cas12	MQCGSLRHNSKSLDSALAYPARLTTGGNEGKTSEAHIENDSLPEITRRPSRLARDFAPSNPFPF MKRIYQGQITGMQFHGAAGEQAVPANQNWEQALWDHHGLFHDAVNYYLVCLLALARPGN PVYAIREKLDAHNGAEPDELMVWRTFRRRGCNRPGLRDSVAKYLTPGNDEPTTEECFAAVLAG NPLGATEEGRAILNEGLAQLLGKCTGESGCRNSAKEYLPRFTKPDFKGNFEEDTARLNRAEASK RLPFYLHDPATTPNSPALDEFGVLSIALPNPKRAELTGAEARDKLLEFSREWSARLPDGSADWR RLEAKITALGDSLAIPGYTSGSAKGENRFQLYAMFLFCFVEKSDFTLGLLRQTTRRPVEGEEPPPR SNHSATAGDPIRIARGGRGYVFRAFTSLKQWGGDTGGDLKWPKFDMAAFCEALKALHQVEA KAKQRAEERSKKQALLDYQRGRIRRFKPTANSEDATPPPVLAGDPRISRLEQLLNTDLQDEYEM SEGVAVAYGLHPRTIRGFREIRKRWISAVGNAPFSEAARATLIACVRSFQSENPGTVGSARLFEA LAEESNWIIWREPSAAEQQSWRENADLPESAEFALDPLQALTDERELKDEIERLSGPIRFTPADA EHSRRQFYFSDVSQIDKRNRFRPRLNEVEVELAVRPNGHWTNVVWVTLQYSAPRLLRDQLPTA DEAGGGWQQAMMAALNLRAPLKKGGEAVSFADCAALSLMPDISPDGEKRLLLNFPVELDGE AIANQLGRSKRWETLQFGGADDESYWLRWPKTWIDETKVRRKAAPPKWWLSKEPFSVLGVD LGQRDAAACALVQVSPGNCPTGVCRHVGSADGVDWWATVRSMNMLRLPGENAKVMRDG RFQEELSGSRGRSASIDELKEAGDICARLGFVADTILGANGRALSFPELNDRLLFSLRSAQSRLAR LQSWSCVAHADVPPARREGILRDISEAKDDPLGLKPLATAGNLEAIASTLREVILQERTSISAQLV RVADRILPLRGRRWEWVARPESPSNHMLRATAPDTDPRRKLVAGQRGLSLARVEQLESLRQR CQSLNRALMQVPGTPSKLGRRSRGVELPDPCPDLLDRLDALKEQRVNQTAHLILAQALGVRLR IHQVSGPQRTRSDSHGEYERIPGREPVDFLVLENLDRYLASQGRSRSENSRLMKWCHRAILLKL KQLCEPYGLRVLETPAAYSSKFSSRDGTAGFRAVEVTPDDLGSHRWRKHSERLADPGASLSRDE REESTRLMAFAERLKALNQDLIARQEAARSSNQPFRPKWRTLLAPQQLGPIFVPAVGKPLQADI NAAINIALRAIASPDVDDIHLRIRAARSGDKFVVRAENTRERARWGSAEAEIGLPTGAGAKEIEE RRSLLTEARVNFFFDPASVAAFDHGKVRDAKLAVTSGRGLWGTLRREEWAIVGKINNDRLAAH GLGRPFAERVDL
122	Cas12	MSQRDPLPSPTPRAYTLRLSTPDADNGAWRERLWKTHEVVNSGAEAFGDWLLSLRGGLDHR LVAVKVRVGRGASKTEREPTEDERRERRIVLALCWLSVESKKGAPQGRVVEDPVDALKRILGQR GLSEADAEQWVFDCRDSLSATIRDDATWVDRSAAFDETVQRLGSSLTREHAEQVIIEFFGDIH DYLALPKNMEEDGVTSPRGGSGKEFRTQARSWLSENWGAGQKGDKAQIVDALRKCSRCIAQ EKPSTGSDLLRVLVRSLGGSPEETLRFDELRKLVGWRTGRRSTGAFALQRTVDMDRLSESDLESL EAKLTVEIDAKSPEASRSVPQWVESMRTAVEREVGMPFRSTRDLIGEFGVMLDHAARRVSATH

[0132]

		SWIKRAEAERRKFEGDAAKLAQIPEEARQWLDQFCEDRSQELNALEPYRIRRRAVEGWESVVR TWAKADCKAEGDRVKAVRALQPEIEKFGDAALFEALAAEDALCVWLLDGKATPRPLLDYSAAT DAQYRKRRFKVPAYRHPDALLHPVFCDFGESRWTIEFSAHRALGRRRKAQQLVDNKTVALQK AQERLRKAKAESSRSRAEEKVRAAEHALEAARKKLAFLQYRRALAVCLWTGKGVESTSLRWHS KRFAKDFAIGSSPEDGASTGVPVARADRLGRASANVPRGASVTISGVFEQKEWNGRLQAPRD ALNAIAKVRDDETLPAADRSRRVQQMLSRLPWFVTFSARLVPQGPWLDYASEHSALGLRVDP KYWPHAEENRQRKGMARLILSRLPSLRVLSVDLGHRYAAACAVWETLSAQEMQRICREMGS APPSPDDLYLHLRRADGNGKQRTTVYRRIGPDTLPDGGQHPAPWARLDRQFLIKLQGEDESA RKASDSEIAVVKKFEADLGRPAMQRRSLRVDDLMSAAVRTARLALRRHGDRARIAFNLIADRR FRPGGAEEPLTDETRVDLLADTLATWHGLFSGGQCHDERAEEQWNEHIAPLLASSGASLSVPS DGDAVAATPARRRRKEVRGKLVPAAMELARRDLSQLSVLWVARWHQDDESWRARLRWLRD WILPRGAKADSGAIRHVGGLSVTRLATIRSLWQLQKAYRTQPEPEDPRKNVPKKGDTSLDDFG RTILDDLEHLRENRVKQLASRICEAALGVGVEQPNGGAKDPKRPQERRFSPCQAVVIENLTRYR PEETRTRRENRQLLNWSAGKVKQYLSEACELHGLHLREVSAAYTSRQDSRTGAPGIRCQDIPV VDFVRENGPCWGRLRSAQQSSGGTAEDQLLLALYERWSEKERTWRDQSGNVWAMDGEGR WVARNGTQLPQGSGLTPHPIRVPQRGGDIFVSAAPRSPAANGIQADLNAAANIGLWALLDP DWEGRWWRLPCSAMDLKPVKGSVNGSAVIHLDAPLKAAATKGAAKKDVVNLWRDISVRSLT EGVWRGYDAYWNLARYRVVQTLRPQVGIGSDE
123	Cas12	MFKGDAFTGLYEVQKTLRFELVPIGLTQSYLENDWVIQKDKEVEENYGKIKAYFDLIHKEFVRQS LENAWLCQLDDFYEKYIELHNSLETRKDKNLAKQFEKVMKSLKKEFVSFFDAKWNEWKQKFSF LKKWWIDVLNEKEVLDLMAEFYPDEKELFDKFDKFFTYFSNFKESRKNFYADDGRAWAIATRAI DENLITFIKNIEDFKKLNSSFREFVNDNFSEEDKQIFEIDFYNNCLLQPWIDKYNKIVWWYSLEN WEKVQWLNEKINNFKQNQNKSNSKDLKFPRMKLLYKQILGDKEKKVYIDEIRDDKNLIDLIDN SKRRNQIKIDNANDIINDFINNNAKFELDKIYLTRQSINTISSKYFSSWDYIRWYFWTGELQEFV SFYDLKETFWKIEYETLENIFKDCYVKGINTESQNNIVFETQGIYENFLNIFKFEFNQNISQISLLE WELDKIQNEDIKKNEKQVEVIKNYFDSVMSVYKMTKYFSLEKWKKRVELDTDNNFYNDFNEY LEGFEIWKDYNLVRNYITKKQVNTDKIKLNFDNSQFLTWWDKDKENERLGIILRREWKYYLWIL KKWNTLNFGDYLQKEWEIFYEKMNYKQLNNVYRQLPRLLFPLTKKLNELKWDELKKYLSKYIQ NFWYNEEIAQIKIEFDIFQESKEKWEKFDIDKLRKLIEYYKKWVLALYSDLYDLEFIKYKNYDDLSI FYSDVEKKMYNLNFTKIDKSLIDGKVKSWELYLFQIYNKDFSESKKEWSTENIHTKYFKLLFNEK NLQNLVVKLSWWADIFFRDKTENLKFKKDKNGQEILDHRRFSQDKIMFHISITLNANCWDKY WFNQYVNEYMNKERDIKIIWIDRWEKHLAYYCVIDKSWKIFNNEIWTLNELNWVNYLEKLEKI ESSRKDSRISWWEIENIKELKNGYISQVINKLTELIVKYNAIIVFEDLNIWFKRWRQKIEKQIYQKL ELALAKKLNYLTQKDKKDDEILWNLKALQLVPKVNDYQDIWNYKQSWIMFYVRANYTSVTCP NCWLRKNLYISNSATKENQKKSLNSIAIKYNDWKFSFSYEIDDKSWKQKQSLNKKKFIVYSDIE RFVYSPLEKLTKVIDVNKKLLELFRDFNLSLDINKQIQEKDLDSVFFKSLTHLFNLILQLRNSDSKD NKDYISCPSCYYHSNNWLQWFEFNWDANWAYNIARKGIILLDRIRKNQEKPDLYVSDIDWD NFVQSNQFPNTIIPIQNIEKQVPLNIKI
124	Cas12	MLSFNWVLFFFFSKMSRSIFSPFTNLYPIQKTLRRELKPLNENFQHDPALSALRNSEIPQRDEQR EKDYQAIKPLLDEFHNQFITESLHSLEPQDRSDFILFYQTYQKKKKNKAEISEKELKSLDEEFESRT

[0133]

		KALRNAIGTSFSVTAELRKSNPDYVSEKGKPFLTQKSYKILTEAGVLWLLEKKYTSDPEKLALIRRF GNFFTYFTGFNQNRENYYATDEKSTAVAYRAINENLLTFANNCELFEKLSVLSLSELEKKTFNPDS YSEYLTQSGIVFYNEMLANIRSKANLYTQEHKAKLPQPKLLYKQIWSPRGDTIPFDLIASEAEFQE TLHTMIRETDQRIPEFNKLLEQIFEEKVDLSQIFFSKTSLNIISNRYFSSWHTLLEKGVELKLFKFKK NDEESFKLPAYLSLAELKELLESAPFQMAEKADADEEKHHQASLFKLQRENLHLEKSHSNWELL LKSMKSDFESFWTWEGEFWSYTLAKKALQSLSALESTNQEHKNLIKMLLDNALYAYRMLKWF KVDTSKLGFVPEGEFYPSLDQLLQDYPLPKWYDMIRNYLTRKTYSQAKLKLNFDCSTLLNGRDK NKEIQNLSVILRKDGKFYLAIMKKDQNKFFENSALYEGNLGTMEKMDYKLLPWANKMLPKCL MPGSDKKKYGASDQVLELYAKGSFKKSEKSFNLADLHTLIDFYKLALPKYEDWKVFNFQFQATE NYQDISQFYREVEQQGYLLNWRKVNEKLIKQGIKDWSLFLFQISSKDFEGKSKTPDLQTLYWQ QLFEFSTNVKLNGEAEIFFRPWSMKKEKKKLKVDNYDVFKHKRYTEDKILFHVPITLWFGNNEV SPSAPSKFNQKLNQELIIPHFDDLHVIGVDRWEKHLAFYSVVSVKTGKIVKQGTLNLLNGTDYE AKLSQKAENRLYARQNRDTIEKIADLKNGYISQVVNKLVELVLEYNAVIVFEDLNAGFKRGRQKI EQSVYQKLELALAKKLNFIVKKEKAVGEPWSVTSAYQLAPQINTFWDIKWKQRGIMLYTRANY TSVTDPLTGWRKQYYFKKGSSEEMKAQFFKSFKNLTRDAGQEAYIFDDGTWLLYSNVERRRGK RGDHRERTQIKYDPSLELDTLFSKYQIEKSDSLFDQLKNRELPQTFWTSFFRIIDLIMQIRNTDDE GRDIILSPIGNPQERFDSRKRYNQLPRDEKGGIIEESAFEYPTSWDANGAYNIARKGVMMLERI KENPEKPDLLIRDAEWDKKITRK
125	Cas12	MLDKFASLYPVTKTLRFRLLPQGRTEENMQVAKVLENDLERSEAAAVVKGLIKKYHLQFISDTLS GSTLSWQALTETLDKFKADHTATAELDSALAAYRCKLAELFTKSPKYKVMATPVSIIKEILKTETD PENIAALNKLNGYTYIIFDYVSTRMLTYSADAKATSLAYRLVDENYLRFYQDISAAAEISAVLEEA GFDNAEVEAFIRTDYNTCLTSEGIASFNAAAGSINQFVNVLLQQNPVLQSEPALRRHLQPLYK MLLDEAESKIIKFEDYGQLRDAVENFRRNFQDLPQSLIDIFAGRYDYSKIYVGYKYLNEASSQIA GGYNWKLLENALEDFYSKPYLVNGKLPVKYKTVVNKKMNQLAYSFTELQEALDAGDSGSSITD LFGKYAELHAAYAAADGNVFYKEYDRKSIASLKNYLDAVNAIARFIKIFAAPEVYVKDEGFYGIV DGAADKLRDFDLLYNMVRNYITKKPYKKSKVALTFNSSSFGRGWDENKIYDELTTIFTYNGKYY LGVINKNDKPDLAAAVSKDEGGYKRMVYKTFDIVKQLPRLSFTKAVKAHFAESDEDFIFDGPKF AKPLRVPKEIYLQSFTDNGDKLADSAKKYTKAYLDMSGDYKGYYEAIIKRIDYTKEFLSAYKSTSI YDLAFLKPAGKAAGSLCWTRHI
126	Cas12	MNRIYQGRVTKVEILNGKNADGQPQELPNWQTALWQHHELFQDAVNYYLFCLAALASSASS PMGKLRNQLGSVWEPFGRTGRRFKGLRDSVGPYLLPDRPTPSIEEAFAAALAGNNSQPELLQL AVDALVEDLGGDAAIQQEGRGYLPRLCSPAYNGQFPRGANSLQKEAAKIRLPTLLHNVATSRN LDALAAELEFGFFANPVPNAGPIAGQEARNKLLEALAWLKAKDTRLTHSANELEKRIGVLPDSV SFPTYSGGSINKEALKHRFFAYLLFQHVERSLVTFEILRDSYPTPKPSARKSSKATPDTMAQLTQF GDDPVKLARGTRGYVFRAFTSLPCWGAKAPSDILWSEFDIAAFKEALKTANQFRLKTKERLDKA DELAGELAWMNGEKSKFKPSEHSEQEPPAVLKGDPRFEVLKQLFEVELAEEHYLAEGESVIYGL HPRTLRCYRELVERWNKTVQPGEVFTEATSKKLVASTDKFQAENKERIGSVTLFKKLLERDYWC LWQTPDVQTVAARQKAGFSSNIIEDYQRYLELQTDIARLKEPIRFTPADAEQSRRLFMFSDLAG KSKHKHLPNATPYGFAVDVALAASEGGVWKETRVRLHYSAPRLRRDGLRKGVGEDLKRTAWL QPMVAALNLSEPAPQDFSKCAVSLMPDKSWKGLRHLLNFPVTLDPTVVQKAIGSQARWANQ

[0134]

		FVAFGKGATEQKFFLRWPEEVSASQKKAGPWWDALRAFSCLSVDLGQRDAGAFALLDVRAN ADWGKKPSRFIGEADGRNWRAALAAAGLLRLPGEDALVWRDGKWQEELYGEKGRLATKEE WLETNAIFSALEQNSEEWIGADPKRRSFPELNSKLLVVARRGQSWLARLHRWLWMLGDENK RERALRELLEQERQEAWRKRAEGKDLLALKQSLTAEIQRLNGLLPEQLVFLANRCLPLRNRKWA WNQHPDKAFAEKGCHLLEMVEAPSHLPLLAGQRGISFERIGQLEELRRRFQSLNRVLQRELGA PPKSGRELRDDLVPDCCPDILAKLDRVKEQRVNQTAHLIVAQVLGVQLRKHQTPESERTERDL HGEYEIMPGRKPVDFIVLEDLSKYLSSQARGRGENVRLMKWCHRQVTAKVKELCEPFGLPVLE TPAAYSSKFCSRTGVAGFRGVEVTLKDRQSFPWSKRLEEDSAEVAELFGWLETASAGHKTKQPR CLLAPMSLGPLFIPVTSQAPIMQADINAAINLGLRAMAAPSVHEIHVRIRSEAKDGQFRVRAQ SKREKARWGNEPPPIKMLVETQRVALAREGGHPNFFVDPLKAATFDRAEVEGLGLPVASGRGL WKSVRDAEWKRCREINLERMRRWGFIMEAPRTLQVSRKEDEDDLTF
127	Cas12	MAVRSVKLKLLVPRDGSAESVRKRKALWATHQFVNDAAAAYAELLLEMRQEDVCRGTDDHG KDVIEPAAHWQAKLRARLAAKQLPPVAVAEALPLLKAFYGSRLIKSFVANDKGVAGTGNATDL NTWLSGLVDPASVAGEKTELRKQLLAELPLCEAADADFEGAARKMLAKSDAREALLEGPGTGV GWPAAYNANPTDSVWLDMLHKAAAKARLELADTTVSELKKLGVFPLLQAASSNRVFGSGVL NPFERMAAAQAAAALLPWETKRHEMRKRRDKFADQLNQWDTEFGASHATALAAIRAFEAEE SERARRESLGNEGTGYRIGGRELRDAWTLLRDWLKGHSTATAAAREDKVRELQAKQGRSFGSH RLLSWLAKPAQQWLADHSAGDVVTRIAVRNARQRKLDTARTLPIWTGADAVKHPRFANFDP PNNTNQPGFDLRAGTQKGRLTLRLSLLTERADGLLLAQDHDFQLVPSRQMAEIVLHKDGKER ALSWQSQDGIGRQVGDVGGSALLFSRDHAECLLERKQITRLERGAWPAALPVWFKLSLDIGAE HKALLKQRFKWGVWLNSALVTRNAKDAKGVPPPVGTRVLAVDLGLRSAATVSVWQVVDAAT PVVAGKWRVPLSDTLSAVHERSAMLALPGEHVDAGVLAARRAANEKLAGLLAATSHLSTVFK LGRAEQGDRRRELLERLGEGDDRRARAAVATTAAERDGLRAVLGATQDAWAGAVAAVVRRL ETDLAGAIAAYRKQQREDVQLRREARHGPGASQLPKQAAAERLLGGKSAWQIEYKERVRKLLT RWIMRQRPGDTAVRRLARKDLGKYCGGLLDHLTALKEDRAKTTADLIVQAARGRVRAHKDAH GRQQDRELWLAKYAPCDLIVMEDLGRYRFATDRPPSENRQLMQWTHREVFRLVQMQAEVE GIQVLETGAEFSSKFDARTWAPGVRCEPITKLWVERYRNGEMPWLADKADEWRREGIELAQL VPGQLLPTGSGEQFVAVSATGGLRVRHADLNAAQCIALRALTGHGTAFRLTARRLGDVFVSAK GLGKRPQGALWREFGSALPPAVVVLRPAGEVRYALRPFASARDAAAALGLQLGALRNVDATD AESDAEDGDLAELLAGADPDRATFFRDPSGDVHGGAWVQAKVFWAEVRRHVRLGLQAQGL LPAAARSSEPRQMQLPLAGALPGDDIPL
128	Cas12	MSTQKNPFNQFTNLYELQKTLRFELRPVPETKKLLEKGEGKNLIQMDLEIDRLYEKEMKPMFNIL HEKFINESLGLVKLDCKKLKKLENLLAEADKLRKQIKEGRKNKNNISEVEKRLKIIIGDNSQGKNK NGEIAVLQDELRVLIVKAFNLTADKWKKELNNKETLLPEKKGKRKIKIKKSGPKILQEENVLAILAY FNPDKADIIKKFAGFFTYFSGFNQNRANYYTVKALATGVANRAINRNFLIFLANRKDFARFKERL PRLAEFDNYFELENYEKYLSQTGIEEYNDQIGKIKQIVNLEHNQQQKDNKFQLKGLATLEKQIG CRTKKQREEGGDKSAPKFLEKVGLGFQVSQDDDGEYLIWECLNYINKELAGKLKSIKDNYQKFF ADWRTGAYDLEKIWFRKEALNTISGRWFGGNNWFIIGKALALTGVGKFDKRENTYKIPEFVSLA EIKTAFEMLENGVNYDFKKSKKKKEGDDTDVVKYSADNLFKEEYKKKGLIKNSLFETMLAVWQ SEIKRKFEQIFDGYKLEKDDVFGRKKGEWVEPFIENFQKVSQEKFDRGVKDENGRSIHTEVVKN

[0135]

		LIEEGYLRLFQLTKYHNLDKKGERDPRPFDGNFYATLDEFWKDNIVVVYHKALQSTLTKKPYSED KIKLNFENGSLLGGFSDGQERSKAGVVLKNKNKFYLGILIDRGFFRTDKANPVYDNAQNNEWE RLILTNLKFQTLAGKGFLGKHGVSYGEMGKDNPMMAVEYLQKFIKLKYLDKYPALNEVAHKKY TIKKEFDADVKNALKDCFTMNFKPVDFGMIRQGLTESLFYLFEIVNKDISSQAKNGKNVHTLY WEALFGDQNLKKPILALNGGAEIFYRESQREKLEKKLDKSGKEVLDHKRYGQDKYFLHASITIN YGQPKNIKFKEVINEKISQNADRVNIIGIDRGEKHLLYYSVVSPEGVLLEQGSFNQIETKNKVDIK AVKAEYGERGELKKVELVPTGKKVKYVDYQILLDYYEKKRNLARRDWQTIGKIKDLKDGYLSQT VHRIYQLILKYNAVVAMEDLNVEFKAKRAAKVEKSVYKNFEMALAKKLNHLILKDRRADEIGG ALRAYQLTPAIPANDVGKFDKAKQWGIMFYVRANYTSTTDPLTGWRKHKYISNSEKIDNIQKFF SPGDGIQIDYDTEKQCFKFSYDHELEGGAKKHWELFACDGLERFYWDNRERQIKKYNLYEEFEK LLGGLRKEENINIQIDGVSEFRWKDLVFFWNLLNQIRNTDRSAQGDENDFLQSPVWSEKYNC FYDSRKAPNNMPNNGDANGAFNIARKGQLILERIKKCSDIPKFGNDNNGKNPENNYFISDAD WDKFAQK
129	Cas12	MAVKSIKVKLRLDDMPEIRAGLWKLHKEVNAGVRYYTEWLSLLRQENLYRRSPNGDGEQECD KTAEECKAELLERLRARQVENGHRGPAGSDDELLQLARQLYELLVPQAIGAKGDAQQIARKFLS PLADKDAVGGLGIAKAGNKPRWVRMREAGEPGWEEEKEKAETRKSADRTADVLRALADFGL KPLMRVYTDSEMSSVEWKPLRKGQAVRTWDRDMFQQAIERMMSWESWNQRVGQEYAKL VEQKNRFEQKNFVGQEHLVHLVNQLQQDMKEASPGLESKEQTAHYVTGRALRGSDKVFEKW GKLAPDAPFDLYDAEIKNVQRRNTRRFGSHDLFAKLAEPEYQALWREDASFLTRYAVYNSILRK LNHAKMFATFTLPDATAHPIWTRFDKLGGNLHQYTFLFNEFGERRHAIRFHKLLKVENGVARE VDDVTVPISMSEQLDNLLPRDPNEPIALYFRDYGAEQHFTGEFGGAKIQCRRDQLAHMHRRR GARDVYLNVSVRVQSQSEARGERRPPYAAVFRLVGDNHRAFVHFDKLSDYLAEHPDDGKLGS EGLLSGLRVMSVDLGLRTSASISVFRVARKDELKPNSKGRVPFFFPIKGNDNLVAVHERSQLLKL PGETESKDLRAIREERQRTLRQLRTQLAYLRLLVRCGSEDVGRRERSWAKLIEQPVDAANHMTP DWREAFENELQKLKSLHGICSDKEWMDAVYESVRRVWRHMGKQVRDWRKDVRSGERPKIR GYAKDVVGGNSIEQIEYLERQYKFLKSWSFFGKVSGQVIRAEKGSRFAITLREHIDHAKEDRLKK LADRIIMEALGYVYALDERGKGKWVAKYPPCQLILEELSEYQFNNDRPPSENNQLMQWSHR GVFQELINQAQVHDLLVGTMYAAFSSRFDARTGAPGIRCRRVPARCTQEHNPEPFPWWLNKF VVEHTLDACPLRADDLIPTGEGEIFVSPFSAEEGDFHQIHADLNAAQNLQQRLWSDFDISQIRL RCDWGEVDGELVLIPRLTGKRTADSYSNKVFYTNTGVTYYERERGKKRRKVFAQEKLSEEEAELL VEADEAREKSVVLMRDPSGIINRGNWTRQKEFWSMVNQRIEGYLVKQIRSRVPLQDSACENT GDI
130	Cas12	MSTQKNPFNQFTNLYELQKTLRFELRPVPETKKLLEKGEGKNLIQMDLEIDRLVEKEMKPMFNIL HEKFINESLGLVKLDCKKLKKLENLLAEADKLRKQIKEGRKNKNNISEVEKRLKIIIGDNSQGKNK NGEIAVLQDELRVLIVKAFNLTADKWKKELNNKETLLPEKKGKRKIKIKKSGPKILQEENVLAILAY FNPDKADIIKKFAGFFTYFSGFNQNRANYYTVKALATGVANRAINRNFLIFLANRKDFARFKERL PRLAEFDNYFELENYEKYLSQTGIEEYNDQIGKIKQIVNLEHNQQQKDNKFQLKGLATLEKQIG CRTKKQREEGGDKSAPKFLEKVGLGFQVSQDDDGEYLIWECLNYINKELAGKLKSIKDNYQKFF ADWRTGAYDLEKIWFRKEALNTISGRWFGGNNWFIIGKALALTGVGKFDKRENTYKIPEFVSLA EIKTAFEMLENGVNYDFKKSKKKKEGDDTDVVKYSADNLFKEEYKKKGLIKNSLFETMLAVWQ

[0136]

		SEIKRKFEQIFDGYKLEKDDVFGRKKGEWVEPFIENFQKVSQEKFDRGVKDENGRSIHTEVVKN LIEEGYLRLFQLTKYHNLDKKGERDPRPFDGNFYATLDEFWKDNIVVVYHKALQSTLTKKPYSED KIKLNFENGSLLGGFSDGQERSKAGVVLKNKNKFYLGILIDRGFFRTDKANPVYDNAQNNEWE RLILTNLKFQTLAGKGFLGKHGVSYGEMGKDNPMMAVEYLQKFIKLKYLDKYPALNEVAHKKY TIKKEFDADVKNALKDCFTMNFKPVDFGMIRQGLTESLFYLFEIVNKDISSQAKNGKNVHTLY WEALFGDQNLKKPILALNGGAEIFYRESQREKLEKKLDKSGKEVLDHKRYGQDKYFLHASITIN YGQPKNIKFKEVINEKISQNADRVNIIGIDRGEKHLLYYSVVSPEGVLLEQGSFNQIETKNKVDIK AVKAEYGERGELKKVELVPTGKKVKYVDYQILLDYYEKKRNLARRDWQTIGKIKDLKDGYLSQT VHRIYQLILKYNAVVAMEDLNVEFKAKRAAKVEKSVYKNFEMALAKKLNHLILKDRRADEIGG ALRAYQLTPAIPANDVGKFDKAKQWGIMFYVRANYTSTTDPLTGWRKHKYISNSEKIDNIQKFF SPGDGIQIDYDTEKQCFKFSYDHELEGGAKKHWELFACDGLERFYWDNRERQIKKYNLYEEFEK LLGGLRKEENINIQIDGVSEFRWKDLVFFWNLLNQIRNTDRSAQGDENDFLQSPVWSEKYNC FYDSRKAPNNMPNNGDANGAFNIARKGQLILERIKKCSDIPKFGNDNNGKNPENNYFISDAD WDKFAQK
131	Cas12	MAIRSIKLKLKTHTGPEAQNLRKGIWRTHRLLNEGVAYYMKMLLLFRQESTGERPKEELQEELIC HIREQQQRNQADKNTQALPLDKALEALRQLYELLVPSSVGQSGDAQIISRKFLSPLVDPNSEG GKGTSKAGAKPTWQKKKEANDPTWEQDYEKWKKRREEDPTASVITTLEEYGIRPIFPLYTNTVT DIAWLPLQSNQFVRTWDRDMLQQAIERLLSWESWNKRVQEEYAKLKEKMAQLNEQLEGGQ EWISLLEQYEENRERELRENMTAANDKYRITKRQMKGWNELYELWSTFPASASHEQYKEALKR VQQRLRGRFGDAHFFQYLMEEKNRLIWKGNPQRIHYFVARNELTKRLEEAKQSATMTLPNAR KHPLWVRFDARGGNLQDYYLTAEADKPRSRRFVTFSQLIWPSESGWMEKKDVEVELALSRQF YQQVKLLKNDKGKQKIEFKDKGSGSTFNGHLGGAKLQLERGDLEKEEKNFEDGEIGSVYLNVVI DFEPLQEVKNGRVQAPYGQVLQLIRRPNEFPKVTTYKSEQLVEWIKASPQHSAGVESLASGFR VMSIDLGLRAAAATSIFSVEESSDKNAADFSYWIEGTPLVAVHQRSYMLRLPGEQVEKQVMEK RDERFQLHQRVKFQIRVLAQIMRMANKQYGDRWDELDSLKQAVEQKKSPLDQTDRTFWEGI VCDLTKVLPRNEADWEQAVVQIHRKAEEYVGKAVQAWRKRFAADERKGIAGLSMWNIEELEG LRKLLISWSRRTRNPQEVNRFERGHTSHQRLLTHIQNVKEDRLKQLSHAIVMTALGYVYDERK QEWCAEYPACQVILFENLSQYRSNLDRSTKENSTLMKWAHRSIPKYVHMQAEPYGIQIGDVR AEYSSRFYAKTGTPGIRCKKVRGQDLQGRRFENLQKRLVNEQFLTEEQVKQLRPGDIVPDDSGE LFMTLTDGSGSKEVVFLQADINAAHNLQKRFWQRYNELFKVSCRVIVRDEEEYLVPKTKSVQA KLGKGLFVKKSDTAWKDVYVWDSQAKLKGKTTFTEESESPEQLEDFQEIIEEAEEAKGTYRTLFR DPSGVFFPESVWYPQKDFWGEVKRKLYGKLRERFLTKAR
132	Cas12	MRKKLFKGYILHNKRLVYTGKAAIRSIKYPLVAPNKTALNNLSEKIIYDYEHLFGPLNVASYARNS NRYSLVDFWIDSLRAGVIWQSKSTSLIDLISKLEGSKSPSEKIFEQIDFELKNKLDKEQFKDIILLNT GIRSSSNVRSLRGRFLKCFKEEFRDTEEVIACVDKWSKDLIVEGKSILVSKQFLYWEEEFGIKIFPHF KDNHDLPKLTFFVEPSLEFSPHLPLANCLERLKKFDISRESLLGLDNNFSAFSNYFNELFNLLSRG EIKKIVTAVLAVSKSWENEPELEKRLHFLSEKAKLLGYPKLTSSWADYRMIIGGKIKSWHSNYTEQ LIKVREDLKKHQIALDKLQEDLKKVVDSSLREQIEAQREALLPLLDTMLKEKDFSDDLELYRFILS DFKSLLNGSYQRYIQTEEERKEDRDVTKKYKDLYSNLRNIPRFFGESKKEQFNKFINKSLPTIDVG LKILEDIRNALETVSVRKPPSITEEYVTKQLEKLSRKYKINAFNSNRFKQITEQVLRKYNNGELPKI

[0137]

		SEVFYRYPRESHVAIRILPVKISNPRKDISYLLDKYQISPDWKNSNPGEVVDLIEIYKLTLGWLLSC NKDFSMDFSSYDLKLFPEAASLIKNFGSCLSGYYLSKMIFNCITSEIKGMITLYTRDKFVVRYVTQ MIGSNQKFPLLCLVGEKQTKNFSRNWGVLIEEKGDLGEEKNQEKCLIFKDKTDFAKAKEVEIFKN NIWRIRTSKYQIQFLNRLFKKTKEWDLMNLVLSEPSLVLEEEWGVSWDKDKLLPLLKKEKSCEE RLYYSLPLNLVPATDYKEQSAEIEQRNTYLGLDVGEFGVAYAVVRIVRDRIELLSWGFLKDPALRKI RERVQDMKKKQVMAVFSSSSTAVARVREMAIHSLRNQIHSIALAYKAKIIYEISISNFETGGNR MAKIYRSIKVSDVYRESGADTLVSEMIWGKKNKQMGNHISSYATSYTCCNCARTPFELVIDND KEYEKGGDEFIFNVGDEKKVRGFLQKSLLGKTIKGKEVLKSIKEYARPPIREVLLEGEDVEQLLKRR GNSYIYRCPFCGYKTDADIQAALNIACRGYISDNAKDAVKEGERKLDYILEVRKLWEKNGAVLR SAKFL
133	Cas12	MSTQKNPFNQFTNLYELQKTLRFELRPVPETKKLLEKGEGKNLIQMDLEIDRLYEKEMKPMFNIL HEKFINESLGLVKLDCKKLKKLENLLAEADKLRKQIKEGRKNKNNISEVEKRLKIIIGDNSQGKNK NGEIAVLQDELRVLIVKAFNLTADKWKKELNNKETLLPEKKGKRKIKIKKSGPKILQEENVLAILAY FNPDKADIIKKFAGFFTYFSGFNQNRANYYTVKALATGVANRAINRNFLIFLANRKDFARFKERL PRLAEFDNYFELENYEKYLSQTGIEEYNDQIGKIKQIVNLEHNQQQKDNKFQLKGLATLEKQIG CRTKKQREEGGDKSAPKFLEKVGLGFQVSQDDDGEYLIWECLNYINKELAGKLKSIKDNYQKFF ADWRTGAYDLEKIWFRKEALNTISGRWFGGNNWFIIGKALALTGVGKFDKRENTYKIPEFVSLA EIKTAFEMLENGVNYDFKKSKKKKEGDDTDVVKYSADNLFKEEYKKKGLIKNSLFETMLAVWQ SEIKRKFEQIFDGYKLEKDDVFGRKKGEWVEPFIENFQKVSQEKFDRGVKDENGRSIHTEVVKN LIEEGYLRLFQLTKYHNLDKKGERDPRPFDGNFYATLDEFWKDNIVVVYHKALQSTLTKKPYSED KIKLNFENGSLLGGFSDGQERSKAGVVLKNKNKFYLGILIDRGFFRTDKANPVYDNAQNNEWE RLILTNLKFQTLAGKGFLGKHGVSYGEMGKDNPMMAVEYLQKFIKLKYLDKYPALNEVAHKKY TIKKEFDADVKNALKDCFTMNFKPVDFGMIRQGLTESLFYLFEIVNKDISSQAKNGKNVHTLY WEALFGDQNLKKPILALNGGAEIFYRESQREKLEKKLDKSGKEVLDHKRYGQDKYFLHASITIN YGQPKNIKFKEVINEKISQNADRVNIIGIDRGEKHLLYYSVVSPEGVLLEQGSFNQIETKNKVDIK AVKAEYGERGELKKVELVPTGKKVKYVDYQILLDYYEKKRNLARRDWQTIGKIKDLKDGYLSQT VHRIYQLILKYNAVVAMEDLNVEFKAKRAAKVEKSVYKNFEMALAKKLNHLILKDRRADEIGG ALRAYQLTPAIPANDVGKFDKAKQWGIMFYVRANYTSTTDPLTGWRKHKYISNSEKIDNIQKFF SPGDGIQIDYDTEKQCFKFSYDHELEGGAKKHWELFACDGLERFYWDNRERQIKKYNLYEEFEK LLGGLRKEENINIQIDGVSEFRWKDLVFFWNLLNQIRNTDRSAQGDENDFLQSPVWSEKYNC FYDSRKAPNNMPNNGDANGAFNIARKGQLILERIKKCSDIPKFGNDNNGKNPENNYFISDAD WDKFAQK
134	Cas12	MAQASSTPAVSPRPRPRYREERTLVRKLLPRPGQSKQEFRENVKKLRKAFLQFNADVSGVCQW AIQFRPRYGKPAEPTETFWKFFLEPETSLPPNDSRSPEFRRLQAFEAAAGINGAAALDDPAFTNE LRDSILAVASRPKTKEAQRLFSRLKDYQPAHRMILAKVAAEWIESRYRRAHQNWERNYEEWKK EKQEWEQNHPELTPEIREAFNQIFQQLEVKEKRVRICPAARLLQNKDNCQYAGKNKHSVLCN QFNEFKKNHLQGKAIKFFYKDAEKYLRCGLQSLKPNVQGPFREDWNKYLRYMNLKEETLRGK NGGRLPHCKNLGQECEFNPHTALCKQYQQQLSSRPDLVQHDELYRKWRREYWREPRKPVFR YPSVKRHSIAKIFGENYFQADFKNSVVGLRLDSMPAGQYLEFAFAPWPRNYRPQPGETEISSVH LHFVGTRPRIGFRFRVPHKRSRFDCTQEELDELRSRTFPRKAQDQKFLEAARKRLLETFPGNAE

[0138]

		QELRLLAVDLGTDSARAAFFIGKTFQQAFPLKIVKIEKLYEQWPNQKQAGDRRDASSKQPRPGL SRDHVGRHLQKMRAQASEIAQKRQELTGTPAPETTTDQAAKKATLQPFDLRGLTVHTARMIR DWARLNARQIIQLAEENQVDLIVLESLRGFRPPGYENLDQEKKRRVAFFAHGRIRRKVTEKAVE RGMRVVTVPYLASSKVCAECRKKQKDNKQWEKNKKRGLFKCEGCGSQAQVDENAARVLGR VFWGEIELPTAIP
135	Cas12	MAVRSVKLKLLVPRDGSAESVRKRKALWATHQFVNDAAAAYAELLLEMRQEDVCRGTDDHG KDVIEPAAHWQAKLRARLAAKQLPPVAVAEALPLLKAFYGSRLIKSFVANDKGVAGTGNATDL NTWLSGLVDPASVAGEKTELRKQLLAELPLCEAADADFEGAARKMLAKSDAREALLEGPGTGV GWPAAYNANPTDSVWLDMLHKAAAKARLELADTTVSELKKLGVFPLLQAASSNRVFGSGVL NPFERMAAAQAAAALLPWETKRHEMRKRRDKFADQLNQWDTEFGASHATALAAIRAFEAEE SERARRESLGNEGTGYRIGGRELRDAWTLLRDWLKGHSTATAAAREDKVRELQAKQGRSFGSH RLLSWLAKPAQQWLADHSAGDVVTRIAVRNARQRKLDTARTLPIWTGADAVKHPRFANFDP PNNTNQPGFDLRAGTQKGRLTLRLSLLTERADGLLLAQDHDFQLVPSRQMAEIVLHKDGKER ALSWQSQDGIGRQVGDVGGSALLFSRDHAECLLERKQITRLERGAWPAALPVWFKLSLDIGAE HKALLKQRFKWGVWLNSALVTRNAKDAKGVPPPVGTRVLAVDLGLRSAATVSVWQVVDAAT PVVAGKWRVPLSDTLSAVHERSAMLALPGEHVDAGVLAARRAANEKLAGLLAATSHLSTVFK LGRAEQGDRRRELLERLGEGDDRRARAAVATTAAERDGLRAVLGATQDAWAGAVAAVWRRL ETDLAGAIAAYRKQQREDVQLRREARHGPGASQLPKQAAAERLLGGKSAWQIEYKERVRKLLT RWIMRQRPGDTAVRRLARKDLGKYCGGLLDHLTALKEDRAKTTADLIVQAARGRVRAHKDAH GRQQDRELWLAKYAPCDLIVMEDLGRYRFATDRPPSENRQLMQWTHREVFRLVQMQAEVE GIQVLETGAEFSSKFDARTWAPGVRCEPITKLWVERYRNGEMPWLADKADEWRREGIELAQL VPGQLLPTGSGEQFVAVSATGGLRVRHADLNAAQCIALRALTGHGTAFRLTARRLGDVFVSAK GLGKRPQGALWREFGSALPPAVVVLRPAGEVRYALRPFASARDAAAALGLQLGALRNVDATD AESDAEDGDLAELLAGADPDRATFFRDPSGDVHGGAWVQAKVFWAEVRRHVRLGLQAQGL LPAAARSSEPRQMQLPLAGALPGDDIPL
136	Cas12	MNRIYQGRVSKIEIKDSEGNFRNVPVGSPDTCPLWRHHRIFQDAVNYYLVALGALAGTGSENA FVGLGSKDRVIHDLYSRLFDSWERFPRDMHGASSLRDSLRRTLPGLSERASLQDAFDAILSGNE ANARERVLSLLSLIQDLGGDIQKGSKRYFPFFCEPATKATFPRARVGLLKVEGKDFVPRLLWSSD LEIAPDQVVEQLKFEYFANPNESVQPIEGNEARVRLIEALDNPQLGIELPIEILSDLRKRVHLIETDI RIPRYFFGGAGAELRKFRLDLFLIAAYVTPDPSILRALRNSFKEPSASKSSKKKDETEEVENLLRSL GDDPLILARGERGFVFPSFTSLPTWVGANAQKPIWRDFDIAAFAEALKSLNQFTAKTEEREEKL KKAEETLHYMLGISDAIPRSSDSETEEQAPSRPGKDPRWPLVAQLEKELGENLSEGTWQLSRSA MRGLRDIIGLWRKHPGASVVTLQKDVKTYQADEKHKREIGSVQLFLLLCEERYHALWQTETDD ERGDESEENDDPARILSDAIEVHQIRREVERFREPIRLTPAEPVFSRRLFMFSDLTDKLAKVKFGET TEENSEVKSQFVEAAIALKEGENLKEARVRITFSAPRLHRDELLGGAESRWLQPITAALGFSNPA PSVKFDSAVALMPDHMDDGRIRHLLNFPVNFDSAWLHQSIGKADLWKSQFNGTKDKNLHL HWAGTARDTTRKNTWWENRTIIENGFTVLSNDLGQRSAGAWALLKVTCSRPDTKHPVRSIGH DGTREWFATVLATGIHRLPGEDQRILKNGKWATEQSGKKGRNATFSEYEAACVLAKNLGCESV ENWLGMSGEKSYPALNDQLVKIANRRITRLGTYHRWSCFSPEKFEDPARRANVIGGQLAELSA YQDENVTVSADILKSGDFEGFRHRAGAAFEALRTELEVHLVNLANLTAPLRQKVWSWQKRPD

[0139]

		SSGYGDLLMVDLDDCHPKIRGQRGLSMARLEQLEGLRRLFLRYNRSLDRSPGIPAKFGREDVG RTSGEPCQALLVKIDRMKEQRVNQTAHLILAQALGVRLCPHRIEENERKSRDLHGEYEKIPGRE PVDFIVIEDLSRYLSSQGRAPSENSRLMKWAHRAVRDKLKMLAEEPFGIPVVETVPAYSSRFHA LNGQAGSRLHELHELEAYQQQSLINLAAKTDFQNRDRSKAAGELFEQFQALAKLNERRRAEG KKVPRTLYYPKSGGPLFLASRDGDTIHADVNAAINLGLRAIAAPACIDIHRRLRATKEKEVYRPRV GNAREKSAFSKDDIIQPSGAPSKKFASSSSPNFFYEPEDLKQANGEPLFDRAMFGEYSLVSGVSL WSMVNNAIYIRCVELNRTRLHGKDPDDQIPM
137	Cas12	MADDLSTQRAYTLRLQGTDPEDQSWRDALWMTHEAVNAGGRAFGDWLLTLRGGIAHELAD TPVKGKKDITDELRKKRRILLALSWLSVESRRGAPDKFIVAGGEEPAGSRNEKVLQALKEILKRRG LSAEESESWMSDCRASLSAAIRDDAVWVNRSAAFDDAQVRIGASLTREDIWDMLDPFFGSRE AYLTPAKKKKEDEDSSEGTGEEKAKDLVQKAGQWLSSRFGTGKGANFDAMAEVYSKISEWAGT AQEGVSGKEGIKNLADALAAFSPVSQNLEGVLKLISGPGYKSATRNLLGELDSLPVVSRDHLSA LHEKAAEDTVKCKESTGTKGRRPYADAILNDVEKRCGFTYLTDSDNRSVSILDTSEFPSDYKWGT ARHSEFAVILDHAARRISVAHSWIKLAEAERDRCEEDAAKVYDLPDKVKEWLDTFCSNRSDISG AQGEGYRIRRKAIEGWKEVVASWGRSSCITAEDRVAAARALQDDPEIDKFGDIQLFEILAQDEA LCVWHKDGDVAKSPDAQMLIDYVLASDAESKKRRFKVPAYRHPDALLHPIFCDFGNSRWDIT YDIHGARGKKKAKRGSKKEEAMPRGVAMKLWTGSDVLSVSLRWQSKKLAADLALDQEAEEV TDTAAVSRADRLGRAAAGIDRGAGVTIAGLFEEAHWNGRLQAPRQQLEAIAAVRDNQKLSSE ERERRIAFMKDRIRWLVTFSAKLRPQGPWHSYAPTQGLQSDPKYWPHSEINKKRKGQAKLILS RLPGLRILSVDLGHRFAAACAVWETMSSEAIQEACRLANHQLPAPADLYLHLKRTVQKNLIDGE KTVEESTVYRRIGADRLPDGTAHPAPWARLDRQFLIKLQGEEKVREASNEEVWQVHLMESALG LSFPLIDRLVYAGWGGTEKQAARLEALREKGWKPTGTPADQDEEGGGYKPSLAVDELMFSAVR TLRLALKYHGDRARIAFALTADYKPMPGDTRYYFSEAKDRSSGADAAEREAKHKDYLLDMLLL WHDLAFSRKWRDEEAKELWNLHIAALPGYQAPAAPIQEEAGQGRKKAREEARAKMTPAAEA LLADGTLREKLHGLWKERWEKDDAQWKKHLRWMKDGILPRGGRAATPSIRYVGGLSLTRLAT LTEFRRKVQVGFYTRLFPSGEKREIKEAFGQTALDALERLREQRVKQLASRIAEAALGAGRVSRT ALKQDPKRPEARVDAACHAVIIENLEHYRPEETRTRRENRGLMNWASSKVKKYLSEACQLHGL FLREVPAGYTSRQDSRTGAPGMRCQDVTVKTFLNSPFWQKQCVQAQKNKSTARDRFLCALK EAVAQGGMEEEKKMGPIRVPVPGGEVFVSADAASPAAKGLQADLNAAANIGLRALLDPDWP GKWWYYVPCDRKTAYPAKEKVEGSAAVDVKQALPFVLPEEKENKGKTKGGKKGKGEVMNLWR DVSAEPLMTGQWLDYTAYRKEVENRVIQVLTAQLKARNPLRFGNLGDEEEIPY
138	Cas12	MAIRSIKLKLKTHTGPEAQNLRKGIWRTHRLLNEGVAYYMKMLLLFRQESTGERPKEELQEELIC HIREQQQRNQADKNTQALPLDKALEALRQLYELLVPSSVGQSGDAQIISRKFLSPLVDPNSEG GKGTSKAGAKPTWQKKKEANDPTWEQDYEKWKKRREEDPTASVITTLEEYGIRPIFPLYTNTVT DIAWLPLQSNQFVRTWDRDMLQQAIERLLSWESWNKRVQEEYAKLKEKMAQLNEQLEGGQ EWISLLEQYEENRERELRENMTAANDKYRITKRQMKGWNELYELWSTFPASASHEQYKEALKR VQQRLRGRFGDAHFFQYLMEEKNRLIWKGNPQRIHYFVARNELTKRLEEAKQSATMTLPNAR KHPLWVRFDARGGNLQDYYLTAEADKPRSRRFVTFSQLIWPSESGWMEKKDVEVELALSRQF YQQVKLLKNDKGKQKIEFKDKGSGSTFNGHLGGAKLQLERGDLEKEEKNFEDGEIGSVYLNVVI DFEPLQEVKNGRVQAPYGQVLQLIRRPNEFPKVTTYKSEQLVEWIKASPQHSAGVESLASGFR

[0140]

		VMSIDLGLRAAAATSIFSVEESSDKNAADFSYWIEGTPLVAVHQRSYMLRLPGEQVEKQVMEK RDERFQLHQRVKFQIRVLAQIMRMANKQYGDRWDELDSLKQAVEQKKSPLDQTDRTFWEGI VCDLTKVLPRNEADWEQAVVQIHRKAEEYVGKAVQAWRKRFAADERKGIAGLSMWNIEELEG LRKLLISWSRRTRNPQEVNRFERGHTSHQRLLTHIQNVKEDRLKQLSHAIVMTALGYVYDERK QEWCAEYPACQVILFENLSQYRSNLDRSTKENSTLMKWAHRSIPKYVHMQAEPYGIQIGDVR AEYSSRFYAKTGTPGIRCKKVRGQDLQGRRFENLQKRLVNEQFLTEEQVKQLRPGDIVPDDSGE LFMTLTDGSGSKEVVFLQADINAAHNLQKRFWQRYNELFKVSCRVIVRDEEEYLVPKTKSVQA KLGKGLFVKKSDTAWKDVYVWDSQAKLKGKTTFTEESESPEQLEDFQEIIEEAEEAKGTYRTLFR DPSGVFFPESVWYPQKDFWGEVKRKLYGKLRERFLTKAR
139	Cas12	MPVRSINLKIVISRNTQGEKSRQSIWTTHAAVNDAVRYYEEQLLIMRGLGYHISDKDVVSKESI QQERLSRIRRAQLENGLPEPLGTDAELNSLVRKFYEFIVPSSVKEDGNAQQANGFLSPLTDPISI GYLSIFEKLGTIPDWVGQLKAGDPQAVENAKKWSATSAGIKRLSETGAPPKWKKLFLTGDPSW PQSFSEDIDKKIKEIEGAPKVICQLMEMGVLPLFPAYFADKLEGSDGSLSRWDRLAFRLAVGHM LSWESWCIKSAEDHFERKRRVESFSEKHTTPSLIICFETLEKYQKERQEKELGQNRSLPMQRPFRI TRRQIRGWEDLRDKWLKNTTRTYDSLKSIASKEQTKKGGRFGDPHLFLWLAKPENHAVWDA DEDALSIFAKMNAMRGLLERSRETAYMTLPDPIEHPRSIQWEAEGGSNFKNYVITHSPVEGLH VQLPLLCKSESGKLIDQTFEFPLAPSDQFKVAQISKTKSEVTITHQSVLDEEYRSKVGAADLLMD WPYLKNRRFESVEHGDIGPVFLKLSLDIERILPDGWTPKRPQAISHFSSASGNSKHKLSVVSGLR VLSVDLGIRSFGACSVFELSEHKPTSGMSFEIEGLNLWANHERSFMLNLPDEDVGNKGRQLQK TKDAELRAMRRVLGRYRKIYALAGIDPEDRKDILELLCQDQDIFEFERTIYKGLVTSTSVSQPLWE GKIKESLKALRNAFGRKVREWRRANRLNSNLKYAGKTMWAIQHLEDTRRFLHSWSHLGRFSG EIRRADRVKRGVFATRLLQHLDSVKRDRLKTGADLLVQSARGFLRDNQGNWKKSYAPCQVILF EDLSRYLMQTDRPRRENSQLMKWSHRSIPLEVAMQGELYGIHVCDTSAAFSSRYHARLATPGI RCHALRKEDLSNQFLIESLQKENPDIDFGICKAGDLIPRGGGEIFVSCDGNGGISRIHADINAAQ NLQRRFWLRHGEAIRIPARKITLKGDEIWVPRSIGKRLQGAMSGCGYLIPTGHESGSCRWERITA SKWESISRSSVAQKEEVNEDLLDIALLEEEALELSNEYTTFFRDPSGITLPSDLWFPMKTFWGMT RAKIKSAIKQ
140	Cas12	MTVKSIKVKLRLDNMPEIRAGLWKLHTEVNAGVRYYTEWLSLLRQENLYRRSPNGDGEQECY KTAEECKVELLERLRARQVENGHRDPAGSDDELLQLARQLYELLVPQAIGAKGDAQQIARKFLS PLADKDAVGGLGIAKAGNKPRWVRMRDAGEPGWEEEKAKAEARKSTDRTADVLRALADFGL KPLMRVYTDSDMSSVQWKPLRKGQAVRTWDRDMFQQAIERMMSWESWNQRVGEAYAKL VEQKSRFEQKNFVGQEHLVQLVNQLQQDMKEASHGLESKEQTAHYLTGRALRGSDKVFEKW EKLDPDAPFDLYDTEIKNVQRRNTRRFGSHDLFAKLAEPKYQALWREDASFLTRYAAYNSILRKL NHAKMFATFTLPDATAHPIWTRFDKLGGNLHQYTFLFNEFGEGRHAIRFQKLLTIEHGVAKEVD DVTVPISMSAQLDDLLPGESNEPTELSFRDHGTDQHFTGEFGGAKIQYRRDQLDHVHRRRGA RDVYLNLSVRVQSQSEARGERRPPYAAVFRLVGDTHRAFAHFDKLSNYLAEHPDDGKLGSEGL LSGLRVMSVDLGLRTSASISIFRVARKDELKPNSEGRVPFFFPIKGNDNLVAVHERSQLLKLPGET ESKDLRAIREERQRILRQLRTQLAYLRLLVRCGSEDVGRRERSWAKLIEQSVDAANHMTPDWR EAFEGELQKLKSLYGICGDREWTEAVYESVRRVWRHMGKQVRDWRKDVRSGERPKIRGYQK DVVGGNSIEQIEYLERQYKFLKSWSFFGKVSGQVIRAEKGSRFATTLREHIDHAKEDRLKKLADR

[0141]

		IIMEALGYVYALDAERGKGTWVAKYPPCQLILEELSEYRFNNDRPPSENNQLMQWSHRGVF QELLNQAQVHDLLVGTMYAAFSSRFDARTGAPGIRCRRVPARCAREQNPEPFPWWLNKFVA EHKLDGCPLRADDLIPTGEGEFFVSPFSAEEGDFHQIHADLNAAQNLQRRLWSDFDISQIRLRC DWGEVDGEPVLIPRLTGKRTADSYGNKVFYTNTGVTYYERERGKKRRKAFAQEELSEEEAELLVE ADEAREKSVVLMRDPSGIINRGDWTRQKEFWSMVNQRIEGYLVKQIRSRVCLPESACENTGDI
141	Cas12	MKNFQDFTNLYELSKTLRFELKPIGGTKKLIEEKNILKLDKKKRENYEKVKPYFNKIHQEFINFALR NPNFDFSQFEEKYLNWLKDKKNKDLLKEKESIDKIFLEKIGKLFENSVKDFLKENGFESIVKEEDQ NLKFFRRKEIFEVLQEKYGSELETQMVNKDGEIKSIFNGWEKWLGYFDKFFNTRDNFYKTDGTS TAIATRIIKDNLKIFLENIVAFGKIKNKKIDFSEVEKNFSVSIDTFFEINNFNNCFLQDGIDFYNKVI GGETLENGEKLKGLNEIINKYRQDTGEKIPYFKKLQKQILSEKDGVFIDKIEDDGGFYEVLKNFYK NAAEKEGFLKNIFENFYTISDKNLEKIYFNKIAFNTISHKFGSALEFERILYEEMKKEKADGIKFEKK ENKYKFPDFIQIIFIKRSLENYDSENLFWKERYYKSEENVDGFLEKNNNNLWGQFCKILNFEFLN ILKRRIIDEAGEEYEVGFEISKNILGEKLENFELNQENKGIIKDFADYSLALYSFGKYFAVEKGRNW DLNIDISDDFYGGEDGYIEKFYNTGYDEIVKPYNLMRNYISKKPWEDNKKWKINFETSSLLSGW DKNLESNGSYIFQKGNKYYLGIINGSKPAKEILEKLYSGDGEKIKRFIYDFQKPDNKNTPRMFIRS KKDSFSPAVEKYNLPINDILEIYDNGLFKTENKGNPNYKESLRKLIDYFKLGFSRHESFKHFNFVW KDSKSYENIADFYRDVEKSCYKIDFEFLNFEELKKLTFEKHLYLFQIYNKDFELDESLQEKGYNFKG EGQKNIHTKYFEALFLEENISRKSGAVFKLSGGGEVFFRKKSIKAKKEKRNSVEVIKNKRYTECKY FLHFPIQVNFKEEISGNFNQEINKFLANNPDINVIGIDRGEKHLAYFSVINQKGEILESGSFNKIE NYNKNGEKLLFPEREIKEIHKDGSLIDLELVETGRKVDYVDYKLLLEYKERKRLLQRQSWKEVEQI KDLKKGYISALVRKIADLIIKHNAIVIFEDLNFRFKQIRGGIEKSIYQQLEKALIDKLNFLVNKNEINL EKAGSILKAYQLTVPVDSLKEIGKQTGVIFYTEAAYTSKIDPITGWRPNLYLKKNNSKINKENILKF DNIVFNSKENRFEFTYDLKKFFGKDSKFPAKTVNTVCSCVERFKWNRNLNNNKGGYIHYENLT DGKLANKEQKEDEFSNFKELFEKYFIDINGNILEQIKNLDTKNNEKFFSSFIDLFTLVCQIRNTNQ NAKGDENDFILSPVEPFFDSRKSQNFGKSLPKNGDENGAFNIARKGLIILNRISENPEKPDLLIF NADWDNFARNI
142	Cas12	MAQAEAPRRLRAYKFALDPTEAQLREFEQHAGSARWAYNHANAILSRYSDTLRNRWNAWIA QHHGLSREQLYALPDRERTAIQAAARAAVKAENAQLAAELRIIDDHRKRVTHKGKPSVEPGEQ PAEDAPERAYQLWRERVELARLHAEDPQAYRAERKRILDEIRPLVNATKRKLIEQGAYRPTAMDI STLWREIRDLPPDEGGSPWWPEVSIYAFTSGFAHAETAWKNYLESLAGRRAGRPVGKPRFKKK RRSRRSFTLYGSVKLVTYRRIQVPSIGSVRLHGSAKRLHRALERRGGIIKSITISQGGHRWYASVL VDELDITPGRETQRGPSRRQRDRGAVGVDLGVHHLVALSDPNEKTLDNPRHLRKARKRLLKA QRAMSRRRGPDKRTGQEPSRRWVKARNRVARLHHELAVRRAGHLHEITKRLATSYELVAIEDL NVAGMTRSARGTIDQPGRGVRAKAGLNRSILDTSPAEFRRQLQYKASWYGATVAVIDRWAPT SRTCSSCGAVKAKLSLAERTFFCEHCGMELDRDINAARNILAFAQSAYPGEGKALNACGGSVS PGSQSVVQAGADEAGRPARKPRRSSRGSDPPATPTTRA
143	Cas12	MKRIAKFRHDKPVKREAWSKGYRVHKNRIINKVTRSIKYPLVVKDEWKKRLIDDAAHDYRWLV

[0142]

		GPINYSDWCRDPNQYSILEFWIDFLCVGGVFQSSHSNICRLAIQLSGGSVFEQEWKDLSPFVR ANLIQGIKPAEFIGFLTAEFRSSSNPKNFISKFFEGSNEDLESLTNEFASIVDFIKAKDISLLRKSLPS CKKIAPNLWEKAVGSHSTNELLKLLTKYTRVMLVAEPSHSDRVFSQTVLQSNDQDDPELTGPLP SHKVGKASYLFIPEFIREVNLDKISKLDLSAKSKLAVEQVKKLSELTSDFKQIENQSEAYFGLSTSF NELSNFLGILIRTLRNAPEAILKDQIALCAPLDKDILKITLDWLCDRAQALPENPRFETNWAEYRS YLGGKIKSWFSNYENFFEIPQAASSQQNNNREKKLGNRSAIRALNLKKEAFEKARETFKGDKGT LEKIDLAYRLLGSISPEVLQCDEGLKLYQQFNDELLVLNETINQKFQDAKRDIKAKKEKESFEKLQ RNLSSPLPRIPEFFGERAKKGYQKARVSPKLARHLLECLNDWLARFAKVEESAFSEKEFQRILDW LRTSDFLPVFIRKSKDPPSWLRYIARVATGKYYFWVSEYSRKRVQIIDKPIAQNPLKELISWFLLN KDAFSRDNELFKGLSSKMVTLARIMAGILRDRGEGLKELQAMTSKLDNIGLLHPSFSVPVTDSL KDAAFYRAFFSELEGLLNIGRSRLIIERITLQSQQSKNKKTRRPLMPEPFINEDKEVFLAFPKFETK NKVKGTRVVYNSPDEVNWLLSPIRSSKGQLSFMFRCLSEDAKIMTTSGGCSYIVEFKKLLEAQE EVLSIHDCDIIPRAFVSIPFTLERESEETKPDWKPNRFMGVDIGEYAVAYCVIEKGTDSIEILDCGIV RNGAHRVLKEKVDRLKRRQRSMTFGAMDTSIAAARESLVGNYRNRLHAIALKHGAKLVYEYE VSAFESGGNRIKKVYETLKKSDCTGETEADKNARKHIWGETNAVGDQIGAGWTSQTCAKCGR SFGADLKAGNFGVAVPVPEKVEDSKGHYAYHEFPFEDGLKVRGFLKPNKIISDQKELAKAVHAY MRPPLVALGKRKLPKNARYRRGNSSLFRCPFSDCGFTADADIQAAYNIAVKQLYKPKKGYPKER KWQDFVILKPKEPSKLFDKQFYRPN
144	Cas12	MAQAEAPRRLRAYKFALDPTEAQLREFEQHAGSARWAYNHANAILSRYSDTLRNRWNAWIA QHHGLSREQLYALPDRERTAIQAAARAAVKAENAQLAAELRIIDDHRKRVTHKGKPSVEPGEQ PAEDAPERAYQLWRERVELARLHAEDPQAYRAERKRILDEIRPLVNATKRKLIEQGAYRPTAMDI STLWREIRDLPPDEGGSPWWPEVSIYAFTSGFAHAETAWKNYLESLAGRRAGRPVGKPRFKKK RRSRRSFTLYGSVKLVTYRRIQVPSIGSVRLHGSAKRLHRALERRGGIIKSITISQGGHRWYASVL VDELDITPGRETQRGPSRRQRDRGAVGVDLGVHHLVALSDPNEKTLDNPRHLRKARKRLLKA QRAMSRRRGPDKRTGQEPSRRWVKARNRVARLHHELAVRRAGHLHEITKRLATSYELVAIEDL NVAGMTRSARGTIDQPGRGVRAKAGLNRSILDTSPAEFRRQLQYKASWYGATVAVIDRWAPT SRTCSSCGAVKAKLSLAERTFFCEHCGMELDRDINAARNILAFAQSAYPGEGKALNACGGSVS PGSQSVVQAGADEAGRPARKPRRSSRGSDPPATPTTRA
145	Cas12	MAIRSIKLKLKTHTGPEAQNLRKGIWRTHRLLNEGVAYYMKMLLLFRQESTGERPKEELQEELIC HIREQQQRNQADKNTQALPLDKALEALRQLYELLVPSSVGQSGDAQIISRKFLSPLVDPNSEG GKGTSKAGAKPTWQKKKEANDPTWEQDYEKWKKRREEDPTASVITTLEEYGIRPIFPLYTNTVT DIAWLPLQSNQFVRTWDRDMLQQAIERLLSWESWNKRVQEEYAKLKEKMAQLNEQLEGGQ EWISLLEQYEENRERELRENMTAANDKYRITKRQMKGWNELYELWSTFPASASHEQYKEALKR VQQRLRGRFGDAHFFQYLMEEKNRLIWKGNPQRIHYFVARNELTKRLEEAKQSATMTLPNAR KHPLWVRFDARGGNLQDYYLTAEADKPRSRRFVTFSQLIWPSESGWMEKKDVEVELALSRQF YQQVKLLKNDKGKQKIEFKDKGSGSTFNGHLGGAKLQLERGDLEKEEKNFEDGEIGSVYLNVVI DFEPLQEVKNGRVQAPYGQVLQLIRRPNEFPKVTTYKSEQLVEWIKASPQHSAGVESLASGFR VMSIDLGLRAAAATSIFSVEESSDKNAADFSYWIEGTPLVAVHQRSYMLRLPGEQVEKQVMEK RDERFQLHQRVKFQIRVLAQIMRMANKQYGDRWDELDSLKQAVEQKKSPLDQTDRTFWEGI VCDLTKVLPRNEADWEQAVVQIHRKAEEYVGKAVQAWRKRFAADERKGIAGLSMWNIEELEG

[0143]

		LRKLLISWSRRTRNPQEVNRFERGHTSHQRLLTHIQNVKEDRLKQLSHAIVMTALGYVYDERK QEWCAEYPACQVILFENLSQYRSNLDRSTKENSTLMKWAHRSIPKYVHMQAEPYGIQIGDVR AEYSSRFYAKTGTPGIRCKKVRGQDLQGRRFENLQKRLVNEQFLTEEQVKQLRPGDIVPDDSGE LFMTLTDGSGSKEVVFLQADINAAHNLQKRFWQRYNELFKVSCRVIVRDEEEYLVPKTKSVQA KLGKGLFVKKSDTAWKDVYVWDSQAKLKGKTTFTEESESPEQLEDFQEIIEEAEEAKGTYRTLFR DPSGVFFPESVWYPQKDFWGEVKRKLYGKLRERFLTKAR
146	Cas12	MVVRSIKLKMKTNSGTDSIYLRKALWRTHRLINEGIVYYMSLLTLYRQDTLGDRTKEEIQSELIKK IREQQRNNGLSEELGSDQEILSLLRHLYELIIPSINGESGDANQLGNKFLYPLVDPNSQSGKGTS NAGRKSKWKRMKEEGNPDWEVEFKKDEERKANDPTIKVFDHLKKYSLLPLFPLFTNNQKDIE WLPMGKRQSVRKWDKDMFIQAIERLLSWESWNRRLGAEREKLEEKIENFYKEHLSGGQIWIE KIREFERVRDRELGETSFSSNDGYLITSRQIRGWDRVYEKWSKISESASKEELWRVVAEQQSKM REGFGDPKVFSFLAELENMDIWRKHPERIYHIATYNGLLKKLSHTKAQATFTLPDAVKHPLWIR YEAQGGTNLNLFKLEETTKKNCKVILSKIIWPTEDGWFEKENVEVDLAPSKQFYRQIKLQDHIK GKQEISFSDYSSGISLKGVLGGSRIQFDRKYIENHQELLPSGDIGPVFFNLVIDLLPIQETRNGRLK SPIGKTLKVVSSEFPKVIDYKPKELTEWINVSSVTGKVGVESITEGMRVMSIDLGQRTSASVSIFE VVKELPKDKEKMLYYNIKDTELFALHKRSFLLNLPGEEVTKRNRQKRKDRRKKLLFIRSQIRMLA SVLKLETKNTPDERKKAINKLVEIVDSYEWTESEKEIWNSEFEYLTNKAVFKQEIWRESLIKSHHR MEPHVGQLVSEWRKSLNEGRRNLAGITMWNIEELEDTRRLLISWSKRSRTPGEANRINNDEPF GAKLLEHIQNVKDDRLKQLANLIVMTALGYKYDKEEKSRDKRWKEKYPACQVILFENLNRYLFS LDRSKRENSKLMKWAHRSIPRTVWMQGEMFGLQVGDVRSEYSSRFHAKSGAPGIRCHSLND EDLKEESFKLKHLIETGFISEEEISSLKKGDIVPWPGGELFVTLSKPYKKGKDIELTVIHADINAAQN LQKRFWQQNSEVYRIPCQLEKAGDDEFFIPKSQTEIVKKYFGKGRFVKINDKKEVYNWEESEK MKIKTESTITLQDLEGFEDIFQTLELAQEQQKKYSTLFRDPSGYFFNEKNWRPQKEFWSIVNNII RSSLKKKILKNKVEV
147	Cas12	MSNPNIPNISPNITLTRDDVVNLLMSSIAMEELGLAHIINAEGEKIQFALGTLQGASGPPATLQQ VLEVNQSTQAMLDTIFRQEMMLDSKLKTATNIPTLRGPTGPVGPTGAPGGVISINGQTGVVTL DASNGVMPFMREQSTSSLDDYKDPGIYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX

		ENPDVLDLALQELLDECDGDGAIQQEGRSMLPRFCSPSYKGDFPQSAAAKDKKSAKEWLPTF LHSAENASNLKLVRQRLKFELFANRDLTGRILDAVESRKRLTEMLGWLTERNPSLAAERERLQKII AALPDTFNLPAWRGGSVNKEALKQRFYAWLIFEHVESSRITFDILRDSFPTPKEKRKSVSETIQSE KPSLELSDDPIKLARGTRGYVFRAFTSLPCWGADNANLLAWKEFDVAAFKEALKALHQVESKS EERNKERERLLQRHSVMRGSIKWKPSPESEEKEPDVLAGDPRIERLEKLLKTELASEYEMSEGQT VEYGLQPRTIRGFRDLRKEWNKIVKPGEPFTEQKKGNLVTALRSYQIENPNVIGSVRLYEALLEK GNWLVWQEADSATVEKWAKQKFASDPLEALTEERQLLRDIERLKQPIRFTPADAVHSRRQFYL AEKGDLSVKNRFDPQNQTLQVPIAIKNDDHWKQQFVKIHFSAPRAVRDQLIDETMEESKEAR WQQPMMEALGLSLKLTKNNAEVSLSECTAVSLMPEELASGDRRILLNFPITLETAPMVKALGKA SLWDGQFAAYGDDNFYLRWPKDKWPAEKESNAWYRRLTEFSLLSVDLGQRDAGAFAVIGATT GKPTRPASRFIGEANGQSWHASVRATGVLRLPGEDAHVFRSGQWQEELYGERGRSADATEW TEAKRICETLGLKFDEILGGDPQWFSFPELNDRLLFAVRRAQTRLARLQSWSWMIADETRRENI REAILAADDDELSLKAAAEKSLWPVLAEKLASEVNRLRNLIPQQLVLLANRILPLRGRRWEWIK RDDTSGCHVLRETNPGTDTTSKKVCGQRGLSMKRLEQLDELRRRFQSLNRALMQTPGQTAGL GKSKRGIELPDPCPDLLDKTEQLREQRVNQTAHLILAQALGVRLRTPQKGDALREQNNVHGEY ETFRLPVDFIVLEDLSRYLSSQGRGRNENSRLMKWCHRAILLKLKQLCESYGLKILETNAAYSSRF CSRTGVAGFRAVELTPDARKEFRWRKHLNRLEKAASGEIKLDREARAESEHVKRLFDMLDQLN AGRKEAGKPLRTLLAPIAGGQIFIPMQGHATQADINAAINLGLRAIAAPDCHAIHVRIRTERKDK TLRVRTGSNREKVRWEGKNPEIQMNKAADLASLTGDRQPNFFPDPSAIACYDRAKIEGVQLPF ASGRGLWGTMNIELQWTRVNQLNNDRAEKKWNLTRSLPEQSSEEDYIPM
149	Cas12	MAVKSIKVKLMLGHLPEIREGLWHLHEAVNLGVRYYTEWLALLRQGNLYRRGKDGAQECYMT AEQCRQELLVRLRDRQKRNGHTGDPGTDEELLGVARRLYELLVPQSVGKKGQAQMLASGFLS PLADPKSEGGKGTSKSGRKPAWMGMKEAGDSRWVEAKARYEANKAKDPTKQVIASLEMVGL RPLFDVFTETYKTIRWMPLGKHQGVRAWDRDMFQQSLERLMSWESWNERVGAEFARLVDR RDRFREKHFTGQEHLVALAQRLEQEMKEASPGFESKSSQAHRITKRALRGADGIIDDWLKLSE GEPVDRFDEILRKRQAQNPRRFGSHDLFLKLAEPVFQPLWREDPSFLSRWASYNEVLNKLEDA KQFATFTLPSPCSNPVWARFENAEGTNIFKYDFLFDHFGKGRHGVRFQRMIVMRDGVPTEVE GIVVPIAPSRQLDALAPNDAASPIDVFVGDPAAPGAFRGQFGGAKIQYRRSALVRKGRREEKAY LCGFRLPSQRRTGTPADDAGEVFLNLSLRVESQSEQAGRRNPPYAAVFHISDQTRRVIVRYGEIE RYLAEHPDTGIPGSRGLTSGLRVMSVDLGLRTSAAISVFRVAHRDELTPDAHGRQPFFFPIHGM DHLVALHERSHLIRLPGETESKKVRSIREQRLDRLNRLRSQMASLRLLVRTGVLDEQKRDRNWE RLQSSMERGGERMPSDWWDLFQAQVRYLAQHRDASGEAWGRMVQAAVRTLWRQLAKQ VRDWRKEVRRNADKVKIRGIARDVPGGHSLAQLDYLERQYRFLRSWSAFSVQAGQVVRAER DSRFAVALREHIDNGKKDRLKKLADRILMEALGYVYVTDGRRAGQWQAVYPPCQLVLEELSE YRFSNDRPPSENSQLMVWSHRGVLEELIHQAQVHDVLVGTIPAAFSSRFDARTGAPGIRCRRV PSIPLKDAPSIPIWLSHYLKQTERDAAALRPGELIPTGDGEFLVTPAGRGASGVRVVHADINAAH NLQRRLWENFDLSDIRVRCDRREGKDGTVVLIPRLTNQRVKERYSGVIFTSEDGVSFTVGDAKT RRRSSASQGEGDDLSDEEQELLAEADDARERSVVLFRDPSGFVNGGRWTAQRAFWGMVHN RIETLLAERFSVSGAAEKVRG

[0145]

150	Cas12	MGLVDTAGGFLIPAALDPAILLSGDGSTNPIRQVXXX

		NFNFDDPNLIILPLAFGKRQGREFIWNDLLSLETGSLKLANGRVIEKTLYNRRTRQDEPALFVALT FERREVLDSSNIKPMNLIGIDRGENIPAVIALTDPEGCPLSRFKDSLGNPTHILRIGESYKEKQRTI QAAKEVEQRRAGGYSRKYASKAKNLADDMVRNTARDLLYYAVTQDAMLIFENLSRGFGRQG KRTFMAERQYTRMEDWLTAKLAYEGLPSKTYLSKTLAQYTSKTCSNCGFTITSADYDRVLEKLK KTATGWMTTINGKELKVEGQITYYNRYKRQNVVKDLSVELDRLSEESVNNDISSWTKGRSGEA LSLLKKRFSHRPVQEKFVCLNCGFETHADEQAALNIARSWLFLRSQEYKKYQTNKTTGNTDKR AFVETWQSFYRKKLKEVWKPAV
153	Cas12	MGKQSTNSSGLKATSGAPSIEKPVTTQRAYTLRLRGIEGDKTWRDSLWATHEAINLGAKAFGD WLLTLRGGLEHTLADATVAGGKGKPARPPSADERRDRRVLLALSWLTVEDERGAPKAPGLIVAY GDDCKSAKDSQDGRDRKVEDALRDILIKRSVAPGAVESWVNDCVVSLKARIRDDAVWVNRS AAFDALRASWRGLTCPNARTVLEQFFGPVADWITLPARAADDGEGDTGGPTAAGSSNDTEFK LVARSFLSENFGTGLKSSKSDISDALMQATRSLAALRGGSPGSAVWSHLCTEFGLLAADDEARA KALRVRIGWTSGRRSKGRLALATAASKASLAQVDIELLIKKLSEEAQEKLAGSTKLPLPWVNDL MAALERSIGFGFVTERNLIDEFGVMLDHAARRVSIACSWIKLAELERRQFEEDAKKLDQVRTQ HADAAAFLDTLGCRRGSESGSAGGASVVIRKRAVLGWNEVVGDWARQGCKSVQERIDAARL LQGELEKFGDIRLFEELAANDAQVVWQNAEGETDPTILARYSAGSVAKANQQRFKVPAYRHP DPLRHPVFGDFGKSRWKIDFAVHESDRAQSGGKRVRSLDAAWQSDVRNMRMALWTGKRV EMVPLRWSSKRLSKDLGISDLSLKDPTVVTRGDRLGRAAVGPGDPVRVASVFAEDNWNGRLQ APRVELNRVARLTQSGNLVQARRLRDRLSWLVSFSPKLAPSGPFIDYAAAHGIEPHKKSGEYW PNSAMNKERKGHHSKLIYSRLPSLRVLSVDLGHRFAAACAVWESMSAAQMRLAASKGKVVR GGIAEGALFIHIESTVADGTVRTTVYRRIGEDALPDGSPHPAPWAKLERQFLIKLQGEETPSRMA ALDELVMIADWERALGYQPVTASSTKQSNGVAGLMGRTVRLFMHASRRHFDRARIAHNLTAE HRTKPGGVPESLTEETRIELLIDTLALWHGLFAGDRWRDPRAQKEWETSGLPSLKLPGRGDDDE TAFGGPGRKAAMVVYRNELKPHAERMAHSDLSNLSKCWTDRWAQDDREWTAKSGRLRSLR RWITPRGLRPVSGDSAQLIERKAAAALRARHVGGLSMQRINTLTDLYRLLKSFKNRPEPSNLRK NIPEKGDARLIGFNQRLLDVRDRLREQRVKQLASRIVEAALGIGRIKIRRVAAGSPRPTLRVDAA CHAVVTENLSNYQPAELQTRRENRQLMAWASSKVHKYLAESCQLHGLHLREVQPNYTSRQC SRTGAAGLRGVAVSATDLLTNPWWMRDVAQAKARIEKALKNGRNGAVADQLLVSAEAWALR IPERDRHDRKADESVKAFHAERVILPRKGGDLFVAESARCNGKGHVPALQADLNAAANVGIR ALLDPDWPGKWWWVPCVGGTYSPSPEKTSGAKVLEHIDQLPHEMVDPPQVAPKSSAPQPK SSRAAKVKAKEFRAIENRWRTCSSELLSQGKWIPSGEYWSKVEAAVCLVLNDQIT
154	Cas12	MAAFQRSYTMNLKPATSEQDKFILWNRLFLTHWSVNEGAKIFGELFLNLRGGLSPELDIFDLDK VKDDKKKKAFVMGRRRLLALGWLSVEDNLSAGEHPFRIREIPVGRNMGKSQASTLLTEILKNK GIKDEAVIKEWIDDCTPSLIANIREDAVWINRASSFNSITPCPTKDEVWIVLSGLLGLRFLDLSLEE VKGKETEYLYDLGEKETQSKSDPSKKARELFGNLFTQNPVLMKNSRDKKDTFAKEFYLAFKEFK DYEKLKEKIESWRKEKEFPLIENPVAEKYPPEVTFTGSPCTVSKRYRKLLVSLELWPSSQDENGNI PKTEKTEDKTHNQVLLDYLLKACNEGNKGTQKIITPVWANNLKAELELKMNEIIRIGESSSTELQ RLMIKMAARRISQTLSWIKINEQTKHDAYQKKNKAFKLLSEIDKNGEACKWLENYELFRTDDS GGEEYHISLRAISCWKQILEEWQKNDSPKALREKVKEVQAEEEKFGDARLFEDLADDNARSVW LLPDGNKTPDILNWWCEYRTAEIDESRFKIPCYCHPHPFKHPVYVEYGKSNPKVIFAMKNNKV

[0147]

		KKGHIEHGWNPQNPRSIALSLFNNGNRESSLVPFIWESKRLWKDLGGEATQIGDIPRSDRMGL SGKRESVKPKAPFQKEVWNARLQSDRRTLEKLEKYWNPESMKWIDDGKFLIQSKWFITFGPD METAEGPWKLYLKEKYVDNKILGNRSKENQKRGYRAKKLLSGYPAGMRILSVDLGHRYAASCA VWETITKKQITEELAYQPDNNSLFEHSCKTIDKKIKNTVYRRIGEDSIDAPWAKLEKQFTIKLQGE DKSCVLLRSDEKELFRSILSKLSCLNNDTGHNILEMIENLLRIVKAKIYRQGILARISYSMTAQYKP GKGGQKSPLSDEDKIHYLSENLAAWSAIMGNQEWNEDVISDWYKTYISHLVSGPKPKEGNRK SDRDKIIEYFLPAARKLYDDNETRIKIHDLFKELWDENNKQLSAVLKEIKKIILPKGIRYFDKNTDN PSKWKNNQSKLKQITHRGGLSMQRIVAIEEYYKLAKAYKNHPEPDDLTKNIPLPGDNSSAGFN QRIRDTLERMKEQRVKQIASRIVESALGLGIEGYKKRPLTPENKPCQAIVIEDLSHYRPDELQTRR ENRRLMQWSSSKVKKYLKEACEMHDVRLVEISPEYTSRQDSRTGAAGLRCIDINIREFLKDSSR WQNKINTIQKKPANKKSNLDQYLIELNESLGNKYKDKVIPSDNFVRIPRKGGDVFVSSSKESPV SKGIQADLNAAANIGLKALLDPDWAGAWWYILIEVKSNHVIPYGEKYKGSECLRAWKFSGLEN QVMKNNMNLWRDLQSQFSGEDKWMSYKEYNELTEKRVINILRERAGLELIKE
155	Cas12	MEDYSGFVNIYSIQKTLRFELKPVGKTLEHIEKKGFLKKDKIRAEDYKAVKKIIDKYHRAYIEEVFD SVLHQKKKKDKTRFSTQFIKEIKEFSELYYKTEKNIPDKERLEALSEKLRKMLVGAFKGEFSEEVAE KYKNLFSKELIRNEIEKFCETDEERKQVSNFKSFTTYFTGFHSNRQNIYSDEKKSTAIGYRIIHQNL PKFLDNLKIIESIQRRFKDFPWSDLKKNLKKIDKNIKLTEYFSIDGFVNVLNQKGIDAYNTILGGKS EESGEKIQGLNEYINLYRQKNNIDRKNLPNVKILFKQILGDRETKSFIPEAFPDDQSVLNSITEFAK YLKLDKKKKSIIAELKKFLSSFNRYELDGIYLANDNSLASISTFLFDDWSFIKKSVSFKYDESVGDP KKKIKSPLKYEKEKEKWLKQKYYTISFLNDAIESYSKSQDEKRVKIRLEAYFAEFKSKDDAKKQFDL LERIEEAYAIVEPLLGAEYPRDRNLKADKKEVGKIKDFLDSIKSLQFFLKPLLSAEIFDEKDLGFYNQ LEGYYEEIDSIGHLYNKVRNYLTGKIYSKEKFKLNFENSTLLKGWDENREVANLCVIFREDQKYYL GVMDKENNTILSDIPKVKPNELFYEKMVYKLIPTPHMQLPRIIFSSDNLSIYNPSKSILKIREAKSF KEGKNFKLKDCHKFIDFYKESISKNEDWSRFDFKFSKTSSYENISEFYREVERQGYNLDFKKVSK FYIDSLVEDGKLYLFQIYNKDFSIFSKGKPNLHTIYFRSLFSKENLKDVCLKLNGEAEMFFRKKSIN YDEKKKREGHHPELFEKLKYPILKDKRYSEDKFQFHLPISLNFKSKERLNFNLKVNEFLKRNKDIN IIGIDRGERNLLYLVMINQKGEILKQTLLDSMQSGKGRPEINYKEKLQEKEIERDKARKSWGTVE NIKELKEGYLSIVIHQISKLMVENNAIVVLEDLNIGFKRGRQKVERQVYQKFEKMLIDKLNFLVFK ENKPTEPGGVLKAYQLTDEFQSFEKLSKQTGFLFYVPSWNTSKIDPRTGFIDFLHPAYENIEKAKQ WINKFDSIRFNSKMDWFEFTADTRKFSENLMLGKNRVWVICTTNVERYFTSKTANSSIQYNSI QITEKLKELFVDIPFSNGQDLKPEILRKNDAVFFKSLLFYIKTTLSLRQNNGKKGEEEKDFILSPVV DSKGRFFNSLEASDDEPKDADANGAYHIALKGLMNLLVLNETKEENLSRPKWKIKNKDWLEFV WERNR
156	Cas12	MKRIAKFRHDKPVKREAWSKGYRVHKNRIINKVTRSIKYPLVVKDEWKKRLIDDAAHDYRWLV GPINYSDWCRDPNQYSILEFWIDFLCVGGVFQSSHSNICRLAIQLSGGSVFEQEWKDLSPFVR ANLIQGIKPAEFIGFLTAEFRSSSNPKNFISKFFEGSNEDLESLTNEFASIVDFIKAKDISLLRKSLPS CKKIAPNLWEKAVGSHSTNELLKLLTKYTRVMLVAEPSHSDRVFSQTVLQSNDQDDPELTGPLP SHKVGKASYLFIPEFIREVNLDKISKLDLSAKSKLAVEQVKKLSELTSDFKQIENQSEAYFGLSTSF NELSNFLGILIRTLRNAPEAILKDQIALCAPLDKDILKITLDWLCDRAQALPENPRFETNWAEYRS YLGGKIKSWFSNYENFFEIPQAASSQQNNNREKKLGNRSAIRALNLKKEAFEKARETFKGDKGT

[0148]

		LEKIDLAYRLLGSISPEVLQCDEGLKLYQQFNDELLVLNETINQKFQDAKRDIKAKKEKESFEKLQ RNLSSPLPRIPEFFGERAKKGYQKARVSPKLARHLLECLNDWLARFAKVEESAFSEKEFQRILDW LRTSDFLPVFIRKSKDPPSWLRYIARVATGKYYFWVSEYSRKRVQIIDKPIAQNPLKELISWFLLN KDAFSRDNELFKGLSSKMVTLARIMAGILRDRGEGLKELQAMTSKLDNIGLLHPSFSVPVTDSL KDAAFYRAFFSELEGLLNIGRSRLIIERITLQSQQSKNKKTRRPLMPEPFINEDKEVFLAFPKFETK NKVKGTRVVYNSPDEVNWLLSPIRSSKGQLSFMFRCLSEDAKIMTTSGGCSYIVEFKKLLEAQE EVLSIHDCDIIPRAFVSIPFTLERESEETKPDWKPNRFMGVDIGEYAVAYCVIEKGTDSIEILDCGIV RNGAHRVLKEKVDRLKRRQRSMTFGAMDTSIAAARESLVGNYRNRLHAIALKHGAKLVYEYE VSAFESGGNRIKKVYETLKKSDCTGETEADKNARKHIWGETNAVGDQIGAGWTSQTCAKCGR SFGADLKAGNFGVAVPVPEKVEDSKGHYAYHEFPFEDGLKVRGFLKPNKIISDQKELAKAVHAY MRPPLVALGKRKLPKNARYRRGNSSLFRCPFSDCGFTADADIQAAYNIAVKQLYKPKKGYPKER KWQDFVILKPKEPSKLFDKQFYRPN
157	Cas12	MAIRSIKLKLKTHTGPEAQNLRKGIWRTHRLLNEGVAYYMKMLLLFRQESTGERPKEELQEELIC HIREQQQRNQADKNTQALPLDKALEALRQLYELLVPSSVGQSGDAQIISRKFLSPLVDPNSEG GKGTSKAGAKPTWQKKKEANDPTWEQDYEKWKKRREEDPTASVITTLEEYGIRPIFPLYTNTVT DIAWLPLQSNQFVRTWDRDMLQQAIERLLSWESWNKRVQEEYAKLKEKMAQLNEQLEGGQ EWISLLEQYEENRERELRENMTAANDKYRITKRQMKGWNELYELWSTFPASASHEQYKEALKR VQQRLRGRFGDAHFFQYLMEEKNRLIWKGNPQRIHYFVARNELTKRLEEAKQSATMTLPNAR KHPLWVRFDARGGNLQDYYLTAEADKPRSRRFVTFSQLIWPSESGWMEKKDVEVELALSRQF YQQVKLLKNDKGKQKIEFKDKGSGSTFNGHLGGAKLQLERGDLEKEEKNFEDGEIGSVYLNVVI DFEPLQEVKNGRVQAPYGQVLQLIRRPNEFPKVTTYKSEQLVEWIKASPQHSAGVESLASGFR VMSIDLGLRAAAATSIFSVEESSDKNAADFSYWIEGTPLVAVHQRSYMLRLPGEQVEKQVMEK RDERFQLHQRVKFQIRVLAQIMRMANKQYGDRWDELDSLKQAVEQKKSPLDQTDRTFWEGI VCDLTKVLPRNEADWEQAVVQIHRKAEEYVGKAVQAWRKRFAADERKGIAGLSMWNIEELEG LRKLLISWSRRTRNPQEVNRFERGHTSHQRLLTHIQNVKEDRLKQLSHAIVMTALGYVYDERK QEWCAEYPACQVILFENLSQYRSNLDRSTKENSTLMKWAHRSIPKYVHMQAEPYGIQIGDVR AEYSSRFYAKTGTPGIRCKKVRGQDLQGRRFENLQKRLVNEQFLTEEQVKQLRPGDIVPDDSGE LFMTLTDGSGSKEVVFLQADINAAHNLQKRFWQRYNELFKVSCRVIVRDEEEYLVPKTKSVQA KLGKGLFVKKSDTAWKDVYVWDSQAKLKGKTTFTEESESPEQLEDFQEIIEEAEEAKGTYRTLFR DPSGVFFPESVWYPQKDFWGEVKRKLYGKLRERFLTKAR
158	Cas12	MTHAKKIPFPVLKRSTLRKARQRIAAGSITAGERPFNSTVTRVVPVKDPVSDQVWAVAREAAM TLRGFGQGSLFDMLIHLHADGFRLFPSGREREAFFLKDLFDPTEFDDGARRAFGDVMPGFTAN SLREILGAPARKCGKVTSVEILLPRLSKGLGVKKSAAPPEVLSSLAAALCEAFPTWSLLTAVDGGV GKVIDDVLRTHGSRLPSLEKAWSTNLPEVPKGLGVPTLAFDDQAPAQSEQTPTGRFAGVVARY LAETFASNPEATAGDASKAVQAKVTTPNGNALSWLFAVGRRAMCSTTLDELAIGLNITSPRGR HALSSLKERMMALPALSVLGERAYPDSRATLQGTVDSLIANYVNRLFELSSSATSIAQTKLILPAA IQGDTAVFDGMPFSAEDVGALFEQLPSEIAKLEHAVKVLVGKERTSTLGYQKAVDDVDEFGVW ASSVDAVIGQINARLKTLERAQEPLGKLMGDGKLKRLVNIHEPEGPAVEIIPVLDQELQDVLTSC RTAFADLEARYPMTVAKAQRHAEAEVRNALELASRKEGGLSLASADVPALAKRKILEPIISIARR SSPAMATAVLTECLRQKLIVKGTGSERSLRGYVLSGEQVIYAHPLSRRRSIVRLDREGLQNFDALE

[0149]

		FLDALQKDATQRTNVRESLIVEMARQSLLLSALPDRIEIGAISWQTPSQNQHAPWANLRPVNG TVGRSETIKSFTAVFHSRISGLLYRLNRQKFMEKYDLRCFIGSTLLFSPKNADWAPPPQYRHGRF SALLARSDFPWEGAEGTHANAVRLAKFLIDETRNATDLQQAIAAKALLAQLPHDWVVCCDFD GAPSYEGAFVSAGEVSAWAKRSGYLLTPPRHFAGAFLEGFKSTKISPHGLTFERMLERDGDSVIE TGRRVTAAFPITQEVAPAAQPWKPRHLAGLDLGEAGLGVCLKNLDNGHEQTLLLKTRKTRLLA HSAEHYRRKDQPRQVFRKQYNQSSENAIKAAIGEVCGLIDNLIARYDAVPVFESQAAAARGSN RMVARVYAGVLQRYTYVVGNGAADATRTSHWLGANRWSYSFGADVIPKVRDLSPEVLRSIKK PENVFRDALGFPGVLANAWRTSMICSVCGTDPIGALEEAIAANQISFVTDNEGEGSLDLGDGR KVTLRVEVPTSSALTKREASRRKRRAPWEAKVGTVWTLTRKSHRDDLLTTIRRSLRRPSSTFQG STTKQWEFHCPCCGQIQQADVNAASNLVRRYFVRASDNARARQHWADDSKRLAFIASMGP DRSAREEKVS
159	Cas12	MNRIYQGRVTKVEKLKNGKSPDDREELKDWQTALWRHHELFQDAVSYYTLALAAMAEGLPD KHPINVLRKRMEEAWEEFPRKTVTPAKNLRDSVRPWLGLSESASFGDALKKILPPAPENKEVRA LAVALLAEKARTLKPQKTSASYWGRFCDDLKKKPNWDYSEEELARKTGSGDWVAGLWSEDAL NKIDELAKSLKLSSLVKCVPDGQINPEGARNLVKEALDHLEGVSNGTKKEKNDPGPAKKTNNW LRQHASDVRNFIHKNKNQFSSLPNGRLITERARGGGININKTYAGVLFKAFPCPFTFDYVRAAV PEPKVKKVDQEKKSEQSATWTELEKRILRIGDDPIELARKNNKPIFKAFTALEKWSDQNSKSCW SDFDKCAFEEALKTLNQFNQKTEEREKRRSEAEAELKYMMDENPEWKPKKETEGDDVREVPIL KGDPRYEKLVKLFGDLDEEGSEHATGKIYGPSRASLRGFGKLRNEWVDLFTKANDNPREQDLQ KAVTGFQREHKLDMGYTAFFLKLCERDYWDIWRDDTEVEVKKIREKRWVKSVVYAAADTREL AEELERLQEPVRYTPAEPQFSRRLFMFSDIKGKQGAKHIREGLVEVSLAVKDQSGKYGTCRVRLH YSAPRLIRDHLSDGSSSMWLQPMMAALGLSSDARGCFTRDSKGNVKEPAVALMSDFVGRKR ELRMLLNFPVDLDISKLEENIGKKARWEKQMNTAYEKNKLKQRFHLIWPGMELKETQEPGQF WWDNPTIQKEGMYCLAIDLSQRRAADYALLHAGVNRDSKTFVELGQAGGQSWFTKLCAAG SLRLPGEDTEVIREGKRQIELSGKKGRNATQSEYDQAIALAKQLLHNENSAELESAARDWLGD NAKRFSFPEQNDKLIDLYYGALSRYKTWLRWSWRLTEQHKELWDKTLDEIRKVPYFASWGELA GNGTNEATVQQLQKLIADAAVDLRNFLEKALLHIAYRALPLRENTWRWIENGKDGKGKPLHLL VSDGQSPAEIPWLRGQRGLSIARIEQLENFRRAVLSLNRLLRHEIGTKPEFGSSTCGESLPDPCP DLTDKIVRLKEERVNQTAHLIIAQSLGVRLKGHSLFTEEREKADMHGEHEVIPGRSPVDFVVLED LSRYTTDKSRSRSENSRLMKWCHRKINEKVKLLAEPFGIPVIEVFASYSSKFDARTGAPGFRAVE VTSEDRPFWRKTIEKQSVAREVFDCLDNLVGKGLNGIHLVLPQNGGPLFIAAVKEDQPLPAIRQ ADINAAVNIGLRAIAGPSCYHAHPKVRLIKGESGTDKGKWLPRKGKEANKRENAQFGNVDLD LEVKFNRLDIDSDVLKGDNTNLFHDPLNIACYGFATIQNLQHPFLAHASAVFSRQKGAVARLQ WEVCRAINSRRLEAWQKKAEKAAVKR
160	Cas12	MSHELAEQPSPPKNKEPTCEESDAIRKNRRILLALSWLSVEDDCSAPTGTFRVASGKDSEAERK NKVLTAFRSILTARRMRSQDVESWIADCAASLSAKIREDAVWINRSACFDQRALDLKVLSREYA KAAVMSFFGPLDEYFKLPDEADDTKPAVGGDGPDFRTLARQWVSTNFGTGKKSDSEAIAQNL RKLADANLAPFSGKPKAALIAHLSVELDGSTADIDGLCRAIGWNTGRPSKGRVAIERLPDPPTET SIQTMQQKFREEAEAKASSKGLRQVPEWMPAFQKSIERDCGMPFKLGEGRDHIGEFSVMLDH AARRVSIGHSWIKRAEAERRRFEADAQRLNHIPAAAKDWLDQFVQFRSGSSGAAAAGGEYRI

[0150]

		RRRAIEGWDEIIKRWKRAACKSPEDRVAAAREVQADPEIEKFGDIQLFEALAADDAECVWRGD GNGTPDPLKDYVAATDALDKMRRFKVPAYRHPDPLAHPVFGDFGNSRGDIRFAVHEAAKATR GTKRIAKDQKEWIRERHGLRMGLWDGQSVRTADLRWSSKRLVDDLALRNHVTTRRTGPVSR ADRLGRAAAGLGADEAACVAGLFELPDWNGRLQAPRAQLDAIAACVAANGGKWDDKARKL RDRIEWLVSFSAKLECCGPFMEYASQNGIQPNGKGEYYPHAERNKGRTGHAKLILSRLPGLRVL AVDLGHRFAAACAVWEALSKIAFDAETKGREVVSGGRAADDLYCHTRHLDCAGKARTTIYRRI GPDKLPDGSDHPAPWARLDRQFLIKLQGEERPARAAGPAETAAVQQIETDLGRARGQEDLPPR PVDSLMREAVRTIRIALRRHGDAARIAYAFKPGAKRLKPGGGAQDHTPETHADAILEALLRWH ELATGARWRDPWAETQWKDWVQPHISATLPELANDADRWERKRHRAALEQVLRPVAQMLI QRPTDALHQVWSKHWADEDLKWPSRLRWLRNWLLPRGPRARSGAARNVGGLSLLRIATLRE LYQTQKAYAMRPEPDDPRKRIAGRNDDRYDELGRSVLQVIERLREQRVKQLASRIVEAALGVG RAKPTRGRQRPQSRVDVPCHAVIIESLRNYRPDELQTRRENRAIMNWSAGKVRKYLEEACQL HGLHLREVMPNYTSREDSRTGLPGVRCVDVPVDPKLGKPKAYWWNSVLSTARKKSIGDAASH DKQGDATSRFIVELAGCLDRLKADGKPLPKTVRVPRIGGDLFVAAPPTSCTAPAHQPHPACDG ARALQADLNAAANIGLRALLDPDFPAKWWYVPCIDDQRGLALPRADKVLGSACFPGDPATFG SLLKTRTAAGPAVDGQAAPDRKPRTGTHRPGSAKSRSLGDGKATTNYWSDRSARDLRPADEG GHWQPTNVYWNWVRKRALLGLYSFNGLSPPSDDRP
161	Cas12	MAIRSIKLKLKTNTGPEAQNLRKGIWRTHRLLNEGVAYYMNMLLLFRQESTDKKTKQEIHEELIR HIRAQQQRNHADEKTQALPLEKALEALRKLYELLVPSSVGQSGDSQIISRKFLSPLVDPNSEGG KGTSKAGAKPAWQKKKEANDPTWKQDYEKWKKRREEDPTASVITTLEEYGIRPLFPLYTNTVAE AWLPLKSGQFVRTWDRDMFQQAIEGMLSWESWNRRVQEEYAKLEGKMAQLNEQLEGGEE WIRLLEQYEEKREQELRENMTAANDKFRITKRQMKGWKELYEVWSTFLPSASQEQYKEAIKRV QQRLRGKFGDFHFFQYLSEEENRLIWKGNPQRIHYFVARNELTKKLEKAKQSARRTLPDANKH PLWVRYDARGGNLQDYYLTAESDKPRSRRFVTFSQLIWPSESGWLEKKDVQAELALSRQFYQ QVTFLKNDKGKQEIEFKDKGSGTTFSGHLGGAKLQLERSVLENKERKFEEGEIGKAYLNVAIDFK PLQEVKNGRVQAPYGQVLQLIRLPNAFPKVRTYKSEELVEWIKASPQHLSGVESLASGFRVMSI DLGLRAAAATSIFSVEESSDKNATKLAYWIEGTPLVAVHQRSYMLRLPGEQVEQHVWEKRDER GDQHKRVRFQIRRLAEIIRLANKQYGDRWDELNRLDEAVSKEKSPLDQADRTFWEGIVSDLTT ALPLNDADWTEAVVQIHRKAELYVGKVVQAWRKRFNADERKGIAGLSMWSIEELDGLRKLLIS WSRRTRNPQEVNRFEPEHTGHKRLLTHIQNVKKDRLKQVSHAIVMTALGYIYDEKKQKWCAK YPACQVILFENLSQYRSNLDRSAKENSTLMKWAHRSIPKYVHMQAEPYGIQIGDVRAEYSSRY YAKTGTPGIRCKKLREHDVKGWRLDHLKKRLVNEQFLTEAQVEQLKAGDIIPDDSGELFMTMT DGSGGKEIVFLQADINAAQNLQKRFWQRNSELFKVSCRVIVRDEAEYLVPQAKKVQEKLGKG VFVKKSDTAWKEVYVWDSQAKLKGKTTFTEESESPEQLEDLQEMIEEAEEAKGTYRTLFRDPSG VFFPDFVWNTPKDFWGEVKRKLYGKLRERLLTKVR
162	Cas12	MNRIYQGRVTKVEVPDGKDEKGNIKWKKLENWSDILWQHHMLFQDAVNYYTLALAAISGSA VGSDEKSIILREWAVQVQNIWEKAKKKATVFEGPQKRLTSILGLEQNASFDIAAKHILRTSEAKP EQRASALIRLLEEIDKKNHNVVCGERLPFFCPRNIQSKRSPTSKAVSSVQEQKRQEEVRRFHNM QPEEVVKNAVTLDISLFKSSPKIVFLEDPKKARAELLKQFDNACKKHKELVGIKKAFTESIDKHGS SLKVPAPGSKPSGLYPSAIVFKYFPVDITKTVFLKATEKLAMGKDREVTNDPIADARVNDKPHF

[0151]

		DYFTNIALIREKEKNRAAWFEFDLAAFIEAIMSPHRFYQDTQKRKEAARKLEEKIKAIEGKGGQF KESDSEDDDVDSLPGFEGDTRIDLLRKLVTDTLGWLGESETPDNNEGKKTEYSISERTLRIFPDIQ KQWSELAEKGETTEGKLLEVLKHEQTEHQSDFGSATLYQHLAKPEFHPIWLKSGTEEWHAENP LKAWLNYKELQYELTDKKRPIHFTPAHPVYSPRYFDFPKKSETEEKEVSKNTHSLTTSLASEHIKN SLQFTAGLIRKTNVGKKAIKARFSYSAPRLRRDCLRSENNENLYKAPWLQPMMRALGIDEEKA DRQNFANTRITLMAKGLDDIQLGFPVEANSQELQKEVSNGISWKGQFNWGGIASLSALRWP HEKKPKNPPEQPWWGIDSFSCLAVDLGQRYAGAFARLDVSTIEKKGKSRFIGEACDKKWYAKV SRMGLLRLPGEDVKVWRDASKIDKENGFAFRKELFGEKGRSATPLEAEETAELIKLFGANEKDV MPDNWSKELSFPEQNDKLLIVARRAQAAVSRLHRWAWFFDEAKRSDDAIREILESDDTDLKQ KVNKNEIEKVKETIISLLKVKQELLPTLLTRLANRVLPLRGRSWEWKKHHQKNDGFILDQTGKA MPNVLIRGQRGLSMDRIEQITELRKRFQALNQSLRRQIGKKAPAKRDDSIPDCCPDLLEKLDH MKEQRVNQTAHMILAEALGLKLAEPPKDKKELNETCDMHGAYAKVDNPVSFIVIEDLSRYRSS QGRSPRENSRLMKWCHRAVRDKLKEMCEVFFPLCERRKAGSAWVSLPPLLETPAAYSSRFCSR SGVAGFRAVEVIPGFELKYPWSWLKDKKDKAGNLAKEALNIRTVSEQLKAFNQDKPEKPRTLL VPIAGGPIFVPISEVGLSSFGLKPQVVQADINAAINLGLRAISDPRIWEIHPRLRTEKRDGRLFARE KRKYGEEKVEVQPSKNEKAKKVKDDRKPNYFADFSGKVDWGFGNIKNESGLTLVSGKALWW TINQLQWERCFDINKRHIEDWSNKQKQ
163	Cas12	MGEENNFSQFTGLYELSKTLRFELKPVWETEKLLIENQVFPKDKIVYESYKKIRPYLDKLHLQFIEE SLSSVKLDFNEIEKKFLEWDKEKDKTTKNKLKEEIFWKNKKWWLNSNLRKDMVSYFNLNWKK WINNFENKTIVNEKWKEEKIKIKWEWYKILLSDSNLNILSDFFTQEKEWDNVLIEKYIENPNFKE NDWEKKFILEKQNLFKSFKWFTTYFTNFNHSRENFYKDDWKSWRIATRIIDENLIFFLKNKKAF DEKYKNNSEITVKFNEKLLNFWEKLEDFFSLDFYNRCYTWKQIEYYNQLIWELNSVVNHEKQA KFSEYTQNKKVSENNKFNKYDFPIFKELYKQILSEKATEQKFIEINDFKELKQNLQELIEKNKQKN KFAINLTKSLIEKIDEYDFEKIYISKLSLNTISSKFFWSNKWFFIQENLEKNIWKKNKNWKIDLPDFI KLSDIKTALENFNKILFEDKENKENIFKEEFDNITENNIFIKFMKIYENEFINLIEWKKNNKWDYEII WYNKSLLDLEKNILNISDFSDKKEEKEKQIEYIKKYLDSSLNIYRVMKYFALEKGKESVEWEFETD DIFYNEFKKFYIDNEIISYYNEFRNYLTKKPYSSNKLKLNFENWTLIDGWDKNKEPDNYWTILRK NWKYFLALQIKWKNNIFYKKKWSWVIDIEEAYKIDLWDEFYEKMDYKFLPDPKKMLPKVIFAKS NVKLFNPSKEILQIKENETFKTWDKFKVNDFYKIVDFYKENIIKYPDWKIFNFKFSDTKTYNNLS DFYKEIELWSYDLNFRKVSKKYILKSIEEKNIYLFEIYNKDFADWKTWSENLHTMYFKWLFEENN LNNIVLKLNWQAEIFRREASLKEKEVNRAKENKEKSHNIIENARYTKDKLFFHCPIKLNFAKHNE KINQEILKYISDNKEINIIWIDRWEKHLAYYSVINRDWNIIKDKNWNLVKWSLNIVWNNQNYH DKLETREKERQDARWSWKTIWNIKDLKQGYISQVVHKLAELVIEHNAIIVFEDLNSWFKRWRQ KIERQVYQKLEKALIEKLNYLTFKDKNFWENWHYLKAYQLTAPFETFEKVWKQTWVIFYTDPSY TSSTCPACWFRKDLYLKYSNLKNALWDIEKIDSIIFDWKRFIFEYNNKKVFTDRDRKRNISSEES WIKWWKTIDNNITEFLEILFKKSNIDYTSWNNLILDIQEINEKELYKWVFDNFNAILNIRNSTIKD NSRTWDFICCPACDFDSRKENKIWIENWDDNWAFNIARKWIIILNKIDSYLNEKWSLDKILW WDMIVKQIDWDDFTHKK
164	Cas12	MAQASSTPAVSPRPRPRYREERTLVRKLLPRPGQSKQEFRENVKKLRKAFLQFNADVSGVCQW AIQFRPRYGKPAEPTETFWKFFLEPETSLPPNDSRSPEFRRLQAFEAAAGINGAAALDDPAFTNE

[0152]

		LRDSILAVASRPKTKEAQRLFSRLKDYQPAHRMILAKVAAEWIESRYRRAHQNWERNYEEWKK EKQEWEQNHPELTPEIREAFNQIFQQLEVKEKRVRICPAARLLQNKDNCQYAGKNKHSVLCN QFNEFKKNHLQGKAIKFFYKDAEKYLRCGLQSLKPNVQGPFREDWNKYLRYMNLKEETLRGK NGGRLPHCKNLGQECEFNPHTALCKQYQQQLSSRPDLVQHDELYRKWRREYWREPRKPVFR YPSVKRHSIAKIFGENYFQADFKNSVVGLRLDSMPAGQYLEFAFAPWPRNYRPQPGETEISSVH LHFVGTRPRIGFRFRVPHKRSRFDCTQEELDELRSRTFPRKAQDQKFLEAARKRLLETFPGNAE QELRLLAVDLGTDSARAAFFIGKTFQQAFPLKIVKIEKLYEQWPNQKQAGDRRDASSKQPRPGL SRDHVGRHLQKMRAQASEIAQKRQELTGTPAPETTTDQAAKKATLQPFDLRGLTVHTARMIR DWARLNARQIIQLAEENQVDLIVLESLRGFRPPGYENLDQEKKRRVAFFAHGRIRRKVTEKAVE RGMRVVTVPYLASSKVCAECRKKQKDNKQWEKNKKRGLFKCEGCGSQAQVDENAARVLGR VFWGEIELPTAIP
165	Cas12	MGEENNFSQFTGLYELSKTLRFELKPVWETEKLLIENQVFPKDKIVYESYKKIRPYLDKLHLQFIEE SLSSVKLDFNEIEKKFLEWDKEKDKTTKNKLKEEIFWKNKKWWLNSNLRKDMVSYFNLNWKK WINNFENKTIVNEKWKEEKIKIKWEWYKILLSDSNLNILSDFFTQEKEWDNVLIEKYIENPNFKE NDWEKKFILEKQNLFKSFKWFTTYFTNFNHSRENFYKDDWKSWRIATRIIDENLIFFLKNKKAF DEKYKNNSEITVKFNEKLLNFWEKLEDFFSLDFYNRCYTWKQIEYYNQLIWELNSVVNHEKQA KFSEYTQNKKVSENNKFNKYDFPIFKELYKQILSEKATEQKFIEINDFKELKQNLQELIEKNKQKN KFAINLTKSLIEKIDEYDFEKIYISKLSLNTISSKFFWSNKWFFIQENLEKNIWKKNKNWKIDLPDFI KLSDIKTALENFNKILFEDKENKENIFKEEFDNITENNIFIKFMKIYENEFINLIEWKKNNKWDYEII WYNKSLLDLEKNILNISDFSDKKEEKEKQIEYIKKYLDSSLNIYRVMKYFALEKGKESVEWEFETD DIFYNEFKKFYIDNEIISYYNEFRNYLTKKPYSSNKLKLNFENWTLIDGWDKNKEPDNYWTILRK NWKYFLALQIKWKNNIFYKKKWSWVIDIEEAYKIDLWDEFYEKMDYKFLPDPKKMLPKVIFAKS NVKLFNPSKEILQIKENETFKTWDKFKVNDFYKIVDFYKENIIKYPDWKIFNFKFSDTKTYNNLS DFYKEIELWSYDLNFRKVSKKYILKSIEEKNIYLFEIYNKDFADWKTWSENLHTMYFKWLFEENN LNNIVLKLNWQAEIFRREASLKEKEVNRAKENKEKSHNIIENARYTKDKLFFHCPIKLNFAKHNE KINQEILKYISDNKEINIIWIDRWEKHLAYYSVINRDWNIIKDKNWNLVKWSLNIVWNNQNYH DKLETREKERQDARWSWKTIWNIKDLKQGYISQVVHKLAELVIEHNAIIVFEDLNSWFKRWRQ KIERQVYQKLEKALIEKLNYLTFKDKNFWENWHYLKAYQLTAPFETFEKVWKQTWVIFYTDPSY TSSTCPACWFRKDLYLKYSNLKNALWDIEKIDSIIFDWKRFIFEYNNKKVFTDRDRKRNISSEES WIKWWKTIDNNITEFLEILFKKSNIDYTSWNNLILDIQEINEKELYKWVFDNFNAILNIRNSTIKD NSRTWDFICCPACDFDSRKENKIWIENWDDNWAFNIARKWIIILNKIDSYLNEKWSLDKILW WDMIVKQIDWDDFTHKK
166	Cas12	MATAINYPTTQRAYTLRLRGIDPQDQSWRDALWATHEAVNRGAKVFGEWLLTLRGGLDHQL ADAPVKVRGGTTRLPSDEERRDRRVLLALSWLSVEDAHGAPPDASLIVAKGTDSADCRARKLA DALIAILQARSVAASEIGDPSKPPEDQPGTWLGDCMGSLSAAIRDDAVWVNRSKAFDAATQS CPSLTRDEIWDFLEPFFASPDAYLKPERAESDEGDSTSAATEDKAKDLVQKAGGWLSKRMGAG GGANFQDLARAYQAIAQWASSAQPGQSAQQAVGSLAGYLSQHGFSPTANDATGVLAVISGP GYKSATRNHITAIATSPEITPQDLSKLQELATKDKAGCSSKIGGKGPRPYATMILQQVEAACGFTY LQSDGPARHREFSVMLDHAARRVNVAHSWIKNAEAERRQFESDARRIKKVPQDALNWLRGY CEERGGASGSLEGYRIRRRAIDGWDQVVIRWSRSDCQSADDRIAAARQLQDDPEIDKFGDIQ

[0153]

		LFEALAAEEALCVWKPDGNPTAQPLKDFVAATEADAKKKRFKVPAYRHPDPLRHPVFTDFGNS RWGIEYSAHRAPAKCDELGQQVDRLTQAVAEAQRNLDGATAAQRASRESKLAEAQSKLVAAQ TEFAAINDPHRVELKLWNGQAVAAIPMRWSSKRLIADLSLRRATQPSSDQRIGVTRADRLGRA AGNADDGRPVTITGLFQQDHWNGRLQAPRAQLDAIAKHVDKHGWDAKARRQIARIRWVV SFSAELSQQGPWFEFCHRFGEDAPARPFVSRHGEYAVKHRDNDQRKGHAKLILSRLPGLRVLA VDLGHRYAAACAVWEAISSDQMRQACAAANAPAPHPLAMYIHLKSTTAKGKPTTTIYRRIGP DKLPDGTPHPAPWARLDRQFLIKLPGEDRPARAASPDEIKAVEDFEDSVGRVRTAVDPPRKRG VDLLMHDAVRTARLALARHGRRARIAFQLISQVRILPGGRPQTLDDAGRRDLLNDTLADWYA LATDSRWTDAAARQLWNERLAALNGGFTIDPPADASQPEAERTRAQRRQAEQELRHRLASL VEALFCNPTLCQQLHQAWTDRWNADDQQWRSRLKWLSRWLLPRGGSRRDGSRRHVGGLS LTRISTLIDFRRKVQVGVFTRLRPDGSRAEIGPQFGQSTLDAIQRLKDQRIKQLTSRIVEAALGIGV EQDRIWDAAKRKWRTVKRPREPRYHVDDQGVQQRDPRFQACHAVVIEDLSHYRPEETRTRR ENRATMDWKSAETRKRLADHCQLYGLHLRDVNPQYTSRQDSRTGAPGCRCVDVSVADFLTK PAWRKQVAQARGKVASNRGDARDRLLVELDHQLTTANSLRGEMDSLRIPVNGGEVFVSADP RSPLAAGIQADLNAAANIGLRALMDPDFLGTWWYVPCDPSTKKPHIEKVKGSILATVGALQAT SEEAAAPPRRGRGGTRSAAPREVINLWRDPSAVRIQDATAGEVWDVTPVYWSIVKDRVVDVL RQRNTKSGD
167	Cas12	MAVRSVKLKLLVPRDGSAESVRKRKALWATHQFVNDAAAAYAELLLEMRQEDVCRGTDDHG KDVIEPAAHWQAKLRARLAAKQLPPVAVAEALPLLKAFYGSRLIKSFVANDKGVAGTGNATDL NTWLSGLVDPASVAGEKTELRKQLLAELPLCEAADADFEGAARKMLAKSDAREALLEGPGTGV GWPAAYNANPTDSVWLDMLHKAAAKARLELADTTVSELKKLGVFPLLQAASSNRVFGSGVL NPFERMAAAQAAAALLPWETKRHEMRKRRDKFADQLNQWDTEFGASHATALAAIRAFEAEE SERARRESLGNEGTGYRIGGRELRDAWTLLRDWLKGHSTATAAAREDKVRELQAKQGRSFGSH RLLSWLAKPAQQWLADHSAGDVVTRIAVRNARQRKLDTARTLPIWTGADAVKHPRFANFDP PNNTNQPGFDLRAGTQKGRLTLRLSLLTERADGLLLAQDHDFQLVPSRQMAEIVLHKDGKER ALSWQSQDGIGRQVGDVGGSALLFSRDHAECLLERKQITRLERGAWPAALPVWFKLSLDIGAE HKALLKQRFKWGVWLNSALVTRNAKDAKGVPPPVGTRVLAVDLGLRSAATVSVWQVVDAAT PVVAGKWRVPLSDTLSAVHERSAMLALPGEHVDAGVLAARRAANEKLAGLLAATSHLSTVFK LGRAEQGDRRRELLERLGEGDDRRARAAVATTAAERDGLRAVLGATQDAWAGAVAAVWRRL ETDLAGAIAAYRKQQREDVQLRREARHGPGASQLPKQAAAERLLGGKSAWQIEYKERVRKLLT RWIMRQRPGDTAVRRLARKDLGKYCGGLLDHLTALKEDRAKTTADLIVQAARGRVRAHKDAH GRQQDRELWLAKYAPCDLIVMEDLGRYRFATDRPPSENRQLMQWTHREVFRLVQMQAEVE GIQVLETGAEFSSKFDARTWAPGVRCEPITKLWVERYRNGEMPWLADKADEWRREGIELAQL VPGQLLPTGSGEQFVAVSATGGLRVRHADLNAAQCIALRALTGHGTAFRLTARRLGDVFVSAK GLGKRPQGALWREFGSALPPAVVVLRPAGEVRYALRPFASARDAAAALGLQLGALRNVDATD AESDAEDGDLAELLAGADPDRATFFRDPSGDVHGGAWVQAKVFWAEVRRHVRLGLQAQGL LPAAARSSEPRQMQLPLAGALPGDDIPL
168	Cas12	MAAFQRSYTMNLKPATSEQDKFILWNRLFLTHWSVNEGAKIFGELFLNLRGGLSPELGIFDLNK DKDDRKKKALVMGRRRLLALGWLSVEDNLSAGDHPFRIREIPVGRNMEIKQATTLLTEILKNKG VKDEAVIKEWIDDCTPSLIANIREDAVWINRAKSFYSMNPCPTKDEVWKILSYVLNTSFLDLSL

[0154]

		NDSSERDNTKNKKGTKENEKDVSNKSKELYGWLFTKNPNKMREAGENKDKFINNFRENFNT FTDYANLKVEIELWRKNNISNTLLITQKAKYPPEVKEANHPSKFSVGYRKLLVHLELWPSSKDEN GDIPKGIEGKDKSHNQILLDYLLEVCNEGNKTTKKVIVPAWADGIKTELESKASIKVGDSTSSVL QRLMIKMAARRISQTLSWIKINEQVRHDAYQKKNKAFKLLCEIDKNGEACKWLENYELFRRDD SGGEEYHISARAISCWKQILEEWQKNDSSKALREKVKVVQAAEDKFGDARLFEDLADDNARS VWLLPDGNKTPDILNWWCEYRTADIDESRFKIPCYCHPHPFKHPVYVEYGKSNPQVIFSLKHD KARKNRIDNGWNPKNPRILALLLLDIVRQKSTLAPFVWESKRLWKDLGGDATVTYKIPRSDRM GLSSIGNIDYARPEVPFLKEKWNARLQSDRRTLEKLEKYWNPESMKWIDDGKFLIQSKWFITFG PDMETAEGPWKLYLKENINDNNYLGNRSKENQKRGYRAKKLLSGYPAGMRILSVDLGHRYAA SCAIWETITKKQITEELAYQPDKNSVFEHSCKTIDKKIKNTVYRRIGDDSIDAPWAKLEKQFTIKL QGEDKSCYLLRSDEKELFRSILSKLSCLNNDTGHNILEMIENLLRIVKAKIYRQGILARISYSMTAQ YKPGKGGQKSPLSDEDKIHYLSENLAAWSALMGNQEWNEDGISDWYKKYISHLVSGPKPKEG NRKSDRDKIIEYFLPAARKLYDDNETRINIHDLFKELWDENNKQLSAVLKEIKKIILPKGIRYFDKN NDSSSRWKNNQSKLKQITHRGGLSLRRIVAIEGYYKLAKAYKNHPEPDNLTKNIPLPGDNSSA GFNQRIRDTLERMKEQRVKQIASRIVESALGLGIEGYKKRPLTPESKPCQAIVIEDLSHYRPDELQ TRRENRRLMQWSSSKVKKYLSEACEMHDVLLVEISPEYTSRQDSRTGVAGLRCIDINIREFLKDS SSWQNKIKTIQMKPTNKKSNLDQYLIELNESLGERYKDKVIPSDKFVRIPRKGGDIFVSSSKESP VSKGIQADLNAAANIGLKALLDPDWAGAWWYILIEAKSNHVIPYGKKYKGAECLRDFKFSGLE NQVMKNNMNLWRDLQSQFSSEDKWMSYKEYNELTEKRVINILRERAGLELIEE
169	Cas12	MPTRTINLKMVLGRKDDTAELRRALWTTHEHVNLAVAEVERVLLRCRGRSYWTLDRRGDPVH VPESQVAEDALAMAREAQRRNGWPVVGEDEEILLALRYLYEQIVPSCLLDDLGKPLKGDAQKI GTNYAGPLFDSDTCRRDEGKDVACCGPFHEVAGKYLGALPEWATPISKQEFDGKDASHLRFKA TGGDDAFFRVSIEKANAWYEDPANQDALKNKAYNKDDWKKEKDKGISSWAVKYIQKQLQLG QDPRTEVRRKLWLELGLLPLFIPVFDKTMVGNLWNRLAVRLALAHLLSWESWNHRAVQDQA LARAKRDELAALFLGMEDGFAGLREYELRRNESIKQHAFEPVDRPYVVSGRALRSWTRVREEW LRHGDTQESRKNICNRLQDRLRGKFGDPDVFHWLAEDGQEALWKERDCVTSFSLLNDADGL LEKRKGYALMTFADARLHPRWAMYEAPGGSNLRTYQIRKTENGLWADVVLLSPRNESAAVEE KTFNVRLAPSGQLSNVSFDQIQKGSKMVGRCRYQSANQQFEGLLGGAEILFDRKRIANEQHG ATDLASKPGHVWFKLTLDVRPQAPQGWLDGKGRPALPPEAKHFKTALSNKSKFADQVRPGLR VLSVDLGVRSFAACSVFELVRGGPDQGTYFPAADGRTVDDPEKLWAKHERSFKITLPGENPSR KEEIARRAAMEELRSLNGDIRRLKAILRLSVLQEDDPRTEHLRLFMEAIVDDPAKSALNAELFKG FGDDRFRSTPDLWKQHCHFFHDKAEKVVAERFSRWRTETRPKSSSWQDWRERRGYAGGKSY WAVTYLEAVRGLILRWNMRGRTYGEVNRQDKKQFGTVASALLHHINQLKEDRIKTGADMIIQ AARGFVPRKNGAGWVQVHEPCRLILFEDLARYRFRTDRSRRENSRLMRWSHREIVNEVGMQ GELYGLHVDTTEAGFSSRYLASSGAPGVRCRHLVEEDFHDGLPGMHLVGELDWLLPKDKDRTA NEARRLLGGMVRPGMLVPWDGGELFATLNAASQLHVIHADINAAQNLQRRFWGRCGEAIRI VCNQLSVDGSTRYEMAKAPKARLLGALQQLKNGDAPFHLTSIPNSQKPENSYVMTPTNAGK KYRAGPGEKSSGEEDELALDIVEQAEELAQGRKTFFRDPSGVFFAPDRWLPSEIYWSRIRRRIW QVTLERNSSGRQERAEMDEMPY

[0155]

170	Cas12	MVTRALNLKLVVPRRPGELTKAEALWSTHDIVNRATSYYESQLLLCRQQDYQTRELTVSAGDQ APDLDALIANARDRNRYRGLEKPQVVREKLRNLYEAIVPPAIGKTGTAQAVGAFVSPLLDADSR GFTEIFDKIEALPNWVDGVRAEEPDALEAAADWLKSPQGKERLRPTGAPPTWIKLAKKKDAG WAAAFVADIDKKLKEVEGTPTLMQELRALGVMPLFPSFFASRIAGHKGAVSTWDRLALRLAVA HLLSWESWVELAAKEHAARVAKLEKFRDDNILGEIADAVEALRLYEKERTEELQQKAQLDAEEV RTTSRTIRGWVDLREKWLKTDASPDALISLVAAEQKRKSGKFGDPQLFRWLAKPENHFVWNK PDFDPPSLFASLRMIEGLVERSKETAWMTLPDARLHPRSSQWEPHGGGNLKTFRLEQGEGGSL SVTLPLLRKSGDDSYVEEEHAFSLAGSKQIPNASLDVRRNKYCLSYRTPTGEEAEAVVGSADLLL DWYFLQQRSEHRPEEGDIGPAFLKLALDITPIDPVWGEREKTPAIHHFKTASGKNTRHADGVAP GFRMLAVDLGIRTLATCSVFELKATAPAGRLSFPIAHLDLHAVHERSFTLTLDGEDPDRDAERWR ENKSAELRRLRMGLTRYRNIRNMREDAPDEREVLLEDLQEKVQEHGWAFEEPLLRELAKHKDT PEPIWEAELTKALAQFRSDFGVIVGEWRRSNRARSTDSHAGKSMWAIDHLTNSRRFLMSWSL LSKPGQIRRLDRDKQGVFAKHLLDHLEGLKADRLKTGSDLIVQAARGFRRDKRGNWHKAYKP CHGILFEDLSRYRMRTDRPRRENSQLMKWAHRAVPKEVGMQAEVYGIRVEDTGAAFSSRFHA ASHTPGIRMHPICQKDLENEWLLDEIEKQNSGVKRRELKLGQLVQLNGGELFACVTASGVKTL HADINAAQNLQRRFFTRHGDAFRIVARKVLVDEEEVWVPRSLGKRLLGALGSHGKLVPTGHES GSCRFEEITTRAWSKLSGEKLSDDRVGNEEDQIIASIEEEALERTGEVVVFFRDPSGQVLPRDLW YPSKTFWSIVKSTTLSKLKAAP
171	Cas12	MEDKQFLERYKEFIGLNSLSKTLRNSLIPVGSTLKHIQEYGILEEDSLRAQKREELKGIMDDYYRN YIEMHLRDVHDIDWNELFEALTEVKKNQTDDAKKCLEKIQEKKRKEIYQYLSDDAVFSEMFKEK MISGILPDFIRCNEEYSEEEKEEKLKTVALFHRFTSSFNDFFLNRKNVFTKEAIATAIGYRVVHENA EIFLENMVAFQNIQKSAESQISIIERKNEHYFMEWKLSHIFTADYYMMLMTQKAIEHYNEMCG VVNQHMKEYCQKEKKNWNLYRMKRLHKQILSNASTSFKIPEKYENDAEVYESVNSFLQNVM EKTVMERIAVLKNNTDNFDLSKIYITAPYYEKISNYLCGSWNTIADCLTHYYEQQIAGKGARKD QKVKAAVKADKWKSLSEIEQLLKEYARAEEVKRKPEEYIAEIENIVSLKEVHLLEYHPEVNLIENEK YATEIKDVLDNYMELFHWMKWFYIEEAVEKEVNFYGELDDLYEEIRDIVPLYNKVRNYVTQKPY SDTKIKLNFGTPTLANGWSKSKEYDYNAILLQKDGKYYMGIFNPVQKPEKEIIEGHSHPLEGNE YKKMVYYYLPSANKMLPKVLLSKKGMEIYQPSEYIINGYKERRHIKSEEKFDLQFCHDLIDYFKS GIERNPDWKVFGFHFSDTDTYQDISGFYREVEDQGYKIDWTYIKEADIDRLNEEGKLYLFQIYN KDFSEKSTGRENLHTMYLKNLFSEENIREQVLKLNGEAEIFFRKSSVKKPIIHKKGTMLVNRTYM EEMHGESVKKNIPEKEYQEIYNYMNHRWKGELSAEAKEYLKKAVCHETKKDIVKDYRYSVDKF FIHLPITINYRASGKEALNSVAQRYIAHQNDMHVIGIDRGERNLIYVSVINMQGEIIEQKSFNVV NKYNYKEKLKEREQNRDEARKNWKEIGQIKDLKEGYLSGVIHEIAKMMIKYHAIVAMEDLNYG FKRGRFKVERQVYQKFENMLIQKLNYLVFKDRSADEDGGVLRGYQLAYIPDSVKKLGRQCGMI FYVPAAFTSKIDPATGFVDIFNHKAYTTDQAKREFILSFDEICYDVERQLFRFTFDYANFATHNVT LARNNWTIYTNGTRTQKEFVNRRVRDKKEVFDPTEKMLKLLELEGVEYQSGANLLPKLEKISDP HLFHELQRIVRFTVQLRNSKNEENDVDYDHVISPVLNEEGKFFDSSKYENKEEKKESLLPVDAD ANGAYCIALKGLYIMQAIQKNWSEEKALSPDVLRLNNNDWFDYIQNKRYR
172	Cas12	MAQASSTPAVSPRPRPRYREERTLVRKLLPRPGQSKQEFRENVKKLRKAFLQFNADVSGVCQW AIQFRPRYGKPAEPTETFWKFFLEPETSLPPNDSRSPEFRRLQAFEAAAGINGAAALDDPAFTNE

[0156]

		LRDSILAVASRPKTKEAQRLFSRLKDYQPAHRMILAKVAAEWIESRYRRAHQNWERNYEEWKK EKQEWEQNHPELTPEIREAFNQIFQQLEVKEKRVRICPAARLLQNKDNCQYAGKNKHSVLCN QFNEFKKNHLQGKAIKFFYKDAEKYLRCGLQSLKPNVQGPFREDWNKYLRYMNLKEETLRGK NGGRLPHCKNLGQECEFNPHTALCKQYQQQLSSRPDLVQHDELYRKWRREYWREPRKPVFR YPSVKRHSIAKIFGENYFQADFKNSVVGLRLDSMPAGQYLEFAFAPWPRNYRPQPGETEISSVH LHFVGTRPRIGFRFRVPHKRSRFDCTQEELDELRSRTFPRKAQDQKFLEAARKRLLETFPGNAE QELRLLAVDLGTDSARAAFFIGKTFQQAFPLKIVKIEKLYEQWPNQKQAGDRRDASSKQPRPGL SRDHVGRHLQKMRAQASEIAQKRQELTGTPAPETTTDQAAKKATLQPFDLRGLTVHTARMIR DWARLNARQIIQLAEENQVDLIVLESLRGFRPPGYENLDQEKKRRVAFFAHGRIRRKVTEKAVE RGMRVVTVPYLASSKVCAECRKKQKDNKQWEKNKKRGLFKCEGCGSQAQVDENAARVLGR VFWGEIELPTAIP
173	Cas12	MAVKSIKVKLRLSECPDILAGMWQLHRATNAGVRYYTEWVSLMRQEILYSRGPDGGQQCYM TAEDCQRELLRRLRNRQLHNGRQDQPGTDADLLAISRRLYEILVLQSIGKRGDAQQIASSFLSPL VDPNSKGGRGEAKSGRKPAWQKMRDQGDPRWVAAREKYEQRKAVDPSKEILNSLDALGLRP LFAVFTETYRSGVDWKPLGKSQGVRTWDRDMFQQALERLMSWESWNRRVGEEYARLFQQK MKFEQEHFAEQSHLVKLARALEADMRAASQGFEAKRGTAHQITRRALRGADRVFEIWKSIPEE ALFSQYDEVIRQVQAEKRRDFGSHDLFAKLAEPKYQPLWRADETFLTRYALYNGVLRDLEKAR QFATFTLPDACVNPIWTRFESSQGSNLHKYEFLFDHLGPGRHAVRFQRLLVVESEGAKERDSV VVPVAPSGQLDKLVLREEEKSSVALHLHDTARPDGFMAEWAGAKLQYERSTLARKARRDKQG MRSWRRQPSMLMSAAQMLEDAKQAGDVYLNISVRVKSPSEVRGQRRPPYAALFRIDDKQR RVTVNYNKLSAYLEEHPDKQIPGAPGLLSGLRVMSVDLGLRTSASISVFRVAKKEEVEALGDGR PPHYYPIHGTDDLVAVHERSHLIQMPGETETKQLRKLREERQAVLRPLFAQLALLRLLVRCGAA DERIRTRSWQRLTKQGREFTKRLTPSWREALELELTRLEAYCGRVPDDEWSRIVDRTVIALWRR MGKQVRDWRKQVKSGAKVKVKGYQLDVVGGNSLAQIDYLEQQYKFLRRWSFFARASGLVV RADRESHFAVALRQHIENAKRDRLKKLADRILMEALGYVYEASGPREGQWTAQHPPCQLIILEE LSAYRFSDDRPPSENSKLMAWGHRGILEELVNQAQVHDVLVGTVYAAFSSRFDARTGAPGVR CRRVPARFVGATVDDSLPLWLTEFLDKHRLDKNLLRPDDVIPTGEGEFLVSPCGEEAARVRQVH ADINAAQNLQRRLWQNFDITELRLRCDVKMGGEGTVLVPRVNNARAKQLFGKKVLVSQDGV TFFERSQTGGKPHSEKQTDLTDKELELIAEADEARAKSVVLFRDPSGHIGKGHWIRQREFWSLV KQRIESHTAERIRVRGVGSSLD
174	Cas12	MSNPNIPNISPNITLTRDDVVNLLMSSIAMEELGLAHIINAEGEKIQFALGTLQGASGPPATLQQ VLEVNQSTQAMLDTIFRQEMMLDSKLKTATNIPTLRGPTGPVGPTGAPGGVISINGQTGVVTL DASNGVMPFMREQSTSSLDDYKDPGIYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXX

		GPRERQVRQGLQGLLEPRAKRERQVRPEPREPQERQAPLVQQALLEPQALLGQAL
175	Cas12	MIKKSNFWQFTGLYELSKTLRFELKPVWETLNILEKDWVSQKDKEVEENYNKIKVFFDSLHREF VKQSLENWYLELLENFYNSYIELNKNIENKKNKSLQKLFEKSSKELKKELVSFFEWKWNDWKQK YSFLKKWWIDVLNEKEVLDLMWEFYPKEKELFKKFDKFFTYFSNFKESRKNFYADDWRAWAIA TRVIDENLITFIKNIEDFKKFKNNFSDFIENGFSDWKIKINWFTLEEKQVFDLDFYNNCLLQDWI DNYNKILWWFSEENWNKIQWINEKINLFKQNQNKTNSKDVKFPRFKLLYKQILSEKEKLIFVDE IENDEKLINFIKESKNNNLIKVEKAIEITENFIKNNETFELDKIYLSKISINTISNKFFSSWDYILKEGF DKWEIKEFISFEDLKNAFGKIKYENLEDIFKSNYITDYIAINWEDLYKNFLNIFLYEFKQNINEINFY NSELEKLFLEKFEKTETQVQIIKNYFDSVLSLYKMTKYFALEKGKKKIEDLETDNNFYNDFFVYYE DFEIWKDYNLVRNFITKKQVKTDKFKLNFENSQFLTGWDKDKEKERLWIILKKDEKYYLWILKN NKIFNSYNYESWDFYEKMSYKQLNNVYRQLPRFAFSKAKREVYWITPELEQIKEEFDIFQKNKE KWEKFDIEKLKKLINCYKKWFIKTYENEFDLEKIKNTDYLDLATFYDEIEQKTYKIDFNKISENFIN AKVNSWELYLFQIYNKDFSETKKAWSKENIHTKYFKLLFDEKNLEKLVIKLSWWAEMFFREKTEK LKTKLDKSWKEVLEHRRYSKDKIMLHLSITLNANKWDSFWFNKMVNEYLNKNEDIKIIWIDRG EKHLAYYSVIDKNWKIEEIDTLNIIKSSDWKITNYLEKLEKIESSRKDSRVSWWEIENIKELKNGYI SQVVNKLAELIIKYNAIIVFEDLNIWFKRWRQKIEKQIYQKLELALAKKLNYLTQKDKNDNEVLW NLKALQLVPKVNDYQDIANYKQSGIMFYTRANYTSTTCPCCWFRKNIYISNSDTKEKQKKDFE KIDIKFDGEKFIFSYEIIQDKKAKQKSNKTNFSVNSNFSRFKYNSKKMLVEEVNLNLELQNLFKDI DLKWDINKQILEKDSYFYKSLTYYFNLILQLRNSDSKNDIDYITCPSCNYHSKDWFQGLEYNAD ANWAYNIARKWIIMLDRIEKNFEKPDLYVSDIDWDNFTQK
176	Cas12	MIKKSNFWQFTGLYELSKTLRFELKPVWETLNILEKDWVSQKDKEVEENYNKIKVFFDSLHREF VKQSLENWYLELLENFYNSYIELNKNIENKKNKSLQKLFEKSSKELKKELVSFFEWKWNDWKQK YSFLKKWWIDVLNEKEVLDLMWEFYPKEKELFKKFDKFFTYFSNFKESRKNFYADDWRAWAIA TRVIDENLITFIKNIEDFKKFKNNFSDFIENGFSDWKIKINWFTLEEKQVFDLDFYNNCLLQDWI DNYNKILWWFSEENWNKIQWINEKINLFKQNQNKTNSKDVKFPRFKLLYKQILSEKEKLIFVDE IENDEKLINFIKESKNNNLIKVEKAIEITENFIKNNETFELDKIYLSKISINTISNKFFSSWDYILKEGF DKWEIKEFISFEDLKNAFGKIKYENLEDIFKSNYITDYIAINWEDLYKNFLNIFLYEFKQNINEINFY NSELEKLFLEKFEKTETQVQIIKNYFDSVLSLYKMTKYFALEKGKKKIEDLETDNNFYNDFFVYYE DFEIWKDYNLVRNFITKKQVKTDKFKLNFENSQFLTGWDKDKEKERLWIILKKDEKYYLWILKN NKIFNSYNYESWDFYEKMSYKQLNNVYRQLPRFAFSKAKREVYWITPELEQIKEEFDIFQKNKE KWEKFDIEKLKKLINCYKKWFIKTYENEFDLEKIKNTDYLDLATFYDEIEQKTYKIDFNKISENFIN AKVNSWELYLFQIYNKDFSETKKAWSKENIHTKYFKLLFDEKNLEKLVIKLSWWAEMFFREKTEK LKTKLDKSWKEVLEHRRYSKDKIMLHLSITLNANKWDSFWFNKMVNEYLNKNEDIKIIWIDRG EKHLAYYSVIDKNWKIEEIDTLNIIKSSDWKITNYLEKLEKIESSRKDSRVSWWEIENIKELKNGYI SQVVNKLAELIIKYNAIIVFEDLNIWFKRWRQKIEKQIYQKLELALAKKLNYLTQKDKNDNEVLW NLKALQLVPKVNDYQDIANYKQSGIMFYTRANYTSTTCPCCWFRKNIYISNSDTKEKQKKDFE KIDIKFDGEKFIFSYEIIQDKKAKQKSNKTNFSVNSNFSRFKYNSKKMLVEEVNLNLELQNLFKDI DLKWDINKQILEKDSYFYKSLTYYFNLILQLRNSDSKNDIDYITCPSCNYHSKDWFQGLEYNAD ANWAYNIARKWIIMLDRIEKNFEKPDLYVSDIDWDNFTQK

[0158]

177	Cas12	MATRSFILKIEPNEEVKKGLWKTHEVLNHGIAYYMNILKLIRQEAIYEHHEQDPKNPKKVSKAEI QAELWDFVLKMQKCNSFTHEVDKDVVFNILRELYEELVPSSVEKKGEANQLSNKFLYPLVDPN SQSGKGTASSGRKPRWYNLKIAGDPSWEEEKKKWEEDKKKDPLAKILGKLAEYGLIPLFIPFTDS NEPIVKEIKWMEKSRNQSVRRLDKDMFIQALERFLSWESWNLKVKEEYEKVEKEHKTLEERIKE DIQAFKSLEQYEKERQEQLLRDTLNTNEYRLSKRGLRGWREIIQKWLKMDENEPSEKYLEVFKD YQRKHPREAGDYSVYEFLSKKENHFIWRNHPEYPYLYATFCEIDKKKKDAKQQATFTLADPINH PLWVRFEERSGSNLNKYRILTEQLHTEKLKKKLTVQLDRLIYPTESGGWEEKGKVDIVLLPSRQFY NQIFLDIEEKGKHAFTYKDESIKFPLKGTLGGARVQFDRDHLRRYPHKVESGNVGRIYFNMTVN IEPTESPVSKSLKIHRDDFPKFVNFKPKELTEWIKDSKGKKLKSGIESLEIGLRVMSIDLGQRQAA AASIFEVVDQKPDIEGKLFFPIKGTELYAVHRASFNIKLPGETLVKSREVLRKAREDNLKLMNQKL NFLRNVLHFQQFEDITEREKRVTKWISRQENSDVPLVYQDELIQIRELMYKPYKDWVAFLKQL HKRLEVEIGKEVKHWRKSLSDGRKGLYGISLKNIDEIDRTRKFLLRWSLRPTEPGEVRRLEPGQRF AIDQLNHLNALKEDRLKKMANTIIMHALGYCYDVRKKKWQAKNPACQIILFEDLSNYNPYEER SRFENSKLMKWSRREIPRQVALQGEIYGLQVGEVGAQFSSRFHAKTGSPGIRCSVVTKEKLQD NRFFKNLQREGRLTLDKIAVLKEGDLYPDKGGEKFISLSKDRKLVTTHADINAAQNLQKRFWTR THGFYKVYCKAYQVDGQTVYIPESKDQKQKIIEEFGEGYFILKDGVYEWGNAGKLKIKKGSSKQ SSSELVDSDILKDSFDLASELKGEKLMLYRDPSGNVFPSDKWMAAGVFFGKLERILISKLTNQYS ISTIEDDSSKQSM
178	Cas12	MAESMYNQQNINQKSTETPTEEDALGIKNPLLTPTTLGQNFLSLQSISPLGSRSINLINWSLISP NQTLLQNFQDNENWQDSSISEFRPFSKNSLTENSPIIEPQSDKTLPSSVPIQLSSELPIQQPPETS FIDSESPIPQPPETPSSDSESPIGQTENIFPFQIDQKTRRNSVIQNSKSSISHFFQKKSEFPREKISQ ENVNKLTKKSAENQDISTTEESVINSIETNDLQTINPTDIPNPEIPVSTLQKQPDSTIDNIPQTESV STINPTDIPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSKNNRIPQLITFLKLNQYQ QLILQIFLTQKFSFQLSKNNRIPPLITFLKLNQYQQLIPRVLLHQKFLFQLFKNNRIPPLITFPKLNQ YQQLIPRIFLTQKFPFQISRNNRIPQLITFPKLNQYQ
179	Cas13	MGAIKNKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS

[0159]

		SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIGSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDLSNDSSA
180	Cas13	MARDNFLNTIKLLADKMKLGAISGFGKDGNEVNDINKLFGDKNTYANIENVVEFYFPWIKALE GRFSLDKGDRNLNDMKMFYKSVLTAFFTAVDSLRNKYTHYSHKDLNIREIKIECTLGGKDYCIGL LNALDCIYDSAVNLLKLRFMVGEDEVAHLRRCKAVNKKVVVRTEKDGFYYRLSDNGGVTEKGV IFIASMFLNRKYGFLFLKQLEGFKRSDEKRYRLTLEAFLAFSNIKPVDRLKSDKLDRASLGLDMLN ELTKIPKELSETLSVDCLYKYLASDGEDDLRSRIRYQDRFVPLALEFISQSDEFKDFRFYTYVGNYV YKGYIKRLIDGTDKERYLSDRLCGFYKSVNDASSDAIAQKYGVEIKDSNEPDYMLPDSFRPHVL RATPHFVINNNNIGIKICGNDCLPIVNGKGVESPEPDYWLSIYELPAMLFYAYLREKNGKRFKDY KSIRELIEGVEKKADEKNDRDKGALMARHIDKEIIWTQTKLDEVKRLEEKKVAAYGKKGRVVLKS GRMADLLAHDMVRLQPATKGSDKITGVNFQALQVSLAYFKRDILADVFSRAMLTTGNHRHPF LYRIDVSHCSSLRDFYVAYLGERRKYFEDVAKKIAKNKLNTPCHILRRLQREGSGEEAGKDVKPK FLPRGIFTDSIKNCLEQSKLNIYIRNARNDVKPAINAAYLILMYYKEIEKGEFQGFYGEKRRYDILE EGKPLDLAERKKALASIKPAKIDVSEANMPMSKEEHLMRKRYHAVCNNESAIRMYQVQDILLL LMAKDIFKKALSEGVMSKKIGLENLNGIFDAPVNFVKNFDNIKLTATGIKIKNYGKVCRLGTDFK FNSLIKAFHKVYSKSVEMDYSDYLKEEEEFEKYRLNMVKLCREVERGITEDLHLSLDGKSHLSFN DDVIKPYNDKYNVFNGDDLTFFINARNMFMHGDYKYECVKYVVSEHFKGSLNDVSFAKETYG HFCNLLESMRKKTGLRIDI
181	Cas13	MKKKISLKEQRNTKKAENKLKYQKAQAERAAAAQQTAAGAESEENPCFDVVKDTKRKALNPL HVEIEAPSAKKSSVKANGLKSLLLTDGKTVMTSFGRGSEANVEKRFDETGTKTFDRDPELFSAK PLETGYRIQRFNASPKDAGLAYRPAGVRPDQIGAKAALEKRYFGKETPGDNIHVQIAYQIQDIEK LLAVYISNIIYAVNNVTGVSAMKDSKGRPVDLLGDYGILGEEGLTKRLQRIPEQADEEAKALQAF LCSERLSYFGKEFCLVRNSPKQPDKEEKRQYKLMRVLCLLGELRQFLVHGKKKEKEFAWLYRLDR QLSQEYRKLLGEFYDAQVDKVNKSFLTNSTVNLEVLFRALKTGTDPERKTVTQEYYQFTVRKED GNLGFSLKTLREILLSAYKHEVRDKEYDSIRHKLYQLFSFALYHYYKTGVGAERREAFVAKLRAVM TAEAKQRAYADEAAEIWNDEGSGIRAAFLEILEAVDFGSAVKGIKARSSVAGDKRFAEWLEEVRI RPEGVSCFTKLMYLLTRFLDGKEINELLTGLINKLENIQSFLDVMQQEHAETGLSDAFSFFEYSGE IAAELRMTRSFARMAAADPEAKRFMVVDGAKLLGFNPKDTESEDEGIIRAIYGDACAEYLQFSE EEKEAFYVQEGLYGKEREKFSPYAYFHTDTSLRNFIAKNVVESARFRYVIRYVSPEIARKYARQEAL VRFALHRVPLLQLRRYYQSCCGPKKDPDAAECVDFLAGVVNRVDFANFTDVRTGDSSKSEQE KKQKYQAIVGLYLTVVYWIVKNLVNVNSRYVMAFHILERDTVLLEGKRLFVGGMKAEDPFLLTD GYVSRQDAYVRKRIGENKRANRHGLNCVLENRNALGSDPASTDAAASLIWSYRNAAAHLTAV AAAQEYVSELREIHSYFEVYHYAMQRYLKSGAEFAELVSKNGPASGKIAAWANAVDRCHSFCK DWLWLLNVPFAYNPARYKNLSIANLFDKNEAAPVTEDASEQKEDE

[0160]

182	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA
183	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPRGYDIPS SLNCIYDSAINIIKERFQAEEKEMEHLRNYTLVNNNGLSEKGYAFFISKFLERKYSYLFLKKLSGFK RGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPIELYQTLEPKYREMYNETL QPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLGNYFHNGYQKTRVDRETK DRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYLVQSTPHYIVNGNNIGIKV LPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHKSHCPLSVKDIIERSIHKSTK QKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHEILKAGRIAETLVRDMLWL QPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSNPHPFLAQIGTNYTSLIEF YIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEEAIFLPRGLFNEAIINCLKKSK LKHLIESPTREKSPALNVSYLIHNYFRAYFEDQSQEFYAQPRNYRLFDKLSPNKGKSKSYLSLEQR IKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQDILLFMMTKEYLPSDLYNR INKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRISSLNKVLSKVKRNNSISS SVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPGNYYDFNELITEYEKRTKQKI DSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKLEDLSNDSSA
184	Cas13	CILDFFTQDKAIAEYQLGVEFLQKNLPVIRYLYLPTSHKRFENVPKNQLISEQRNYFKNSLKVLKN LIRDYRNFYTHHFHKPIPVFPETYKLLDDLFLAVANDVKKHRMKTDASKQLLKKGLIEELAQLEK LKLEDLKKLKREGKKVNLNDKEAITNAILNDSFSHLLPKENTISKYYSAVPTEDIDTENGVTISESG IIFLLGLFLTKKQSEDLRSRVKGFKAKLIVNPENPINKKNNSLKYMATHWVFGYLGFKGLKNRFT TTFTKDTLLAQIVDELSKVPDELYQVLPEELKNEFLEDMNEYLKEENSESLDKATVIHPVIRKRYE NKFAYFALRFLDEFVDFPTLRFQLHLGNYVHDKREKPIEGTKYVTERIVKEKIKAFAKLSEAAQLK QKYFEEKENHQSIGLQLYPNPSYNFVGNNIPIHLNLNEHFFPKEVKIVAGRLKKRNSSYKSDHP

[0161]

		EEYKVRTDNKIKPDAILQDLGKPEKLAPVAMLSLNELPALLHLVLTKKTPEEIEIIIAQKIAERYNVL TNYKAGDDISKGQITKNLLKAKQKKEVNLDKLQLAIEKEIAVTNDKLQTIALHIKERNDPKQKRK YVFTNKEIGLQVTWLANDLKRFMPKGSRQNWRGQHHSQLQKSLAFYDIQPKEPLSLLEEVW DFKNEAYLWNNGIRRSFDKRDFISFYTSYLNNRKETFQRFKDQLNGIRSNKKILDKFIKQQHLW NLFHKRLYVIDTIEEQVEKLLVKPMQFPKGVFDHKPTYIKGKSIQENPECFADWYVAWNQHTD YQKFYSWDRDYKSAYLSGEQEKTEKRFIRVQGSKINKVKQQDVLLAKMASIIFNELYLPEDAEH LDLNLSDIYKTQTERKAEIEAALIQSHKTTGDNSANIIKSTSAWTLTVPYCSKNIYEPQVKLKELG KFKKFIASQKVQTLFEYKPQKIWNKTELEEVLELKANSYEVIRRDYLLKSIQEFEKYMIKKLPTLIDT NEHPNFNKYLTTFLKSLELVSEEDAKWLISKKDFDTTPIDELKKQSKIMEKAFLLVMIRNKFSHN QLPRKIYYDEIYKNVPNAVSINFNELFLEYTNQTILEFK
185	Cas13	NRRDMEASPGRLARYIVLKTLYERAFPRWLEAREAETLNGWIGRAADRATVAARHINKDENA AARMAGLVRLADGKGIADFTDRLAAETASEYRVQRGYDSDPAVARKQAKHIEDLRCDVVGQA FEAYLADVARKLAWTMNDPPGGPLPDEKKASLETAAPPAEDAGAEAEEDWLARLYFLLHMLP VEEVGGLRHQLRKWSVLEREPDSVLEREPDADVEAIERILGLYLDMHDAKFEGGDGVAGAEAL TDLFTSPAQFRRVCPEDGAGNGGHVPWRGLREMLRFGGGEPRLMWAFRKWPIGDGMVDG LNALEATVAEAHKQREDLHAKWAGKKGFSRKDKDEYRAALETVVVHRHLAAHVQLVNHARL HRLAMAVLARLADYAGLWERDLYFTTLALIRLENGKPEDVFRSRELEWLREGRIVDALKELKKN ADGSEPAVGTALQRLFGKGILTGGGTVSVRRDLLHFNMLQRKANEPFNLTTAVNDTRKLMAYD RKLKNAVSRSIIELLAREGLDLAWEMKDHQLAGAVLKTRQAVHLGGAKVGGGPITEDLHGPEF TAMAAALFGGEARAATDAAEAATGRPDRRERKSGGASPRPARPAKTLPAPTPRLLPAAGERVE GVLVEEKTRKGGWKAAVEIGGPRIVGDIFNSGEVPSDAEPGLEAEFVVRVANPANASFMWLSP DVEERLKKAAAPRRGGRPAGRQR
186	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA

[0162]

187	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPRGYDIPS SLNCIYDSAINIIKERFQAEEKEMEHLRNYTLVNNNGLSEKGYAFFISKFLERKYSYLFLKKLSGFK RGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPIELYQTLEPKYREMYNETL QPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLGNYFHNGYQKTRVDRETK DRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYLVQSTPHYIVNGNNIGIKV LPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHKSHCPLSVKDIIERSIHKSTK QKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHEILKAGRIAETLVRDMLWL QPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSNPHPFLAQIGTNYTSLIEF YIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEEAIFLPRGLFNEAIINCLKKSK LKHLIESPTREKSPALNVSYLIHNYFRAYFEDQSQEFYAQPRNYRLFDKLSPNKGKSKSYLSLEQR IKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQDILLFMMTKEYLPSDLYNR INKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRISSLNKVLSKVKRNNSISS SVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPGNYYDFNELITEYEKRTKQKI DSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKLEDLSNDSSA
188	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA
189	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPRGYDIPS SLNCIYDSAINIIKERFQAEEKEMEHLRNYTLVNNNGLSEKGYAFFISKFLERKYSYLFLKKLSGFK RGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPIELYQTLEPKYREMYNETL QPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLGNYFHNGYQKTRVDRETK DRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYLVQSTPHYIVNGNNIGIKV LPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHKSHCPLSVKDIIERSIHKSTK

[0163]

		QKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHEILKAGRIAETLVRDMLWL QPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSNPHPFLAQIGTNYTSLIEF YIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEEAIFLPRGLFNEAIINCLKKSK LKHLIESPTREKSPALNVSYLIHNYFRAYFEDQSQEFYAQPRNYRLFDKLSPNKGKSKSYLSLEQR IKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQDILLFMMTKEYLPSDLYNR INKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRISSLNKVLSKVKRNNSISS SVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPGNYYDFNELITEYEKRTKQKI DSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKLEDLSNDSSA
190	Cas13	MEEANRYIYGAYFNMARDNFLNTIKLLADKMKLGATSGFGKDGNEVNDINELFGDKNTYANI ENVVEFYFPWIKALEGRFSLDKGDRNLNDMKMFYKSVLTAFFTAVDSLRNKYTHYSHKDLNIR EIKIECTLGGKDYCIGLLNALDCIYDSAVNLLKLRFMAGEYEVAHLRRCKAVNKKVVVRTEKDGF YYRLSDNGGVTEKGVIFIASMFLNRKYGFLFLKQLEGFKRSDEKRYRLTLETFLAFSNIKPVDRLK SDKLDRASLGLDMLNELTKIPRELSETLSVDCLYKYLTSDGEDDLRSRIRYQDRFVPLALEFISQS DEFKDFRFYTYVGNYVYKGYIKRLIDGTDKERYLSDRLCGFYKSVNDASSDAIAQKYGVEIKDSN EPDYMLPDSFRPHVLRATPHFVINNNNIGIKICGNDCLPIVNGKGVESPEPDYWLSIYELPAML FYAYLREKNGKLLKDYKSIRELIEDVEKKADEKNDRDKGALMARHIDKEIIWTQTKLDEVKRLEEK KVAAYGKKGRVVLKSGRMADLLAHDMVRLQPATKGSDKITGANFQALQVSLAYFKRDILADV FSRAMLTTGNHRHPFLYRIDVSHCSSLRDFYVAYLGERRKYFEDVAKKIAKNKLNTPCHILRRLQ REGSGEEAGKDVKPKFLPRGIFTGSIKSCLEKSALNINIRNARNDVKPAINAAYLILMYYKEIEKGE FQGFYGEKRRYDILEEGKPLDLDERKKALASIKPAKIDVSEANMPMSKEEHLMRKRYHAVCNN ESAIRMYQVQDILLLLMAKDIFKKALSEGVMSKKIGLENLNGIFDAPVNFVKNFDNIKLTATGIKI KDYGKVCRLGTDFKFNSLVKAFHKVYSKSVEMDYSDYLKEEEEFEKYRLNMVKLCREVERGITE DLHLSLDGKSHLGFNDDVIKPYNDKYNVFNGGDLTFFINARNMFMHGDYKYECVKYVVSEH FKGSLNDVSFAKETYGHFCNLLESMRKKTGLRIDI
191	Cas13	MGAIKNKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIGSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE

[0164]

		NIKLEDLSNDSSA
192	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA
193	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEIEHLRRYTRKKGRVVLKTEDDHFYYTLVNNNDLSEKGYAFFIS MFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPI ELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLG NYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYL VQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHK SHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHE ILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSN PHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEEAIF LPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRLFD KLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQD ILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRI SSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPG NYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKL EDLSNDSSA
194	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI

[0165]

		PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA
195	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFETFALHFLDKQPDFKEIGFYTYLG NYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYL VQSMPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIH KSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQH EILKAGRIAEMLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDLSNDSSA
196	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPRGYDIPS SLNCIYDSAINIIKERFQAEEKEMEHLRNYTLVNNNGLSEKGYAFFISKFLERKYSYLFLKKLSGFK RGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPIELYQTLEPKYREMYNETL QPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLGNYFHNGYQKTRVDRETK DRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYLVQSTPHYIVNGNNIGIKV LPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHKSHCPLSVKDIIERSIHKSTK QKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHEILKAGRIAETLVRDMLWL QPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSNPHPFLAQIGTNYTSLIEF YIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEEAIFLPRGLFNEAIINCLKKSK LKHLIESPTREKSPALNVSYLIHNYFRAYFEDQSQEFYAQPRNYRLFDKLSPNKGKSKSYLSLEQR IKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQDILLFMMTKEYLPSDLYNR

[0166]

		INKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRISSLNKVLSKVKRNNSISS SVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPGNYYDFNELITEYEKRTKQKI DSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKLEDLSNDSSA
197	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEIEHLRRYTRKKGRVVLKTEDDHFYYTLVNNNDLSEKGYAFFIS MFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPI ELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLG NYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYL VQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHK SHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHE ILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSN PHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEEAIF LPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRLFD KLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQD ILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRI SSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPG NYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKL EDLSNDSSA
198	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLILNYFRTYFEDQSQEFYAQPRNYRLF DKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQ DILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDT RINSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATP GNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIK LEDFSNDSSA
199	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP

[0167]

		SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRIINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDLSNDSSA
200	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSKKGYAFF ISMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLILNYFRTYFEDQSQEFYAQPRNYRLF DKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQ DILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDT RINSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATP GNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIK LEDFSNDSSA
201	Cas13	MKHVFAAYFSDARLNIMASLNDVREKSGLKRYKNEAENVQNFEGIFPKNIASDIRDKRITLLRIR FPFIETIVDPGRGKENPASKYGELSWLFQLVNDMRNVFIHSTGSEEEIDYQHHKKIFNALRKVYD CGLRTVKSRFQLENDTTMPLLRCDNRGRPKPFNKFSLALCTSPERNGNKKQSDVLHDFGRVLL CSLFLEKRQISGLVSHFWDKNGYGTDWNDSEQTIIRELLYVNRIRLPSQRLRTDSTLTSVTLDTIS ELARCPRPLFELLDADGQENFRVGRSPKNPQNRNDDPSYLLLRGHQSRFIPLAMRHLDFDSK CKLRFAVDLGQYYHSVRLKPAESFIDGNPGIRRLGQKIIAFGRLKDFEDAEKPEIWKKLEENGQK FAEEEEELLKRASITGSPEELKPYIIKTFPHYHLYRDKIGFCIDWEEKKDQKVKYPNLGVRGEDSKS TDSGGIKKRENRQLSRHQFWISPNKIIDLAFYHYLQTEIKQEITASVKTGRKKCPYPSVENILKEYY EGMVVLIKELKEQGPLPPWTEIPQISERRAECHRWINKEIIKAENFTISLADLPKAIRRHLKVLDS RETSVSDIIKRTKTMIEETCKKQKEIEYLLKYPKKRGKKGFRPIKHGNIADFLTEDLLRFQPKDSSKK

[0168]

		NGGKLTSKNYQILQKAIAYYDKPYCIVDLLKKSGLLEGEFKHPFLCKIITEENHEQYSTLIDFYQKY LEERKAFLEGFIDTFVAGSSIPGWLRLRKPSTFESWLDQQLDEDEKLCQPLPVPKSLFYQMLLKM TAEKLDLTPEMLCKKGTQRFIRDSQEVEVKPSVSWFIRQYMEHRDDTAQEMYMFKRRHELFDF FHDKKKTTKKLHEEKTCCLSEKVRQEELESVHKGIEKLKKLLRTYKRSEKKIRHFSTMDMVLYLLA KKNFEKLILCDETSGPDWSLKTLETKILSTKIKYELNVPGTDRTIVHRACAIKKTGELRLLVRDRRL PSLLDYYPKTEKSIDQEEIKVELADYSCKRIEAMKLISDLEQKIEESCNRGFCKPVPDKLKKIFGAK KHGTLLYALYHRFHEEKDKSVDEQGFNKDCFAHARQIRNAFAHNEYPVSEQFNQIVRQVNET SQPHNHNSPVNHPKIADQLVKELDKLYKPWRNFLKRIAG
202	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPRGYDIPS SLNCIYDSAINIIKERFQAEEKEMEHLRNYTLVNNNGLSEKGYAFFISKFLERKYSYLFLKKLSGFK RGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPIELYQTLEPKYREMYNETL QPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLGNYFHNGYQKTRVDRETK DRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYLVQSTPHYIVNGNNIGIKV LPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHKSHCPLSVKDIIERSIHKSTK QKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHEILKAGRIAETLVRDMLWL QPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSNPHPFLAQIGTNYTSLIEF YIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEEAIFLPRGLFNEAIINCLKKSK LKHLIESPTREKSPALNVSYLIHNYFRAYFEDQSQEFYAQPRNYRLFDKLSPNKGKSKSYLSLEQR IKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQDILLFMMTKEYLPSDLYNR INKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRISSLNKVLSKVKRNNSISS SVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPGNYYDFNELITEYEKRTKQKI DSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKLEDLSNDSSA
203	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPRGYDIPS SLNCIYDSAINIIKERFQAEEKEMEHLRNYTLVNNNGLSEKGYAFFISKFLERKYSYLFLKKLSGFK RGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPIELYQTLEPKYREMYNETL QPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLGNYFHNGYQKTRVDRETK DRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYLVQSTPHYIVNGNNIGIKV LPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHKSHCPLSVKDIIERSIHKSTK QKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHEILKAGRIAETLVRDMLWL QPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSNPHPFLAQIGTNYTSLIEF YIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEEAIFLPRGLFNEAIINCLKKSK LKHLIESPTREKSPALNVSYLIHNYFRAYFEDQSQEFYAQPRNYRLFDKLSPNKGKSKSYLSLEQR IKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQDILLFMMTKEYLPSDLYNR INKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRISSLNKVLSKVKRNNSISS SVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPGNYYDFNELITEYEKRTKQKI DSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKLEDLSNDSSA

[0169]

204	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA
205	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPRGYDIPS SLNCIYDSAINIIKERFQAEEKEMEHLRNYTLVNNNGLSEKGYAFFISKFLERKYSYLFLKKLSGFK RGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPIELYQTLEPKYREMYNETL QPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLGNYFHNGYQKTRVDRETK DRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYLVQSTPHYIVNGNNIGIKV LPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHKSHCPLSVKDIIERSIHKSTK QKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHEILKAGRIAETLVRDMLWL QPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSNPHPFLAQIGTNYTSLIEF YIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEEAIFLPRGLFNEAIINCLKKSK LKHLIESPTREKSPALNVSYLIHNYFRAYFEDQSQEFYAQPRNYRLFDKLSPNKGKSKSYLSLEQR IKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQDILLFMMTKEYLPSDLYNR INKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRISSLNKVLSKVKRNNSISS SVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPGNYYDFNELITEYEKRTKQKI DSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKLEDLSNDSSA
206	Cas13	MGAIKNKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS

[0170]

		SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIGSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDLSNDSSA
207	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSKKGYAFF ISMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLILNYFRTYFEDQSQEFYAQPRNYRLF DKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQ DILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDT RINSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATP GNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIK LEDFSNDSSA
208	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMKHLRNYTLVNNNGLSEKGYAFFISKFLERKYSYLFLKKLSGF KRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKIPIELYQTLEPKYREMYNET LQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLGNYFHNGYQKTRVDRET KDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYLVQSTPHYIVNGNNIGIK VLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHKSHCPLSVKDIIERSIHKST KQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHEILKAGRIAETLVRDMLW LQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSNPHPFLAQIGTNYTSLIEF YIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEEAIFLPRGLFNEAIINCLKKSK LKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRLFDKLSPNKGKSKSYLSLEQR IKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQDILLFMMTKEYLPSDLYNR INKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRINSLNKVLSKVKRNNSIS SSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPGNYYDFNELITEYEKRTKQ KIDSSFLIKTRNMFLHDKYEAECIKEISDDLVYAKKIIAEFKMKIENIKLEDLSNDSSA

[0171]

209	Cas13	MGAIKNKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIGSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDLSNDSSA
210	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLILNYFRTYFEDQSQEFYAQPRNYRLF DKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQ DILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDT RINSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATP GNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIK LEDFSNDSSA
211	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ

[0172]

		HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA
212	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPRGYDIPS SLNCIYDSAINIIKERFQAEEKEMEHLRNYTLVNNNGLSEKGYAFFISKFLERKYSYLFLKKLSGFK RGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPIELYQTLEPKYREMYNETL QPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLGNYFHNGYQKTRVDRETK DRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYLVQSTPHYIVNGNNIGIKV LPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHKSHCPLSVKDIIERSIHKSTK QKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHEILKAGRIAETLVRDMLWL QPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSNPHPFLAQIGTNYTSLIEF YIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEEAIFLPRGLFNEAIINCLKKSK LKHLIESPTREKSPALNVSYLIHNYFRAYFEDQSQEFYAQPRNYRLFDKLSPNKGKSKSYLSLEQR IKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQDILLFMMTKEYLPSDLYNR INKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRISSLNKVLSKVKRNNSISS SVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPGNYYDFNELITEYEKRTKQKI DSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKLEDLSNDSSA
213	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRI PIELYQTLEPKYREMYNATLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLILNYFRTYFEDQSQEFYAQPRNYRLF DKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQ DILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDT RINSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATP GNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIK LEDFSNDSSA

[0173]

214	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFETFALHFLDKQPDFKEIGFYTYLG NYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYL VQSMPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIH KSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQH EILKAGRIAEMLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDLSNDSSA
215	Cas13	MGAIKNKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIGSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDLSNDSSA
216	Cas13	MGKLYGYKRWYEIEQNNGEKGSFKRKIRVKRVYDEESKSYVVRRDEVEDTELIKNKNFIINLKDY KTRNSNIQKFYDKFHVGNILFKLKASVKKGKKTFYKDLEKAETVLTNVEILEQTIKLANNSKINRK KLEKELTQLNINEKSEEVTIDNIKIYLRQGEKFDKKENINAIKWRKLTSEELTIKVEIYRECQSINSNL YSLLDYVLSNEEYDDRYYLEEVENKLLIFGTGNKNKNGRNYYYFDYVLKSLSKIKGLIKKDDRNL NYLMFLFNIQKTSENKEHFINKIFNYFKYEVRIEKEDIVEFLVGELEYYDLIKRIEKKPSENQNQTN LEKTYILLDKHEKLKETIDTKNEIVQKLTIELKNNNLRNRIEIILHKYKILELVDKLNKNIKNGKINTE

[0174]

[0175]

		LVGIYKEHYGQCIEYINFNELALEEKELYKIIYRYLKGRIEKLLQNRNKIKIGELRIEDIFIFQKLLEKIEI RVKQYLLEHILYLGKLKHHNIDEVNTIRFVEEHANEELSLELITLFSATNVELNRLLKVKGENGSYE KDYDFFSAKPDKGKIKIKDTNSVMKFELLKKLKFINSEATETNQEAIDFLKEAYNLRNNILHGKNE EIIEDNKKNLSKSYKNINELIEELRPSDNEICKSLNLDIIFKGNRKINDINAKLFGNNREKIYLPSFS KLVPEIKNIIESYDKNGTFNDERIKKIVLNGAIYVNKILYLKECSNKDGEFIKNLKEELNKDSKEKSK YVSIEELYKKSQISASKGNKKAIYKYQRKIIEIYLKYLKENYVEILDFSKLNLNIEQIENDIKNRKNSE NKVLIESIKQKVFPENDFEYIISIFALLNDNIFINKIRNRFFSTDTWLKNNRYSNIIKILDEVISVNLL RTELLNTSIDIEEIKDDVLTEDIENIIPEIREEILQRTKKDFKTLLGNNAISKEGLSNEDIDKIRNIEDA KINLDFVNNEIKVSLKEYGSLPPNGVLSRNTSKYYNNEIAKKIDQISILTFTKKSIGTISDEKFRNIY WQERKESDESKKIFVYNKNILYLVTKHSFEKLYKNFLEEELNNLKLEDTKYLRDLDLRREKNLKVD NTLKEINEKVRGYSKEYKKKFIENLKNNDEYFGKVVSGRFKNYQEFKEIYDEVSEYKKIRDVVNF NPLNKVYNYLIEINWKLAIQMARAERDLHYIVNGLNELKLIELNQGQNDGISRAYPKYKLNKEK NKKELRLEECHYNFDIDNYKKFEKICEKLGIDLSENGELQQENETNIRNYISHFYILRKPFVDISISE AIKRVSKLLSYRTRYNNSTYSSVFEVFKKDVELNYDFLKKKIELNGKTYDEVVQRKKISCLELESYL DYKPIIKKILF
217	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA
218	Cas13	MGAIKNKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS

		SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIGSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDLSNDSSA
219	Cas13	MGAIKNKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIGSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDLSNDSSA
220	Cas13	MGKLYGYKRWYEIEQNNGEKGSFKRKIRVKRVYDEESKSYVVRRDEVEDTELIKNKNFIINLKDY KTRNSNIQKFYDKFHVGNILFKLKASVKKGKKTFYKDLEKAETVLTNVEILEQTIKLANNSKINRK KLEKELTQLNINEKSEEVTIDNIKIYLRQGEKFDKKENINAIKWRKLTSEELTIKVEIYRECQSINSNL YSLLDYVLSNEEYDDRYYLEEVENKLLIFGTGNKNKNGRNYYYFDYVLKSLSKIKGLIKKDDRNL NYLMFLFNIQKTSENKEHFINKIFNYFKYEVRIEKEDIVEFLVGELEYYDLIKRIEKKPSENQNQTN LEKTYILLDKHEKLKETIDTKNEIVQKLTIELKNNNLRNRIEIILHKYKILELVDKLNKNIKNGKINTE LYGIYKEHYGQCIEYINFNELALEEKELYKIIYRYLKGRIEKLLQNRNKIKIGELRIEDIFIFQKLLEKIEI RVKQYLLEHILYLGKLKHHNIDEVNTIRFVEEHANEELSLELITLFSATNVELNRLLKVKGENGSYE KDYDFFSAKPDKGKIKIKDTNSVMKFELLKKLKFINSEATETNQEAIDFLKEAYNLRNNILHGKNE EIIEDNKKNLSKSYKNINELIEELRPSDNEICKSLNLDIIFKGNRKINDINAKLFGNNREKIYLPSFS KLVPEIKNIIESYDKNGTFNDERIKKIVLNGAIYVNKILYLKECSNKDGEFIKNLKEELNKDSKEKSK YVSIEELYKKSQISASKGNKKAIYKYQRKIIEIYLKYLKENYVEILDFSKLNLNIEQIENDIKNRKNSE NKVLIESIKQKVFPENDFEYIISIFALLNDNIFINKIRNRFFSTDTWLKNNRYSNIIKILDEVISVNLL RTELLNTSIDIEEIKDDVLTEDIENIIPEIREEILQRTKKDFKTLLGNNAISKEGLSNEDIDKIRNIEDA KINLDFVNNEIKVSLKEYGSLPPNGVLSRNTSKYYNNEIAKKIDQISILTFTKKSIGTISDEKFRNIY WQERKESDESKKIFVYNKNILYLVTKHSFEKLYKNFLEEELNNLKLEDTKYLRDLDLRREKNLKVD NTLKEINEKVRGYSKEYKKKFIENLKNNDEYFGKVVSGRFKNYQEFKEIYDEVSEYKKIRDVVNF NPLNKVYNYLIEINWKLAIQMARAERDLHYIVNGLNELKLIELNQGQNDGISRAYPKYKLNKEK

[0176]

		NKKELRLEECHYNFDIDNYKKFEKICEKLGIDLSENGELQQENETNIRNYISHFYILRKPFVDISISE AIKRVSKLLSYRTRYNNSTYSSVFEVFKKDVELNYDFLKKKIELNGKTYDEVVQRKKISCLELESYL DYKPIIKKILF
221	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEIEHLRRYTRKKGRVVLKTEDDHFYYTLVNNNDLSEKGYAFFIS MFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPI ELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLG NYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYL VQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHK SHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHE ILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSN PHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEEAIF LPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRLFD KLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQD ILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRI SSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPG NYYDFNELITEYEKRTKQKIDSSFRIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKL EDLSNDSSA
222	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA
223	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP

[0177]

		SSLNCIYDSAINIIKERFQAEEKEMEHLRRYIRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPVLNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA
224	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMKHLRNYTLVNNNGLSEKGYAFFISKFLERKYSYLFLKKLSGF KRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKIPIELYQTLEPKYREMYNET LQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLGNYFHNGYQKTRVDRET KDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYLVQSTPHYIVNGNNIGIK VLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHKSHCPLSVKDIIERSIHKST KQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHEILKAGRIAETLVRDMLW LQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSNPHPFLAQIGTNYTSLIEF YIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEEAIFLPRGLFNEAIINCLKKSK LKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRLFDKLSPNKGKSKSYLSLEQR IKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQDILLFMMTKEYLPSDLYNR INKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRINSLNKVLSKVKRNNSIS SSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPGNYYDFNELITEYEKRTKQ KIDSSFLIKTRNMFLHDKYEAECIKEISDDLVYAKKIIAEFKMKIENIKLEDLSNDSSA
225	Cas13	MGAIKNKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRL

[0178]

		FDKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIGSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDLSNDSSA
226	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLILNYFRTYFEDQSQEFYAQPRNYRLF DKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQ DILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDT RINSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATP GNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIK LEDFSNDSSA
227	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA

[0179]

228	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSKI PIELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKHLIESPTREKSPALNVSYLIQNYFRAYFEDQSQEFYAQPRNYRL FDNLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQI QDILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHH DTRISSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKA TPGNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIE NIKLEDFSNDSSA
229	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
230	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL

[0180]

		EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
231	Cas13	MDTPNFSERIPVSLQSHPYYFAHYLNMARHNAYVILEYVNRELIKPGKNLDEDNLIQSTVLKDG YFDRKPDELSHRNRLLVQHFPFLREAENEGARTCNPVSYKLKTALAALNQWRNNASHYPLNQ NHEKDFDLQPFFSFAIEACKKRMREVFQPDDFYLLETNEKQFYTLHNENGFTEKGLYCFICFFLE KKYAFQFLAGIKGFKNTTDNKFRATLETFTEHCCRLPKPKLDSSDIKLDMLGELSRCPAPLFDLLD IEERKKFIREPEEVKPDESGDREEVQQVLMKRYDDRFPYFALRYFEEKNLLKGISFHIHIGRWIKSE HTKKIMGAERDRRLLKDIRTFGELKEFSPEHAPDYWLRDGITPDDVDQFSPQYRIVGNRIGIKL NYNGHNRWSVPDKEINVKPDAIISTYEFLNLFLYEHLYQKKLTGLSPAEFIQDYLDRFNNFLSEF KAGHIRPVGDFSLEKRRGQGDEPDLTARRKSLQKELDRFVLKGKDLPDKIREYLLGYKQKSEKKQ AKWILGGMIKETVYWRNKAEQSPEKMRSGDMAQQLARDIIFLTPPHTVKEHKQKLNSLEYDV LQYALAYFSSNREKLYSFFKEHQLTVKGDRAHPFLYKIRLDECQGILDFFIVYMQQKEKWLGWL DRNLKSPRLNEEEFFNTYSYFIKTDTKRAIEMDYESCPNYLPRGIFNEPIAKALQKAGVKIKDED NASYALSVYSNGKTQPFYNKERYYNKGIFRMEELPEKLQPKELLGKIQWTIKSSGKDTEEFRSLQ NLKNRILNTEKEIRYVQSTDRALWIMVADLFPETFELRPDDLECIGHDLSDDLLSRPYQMKEKV YNYTITDYLPIKRYGEFRRFLKDRRLENLLTYFEEGVPLHREALVAELEAYDLQRKNLLEIIYRFEKL VFDRHRHELTFSGEGENQYVNHWDYLDFVARKYGLSAEVKELNSERFTELRNKMLHNQIPYQ LWIKEAIAAREENTVCGRIMGMIGEIYERMTTEIEKQMQV
232	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW

[0181]

		QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
233	Cas13	MENKTSLGNNIYYNPFKPQDKSYFAGYFNAAMENTDSVFRELGKRLKGKEYTSENFFDAIFKE NISLVEYERYVKLLSDYFPMARLLDKKEVPIKERKENFKKNFKGIIKAVRDLRNFYTHKEHGEVEIT DEIFGVLDEMLKSTVLTVKKKKVKTDKTKEILKKSIEKQLDILCQKKLEYLRDTARKIEEKRRNQRE RGEKELVAPFKYSDKRDDLIAAIYNDAFDVYIDKKKDSLKESSKAKYNTKSDPQQEEGDLKIPIS KNGVVFLLSLFLTKQEIHAFKSKIAGFKATVIDEATVSEATVSHGKNSICFMATHEIFSHLAYKKLK RKVRTAEINYGEAENAEQLSVYAKETLMMQMLDELSKVPDVVYQNLSEDVQKTFIEDWNEYL KENNGDVGTMEEEQVIHPVIRKRYEDKFNYFAIRFLDEFAQFPTLRFQVHLGNYLHDSRPKENL ISDRRIKEKITVFGRLSELEHKKALFIKNTETNEDREHYWEIFPNPNYDFPKENISVNDKDFPIAG SILDREKQPVAGKIGIKVKLLNQQYVSEVDKAVKAHQLKQRKASKPSIQNIIEEIVPINESNPKEA IVFGGQPTAYLSMNDIHSILYEFFDKWEKKKEKLEKKGEKELRKEIGKELEKKIVGKIQAQIQQIID KDTNAKILKPYQDGNSTAIDKEKLIKDLKQEQNILQKLKDEQTVREKEYNDFIAYQDKNREINKV RDRNHKQYLKDNLKRKYPEAPARKEVLYYREKGKVAVWLANDIKRFMPTDFKNEWKGEQHSL LQKSLAYYEQCKEELKNLLPEKVFQHLPFKLGGYFQQKYLYQFYTCYLDKRLEYISGLVQQAENF KSENKVFKKVENECFKFLKKQNYTHKELDARVQSILGYPIFLERGFMDEKPTIIKGKTFKGNEALF ADWFRYYKEYQNFQTFYDTENYPLVELEKKQADRKRKTKIYQQKKNDVFTLLMAKHIFKSVFK QDSIDQFSLEDLYQSREERLGNQERARQTGERNTNYIWNKTVDLKLCDGKITVENVKLKNVG DFIKYEYDQRVQAFLKYEENIEWQAFLIKESKEEENYPYVVEREIEQYEKVRREELLKEVHLIEEYIL EKVKDKEILKKGDNQNFKYYILNGLLKQLKNEDVESYKVFNLNTEPEDVNINQLKQEATDLEQK AFVLTYIRNKFAHNQLPKKEFWDYCQEKYGKIEKEKTYAEYFAEVFKKEKEALIK
234	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV

[0182]

		TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKSQI
235	Cas13	MTEQSERPYNGTYYTLEDKHFWAAFLNLARHNAYITLTHIDRQLAYSKADITNDQDVLSFKALWKNLDNDLERKSRLRSLILKHFSFLEGAAYGKKLFESKSSGNKSSKNKELTKKEKEELQANALSLDNLKSILFDFLQKLKDFRNYYSHYRHSGSSELPLFDGNMLQRLYNVFDVSVQRVKRDHEHNDKVDPHYHFNHLVRKGKKDRYGHNDNPSFKHHFVDSEGMVTEAGLLFFVSLFLEKRDAIWMQKKIRGFKGGTGPYEQMTNEVFCRSRISLPKLKLESLRTDDWMLLDMLNELVRCPKPLYDRLREKDRACFRVPVDILPDEDDTDGGGEDPFKNTLVRHQDRFPYFALRYFDLKKVFTSLRFHIDLGTYHFAIYKKMIGEQPEDRHLTRNLYGFGRIQDFAEEHRPEEWKRLVRDLDYLETGDKPYISQTTPHYHIEKGKIGLRFVPEGQHLWPSPEVGTTRTGRSKCAQDKRLTAEAFLSVHELMPMMFYYFLLREKYSEEVSAEKVQGRIKRVIEDVYAIYDAFARDEINTLKELDTCLADKGIRRGHLPKQMITILSQERKDMKEKIRKKLQEMIADTDHRLDMLDRQTDRKIRIGRKNAGLPKSGVIADWLVRDMMRFQPVAKDASGKPLNNSKANSTEYRMLQRALALFGGEKERLTPYFRQMNLTGGNNPHPFLHETRWESHTNILSFYRSYLRARKAFLERIGRSDRVENCPFLLLKEPKTDRQTLVAGWKDEFHLPRGIFTEAVRDCLIEMGYDEVGSYREVGFMAKAVPLYFERACEDRVQPFYDSPFNVGNSLKPKKGRFLSKEDRAEEWERGMERFRDLEAWSHSAARRIKDAFAGIEYASPGNKKKIEQLLRDLSLWEAFESKLKVRADKINLAKLKKEILEAQEHPYHDFKSWQKFERELRLVKNQDIITWMMCRDLMEENKVEGLDTGTLYLKDIRPNVQEQGSLNVLNRVKPMRLPVVVYRADSRGHVHKEAPLATVYIEERNTKLLKQGNFKSFVKDRRLNGLFSFVDTGGLAMEQYPISKLRVEYELAKYQTARVCVFELTLRLEESLLSRYPHLPDESFREMLESWSDPLLAKWPELHGKVRLLIAVRNAFSHNQYPMYDEAVFSSIRKYDPSSPDAIEERMGLNIAHRLSEEVKQAKETVERIIQA
236	Cas13	MEKPLPPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLTTPPNDDKIADVVCGTWNNILNNDHDLLKKSQLTELILKHFPFLAAMCYHPPKKEGKKKGSQKEQQKEKENEAQSQAEALNPSELIKALKTLVKQLRTLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTQDFAHLNRKGKNKQDNPKFDRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQSEKMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEKDKKHFQVEADGFLDEIEEEQNPFKDALIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTRTLLSFGRLQDFTEINRPQEWKALTKDLDYKETSKQPFISKTTPHYHITDNKIGFRLGTSKELYPSLEVKDGANRIAKYPYNSDFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERINTIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLGKRREKLIKTGDWLVKDFMRFQPVAYDVQNQPIESSKANSTEFQLIQRALALYGGEKNRLEGYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKIPKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLTLSKPIRKEIKKHGRVGFISRAITLYFRERYQDDHQSFYNLPYELEAKASTPKPPLPKKREYVLRAEHYEYWQQNKPQSPTELQRLELHTSDRWKDYLLYKRWQHLEKKLRLYRNQDVMLWLMTLELTKNHFKELKLNYHQLKLENLAVNVQEADAKLNPLNQTLPMVLPVKVYPATAFGEVQYQETPIRTVYIREEQTKALKMGNFKALVKDRRLNGLFSFIKEENDTQKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHASLSSLENEFRTLLEEWKKKYAASSMVTDEHIAFIASVRNAFCHNQYPFYKETLHAPILLFTVAQPTTEEKDGLGIAEALLRVLREYCEIVKSQI

[0183]

237	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
238	Cas13	MENKTSLGNNIYYNPFKPQDKSYFAGYFNAAMENTDSVFRELGKRLKGKEYTSENFFDAIFKE NISLVEYERYVKLLSDYFPMARLLDKKEVPIKERKENFKKNFKGIIKAVRDLRNFYTHKEHGEVEIT DEIFGVLDEMLKSTVLTVKKKKVKTDKTKEILKKSIEKQLDILCQKKLEYLRDTARKIEEKRRNQRE RGEKELVAPFKYSDKRDDLIAAIYNDAFDVYIDKKKDSLKESSKAKYNTKSDPQQEEGDLKIPIS KNGVVFLLSLFLTKQEIHAFKSKIAGFKATVIDEATVSEATVSHGKNSICFMATHEIFSHLAYKKLK RKVRTAEINYGEAENAEQLSVYAKETLMMQMLDELSKVPDVVYQNLSEDVQKTFIEDWNEYL KENNGDVGTMEEEQVIHPVIRKRYEDKFNYFAIRFLDEFAQFPTLRFQVHLGNYLHDSRPKENL ISDRRIKEKITVFGRLSELEHKKALFIKNTETNEDREHYWEIFPNPNYDFPKENISVNDKDFPIAG SILDREKQPVAGKIGIKVKLLNQQYVSEVDKAVKAHQLKQRKASKPSIQNIIEEIVPINESNPKEA IVFGGQPTAYLSMNDIHSILYEFFDKWEKKKEKLEKKGEKELRKEIGKELEKKIVGKIQAQIQQIID KDTNAKILKPYQDGNSTAIDKEKLIKDLKQEQNILQKLKDEQTVREKEYNDFIAYQDKNREINKV RDRNHKQYLKDNLKRKYPEAPARKEVLYYREKGKVAVWLANDIKRFMPTDFKNEWKGEQHSL LQKSLAYYEQCKEELKNLLPEKVFQHLPFKLGGYFQQKYLYQFYTCYLDKRLEYISGLVQQAENF KSENKVFKKVENECFKFLKKQNYTHKELDARVQSILGYPIFLERGFMDEKPTIIKGKTFKGNEALF ADWFRYYKEYQNFQTFYDTENYPLVELEKKQADRKRKTKIYQQKKNDVFTLLMAKHIFKSVFK QDSIDQFSLEDLYQSREERLGNQERARQTGERNTNYIWNKTVDLKLCDGKITVENVKLKNVG DFIKYEYDQRVQAFLKYEENIEWQAFLIKESKEEENYPYVVEREIEQYEKVRREELLKEVHLIEEYIL EKVKDKEILKKGDNQNFKYYILNGLLKQLKNEDVESYKVFNLNTEPEDVNINQLKQEATDLEQK AFVLTYIRNKFAHNQLPKKEFWDYCQEKYGKIEKEKTYAEYFAEVFKKEKEALIK

[0184]

239	Cas13	MFFSFHNAQRVIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFAHLNRKGKNKQDNPDFNR YRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQREKMTTEVFCRSRILLPKLRLE SRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLDEIEEEQNPFKDTLIRHQDRF PYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTRTLLSFGRLQDFTEINRPQEW KALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSLEIKDGANRIAKYPYNSGFVA HAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERINTIEDLEKANQGRLPLGAFPK QMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLGKRREKLIKTGVLADWLVKDF MRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLEGYFKQTNLIGNTNPHPFLNK FNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKIPKENRKNLVKGWEQGGISLP RGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKYQDKHQSFYNLSYKLEAKAPLL KREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRWQHLEKKLRLYRNQDVMLWLM TLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQTLPMVLPVKVYPATAFGEVQYHK TPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDTQKHPISQLRLRRELEIYQSLRVD AFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMVTDEHIAFIASVRNAFCHNQYPF YKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKSQI
240	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
241	Cas13	MEKPLPPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLTTPPNDDKIADVVCGTWNNIL NNDHDLLKKSQLTELILKHFPFLAAMCYHPPKKEGKKKGSQKEQQKEKENEAQSQAEALNPS ELIKALKTLVKQLRTLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTQDF AHLNRKGKNKQDNPKFDRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQS EKMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEKDKKHFQVEADGFL DEIEEEQNPFKDALIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLT RTLLSFGRLQDFTEINRPQEWKALTKDLDYKETSKQPFISKTTPHYHITDNKIGFRLGTSKELYPSL

[0185]

		EVKDGANRIAKYPYNSDFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERI NTIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKL GKRREKLIKTGVLADWLVKDFMRFQPVAYDVQNQPIESSKANSTEFQLIQRALALYGGEKNRL EGYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLK IPKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLTLSKPIRKEIKKHGRVGFISRAITLYFRERY QDDHQSFYNLPYELEAKASTPKPPLPKKREYVLRAEHYEYWQQNKPQSPTELQRLELHTSDR WKDYLLYKRWQHLEKKLRLYRNQDVMLWLMTLELTKNHFKELKLNYHQLKLENLAVNVQEA DAKLNPLNQTLPMVLPVKVYPATAFGEVQYQETPIRTVYIREEQTKALKMGNFKALVKDRRLN GLFSFIKEENDTQKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHASLSSLENEFRTLLEEW KKKYAASSMVTDEHIAFIASVRNAFCHNQYPFYKETLHAPILLFTVAQPTTEEKDGLGIAEALLR VLREYCEIVKSQI
242	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITCHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
243	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITCHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI

[0186]

		PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
244	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
245	Cas13	MFFSFHNAQRVIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFAHLNRKGKNKQDNPDFNR YRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQREKMTTEVFCRSRILLPKLRLE SRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLDEIEEEQNPFKDTLIRHQDRF PYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTRTLLSFGRLQDFTEINRPQEW KALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSLEIKDGANRIAKYPYNSGFVA HAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERINTIEDLEKANQGRLPLGAFPK QMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLGKRREKLIKTGVLADWLVKDF MRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLEGYFKQTNLIGNTNPHPFLNK FNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKIPKENRKNLVKGWEQGGISLP RGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKYQDKHQSFYNLSYKLEAKAPLL KREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRWQHLEKKLRLYRNQDVMLWLM TLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQTLPMVLPVKVYPATAFGEVQYHK TPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDTQKHPISQLRLRRELEIYQSLRVD AFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMVTDEHIAFIASVRNAFCHNQYPF

[0187]

		YKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKSQI
246	Cas13	MDTPNFSERIPVSLQSHPYYFAHYLNMARHNAYVILEYVNRELIKPGKNLDEDNLIQSTVLKDG YFDRKPDELSHRNRLLVQHFPFLREAENEGARTCNPVSYKLKTALAALNQWRNNASHYPLNQ NHEKDFDLQPFFSFAIEACKKRMREVFQPDDFYLLETNEKQFYTLHNENGFTEKGLYCFICFFLE KKYAFQFLAGIKGFKNTTDNKFRATLETFTEHCCRLPKPKLDSSDIKLDMLGELSRCPAPLFDLLD IEERKKFIREPEEVKPDESGDREEVQQVLMKRYDDRFPYFALRYFEEKNLLKGISFHIHIGRWIKSE HTKKIMGAERDRRLLKDIRTFGELKEFSPEHAPDYWLRDGITPDDVDQFSPQYRIVGNRIGIKL NYNGHNRWSVPDKEINVKPDAIISTYEFLNLFLYEHLYQKKLTGLSPAEFIQDYLDRFNNFLSEF KAGHIRPVGDFSLEKRRGQGDEPDLTARRKSLQKELDRFVLKGKDLPDKIREYLLGYKQKSEKKQ AKWILGGMIKETVYWRNKAEQSPEKMRSGDMAQQLARDIIFLTPPHTVKEHKQKLNSLEYDV LQYALAYFSSNREKLYSFFKEHQLTVKGDRAHPFLYKIRLDECQGILDFFIVYMQQKEKWLGWL DRNLKSPRLNEEEFFNTYSYFIKTDTKRAIEMDYESCPNYLPRGIFNEPIAKALQKAGVKIKDED NASYALSVYSNGKTQPFYNKERYYNKGIFRMEELPEKLQPKELLGKIQWTIKSSGKDTEEFRSLQ NLKNRILNTEKEIRYVQSTDRALWIMVADLFPETFELRPDDLECIGHDLSDDLLSRPYQMKEKV YNYTITDYLPIKRYGEFRRFLKDRRLENLLTYFEEGVPLHREALVAELEAYDLQRKNLLEIIYRFEKL VFDRHRHELTFSGEGENQYVNHWDYLDFVARKYGLSAEVKELNSERFTELRNKMLHNQIPYQ LWIKEAIAAREENTVCGRIMGMIGEIYERMTTEIEKQMQV
247	Cas13	MTEQNEKPYNGTYYTLEDKHFWAAFLNLARHNAYITLTHIDRQLAYSKADITNDEDILFFKGQ WKNLDNDLERKARLRSLILKHFFFLEGAAYGKKLFESQSSGNKSSKKKELTKKEKEELQANALSL DNLKSILFDFLQKLKDFRNYYSHYRHPESSELPLFDGNMLQRLYNVFDVSVQRVKRDHEHND KVDPHRHFNHLVRKGKKDKYGNNDNPFFKHHFVDREGKVTEAGLLFFVSLFLEKRDAIWMQ KKIRGFKGGTETYQQMTNEVFCRSRISLPKLKLESLRTDDWMLLDMLNELVRCPKSLYDRLREE DRARFRVPVDILSDEDDTDGAEEDPFKNTLVRHQDRFPYFALRYFDLKKVFTSLRFHIDLGTYHF AIYKKNIGEQPEDRHLTRNLYGFGRIQDFAEEHRPEEWKRLVRDLDYFETGDKPYITQTTPHYHI EKGKIGLRFVPEGQHLWPSPEVGATRTGRSKYAQDKRFTAEAFLSVHELMPMMFYYFLLREKYS EEASAERVQGRIKRVIEDVYAVYDAFARDEINTRDELDACLADKGIRRGHLPRQMIAILSQKHK DMEEKVRKKLQEMIADTDHRLDMLDRQTDRKIRIGRKNAGLPKSGVIADWLVRDMMRFQPV AKDTSGKPLNNSKANSTEYRMLQRALALFGGEKERLTPYFRQMNLTGGNNPHPFLHETRWES HTNILSFYRSYLKARKAFLQSIGRSDRVENHRFLLLKEPKTDRQTLVAGWKGEFHLPRGIFTEAV RDCLIEMGLDEVRSYKEVGFMAKAVPLYFERASKDRVQPFYDYPFNVGNSLKPKKGRFLSKEKR AEEWESGKERFRDLEAWSHSAARRIEDAFAGIENASRENKKKIEQLLQDLSLWETFESKLKVKA DKINIAKLKKEILEAKEHPYLDFKSWQKFERELRLVKNQDIITWMMCRDLMEENKVEGLDTGTL YLKDIRTDVQEQGSLNVLNHVKPMRLPVVVYRADSRGHVHKEQAPLATVYIEERDTKLLKQG NFKSFVKDRRLNGLFSFVDTGGLAMEQYPISKLRVEYELAKYQTARVCAFEQTLELEESLLTRYP HLPDKNFRKMLESWSDPLLAKWPELHEKVRLLIAVRNAFSHNQYPMYDEAVFSPIRKYDPSSP DAIEERMRLNIAHRLSEEVKQAKETVERIIQA
248	Cas13	MDTPNFSERIPVSLQSHPYYFAHYLNMARHNAYVILEYVNRELIKPGKNLDEDNLIQSTVLKDG

[0188]

		YFDRKPDELSHRNRLLVQHFPFLREAENEGARTCNPVSYKLKTALAALNQWRNNASHYPLNQ NHEKDFDLQPFFSFAIEACKKRMREVFQPDDFYLLETNEKQFYTLHNENGFTEKGLYCFICFFLE KKYAFQFLAGIKGFKNTTDNKFRATLETFTEHCCRLPKPKLDSSDIKLDMLGELSRCPAPLFDLLD IEERKKFIREPEEVKPDESGDREEVQQVLMKRYDDRFPYFALRYFEEKNLLKGISFHIHIGRWIKSE HTKKIMGAERDRRLLKDIRTFGELKEFSPEHAPDYWLRDGITPDDVDQFSPQYRIVGNRIGIKL NYNGHNRWSVPDKEINVKPDAIISTYEFLNLFLYEHLYQKKLTGLSPAEFIQDYLDRFNNFLSEF KAGHIRPVGDFSLEKRRGQGDEPDLTARRKSLQKELDRFVLKGKDLPDKIREYLLGYKQKSEKKQ AKWILGGMIKETVYWRNKAEQSPEKMRSGDMAQQLARDIIFLTPPHTVKEHKQKLNSLEYDV LQYALAYFSSNREKLYSFFKEHQLTVKGDRAHPFLYKIRLDECQGILDFFIVYMQQKEKWLGWL DRNLKSPRLNEEEFFNTYSYFIKTDTKRAIEMDYESCPNYLPRGIFNEPIAKALQKAGVKIKDED NASYALSVYSNGKTQPFYNKERYYNKGIFRMEELPEKLQPKELLGKIQWTIKSSGKDTEEFRSLQ NLKNRILNTEKEIRYVQSTDRALWIMVADLFPETFELRPDDLECIGHDLSDDLLSRPYQMKEKV YNYTITDYLPIKRYGEFRRFLKDRRLENLLTYFEEGVPLHREALVAELEAYDLQRKNLLEIIYRFEKL VFDRHRHELTFSGEGENQYVNHWDYLDFVARKYGLSAEVKELNSERFTELRNKMLHNQIPYQ LWIKEAIAAREENTVCGRIMGMIGEIYERMTTEIEKQMQV
249	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEMEHLRRYTRKKGRVVLKTEDDHFYYTLANNNDLSEKGYAFFI SMFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRI PIELYQTLEPKYREMYNATLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYL GNYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEP YLVQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNI HKSHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQ HEILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINS SNPHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQEKEE AIFLPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLILNYFRTYFEDQSQEFYAQPRNYRLF DKLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQ DILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDT RINSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATP GNYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIK LEDFSNDSSA
250	Cas13	MEKPLPPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLTTPPNDDKIADVVCGTWNNIL NNDHDLLKKSQLTELILKHFPFLAAMCYHPPKKEGKKKGSQKEQQKEKENEAQSQAEALNPS ELIKALKTLVKQLRTLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTQDF AHLNRKGKNKQDNPKFDRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQS EKMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEKDKKHFQVEADGFL DEIEEEQNPFKDALIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLT RTLLSFGRLQDFTEINRPQEWKALTKDLDYKETSKQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EVKDGANRIAKYPYNSDFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERI NTIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKL

[0189]

		GKRREKLIKTGVLADWLVKDFMRFQPVAYDVQNQPIESSKANSTEFQLIQRALALYGGEKNRL EGYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLK IPKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLTLSKPIRKEIKKHGRVGFISRAITLYFRERY QDDHQSFYNLPYELEAKASTPKPPLPKKREYVLRAEHYEYWQQNKPQSPTELQRLELHTSDR WKDYLLYKRWQHLEKKLRLYRNQDVMLWLMTLELTKNHFKELKLNYHQLKLENLAVNVQEA DAKLNPLNQTLPMVLPVKVYPATAFGEVQYQETPIRTVYIREEQTKALKMGNFKALVKDRRLN GLFSFIKEENDTQKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHASLSSLENEFRTLLEEW KKKYAASSMVTDEHIAFIASVRNAFCHNQYPFYKETLHAPILLFTVAQPTTEEKDGLGIAEALLR VLREYCEIVKSQI
251	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
252	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW

[0190]

		QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
253	Cas13	MFFSFHNAQRVIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFAHLNRKGKNKQDNPDFNR YRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQREKMTTEVFCRSRILLPKLRLE SRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLDEIEEEQNPFKDTLIRHQDRF PYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTRTLLSFGRLQDFTEINRPQEW KALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSLEIKDGANRIAKYPYNSGFVA HAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERINTIEDLEKANQGRLPLGAFPK QMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLGKRREKLIKTGVLADWLVKDF MRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLEGYFKQTNLIGNTNPHPFLNK FNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKIPKENRKNLVKGWEQGGISLP RGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKYQDKHQSFYNLSYKLEAKAPLL KREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRWQHLEKKLRLYRNQDVMLWLM TLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQTLPMVLPVKVYPATAFGEVQYHK TPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDTQKHPISQLRLRRELEIYQSLRVD AFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMVTDEHIAFIASVRNAFCHNQYPF YKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKSQI
254	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI

[0191]

255	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
256	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
257	Cas13	MDTPNFSERIPVSLQSHPYYFAHYLNMARHNAYVILEYVNRELIKPGKNLDEDNLIQSTVLKDG YFDRKPDELSHRNRLLVQHFPFLREAENEGARTCNPVSYKLKTALAALNQWRNNASHYPLNQ NHEKDFDLQPFFSFAIEACKKRMREVFQPDDFYLLETNEKQFYTLHNENGFTEKGLYCFICFFLE KKYAFQFLAGIKGFKNTTDNKFRATLETFTEHCCRLPKPKLDSSDIKLDMLGELSRCPAPLFDLLD

[0192]

		IEERKKFIREPEEVKPDESGDREEVQQVLMKRYDDRFPYFALRYFEEKNLLKGISFHIHIGRWIKSE HTKKIMGAERDRRLLKDIRTFGELKEFSPEHAPDYWLRDGITPDDVDQFSPQYRIVGNRIGIKL NYNGHNRWSVPDKEINVKPDAIISTYEFLNLFLYEHLYQKKLTGLSPAEFIQDYLDRFNNFLSEF KAGHIRPVGDFSLEKRRGQGDEPDLTARRKSLQKELDRFVLKGKDLPDKIREYLLGYKQKSEKKQ AKWILGGMIKETVYWRNKAEQSPEKMRSGDMAQQLARDIIFLTPPHTVKEHKQKLNSLEYDV LQYALAYFSSNREKLYSFFKEHQLTVKGDRAHPFLYKIRLDECQGILDFFIVYMQQKEKWLGWL DRNLKSPRLNEEEFFNTYSYFIKTDTKRAIEMDYESCPNYLPRGIFNEPIAKALQKAGVKIKDED NASYALSVYSNGKTQPFYNKERYYNKGIFRMEELPEKLQPKELLGKIQWTIKSSGKDTEEFRSLQ NLKNRILNTEKEIRYVQSTDRALWIMVADLFPETFELRPDDLECIGHDLSDDLLSRPYQMKEKV YNYTITDYLPIKRYGEFRRFLKDRRLENLLTYFEEGVPLHREALVAELEAYDLQRKNLLEIIYRFEKL VFDRHRHELTFSGEGENQYVNHWDYLDFVARKYGLSAEVKELNSERFTELRNKMLHNQIPYQ LWIKEAIAAREENTVCGRIMGMIGEIYERMTTEIEKQMQV
258	Cas13	MFFSFHNAQRVIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFAHLNRKGKNKQDNPDFNR YRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQREKMTTEVFCRSRILLPKLRLE SRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLDEIEEEQNPFKDTLIRHQDRF PYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTRTLLSFGRLQDFTEINRPQEW KALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSLEIKDGANRIAKYPYNSGFVA HAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERINTIEDLEKANQGRLPLGAFPK QMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLGKRREKLIKTGVLADWLVKDF MRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLEGYFKQTNLIGNTNPHPFLNK FNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKIPKENRKNLVKGWEQGGISLP RGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKYQDKHQSFYNLSYKLEAKAPLL KREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRWQHLEKKLRLYRNQDVMLWLM TLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQTLPMVLPVKVYPATAFGEVQYHK TPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDTQKHPISQLRLRRELEIYQSLRVD AFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMVTDEHIAFIASVRNAFCHNQYPF YKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKSQI
259	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW

[0193]

		QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
260	Cas13	MTNTPKRRTLHRHPSYFGAFLNIARHNAFMIMEHLSTKYDMEDKNTLDEAQLPNAKLFGCLK KRYGKPDVTEGVSRDLRRYFPFLNYPLFLHLEKQQNAEQAATYDINPEDIEFTLKGFFRLLNQM RNNYSHYISNTDYGKFDKLPVQDIYEAAIFRLLDRGKHTKRFDVFESKHTRHLESNNSEYRPRS LANSPDHENTVAFVTCLFLERKYAFPFLSRLDCFRSTNDAAEGDPLIRKASHECYTMFCCRLPQ PKLESSDILLDMVNELGRCPSALYNLLSEEDQARFHIKREEITGFEEDPDEELEQEIVLKRHSDRFP YFALRYFDDTEAFQTLRFDVYLGRWRTKPVYKKRIYGQERDRVLTQSIRTFTRLSRLLPIYENVKH DAVRQNEEDGKLVNPDVTSQFHKSWIQIESDDRAFLSDRIEHFSPHYNFGDQVIGLKFINPDR YAAIQNVFPKLPGEEKKDKDAKLVNETADAIISTHEIRSLFLYHYLSKKPISAGDERRFIQVDTETFI KQYIDTIKLFFEDIKSGELQPIADPPNYQKNEPLPYVRGDKEKTQEERAQYRERQKEIKERRKELN TLLQNRYGLSIQYIPSRLREYLLGYKKVPYEKLALQKLRAQRKEVKKRIKDIEKMRTPRVGEQAT WLAEDIVFLTPPKMHTPERKTTKHPQKLNNDQFRIMQSSLAYFSVNKKAIKKFFQKETGIGLSN RETSHPFLYRIDVGRCRGILDFYTGYLKYKMDWLDDAIKKVDNRKHGKKEAKKYEKYLPSSIQH KTPLELDYTRLPVYLPRGLFKKAIVKALAAHADFQVEPEEDNVIFCLDQLLDGDTQDFYNWQR YYRSALTEKETDNQLVLAHPYAEQILGTIKTLEGKQKNNKLGNKAKQKIKDELIDLKRAKRRLLD REQYLRAVQAEDRALWLMIQERQKQKAEHEEIAFDQLDLKNITKILTESIDARLRIPDTKVDITD KLPLRRYGDLRRVAKDRRLVNLASYYHVAGLSEIPYDLVKKELEEYDRRRVAFFEHVYQFEKEVY DRYAAELRNENPKGESTYFSHWEYVAVAVKHSADTHFNELFKEKVMQLRNKFHHNEFPYFDW LLPEVEKASAALYADRVFDVAEGYYQKMRKLMRQ
261	Cas13	MTNTPKRRTLHRHPSYFGAFLNIARHNAFMIMEHLSTKYDMEDKNTLDEAQLPNAKLFGCLK KRYGKPDVTEGVSRDLRRYFPFLNYPLFLHLEKQQNAEQAATYDINPEDIEFTLKGFFRLLNQM RNNYSHYISNTDYGKFDKLPVQDIYEAAIFRLLDRGKHTKRFDVFESKHTRHLESNNSEYRPRS LANSPDHENTVAFVTCLFLERKYAFPFLSRLDCFRSTNDAAEGDPLIRKASHECYTMFCCRLPQ PKLESSDILLDMVNELGRCPSALYNLLSEEDQARFHIKREEITGFEEDPDEELEQEIVLKRHSDRFP YFALRYFDDTEAFQTLRFDVYLGRWRTKPVYKKRIYGQERDRVLTQSIRTFTRLSRLLPIYENVKH DAVRQNEEDGKLVNPDVTSQFHKSWIQIESDDRAFLSDRIEHFSPHYNFGDQVIGLKFINPDR YAAIQNVFPKLPGEEKKDKDAKLVNETADAIISTHEIRSLFLYHYLSKKPISAGDERRFIQVDTETFI KQYIDTIKLFFEDIKSGELQPIADPPNYQKNEPLPYVRGDKEKTQEERAQYRERQKEIKERRKELN TLLQNRYGLSIQYIPSRLREYLLGYKKVPYEKLALQKLRAQRKEVKKRIKDIEKMRTPRVGEQAT WLAEDIVFLTPPKMHTPERKTTKHPQKLNNDQFRIMQSSLAYFSVNKKAIKKFFQKETGIGLSN RETSHPFLYRIDVGRCRGILDFYTGYLKYKMDWLDDAIKKVDNRKHGKKEAKKYEKYLPSSIQH KTPLELDYTRLPVYLPRGLFKKAIVKALAAHADFQVEPEEDNVIFCLDQLLDGDTQDFYNWQR YYRSALTEKETDNQLVLAHPYAEQILGTIKTLEGKQKNNKLGNKAKQKIKDELIDLKRAKRRLLD REQYLRAVQAEDRALWLMIQERQKQKAEHEEIAFDQLDLKNITKILTESIDARLRIPDTKVDITD KLPLRRYGDLRRVAKDRRLVNLASYYHVAGLSEIPYDLVKKELEEYDRRRVAFFEHVYQFEKEVY DRYAAELRNENPKGESTYFSHWEYVAVAVKHSADTHFNELFKEKVMQLRNKFHHNEFPYFDW

[0194]

		LLPEVEKASAALYADRVFDVAEGYYQKMRKLMRQ
262	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
263	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI

[0195]

264	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
265	Cas13	MESIKNSQKSTGKTLQKDPPYFGLYLNMALLNVRKVENHIRKWLGDVALLPEKSGFHSLLTTD NLSSAKWTRFYYKSRKFLPFLEMFDSDKKSYENRRETTECLDTIDRQKISSLLKEVYGKLQDIRN AFSHYHIDDQSVKHTALIISSEMHRFIENAYSFALQKTRARFTGVFVETDFLQAEEKGDNKKFFAI GGNEGIKLKDNALIFLICLFLDREEAFKFLSRATGFKSTKEKGFLAVRETFCALCCRQPHERLLSVN PREALLMDMLNELNRCPDILFEMLDEKDQKSFLPLLGEEEQAHILENSLNDELCEAIDDPFEMI ASLSKRVRYKNRFPYLMLRYIEEKNLLPFIRFRIDLGCLELASYPKKMGEENNYERSVTDHAMAF GRLTDFHNEDAVLQQITKGITDEVRFSLYAPRYAIYNNKIGFVRTGGSDKISFPTLKKKGGEGHCV AYTLQNTKSFGFISIYDLRKILLLSFLDKDKAKNIVSGLLEQCEKHWKDLSENLFDAIRTELQKEFP VPLIRYTLPRSKGGKLVSSKLADKQEKYESEFERRKEKLTEILSEKDFDLSQIPRRMIDEWLNVLPT SREKKLKGYVETLKLDCRERLRVFEKREKGEHPVPPRIGEMATDLAKDIIRMVIDQGVKQRITSA YYSEIQRCLAQYAGDDNRRHLDSIIRELRLKDTKNGHPFLGKVLRPGLGHTEKLYQRYFEEKKE WLEATFYPAASPKRVPRFVNPPTGKQKELPLIIRNLMKERPEWRDWKQRKNSHPIDLPSQLFE NEICRLLKDKIGKEPSGKLKWNEMFKLYWDKEFPNGMQRFYRCKRRVEVFDKVVEYEYSEEGG NYKKYYEALIDEVVRQKISSSKEKSKLQVEDLTLSVRRVFKRAINEKEYQLRLLCEDDRLLFMAVR DLYDWKEAQLDLDKIDNMLGEPVSVSQVIQLEGGQPDAVIKAECKLKDVSKLMRYCYDGRVK GLMPYFANHEATQEQVEMELRHYEDHRRRVFNWVFALEKSVLKNEKLRRFYEESQGGCEHRR CIDALRKASLVSEEEYEFLVHIRNKSAHNQFPDLEIGKLPPNVTSGFCECIWSKYKAIICRIIPFIDP ERRFFGKLLEQK
266	Cas13	MEKPLPPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLTTPPNDDKIADVVCGTWNNIL NNDHDLLKKSQLTELILKHFPFLAAMCYHPPKKEGKKKGSQKEQQKEKEKEKENEAQSQAEAL NPSELIKVLKTIVKQLRTLRNYYSHHSHKKPDTEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLT RDFAHLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASH

[0196]

		KQREKMTTEVFCRSHILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEAD GFLDEIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKR HLTRTLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKEL YPSLEIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEE ERINTIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSS PKLGKRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEK NRLEGYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYC LLLKIPKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYF KEKYQDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYK RWQHLEKKLRLYRNQDIMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLN QTLPMVLPVKVYPATAFGEVQYQETPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEEN DTQKHPISQLRLRRELEIYQSLRVDAFKETLDLEEKLLKKHTSLSSLENKFRILLEEWKKEYAASSM VTDEHIAFIASVRNAFCHNQYPFYEEALHAPIPLFTVAQQTTEEKDGLGIAEALLRVLREYCEIVK SQI
267	Cas13	MFFSFHNAQRVIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFAHLNRKGKNKQDNPDFNR YRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQREKMTTEVFCRSRILLPKLRLE SRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLDEIEEEQNPFKDTLIRHQDRF PYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTRTLLSFGRLQDFTEINRPQEW KALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSLEIKDGANRIAKYPYNSGFVA HAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERINTIEDLEKANQGRLPLGAFPK QMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLGKRREKLIKTGVLADWLVKDF MRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLEGYFKQTNLIGNTNPHPFLNK FNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKIPKENRKNLVKGWEQGGISLP RGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKYQDKHQSFYNLSYKLEAKAPLL KREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRWQHLEKKLRLYRNQDVMLWLM TLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQTLPMVLPVKVYPATAFGEVQYHK TPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDTQKHPISQLRLRRELEIYQSLRVD AFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMVTDEHIAFIASVRNAFCHNQYPF YKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKSQI
268	Cas13	MEKPLPPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLTTPPNDDKIADVVCGTWNNIL NNDHDLLKKSQLTELILKHFPFLAAMCYHPPKKEGKKKGSQKEQQKEKEKEKENEAQSQAEAL NPSELIKVLKTIVKQLRTLRNYYSHHSHKKPDTEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLT RDFAHLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASH KQREKMTTEVFCRSHILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEAD GFLDEIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKR HLTRTLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKEL YPSLEIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEE ERINTIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSS PKLGKRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEK NRLEGYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYC

[0197]

		LLLKIPKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYF KEKYQDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYK RWQHLEKKLRLYRNQDIMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLN QTLPMVLPVKVYPATAFGEVQYQETPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEEN DTQKHPISQLRLRRELEIYQSLRVDAFKETLDLEEKLLKKHTSLSSLENKFRILLEEWKKEYAASSM VTDEHIAFIASVRNAFCHNQYPFYEEALHAPIPLFTVAQQTTEEKDGLGIAEALLRVLREYCEIVK SQI
269	Cas13	MGAIENKHIFAAYANLAIDGLIKTLNFIAKKLDTQKQLSSWDIKHVITLIDSIFDQNPQNNLEQV VEGYLPWIKPIIEMKTPKKGERQSDKLCIEYKTIITAFASLLNDVRNYYTHYYHDPICIYPGGYDIP SSLNCIYDSAINIIKERFQAEEKEIEHLRRYTRKKGRVVLKTEDDHFYYTLVNNNDLSEKGYAFFIS MFLERKYSYLFLKKLSGFKRGDSLQYRLTLEVFTALSTKPPVERLRTTKDTKQDRALDILNELSRIPI ELYQTLEPKYREMYNETLQPTDAEDPYGLPDRSRIRFRSRFEAFALHFLDKQADFKEIGFYTYLG NYFHNGYQKTRVDRETKDRYINFQLAGFCKNIQDISAKKLSEALNVKSIDISTDSIPDINSFEPYL VQSTPHYIVNGNNIGIKVLPEGKDTYPTIDEKGAKMPIADFWLSKYELPAMLFYTYLRNNNIHK SHCPLSVKDIIERSIHKSTKQKHPEERSELMLRRVMKAIFWTDSKLNEVERIKSQKSAFGKRQHE ILKAGRIAETLVRDMLWLQPSKNNGRDKVTEPNFQAIQVSLAYFGIRRNDLTEIFTRAGLINSSN PHPFLAQIGTNYTSLIEFYIAYLKERKVYFSRIQKKILQGKLNIQCHPLRDLQREPNKPQDKEEAIF LPRGLFNEAIINCLKKSKLKQLIESPTREKSPALNVSYLIQNYFRTYFEDQSQEFYAQPRNYRLFD KLSPNKGKSKSYLSLEQRIKKMEELRPSKIPVAEANKLLEKEDRLYRKNYNEICDNESIIRLYQIQD ILLFMMTKEYLPSDLYNRINKYKLENVKGILNERVSYLIDLNPLKIQGEDIKIKDYGKLFYIHHDTRI SSLNKVLSKVKRNNSISSSVKIQPYENYKRECLDFEEAQIQIIPIIHSFEIAMVSMFPDLKKATPG NYYDFNELITEYEKRTKQKIDSSFLIKTRNMFLHDKYEAECIKEISDDFVYAKKIIAEFKMKIENIKL EDLSNDSSA
270	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKDWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS

[0198]

		QI
271	Cas13	MEKPLPPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLTTPPNDDKIADVVCGTWNNIL NNDHDLLKKSQLTELILKHFPFLAAMCYHPPKKEGKKKGSQKEQQKEKENEAQSQAEALNPS ELIKALKTLVKQLRTLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTQDF AHLNRKGKNKQDNPKFDRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQS EKMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEKDKKHFQVEADGFL DEIEEEQNPFKDALIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLT RTLLSFGRLQDFTEINRPQEWKALTKDLDYKETSKQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EVKDGANRIAKYPYNSDFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERI NTIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKL GKRREKLIKTGVLADWLVKDFMRFQPVAYDVQNQPIESSKANSTEFQLIQRALALYGGEKNRL EGYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLK IPKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLTLSKPIRKEIKKHGRVGFISRAITLYFRERY QDDHQSFYNLPYELEAKASTPKPPLPKKREYVLRAEHYEYWQQNKPQSPTELQRLELHTSDR WKDYLLYKRWQHLEKKLRLYRNQDVMLWLMTLELTKNHFKELKLNYHQLKLENLAVNVQEA DAKLNPLNQTLPMVLPVKVYPATAFGEVQYQETPIRTVYIREEQTKALKMGNFKALVKDRRLN GLFSFIKEENDTQKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHASLSSLENEFRTLLEEW KKKYAASSMVTDEHIAFIASVRNAFCHNQYPFYKETLHAPILLFTVAQPTTEEKDGLGIAEALLR VLREYCEIVKSQI
272	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI

[0199]

273	Cas13	MEKPLLPNVYTLKHKFFWGAFLNIARHNAFITICHINEQLGLKTPSNDDKIVDVVCETWNNIL NNDHDLLKKSQLTELILKHFPFLTAMCYHPPKKEGKKKGHQKEQQKEKESEAQSQAEALNPSK LIEALEILVNQLHSLRNYYSHYKHKKPDAEKDIFKHLYKAFDASLRMVKEDYKAHFTVNLTRDFA HLNRKGKNKQDNPDFNRYRFEKDGFFTESGLLFFTNLFLDKRDAYWMLKKVSGFKASHKQRE KMTTEVFCRSRILLPKLRLESRYDHNQMLLDMLSELSRCPKLLYEKLSEENKKHFQVEADGFLD EIEEEQNPFKDTLIRHQDRFPYFALRYLDLNESFKSIRFQVDLGTYHYCIYDKKIGDEQEKRHLTR TLLSFGRLQDFTEINRPQEWKALTKDLDYKETSNQPFISKTTPHYHITDNKIGFRLGTSKELYPSL EIKDGANRIAKYPYNSGFVAHAFISVHELLPLMFYQHLTGKSEDLLKETVRHIQRIYKDFEEERIN TIEDLEKANQGRLPLGAFPKQMLGLLQNKQPDLSEKAKIKIEKLIAETKLLSHRLNTKLKSSPKLG KRREKLIKTGVLADWLVKDFMRFQPVAYDAQNQPIKSSKANSTEFWFIRRALALYGGEKNRLE GYFKQTNLIGNTNPHPFLNKFNWKACRNLVDFYQQYLEQREKFLEAIKNQPWEPYQYCLLLKI PKENRKNLVKGWEQGGISLPRGLFTEAIRETLSEDLMLSKPIRKEIKKHGRVGFISRAITLYFKEKY QDKHQSFYNLSYKLEAKAPLLKREEHYEYWQQNKPQSPTESQRLELHTSDRWKDYLLYKRW QHLEKKLRLYRNQDVMLWLMTLELTKNHFKELNLNYHQLKLENLAVNVQEADAKLNPLNQT LPMVLPVKVYPATAFGEVQYHKTPIRTVYIREEHTKALKMGNFKALVKDRRLNGLFSFIKEENDT QKHPISQLRLRRELEIYQSLRVDAFKETLSLEEKLLNKHTSLSSLENEFRALLEEWKKEYAASSMV TDEHIAFIASVRNAFCHNQYPFYKEALHAPIPLFTVAQPTTEEKDGLGIAEALLKVLREYCEIVKS QI
274	Cas12a	MKSLAQFQNLYALQKTLRFELKPEGHTRETFNRWLEEIEKEQASENENIVYQDLLRAKKYEKIKII LDEYHKDFIEQALAYANLTELEKYEELYRKSNRTSEEEEEFENTKESLRKQIANIFIKNPNKTVQER WKFLFSKKLIQNELIVWVKGNYELLSEKLKNEFPDESSIISTIEDFKYFTTVFRNYHENRKNLYSNE DKFSTIAHRLIHENLPKFIDNIAIYQKAKAVLNINEVEKELGLPEDTLDKIFSLDFFSKALTQKGIDQ YNYFLGGKTENEVKKIKGLNEFINLYNQQQQDKNQRLPFLKVLYKLPLFERTSTSFRFEPIENDR DLIERIGKFYYNDLKQYRDDSQGDTTDILSGINTLLRHVHDYRDGLYVNGGITLTQISQKIFGSW SYINNALAYFYDTYIDASGVDHQGERKPKKQKQIQEKTKWLKQKQFPVILVEKALSEYKSIETNE DLKTRISDTTLCDFFKRCGNDDNGQDLFDRIEARLREKNEEGYSLEDLLKKEFTTERKLMQDKT KTLLIKNFLDVIQGDKDDITAGLLHFVKCLIPRTEISEKNELFYSGMEKYLNILSEVTPLYNKARNY LTQKPYSIEKVKLNFENSTLLDGWDENEESDNSCVLLRKRGYYYLGIMNKKHNMIFDRKIYPKA TEGEAYYEKMIYKLLPGAYKMLPKVFFSEKNIDYFKPSEEILRIRNTASYSKNGQPQEGYQKASFS IEDCRKYIDFFKKCIANHWDWQKFNFNFSPTEYYQSIDEFYREIERQGYKIDFVKIPESYINQLIKE NKLYLFKIYNKDFSEKKKSKGKDNLHTLYWKMLFDEKNLKDVVLKLNGEAEVFFRQKSILYNEEI VNKGHHYSELKDRFSYPIISNKRYAEDKFFLHVPITLNFKADGINNVNNMVNEFIKDNRDIHII GIDRGERHLLYVSVINQKGDIVEQCSLNEIVTEYNGKIFKKNYHEELDNLEKERDRARKDWQTI ANIKELKEGYLSHVIHKISKLILKYNAIVVMEDLNSGFKRGRQKVEKQVYQNFEKQLIEKLNYLVL KESNVDEPGGVLRAYQLANKFETFKKLGKQSGIIFYVPAAYTSAIDPVTGYIQYLYPLKQADSVEK ARKFYSQFKRISYNPHKQWFEFSFDYNDFNIIYHGKSSWTICTTNTERYMWNRLLNNGHGGE ELVYVTNELELLFGEYNIIYGDGKDIKQQITDVQDIDVDRTAKQFYKRINELLNLTLKLRHNNGKK GADEEDYILSPVEPYFDSRFESRKPSMQQTLPINADANGAFNIARKGLLLLERLNQLGVEEFEKT KKSNNKKTQWLPHELWVEYAQNHTRK

[0200]

275	Cas12a	MQDKTGWSSFTNKYSLSKTLRFELKPVGNTQKMLEDDGVFQKDRERQENYKKVKPFMDKLH REFIKEALNNLKLEGLTEYFEIFKKFRKDKNNKELKNAEKKLRQIIGRCYTETAQIWVEKYKEFGFK KKNIGFLFEEGVFELMKLKYGNDEASQIEKNGEVLSIFDGWKGFLGYFKKFFETRNNFYKDDGT STAVSTRIINENLKIYLDNLIKYNKIKDKVDFKEADILQENKLNLSDFFNVESYAKYSLQKGIDYYN EILGGKTLKNGTKLKGLNEVINEYKQKNKSGELSKFKMLKKQILGEGEDRTLFEEIENEDELKDVL KDFFYNADPKITLFKTLLEDFFSNTEKYKDELDKIYFNTVAINGILHRWVDDSGVFQKYLFEVLKS NKLVKSNHYDKKEDSYKFPDFISFEHIKVALENCERDGLKDKFWKEKYYTKECLTENGLANLW QEFLEIYKCEFKKLYDYKTDDNDCYLQYRDNYKKYILDANFNPKEKSAKDIIKDYLDSVLSIYQLA KYFALEKKKVWTTDYETGDFYYEYIKFYEDTYEQIIKPYNLVRNYLTRKPINTAKKWKLNFDNAYL ASGWDKDKEVSNLTVILRRDEQYYLAIMKKGKNKIFEKKFSCGEFEKMEYKQIAEASSDIHNLVL MNDGSCRRCIKMHDKRKYWPLDISIIKEKKSYAKENFVRRDFERFVNYMKKCSLLYWKEYDLK FSDTSTYKNINDFTNEIASQGYKLSFSAIPESYINEKNNNGELYLFQIYNKDFGIKTEGNKNLHT MYWESIFSEENRFRNFIVKLNGKAEIFYRPKSEQVEKEQRNFTREIIKNRRYTENKIYFHCPITLN RISRENVKKFNNGINNYIATNPNINILGVDRGEKHLVYYAIVDQDGKLIDAEDATGSFNTIGSTD YHRLLEEKAKDREKERKDWDLIRGIKDLKKGYISLVVRKIADLAIKYNAIIIFEDLNTRFKQIRGGM EKSVYQQLEKALINKLSFLVNKGEKDPEQAGHLLKAYQLAAPFQTFDKMGRQTGIIFYTQASYT SKIDPITGWRPNLYLKYRNIDDSKESIKKFKSILFNKEKNRFEFTYDLKDFVDFEEDKIPEKTEWTL CSSVERHKWNRHMNNNKGGYEVYKDLTENFYKLFDENNISMNKDIVDQVESISNGNFFRQF IYLFNLVCQIRNTDEKAEDVDKRDFILSPVEPFFDSRRAKDFKAYGDNLPKNGDENGAYNIARK GVLIIKKIKEYYNQNGSCDKLGWGDLSISHKEWDDFATNN
276	Cas12a	MDSYEQFTKLYPIQKTIRFELKPQGRTKEHFDNSNFLEKDRERDDNYKILKEVIDDYHREFIDEC LSNIQLNWDDLKKFSEEYRRSKEKKNNRDSESEQKRMSTTSETRAINKKNLEAEQKRMRGEIV SAFKKDDRFKHLFSEKLFSILLKNQIYEKGTLEEIEAFDCFNKFSGYFKSFHENRKNMYSDEDKET AISYRIINENFPKLLDNFEKYQYVCREYPEQIREAESTLAEAGCYIKMDEIFSIDNFNNVMMQGG KESGISRYNLAIGGIVQGTGEKPKGLNEFLNLAYQNEPNGRKKIRMEPLYKQILSKEESFSYRLEA FTDDSQLLSAIRSFFDIVEKDKNGNIFDRAVNLMSSFSNYDTSKIYIRKAYLNQVSKEIFGYRGKS DSKPAKTADESLNKSGGWEKLGQMLRDYKADSIGDRNLEKTCKKVDKWLDSDEFTLSDILGAI SLAGSNETFEAYVSEICVARRNIDKEKEKEKNINVEKISGDTESIQIIKALLDSVQEFFHLLSPFQLH PNTPHDWTFYAEFNDIYDKLSAITPLYNQARNHLTKKNLDTSKIKLNFNNPTLANGWDVNKE YENTAVILIRDGKYYLGIMNPKNKRKIKFDEGSGAGPFYQKMVYKLLPGPYRMLPKVFFAKKNI DYYNPSQEIREGYKAGKHKKGKEFDKGFCHKLIDFFKESIQKNENWKVFDFKFSPTESYDDISEF YQEVEKQGYRMYFVNIPSDTIDRYVEGGDMFLFQIYNKDFAKGAKGNKDMHTLYWNAVFSEE NLQKGVMKLSGEAELFYRKKSDIKDPPHREGEILVNRTYIDRTHVSGVMGEQNTVKESRIPVPD EIHKNLFDYYNHGRELTKEEKEYCDKVGSFKAYYGIVKDRRYLENKMYFHVPLTLNFKAIGEKRI NKMAIEKFLTDENACIIGIDRGERNLLYYSIIDRNGKIIDQKSLNVIDGFDYHEKLSQRQTEREVA RQSWNSIGKIKDLKEGYLAKAVHEISKMAIKYNAIVVLEDLHFGFKKGRLKVEKQIYQKFEEMLI NKLNYLVFKDVSDSSDAGGVLNAYQLTAPLESFSKLGKQSGILFYVPAAFTSVIDPTTGFVDLFN SSSITSTQKKKEFLQRFESIVYSARDGGIFAFTFDYRNFSKIATDHRNMWTVYTHGERIRYVRDE KCYKTTDPTKRIKEALSGIEYDDGSDIRDKITQSGDNNLINTVYHSFMDTIKMRNKDGRIDYIIS PVKNRNGEFFRSDYKHRDFPVDADANGAYHIALKGELLMRMIGKTYDSNSDKMPKLEHKDW FEFMQTRGDQ

[0201]

277	Cas12b	MCVSRLPWFNITLTGKLNRQRLNQMCVSRLPWFCTPKGQLAATPKTVVAQQENAMLAIIRD VHEAAPADLKTVAQRLEPGYFVTQFPKQQMTGDEARAEAERLFAACQKKFKELAEYEDGYRQ CLDALGPNLSLPRLGRKPKGAYPYAVVFKLMPTNATWECFKRVTASLYKRAQKGVVSPVSADSI ADVRTNDEPLFEYFTNLALVRPPGNKDRAVWFEFDLAAFIEAIKSPHQFFQDTIKREQAVAQIK AKLDAMDGQGRAAASGEEDALPGFEGDDRITLLRELVTDTLGYLAEADASTSPGGKIEYSIQERT VRGFAEVKRRWRDLVEKGKATEDALLKVLAEEQTEHRDDFGSATLYRELAKPKFQPIWRDPGT QPWHADDPLRAWLEYRELGRELEDKQRPIRFTPVHPVHSPRFFIFPKKKGGGRFGTVHEPGQL RVMAGIVAQTQHGWEPVPVRITYAAPRLRRDQLRDDVETDLESRPWLQPMMQALGLPEPDT ADFSNCRVTLQPSAPDDIQLTFPVDVSADKLTTAIGKAARWAKQFNLFPDGDNFYNASLRWP HEKKPSKPPVPWHEALDNFSVLAADLGQRCAGAFARLEVRANDDFAGKPSRFIGETPGKKWR AALVAAGMLRLPGEEQTVWRPGATGPNFHTELSGSRGRMARPHEADDTADLLRAFDCPEESL MPADWRTSLSFPEQNDKLLVAARRYQSRLARLHRWCWFLTDEKKRQTALDEIREAEDMPAAD DPQLTDKLRALLLQKQAALPGLLVRLANRILPLRGRSWQWETHPDKADCHLLTQTGPALPDV WIRGQRGLSMQRIEQIEELRRRFQSLNQMQRREIGGKPPIRRDDSIPDCCPDLLDKLDQIKEQ RANQAAHMILAEALGLRLAPPPADKRQLRASRDVHGQYVKSREPVDFIVIEDLSRYRSSQGRA PRENSRLMKWCHRAVRDKLRELCEPFGIPVVETPAAYSSRFCSRSGVAGFRAVEVGPGFDREFP WMMLKDREDEGEPVRQLILQVATLNQGRDGKPPRTLLAPLAGGPIFVPIVDKLNGADIQPALA QADINAAINLGLRAIADPRLWSIHPRCRTQRQGDQMLTREKRKFGETGQPLAVHRADGVKPD DTRNPNFFADISGSLPAWESATLDGQHLLSGRCLRSEIKKRQWQRCAEINDRRMNRWMKGE
278	Cas12b	MTELQTQRAYTLRLKGIDEKDQSWRDALWKTHEAVNKGAKVFGDWLLTLRGGLDHTLADAEI PGEKGKPDRAPTQEERKHRRILLALSWLSVESERGAPEEFIVATGKEPAATRNDKVIAALKDILRG RNLTEEKISEWTEVCTPSLSAAIREDAVWVNRSRAFDEAVKRIGSSLTREEVWDMLECFFGSRN AYLAPVKISEDESSDGEQEEKAKDLVQKAGQWLSSRFGTGEGADFAKMAAVYAKIAAWAGNA QAGTTGNEVINNLATALREFTPKSNDLKGVLDLISGPGYKSATRNLLKQIANTKTVTREDISKLQ ETAGEDSEECATKTGSKGKRAYADAILKDVESVCGFTYRIDKDGQPVSVADYSKYDEDYKWGSS RHKEFAVMLDHAARRVSLAHTWIKRAEAERRKFEEDSKKIMQVPQAAKDWLDAYCAQRSEA SGALEPYRIRKRAIQGWKEIIASWNKPDCKTAEDRIAAARQLQDDPEIEKFGDIQLFEALAEDD AQCVWKKEDGTLDPEILINYTLASEAMFKKQHFKVPSYRHPDAFLYPVFCDFGNSRWELDFSI REAATKLKEIEAKIEKQRQEVHKVQQALEKCENDEKRPKMEERLKEAQKKLQESQNYGEYLHS NNKITMVLFDGTFVKKHIFAWQSKRLTKDLALYQEPSADPKNVVSRADRLGRAVASVGINDAV KVAGLFEQENWNGRLQAPRQQLEAIAQYVEKHGWDNKAEKMRASIKWFITFSAKLQSKGPW NEFARKHGLKEDPHYWPHAEKNENRTAHSRLILSRLPGLRVLSVDLGHRYAAACAVWEALGSE AFKKDIEGKRIIRGDTDENALYCHTEHEANGKKHITIYRRIGADTLPDGAHHPAPWARLDRQFLI KLQGEDEQAREASNEEIWKVHQLENTLGRRTPLIDRLIAGGWGYTEKQKARLEVLTNLGWCPT NKTDNQEEGDEEETAILSKPSLLVDDLMFSAVRTLRLALKRHGDRARIAHYLITDEKTKPGGVKE KLDKNGRVELLLDALGLWHDLFSSPGWHDEKAKQLWNAYIAGLLPEGELQQAKSVTTSAALG GQQKKEKKEKLRAVAEALYLNSDLCHSLNEVWRKRWEEDDKQWRIYIRWFKDWIMPRGANA KSPAIRHVGGLSLTRLATLTEFRRKVQVGFFTRLHPDGTKTETREDFGQKTLDTLEHLREQRVKQ LASRIVEAALGIGSEDKRHWDGKKRPRQRIADPRFVPCHAVVIENLTHYRPEETRTRRENRQIM EWASSKVKKYLSEICQLHGLHLREVSAAYTSHQDSRTGAPGIRCQDVSLIEFMKSPFWRKQVA

[0202]

		QAEKKQKEGKGDAVERYLCELNQKWKGASEEEWRKAGFVRIPLRGGEIFVSAAGHDSPAAKGI HADLNAAANIGLRALLDPDWSGKWWYVPCNSSTMCPARDKVTGSAAVNPGQPLQVSAQL ESDDAAKDTKKRKKKGDGKSKEIINLWRDISSYPLEDTRGGTWSNKTVYWNRVQSNVVHILQ NQMKG
279	Cas12b	MPETTQRAYTLRLQGHDPKDASWREALWKTHEAVNRGAKAFGDWLLTLRGGLDHSLADEG APGQTPTEEQRKQRRILLALSWLSVESENGAPQEYIVPHDRDNESGARQNWKTREALREILKN RGCRDDEIESWCHDCEPSLTSAIRKDAVWVNRSKAFDNAVQSIPNFSREEIWDLLGCFFVSSQ AYLAPLESPKDDKPDASKKDSSKDLIQSAGQWLSRRFGRGKGLNFARLAETYEAIARWASVAN PGDTNDLIADLAKTLNAETPELDGILKVVSGPGHKSKTRNLLRSLSAVNHITKDTLQRLKDTANE DAKKAKLKKGEKGHRAYAYKVLEAVEDACGFTYLQEGDRAKHCEFAVMLDHAARRVSSLHTW IKRAEAERRRFEIDTKKKDQLPPSVKEWLDTYCQKRSKETGAVEPYRIRRGAIEGWKEIVEAWSK AGTTTAEDRKHEARRLPDNPHIDKSGDIKLFEDLALEDALPVWHANGDPNNPPDPQLLIDYV EGSEAEFKKRAFKVPTYCHPDPLVHPVFCDYGCSRWNVSFAIQPVKKQKLSSEEKLPAKGLLLD LLHGTAIRPVALRWQSKRFARDLALNTTDSSDKPNEVTRADRFGCALAKCPSSQKIRIRGLFEE KYWNGRLQAPRPELTALAKRVAKYGWDKKARKLRNSLNWFITFSANLRPSGPWEEYTKYAEK AFSSNASAKPSVSRGGFWVVHASPNKRGKMAQLRLCRLPELRVLSVDLGHRYAAACAVWETL SKSAFEQEIHERKILRGGTGPNDLFCHTQHDTNGQSKVTIYRRIGADTLPNGTPHPAPWARLD RQFLIKLPGEEREARKASPTELANVEKLEKELGLKTSENRVKRIDDLMSDTLRTVRQALRRHSLR ARIAFNLATLRDQSDGDEESQSKQKRDTRWNNTVKIWHSLLESNEWTDDWAKALWDELGP LSDPQKADDAEWLKLAAEKFYTRWQEDEQTWRERLRWLRRWILPRGSQAASQKGSIRHVGG LSLTRLATIKTLYQVLKAYHMRLKPDNSRKNIPAEGDEALQNFGQKILDDLEHMREQRVKQLAS RIVEAALGLGRMKQVTIGKDPKRPREPVDQSCHAVVIENLTHYRPEKRQTRRENRQLMDWSA AKVKKYLKECCQLHGLHLVEVSASYTSRQDSRTGAPGIRCQEVPLTDFLKKNFWREQVKQAKQ RLSEGKANARDRYLCQLNERWGNAPAPVTQTAIRLRIPLNGGELFVSADQNSPASKGIQADLN AAANIGLRAITDPDWPGAWWYVPCEANTFKPVKDKVAGSAAIDSNVSLKKDSPNSEKPASD RKSRTSKSMINLWCDTSSKSLSEKDQWQESAPYWEDVAARTINILQASLACSTTNSQ
280	Cas12a	MKSLAQFQNLYALQKTLRFELKPEGHTRETFNRWLEEIEKEQASENENIVYQDLLRAKKYEKIKII LDEYHKDFIEQALAYANLTELEKYEELYRKSNRTSEEEEEFENTKESLRKQIANIFIKNPNKTVQER WKFLFSKKLIQNELIVWVKGNYELLSEKLKNEFPDESSIISTIEDFKYFTTYFRNYHENRKNLYSNE DKFSTIAHRLIHENLPKFIDNIAIYQKAKAVLNINEVEKELGLPEDTLDKIFSLDFFSKALTQKGIDQ YNYFLGGKTENEVKKIKGLNEFINLYNQQQQDKNQRLPFLKVLYKLPLFERTSTSFRFEPIENDR DLIERIGKFYYNDLKQYRDDSQGDTTDILSGINTLLRHVHDYRDGLYVNGGITLTQISQKIFGSW SYINNALAYFYDTYIDASGVDHQGERKPKKQKQIQEKTKWLKQKQFPVILVEKALSEYKSIETNE DLKTRISDTTLCDFFKRCGNDDNGQDLFDRIEARLREKNEEGYSLEDLLKKEFTTERKLMQDKT KTLLIKNFLDVIQGDKDDITAGLLHFVKCLIPRTEISEKNELFYSGMEKYLNILSEVTPLYNKARNY LTQKPYSIEKVKLNFENSTLLDGWDENEESDNSCVLLRKRGYYYLGIMNKKHNMIFDRKIYPKA TEGEAYYEKMIYKLLPGAYKMLPKVFFSEKNIDYFKPSEEILRIRNTASYSKNGQPQEGYQKASFS IEDCRKYIDFFKKCIANHWDWQKFNFNFSPTEYYQSIDEFYREIERQGYKIDFVKIPESYINQLIKE NKLYLFKIYNKDFSEKKKSKGKDNLHTLYWKMLFDEKNLKDVVLKLNGEAEVFFRQKSILYNEEI WNKGHHYSELKDRFSYPIISNKRYAEDKFFLHVPITLNFKADGINNVNNMVNEFIKDNRDIHII

[0203]

		GIDRGERHLLYVSVINQKGDIVEQCSLNEIVTEYNGKIFKKNYHEELDNLEKERDRARKDWQTI ANIKELKEGYLSHVIHKISKLILKYNAIVVMEDLNSGFKRGRQKVEKQVYQNFEKQLIEKLNYLVL KESNVDEPGGVLRAYQLANKFETFKKLGKQSGIIFYVPAAYTSAIDPVTGYIQYLYPLKQADSVEK ARKFYSQFKRISYNPHKQWFEFSFDYNDFNIIYHGKSSWTICTTNTERYMWNRLLNNGHGGE ELVYVTNELELLFGEYNIIYGDGKDIKQQITDVQDIDVDRTAKQFYKRINELLNLTLKLRHNNGKK GADEEDYILSPVEPYFDSRFESRKPSMQQTLPINADANGAFNIARKGLLLLERLNQLGVEEFEKT KKSNNKKTQWLPHELWVEYAQNHTRK
281	Cas12b	MAYQNGKEQPTVTNQRAYTLRLSGTNDQDSIWRNRLWHTHEAVNKGAKTFGDWLLTMRG GLCHTLAEADVPGKGNKPARHPTPQEIRSRRVVLALSWLSVESQHGAPERHLVSHDLDIATGE RKNWKTVEALREILHGRCLCKELIDEWANDCRDSLSATIREDAVWVNRSKAFDLAAKKIGASLT REELWDFLQPFFANKHGYLQMDTVAGVTNGDSETDAEEAKEDSSEEKAKDLSQKAGQWLSS RFGTGTGADFSRFSKVYEVLAARCGSVAVGVSGVEAIRILAGTLADFSPGSNDIEGMLGLMSGP GYKSATRNILQKINTLQTVSQQDLDRLREASEKDALQSKQKVGGKGSRPYANAILQDVEAACGI CYAGTGESPARHWQYAVILDHAARRVSMAHSWIKRAEEQRSKFEIEKDKLDHVPKDALAWLD AFCARRSSESGASDAYRIRRSAVDGWKQVVAAWAALPPKPENQGSELLSDAESARIQAAREL QDTVEKFGDIQLFEALSLTGAKCVWQPDGRPDAQPLLDYVAGTDAISKKQRFKVPAYRHPDAL LHPVFCDFGNSRWNINYAIHRAPEKLTPAQQLLEKKKAEIDKAELTLAKAGDAAKQANISEKIN GLRAAFIQQQEKVAWLNSRHAMTMSLWDGTHIEDTPLIWQSKRFGSDIGQPVEAQPLPVSR ADRFGRAVALAQDNVPVIPSGLFDLSDWNGRLQAPRRQLEAIAAIRDSAKLSVNEKQQLVAK RIQSIRWLLTFSAKLQSHGPFIAYAAQHGFDWRYGAHGPENKSRQGLAKLILCRLPGLRILSVDL GHRYAAACAVWETLNAGQIQKACLDAGKEAPGPCTLYLHLKQIANGKEKKTIFRRIAADTLPD GSPHPAPWARLDRQFLIKLQGEDRDARLATSEEIAAVEQMENELGVVRQLKRKGRELLVDELM SDALRTLRLGLRRHGVRARIAFNLTANKRIRPGGKEEVLDQEGRVLLLTETLLAWYELYTAERWT DEPARELWNRHIQPLLGATILQNTVNQEDTPSAAKRRKLREETSGKLKHVAEEIAKNDSLCRQL HVLWSAQWQTEDVIWRTRLRMMRRWLLPRGVKRNAQLRISIRDVGGLSLTRIASFKSLYQVQ KAYQMRPHPEDPRLNIPERGDSRLENFGQRVLDAMERMRENRVKQLASRIAEAALGIGGETGI SSKDGSQKKRPTERSSDPRFAPCHAVVIEDLTHYRPDETQTRRENRQLMSWSSSKVKKYLGEA CELNGLYLREVSPAYTSRQDSRTGAPGLRCNDVTVVEFNNSPFWRKQVGAAEKNQKEGNKG DARERYLLSIEEGIRGAANDRDIFRIPVKGGEIFVSACITDGGNNAKKNAPPGLQADLNAAANI GLRAIFDPDWEGRWWYIPCDAATLCPDAKKFIGCKAVDPTKPLRVVAEEGAISASGIGSKKSGR KKNAATDGTRIVNLWRDPSGAPIHRDVLRSPEWQDYAGYWNEVQHRVIRNLKTCYEQTSQQ EDPFVSQDADKPF
282	Cas12b	MKRLAETALADKVKCETNSRPKGERAYANSILHDVESACGFTYRVDKGEQPVPVSDYSHYAND YRWGPANHSEFAVMLDHAARRVSLAHTWIKRAEAERRQFEENAKKIDKVPKVAREWLDSLC AERSIVLGALEPYRIRRRAVDGWKHVVAAWSKSDCKTAQDRITAARLLQEDPEIDKFGDIQLFE ALAEDHAVCVWQRDGEAGKTSDPQLLIDYALAAEAEFKKRHFKVPAYRHPEAFWHPVFCDFG QSRWKICFDVHKNRQSRRQRACANRISRKICFDVHKKRQTLRLSLEVWTGSKMLDMPLCWQ CKRLARDLALGQDHKKDRSCQVTRADRLGRAVSNVARNQEVQILGLFEQEYWNGRLQAPRP QLEALGRYIEKHGWDAKAQKSCRAIRWMISFSPRLQPAGPWGKFAEKLQLNPNPKYWPHAE DNKDRGSRSKLILCRLPGLRVLSVDLGHRYAAACAVWEAVDAEQVKEACQAAGHREPNENDL

[0204]

		YLHLKKRTTKQKKGSQGVVEETTIYRRIGADTLPDCTPHPAPWARLDRQFLIRLQGEEDEARAA SNEEVWAVHKLEAELGRTIPLIDRLLGAGWGQTEKQKARLKALRELGWTPANKCQAFNSTDET ELRRPSLAVDELMLDAVGTLRLALKRHGDRARIARYLITDERTKPGGVKEKLDENGRIELLQDAL IIWHGLFSSPRWRDDAAKQLWNEHIAKLVGEQNLVEVSEDASGSERRTKQKQNREKLREAAK ALVDDVALRQALHDMWKRRWEEEDREWRRRLRWFKDWVLPRREQARKAYSRPAETGSSSH PKRRARYAAIRRVGGLSLTRLATLTEFRRKVQVGFFTRLKPDGTKAEAKEGFGQSTLDALEHLRA QRVKQLASRIVEAALGVGRIRRFPGVKNPKRPDTPVDKPCHAIVIENLTHYRPEETRTRRENRQ LMTWSSSKIKKYLAEACQLYGLHLREVTAAYTSRQDSRTGAPGLRCQDVPVKEFMRSLFWRKE VAQAEKKLTAGKGSSYERLLCELNQRWKDNSPGDGKRAELLRLPHKGGEIFVSAAPDSPAARG LQADLNAAANIGLRALTDPDWPGKWWHVPCNAVTFRPVEDKVKGSAAVKLDQSLRQVAHP QSKDPGAKKSKEIVNLWCDISSLPLEHREWKLDWEPYPAYWNNVQCRVIRVLQGKV
283	Cas12b	MANAKVKTTTRSYTLSLNAPSDTTDRSPLWHRIFRTHYAICCGAREFGKLLLDLRGGLPTSLAQ LGEGIAENDRRQTQRGTRRILALGWLSVEDLDHARNDPHRVQDTAPGSPLDQDLAEKILRKILI TKGIKSEEEQSNWISDCLPALTANIRPDAVWVNRAESFAQWQRGTQPGAQPPTPEEAQQILFS LCGESLVTLTLPEQPAAAGQKQPDQETSPDPEEQTDRPPAAPSADDEMDPSNASRGIFGDLFG ENAEGKRSRSQGKDNFACAVRDFLCANPTPSADAITEFREKQKPREPNPPGPEKYPPEVSTSG APTAVAKRYRKLLVCAGLWPKSADEDGSSRNSAKTKFADPKEPQKTEIQINALDLIDACNQAAP ADDSGTSPKAGRVFAPAWASNIAEKVASATQMPANAKSLNEFKRLMFALAARRFSQTQSWTR RNEAERHMAAARQDAAVARLREIDPDHKAQDWLRGYEQRRADQSGSNGEFRITRRMIGEA EAVFKAWAGTNSAAERELKTVAVQTTAEKFGDAALYSEIARNTAAEAVWRSGSAPEILDQWVK LRKAQSDQQRTRVPRFCHPNAFRHPTWCEFGESSKPGVWYAWNPKSKPRKPEVGGEGDGT RRLWVLLPDFNSGIGQAVPLRWRSKRLSKDLGEALQPSDAPIPRADRVSIAAAGLNLEGANGV PARYRPSLPFSENTKGWNARLQANRTALLHLESKWDAEAATWRDGGRSLLALKWFTTFSPEL AMSEGPGRAIHPKLGWNSEPHSDLNRAQKRGGNAKLILSRLPGLRVLSVDLGHRYAAACAV WETLTTEQMNAACQAKNHTQPAESDMYVHLAHPTERVVKSGRKKGQNLIQTTVYRRIAADT LPDGTPHPAPWGRLDRQFLIKLQGEQRPTRAASKNEADLANALFHRLGLRSDADSENKSRAV DKLMARTVRVATLGLKRHARRAKIAYALDPNTKAIPGMGGSSAAFTPGDEPHIHLLTDALFDW QSLATDAKWDDAHARSLWNHHIATLPGGFHLENPTPRDESAHEPSRQRQRSGDDALRATLK PIAEKLSKADRQEVHAAWKKYWGDSDGQSAIVPKVLQGQRGPEKTTPSASASGWHGKIRWI TDWIMGKYLEGCTGHAWKHDVGGLSVSRITTMKSLYQLHKAFAMRATPEKPRGAPEKGESNL GAAQGILTAMESMRQQRVKQLASRIAEAALGAGIERRSDNGRELQRPRERVDDPRFAACHAV VVEDLTNYRPDEMQTRRENRQLMQWASSKVKKYLSEACQLHGLYLRGVPAGYTSRQDSRTG APGVRCGDIPVEELMAAPRWRRQILTAEKTRRENNTGTARDRYILTLDEKYRLLTAEQRKKTPPA RIPVKGGDLFVSADPDSPAASGIQADLNAAANIGLKALIDPDWPGRWWYIPCDATTHKPSPER TRGSAAVDCDVPLGPDSTGTPEDRDAKPKKNQRNSKIAGRGQSAIINLWRDPTHLPIKENPSA WCESKKYWNQVEHNVVKVIESKGQKLTQTAEAATGESASSPPIAPTDVPW

[0205]

[0206] 당업자는 아미노산 서열이 공지되어 있다는 점을 감안할 때 이들 효소가 용이하게 (예를 들어, 다양한 상업적 공급원 중 임의의 것으로부터 수축될 수 있기 때문에 공급원 유기체의 배양을 통해 및/또는 재조합 발현/정제에 의해) 제조될 수 있음을 이해할 것이다. 제조된 효소는 이어서 다양한 온도(들)에서의 직접적 및/또는 부수적 절단 및/또는 관련 온도(들)에서의 안정성 및/또는 기능성의 다른 증거에 대해 평가될 수 있다.

[0207] 실시예 4: Cas13의 열안정성

[0208] 이 실시예는 Cas13 효소의 열안정성을 확인하고 추가로 입증한다. 이 실시예는 본원에 기술된 바와 같이 개선된 부수적 활성 검정에 사용하기 위한 특정 열안정성 Cas13 후보를 제공한다. TccCas13a 및 ThpCas13a의 열안정성을 테스트하였다. 간단히 말해서, 다양한 범위의 표지된 RNA 표적을 TccCas13a 또는 ThpCas13a; Rnase 억제제; T7 RNA 중합효소, MgCl2 및 cRNA (정방향 또는 역상보체 방향)과 함께 인큐베이션하였다. 도 3a는 65℃에서 TccCas13a의 상당한 활성을 입증한다. 도 3a의 데이터는 또한 cRNA의 구조가 열안정성 효소의 활성에 영향을 미칠 수 있음을 시사한다. 또한, 도 3b는 TccCas13a가 40℃ 내지 65℃ 범위를 포함한 광범위한 온도에 걸쳐 활성임을 보여준다.

[0209] 검정 내 배경에 기여하는 매개변수를 확인하기 위해 일부 구성성분이 있거나 없는 TccCas13a를 사용하여 추가 검정을 수행하였다. 도 3c는 Cas 효소와 cRNA의 복합체의 존재가 검정의 배경에 기여한다는 것을 보여준다.

[0210] 실시예 5: 열안정성 Cas 효소에 대한 예시적인 발견 및 스크리닝

[0211] 본 실시예는 열안정성 Cas 효소 후보 (예를 들어 Cas12 및 Cas13 효소) 발견하고 스크리닝하는 예시적인 방법을 입증한다 (도 4). 신규한 Cas12 및 Cas13 효소는 맞춤형 인실리코 파이프라인을 사용하여 발견되었다. 간단히 말해서, 공개적으로 이용 가능한 미생물 게놈 및 메타게놈 데이터베이스는 먼저 샘플 수집 온도 및 시퀀싱 판독

품질과 같은 환경적 메타데이터를 기반으로 필터링되었다. CRISPR 반복부는 공개된 반복 주석 방법을 사용하여 필터링된 게놈 데이터 세트에서 이후에 식별되었다. 다음으로, 모든 코딩 서열은 공개된 개방형 판독 프레임(open-reading-frame, ORF) 발견 방법을 사용하여 CRISPR 반복부를 갖는 게놈에 주석을 달았고, 이러한 ORF는 공지된 Cas12 및 Cas13 효소에 대해 사전 훈련된 은닉 마르코프 모델 (Hidden Markov Model, HMM)을 사용하여 이후에 분류되었다. 효소는 그의 직접 반복부가 보존되고 (>95%) 예측된 효소가 이전에 발견된 효소와 일치하는 도메인 토폴로지를 갖는 경우 및 그 경우에만 추정 후보로서 주석이 달렸다.

[0212] 후보 효소는 제조사의 지침에 따라 *시험관내* 단백질 합성 (예를 들어, New England BioLabs의 PURExpress *시험관내* 단백질 합성 키트)에 의해 발현되었다. Cas12a 후보 효소의 초기 풀은 52℃ 에서 활성에 대한 음성 대조군으로 주형을 사용하지 않는 엔드포인트 (도 5) 및 동역학 분석 (도 6)에 의해 평가되었다. 각 후보는 52℃에서 3개의 상이한 가이드/표적 쌍으로 테스트되었다 (도 5).

[0213] 52℃에서 44개의 초기 후보 중에서 가장 높은 활성을 나타내는 후보의 서브세트 (예를 들어, 12개의 후보)는 더 높은 온도 (예를 들어, 58℃, 60℃, 62℃)에서 추가 평가를 위해 가장 효율적인 가이드 및 표적과 조합하여 선택되었다.

[0214] 엔드포인트 및 동역학 분석 둘 다 58℃에서 일부 활성을 나타내는 후보 효소의 서브세트 (예를 들어, 12개의 후보 효소 중 9개)를 나타내었다. 일부 활성을 갖는 9개 중 5개는 높은 활성 (RS9, RS12, RS38, RS54, 및 RS56)으로 분류되었고, 나머지 4개는 낮은 활성 (RS31, RS39, RS47 및 RS50)으로 분류되었다 (도 7).

[0215] 엔드포인트 및 동역학 분석 둘 다 60℃에서 일부 활성을 나타내는 서브세트 (예를 들어, 12개의 후보 효소 중 5개)를 나타내었다. 일부 활성을 갖는 5개 중 3개는 높은 활성 (RS50, RS56, 및 RS9)으로 분류되었고, 나머지 2개는 낮은 활성 (RS28 및 RS29)으로 분류되었다 (도 8).

[0216] 엔드포인트 및 동역학 분석 둘 다 62℃에서 일부 활성을 나타내는 서브세트 (예를 들어, 12개의 후보 효소 중 2개) (RS9 및 RS54)를 나타내었다 (도 9).

[0217] 12개의 후보 효소의 정제된 목록이 다양한 온도에서 평가되는 동안, 4개의 우선 순위 후보 효소 (RS10, RS28, RS38, 및 RS54)가 정제되고 다양한 온도 (예를 들어, 대략 35℃ 내지 65℃)에서 활성에 대해 평가되었다. RS54는 LAMP 온도 (예를 들어, 61℃)에서 활성을 보였다 (도 10).

[0218] Cas12a 후보의 서브세트는 58℃ 및 70℃ 둘 다에서 주형이 없는 대조군과 비교하여 3개의 상이한 가이드 및 표적 세트를 사용하여 추가로 조사되었다 (도 11). Cas12bcdf는 또한 52 및 58℃ 둘 다에서 모든 가이드/표적 쌍으로 평가되었다 (도 12). 52℃에서 활성을 보인 Cas12a 후보인 RS62에 대해서도 동역학 분석을 수행하였다 (도 13).

[0219] Cas13 후보 효소의 초기 풀은 37℃ 및 52℃ 둘 다에서 활성에 대한 음성 대조군으로 주형을 사용하지 않는 엔드포인트 분석 (도 14)에 의해 평가되었다. 단일 Cas13 후보 효소 (RS73)는 열안정성을 나타내는 것으로 확인되었다.

[0220] 실시예 6: 열안정성 Cas12a 효소의 예시적인 특성 분석

[0221] 본 실시예는 예시적인 열안정성 Cas12a 효소인 RS9의 특성 분석을 입증한다. RS9가 표적 핵산의 증폭을 위해 열안정성 무기 피로포스파타제 (TIPP)의 사용을 필요로 하는지를 결정하기 위해, ORF1ab 증폭의 실시간 검출은 TIPP의 유무에 따라 ORF1ab의 시작 농도 범위 (4.5 카피/μL 내지 4,500 카피/μL)에 걸쳐 완료되었다. 예시적인 반응은 표시된 바이러스성 RNA 주형 농도가 존재하는 1 U 열안정성 무기 피로포스파타제 (TIPP)가 있거나 없는, 30 ng/ul RS9, 112.5 XL-213 (ORF1ab 가이드), 1x HKFB (ORF1ab) 프라이머 세트, 1x wsLAMP 믹스, 125 nM DNase Alert를 포함한다. 예시적인 반응은 QS5에서 120분 동안 58℃에서 인큐베이션되고 VIC 채널에서 검출되었다. TIPP를 함유하지 않은 실시간 반응은 주형의 시작 농도에 관계 없이 주형이 없는 대조군과 비교하여 ORF1ab의 통계적으로 상당한 증폭을 초래하지 않았다. TIPP를 함유하는 실시간 반응은 주형의 시작 농도가 4.5 카피/μL인 것을 제외하고는 주형이 없는 대조군과 비교하여 ORF1ab의 상당한 증폭을 보여주었으며, 이는 RS9가 증폭을 위해 TIPP의 사용을 필요로 함을 시사한다 (도 15).

[0222] RS9의 특이성은 또한 실시간 분석을 사용하여 평가되었다. 증폭은 4,500 카피/μL ORF1ab 주형의 시작 농도와 ORF1ab에 특이적인 프라이머 및 가이드 또는 ORF1ab 가이드가 있는 비-표적화 프라이머로 실시되었다. 각 반응 조건 또한 TIPP의 유무에 따라 실시되었다. 예시적인 반응은 4,500 카피/μl 바이러스성 RNA가 존재하는 1 U 열안정성 무기 피로포스파타제 (TIPP)가 있거나 없는, 30 ng/ul RS9, 112.5 XL-213(ORF1ab 가이드), 1x HKFB

(ORF1ab) 또는 CFB (N) 프라이머 세트, 1x wsLAMP 믹스, 125 nM DNase Alert를 포함한다. 예시적인 반응은 QS5에서 120분 동안 58℃에서 인큐베이션되었고 VIC 채널에서 검출되었다. 비-표적화 프라이머를 함유하고/하거나 TIPP를 함유하지 않는 반응에 대해 증폭이 감지되지 않았다. ORF1ab 프라이머, ORF1ab 가이드, 및 TIPP를 함유하는 반응에서 강력한 증폭이 감지되었으며, 이는 RS9가 그의 표적에 특이적이며 증폭을 위해 TIPP를 필요로 함을 나타낸다 (도 16).

[0223] RS9 부수적 절단 활성은 100 nM의 단일 가닥 DNA 표적 및 DNaseAlert 또는 RNaseAlert를 리포터로 사용하여 평가되었다. 표적이 없는 조건을 음성 대조군으로 이용하였다. RS9는 DNaseAlert를 절단할 수 없었고, 결과적으로 표적이 없는 대조군 조건보다 강도 측정이 상당히 높게 나타났다. RS9는 RNaseAlert를 절단할 수 있었고, 결과적으로 표적이 없는 대조군 조건의 강도과 유사한 측정된 강도를 얻었으며, 이는 RS9가 RNA-특이적 부수적 절단 활성을 갖는다는 것을 나타낸다 (도 17).

[0224] RS9 부수적 절단 활성은 ORF LAMP 제품을 표적으로 사용하고 RNaseAlert, PolyrA, PolyrC, 또는 PolyrU 리포터를 사용하여, 공지된 Cas12a, LbaCas12a와 함께 추가로 평가되었다. 표적이 없는 조건을 음성 대조군으로 이용하였다. RS9 및 LbaCas12a 둘 다 PolyrA, PolyrC, 또는 PolyrU보다 RNaseAlert를 더 효율적으로 절단할 수 있었다 (도 18).

[0225] 실시예 7: 열안정성 Cas13a의 예시적인 특성 분석

[0226] 본 실시예는 예시적인 열안정성 Cas13a 효소인 TccCas13a의 특성 분석을 입증한다. TccCas13a 활성을 위한 최적 온도를 결정하기 위해, Cas 반응은 10nM 표적 및 RNaseAlert를 리포터로 사용하여 다양한 온도에서 실시되었다. 표적이 없는 조건을 음성 대조군으로 이용하였다. 온도 프로파일은 TccCas13a이 대략 62℃에서 가장 높은 활성을 보임을 시사한다 (도 19).

[0227] TccCas13a가 RNA외에 ssDNA에 의해 활성화될 수 있는지 결정하기 위해, Cas 반응은 RNaseAlert를 리포터로 사용하여 62℃에서 완료되었다. 상이한 표적은 상이한 농도에서 이용되었다 (예를 들어, 10 nM, 100 nM, 또는 1,000 nM ssDNA 또는 10 nM RNA). 표적이 없는 조건을 음성 대조군으로 이용하였다. 결과는 TccCas13a가 RNA에 의해 활성화될 수 있지만, 62℃에서 가장 높은 농도의 ssDNA 주형에서도 ssDNA에 의해 활성화될 수 없음을 나타낸다 (도 20).

[0228] ssDNA에 의한 TccCas13a 활성화 또한 58℃에서 평가되었다. TccCas13a는 표적이 없는 대조군과 비교하여 1 nM, 10 nM, 및 100 nM RNA 표적의 존재하에 58℃에서 활성화된 반면, 58℃에서 ssDNA에 의한 TccCas13a 활성화는 100 nM 또는 1,000 nM의 ssDNA 표적이 이용될 때만 검출되었다. 58℃에서 10 nM의 ssDNA 표적은 표적이 없는 대조군과 비교하여 차이를 보이지 않았으며, 이는 TccCas13a 활성화가 LwaCas13 ssDNA 활성화에 대해 관찰된 것과 유사한 RNA보다 더 높은 농도의 ssDNA를 필요로 함을 시사한다. 흥미롭게도, TccCas13a는 대조군 (표적이 없음)과 비교하여 임의의 농도 (10 nM, 100 nM, 또는 1,000 nM)에서도 ssDNA*에 의해 활성화되지 않았다 (도 21).

[0229] TccCas13a가 LwaCas13의 것과 상이한 특이적 부수적 활성을 보이는지를 결정하기 위해, Cas 반응은 2개의 상이한 리포터, 즉 여러 개의 상이한 염기 ("NN")를 함유하는 RNaseAlert 및 단 2개의 "UU" 염기와 DNA 백본이 있는 "UU"-특이적 리포터를 사용하여 수행되었다. 반응은 60℃에서 실시되었다. LwaCas13a는 다른 리포터보다 어느 한 리포터에서 부수적 활성에 대한 선호도를 보이지 않은 반면, TccCas13a는 "UU" 부위에 비해 "NN" 부위에서 증가된 부수적 활성을 보였다 (도 22).

[0230] 실시예 8: 추가 후보 열안정성 Cas 효소의 예시적인 특성 분석

[0231] 본 실시예는 예시적인 열안정성 Cas 효소인 Pal1 (서열번호 274), Pal2 저 MW, Pal2 고 MW (서열번호 275), 및 Pal3 (서열번호 276)의 특성 분석을 입증한다. 각 효소는 DnaseAlert를 리포터로 사용하는 Cas-단독 반응에서 37℃ 및 56℃ 둘 다에서 4개의 가이드 (342-353으로 지정됨)를 사용하여 테스트되었다. 형광 신호는 각 반응에 대한 시간에 대해 플롯팅되었다 (도 23). Pal1은 56℃에서 2개의 가이드에 대해 낮은 활성을 보였다. Pal2 저 MW 또는 Pal3에 대해서는 활성이 관찰되지 않은 반면, Pal2 고 MW에 대해 56℃에서 2개의 가이드에 대해서는 활성이 관찰되었다. 56℃에서의 Pal1 및 Pal2 활성은 도 24에 도시되어 있다. 이들 효소에 대한 추가 연구 결과는 도 25-30에 도시되어 있다. 보다시피, Pal1은 56℃ 및 70℃에서 2개의 가이드에 대해 활성을 보였고; Pal1은 57℃에서 최대 활성을 보였고 적어도 67℃까지 상당한 활성을 보였다. Pal2 고 MW는 56℃에서 2개의 가이드에 대해 활성을 보였고; Pal2 고 MW는 또한 47-52℃에서 최대 활성을 보였고 적어도 57℃까지 상당한 활성을 보였다. 37℃, 56℃, 또는 70℃에서 Pal2 저 MW, 또는 Pal3-6 중 어느 것에서도 상당한 활성이 관찰되지 않았다.

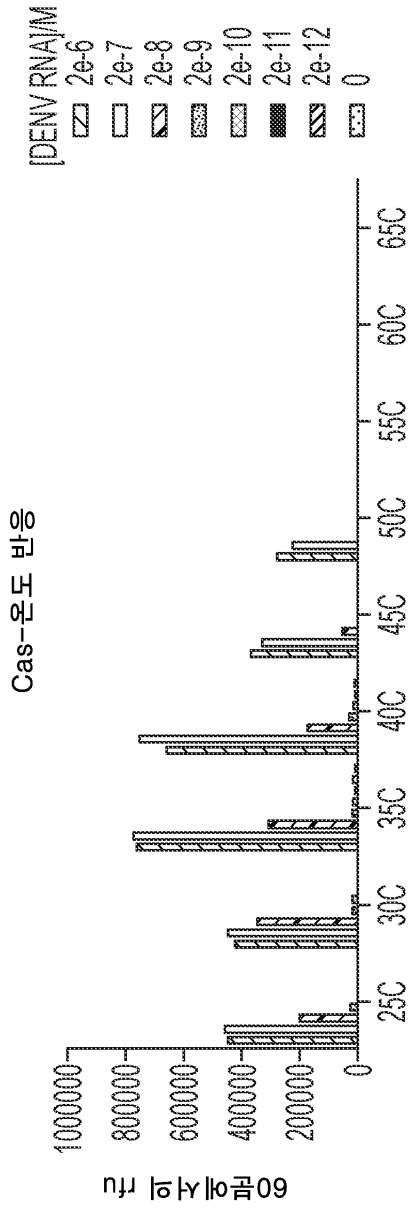
따라서, 당업자는 이들 효소가 적어도 약 56℃ 및/또는 56℃ 및 70℃ 범위 내에서 열안정성임을 이해한다. 이들 특정 예시된 효소는 또한 관련 활성(들)이 37℃에서와 같은 더 낮은 온도에서 극적으로 감소되고/되거나 검출되지 않기 때문에 열활성인 것으로 기술될 수 있다. 임의의 특정 이론에 얽매이는 것은 아니지만, 호열성 유기체의 효소는 종종 그러한 온도에서 감소된 (또는 검출할 수 없는) 활성을 나타낼 수 있음을 주목해야 한다.

[0232] **등가물**

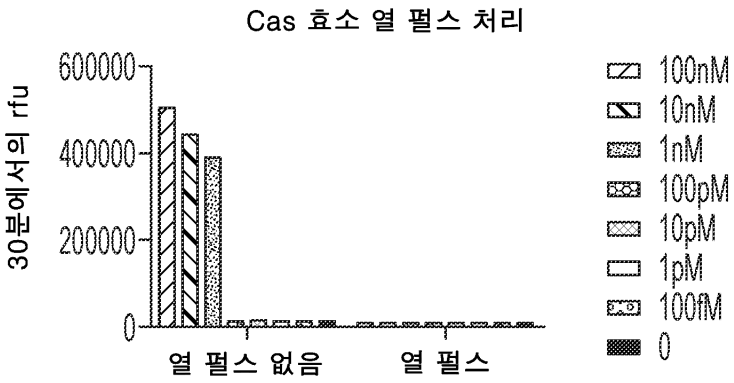
[0233] 당업자는 단지 일상적인 실험을 사용하여 본원에 기술된 발명의 특정 구현예에 대한 많은 등가물을 인식하거나 확인할 수 있을 것이다. 본 발명의 범위는 상기 설명으로 제한되는 것으로 의도되지 않으며, 오히려 하기 청구범위에 제시된 바와 같다:

도면

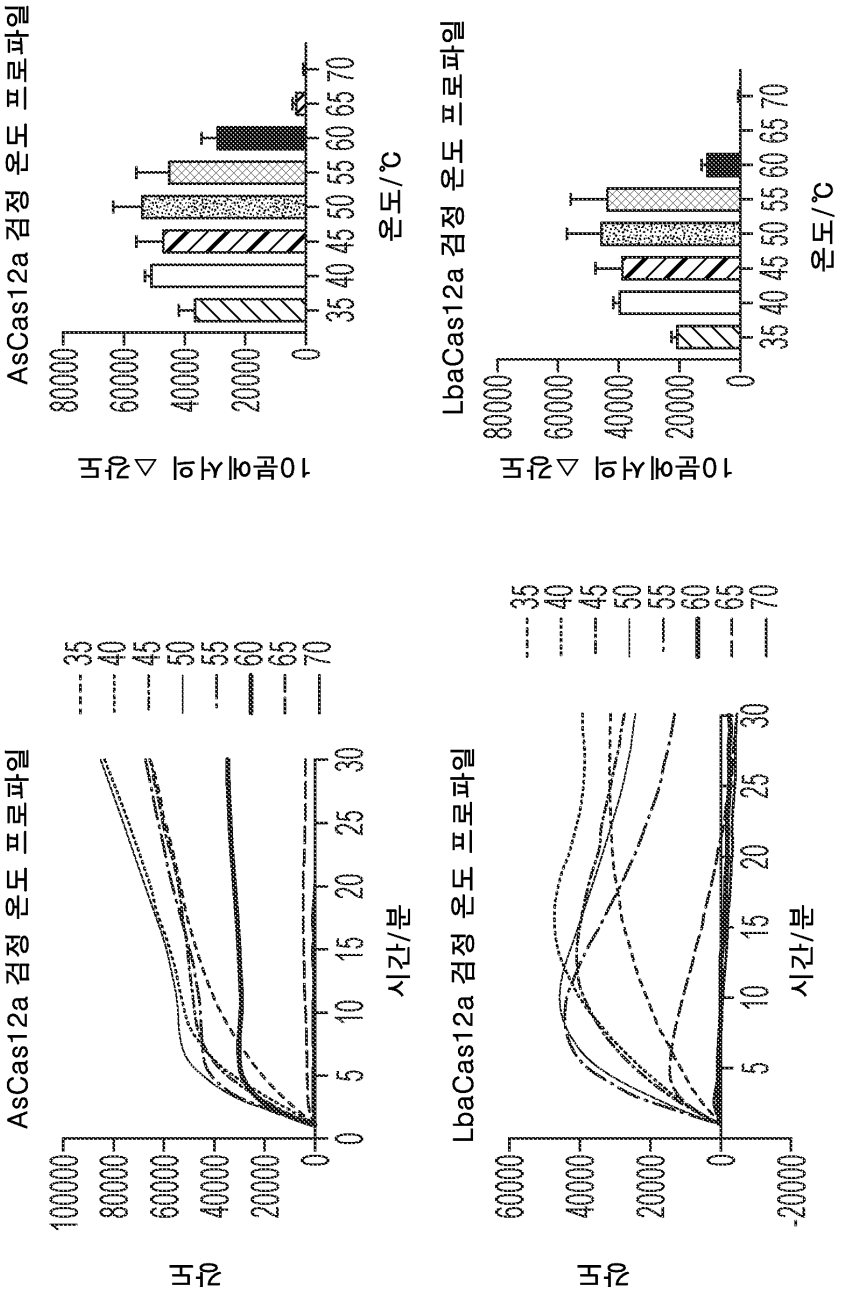
도면1a



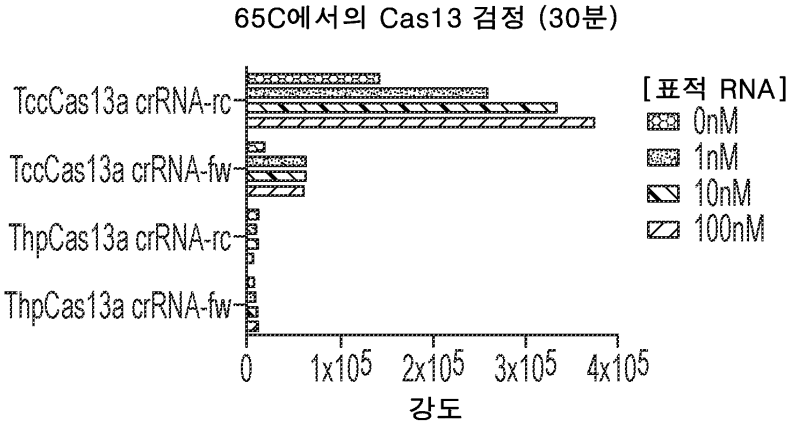
도면1b


Cas 효소 열 펄스 처리
30분에서의 rfu
600000
400000
200000
0
열 펄스 없음
열 펄스
100nM
10nM
1nM
100pM
10pM
1pM
100fM
0

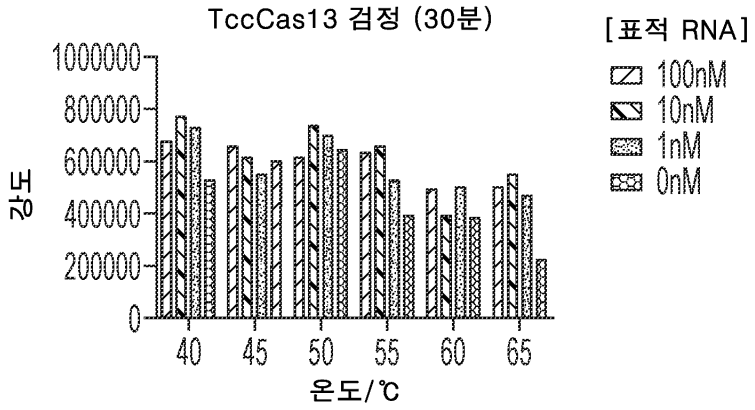
도면2


AsCas12a 검정 온도 프로파일
LbaCas12a 검정 온도 프로파일
10분에서의 △강도
온도/℃
0
20000
40000
60000
80000
35 40 45 50 55 60 65 70
AsCas12a 검정 온도 프로파일
LbaCas12a 검정 온도 프로파일
강도
시간/분
35
40
45
50
55
60
65
70
0
5
10
15
20
25
30
-20000
100000

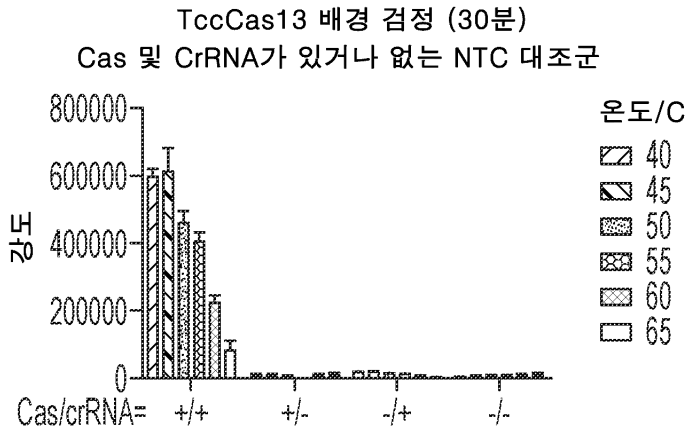
도면3a



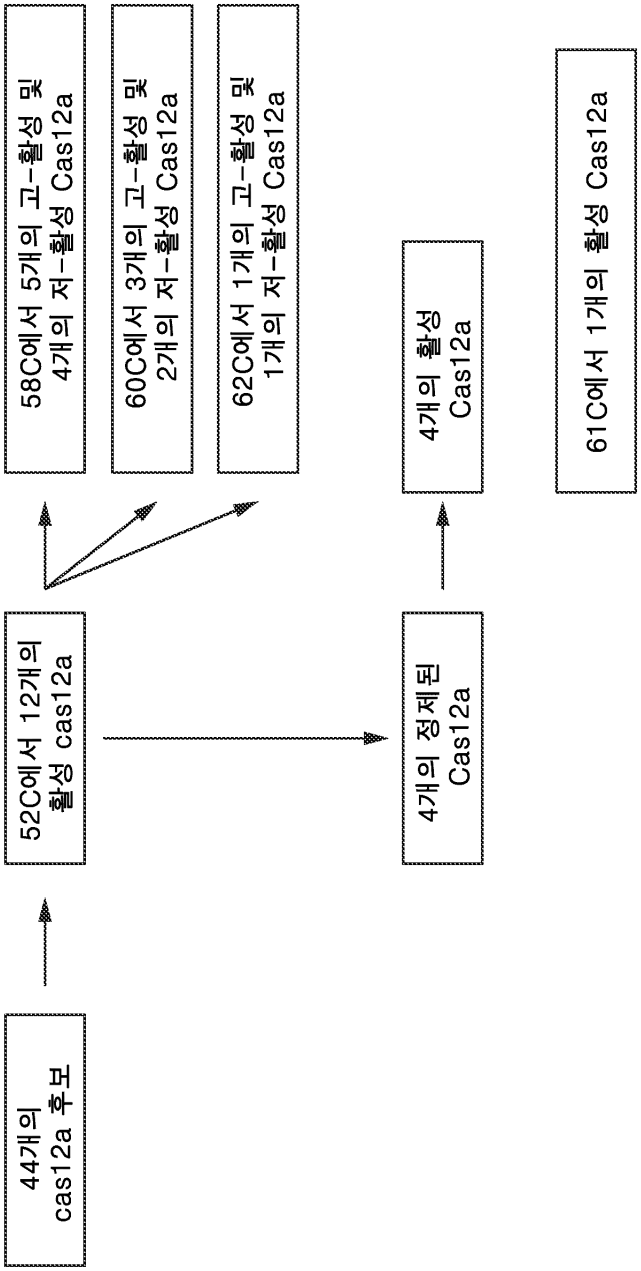
도면3b



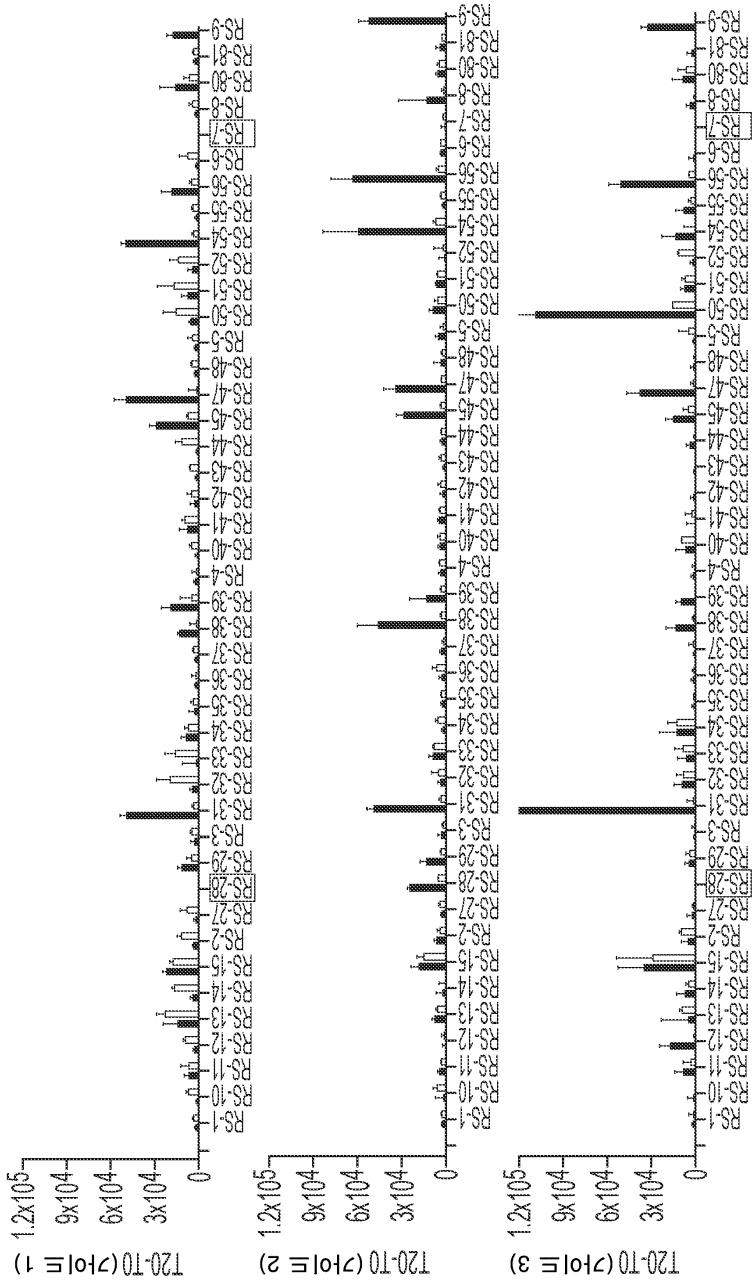
도면3c



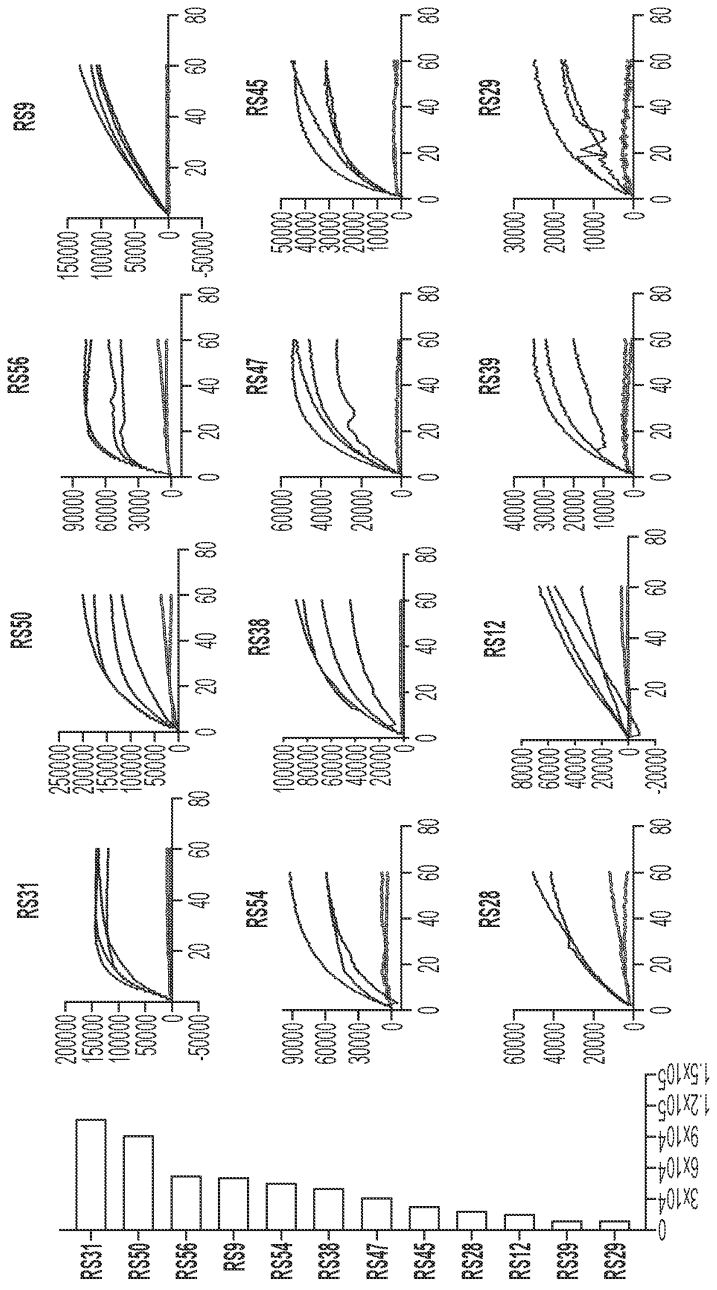
도면4


44개의 cas12a 후보
52C에서 12개의 활성 cas12a
58C에서 5개의 고-활성 및 4개의 저-활성 Cas12a
60C에서 3개의 고-활성 및 2개의 저-활성 Cas12a
62C에서 1개의 고-활성 및 1개의 저-활성 Cas12a
47개의 정제된 Cas12a
4개의 활성 Cas12a
61C에서 1개의 활성 Cas12a

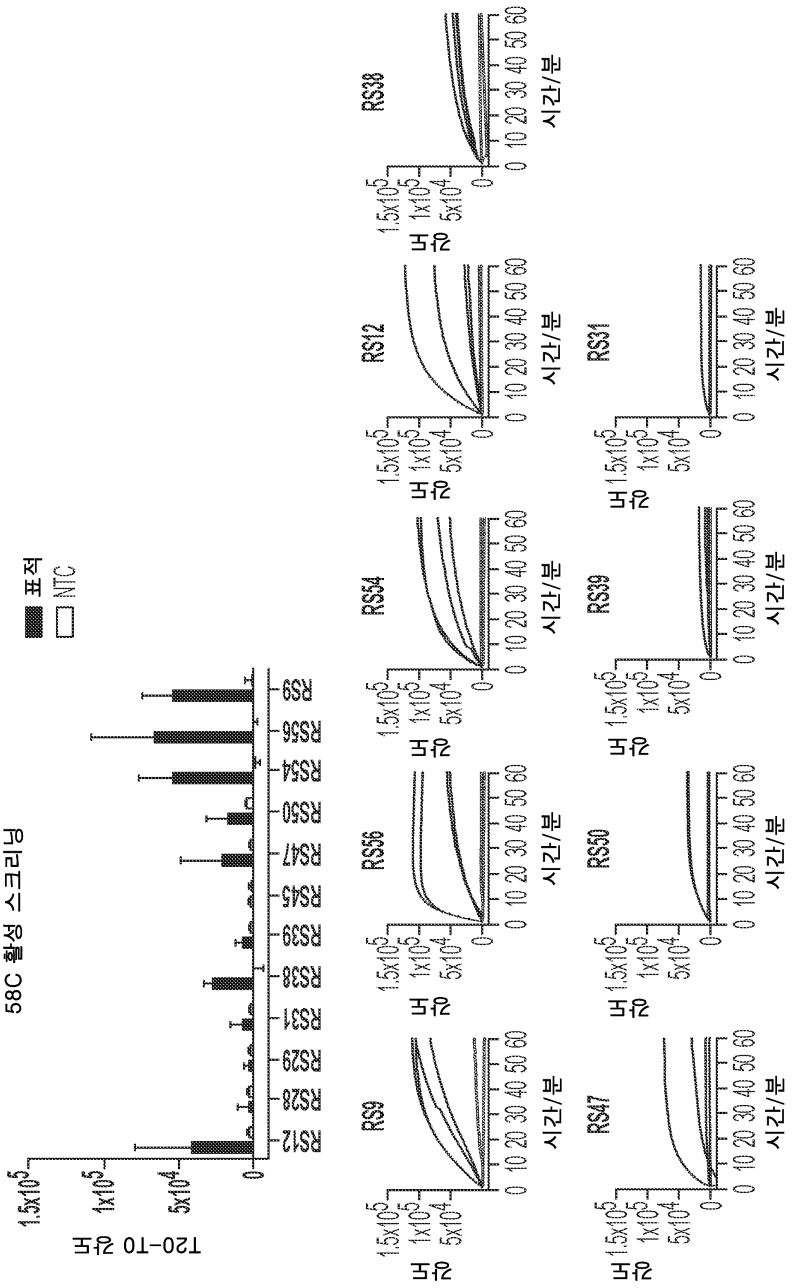
도면5



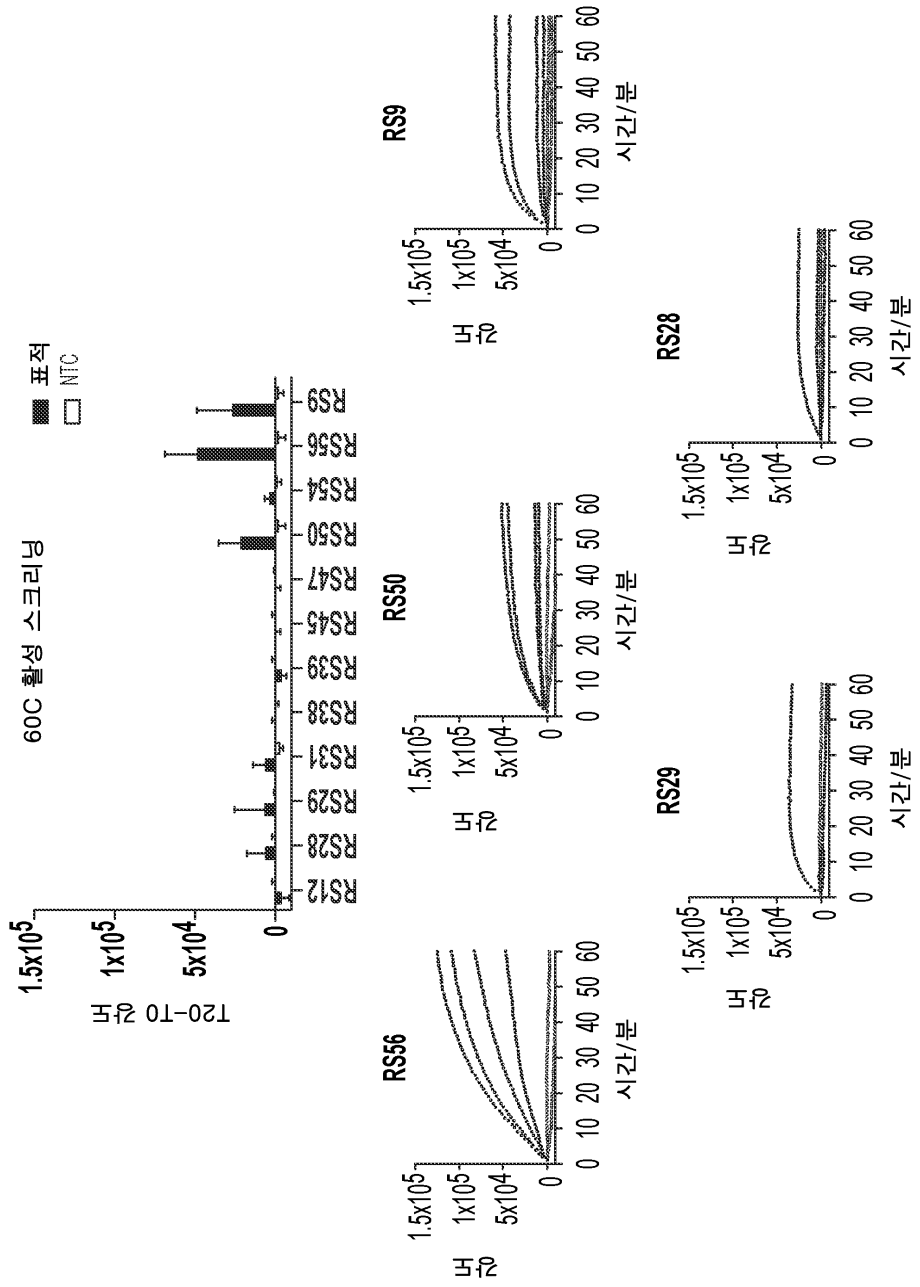
도면6


RS31
RS50
RS56
RS9
RS54
RS38
RS47
RS45
RS28
RS12
RS39
RS29
3X10⁴
6X10⁴
9X10⁴
1.2X10⁵
1.5X10⁵

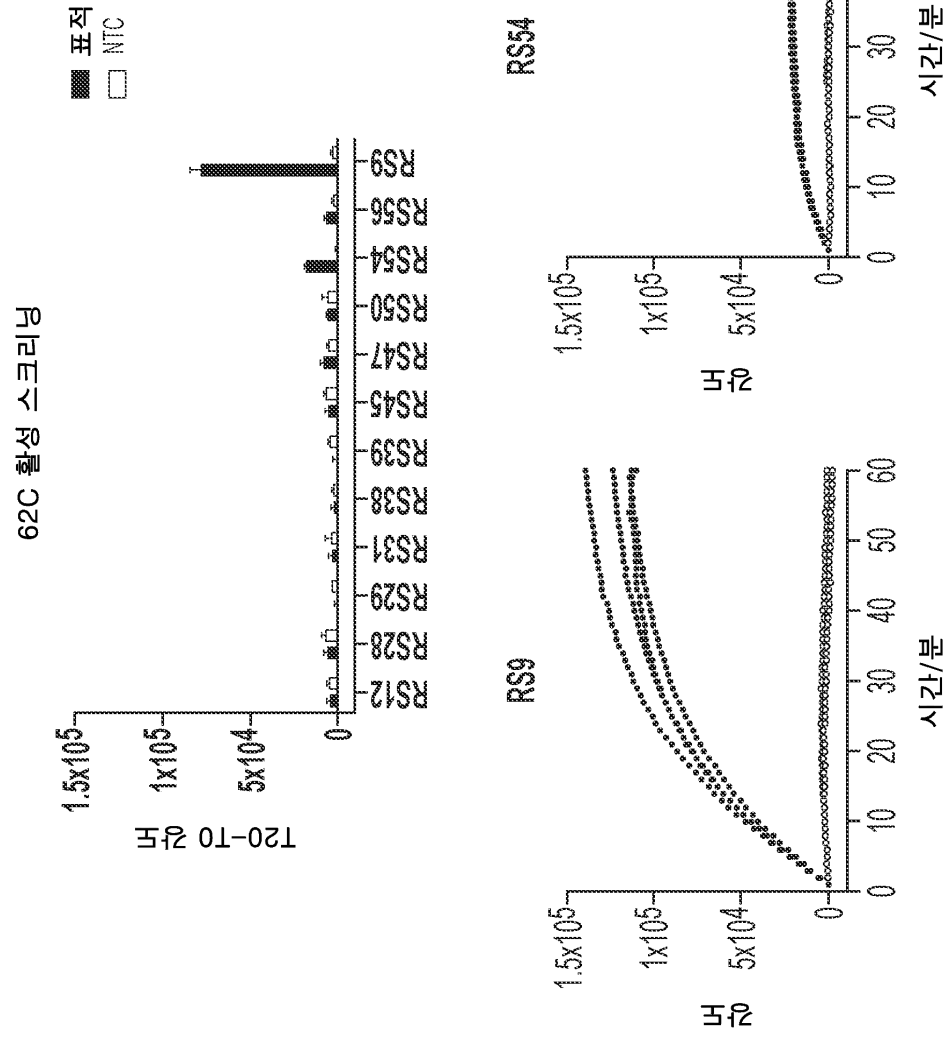
도면7


58C 활성 스크리닝
표적
NTC
T20-T0 강도
RS12
RS28
RS29
RS31
RS38
RS39
RS45
RS47
RS50
RS54
RS56
RS9
RS36
RS54
RS12
RS38
RS39
RS31
RS47
RS50
강도
시간/분

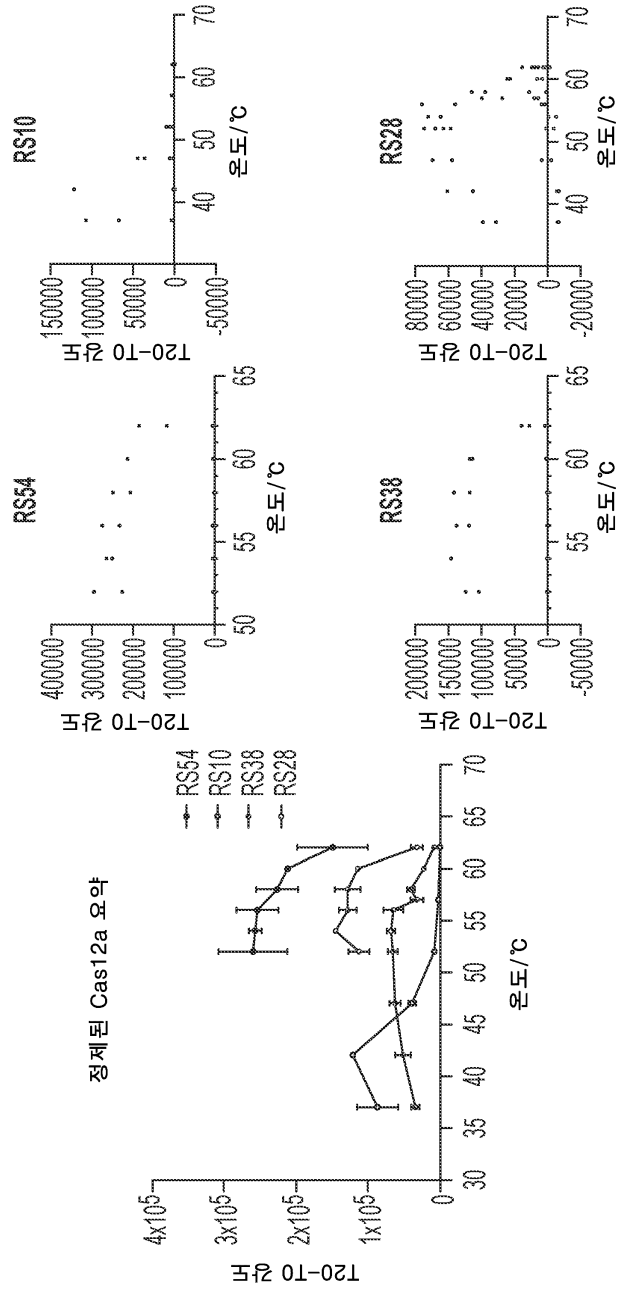
도면8


60C 활성 스크리닝
표적
NTC
T20-T0 값
RS12
RS28
RS29
RS31
RS38
RS39
RS45
RS47
RS50
RS54
RS56
RS9
RS56
RS50
RS9
RS28
RS29
값
시간/분

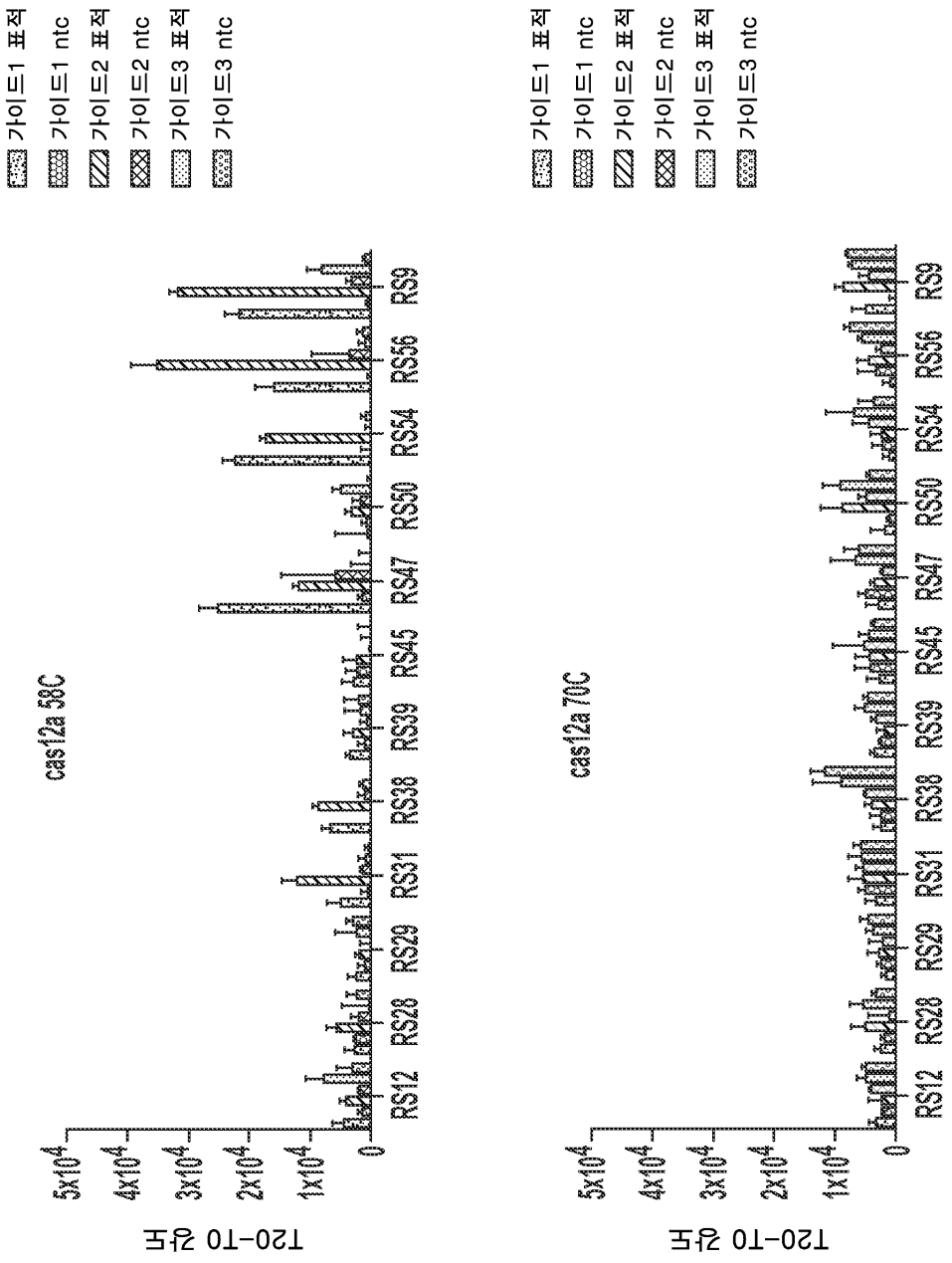
도면9


62C 활성 스크리닝
표적
NTC
T20-T0 강도
1.5x10^5
1x10^5
5x10^4
0
RS9
RS54
RS56
RS50
RS47
RS45
RS39
RS38
RS31
RS29
RS28
RS12
RS54
RS9
강도
시간/분
0
10
20
30
40
50
60

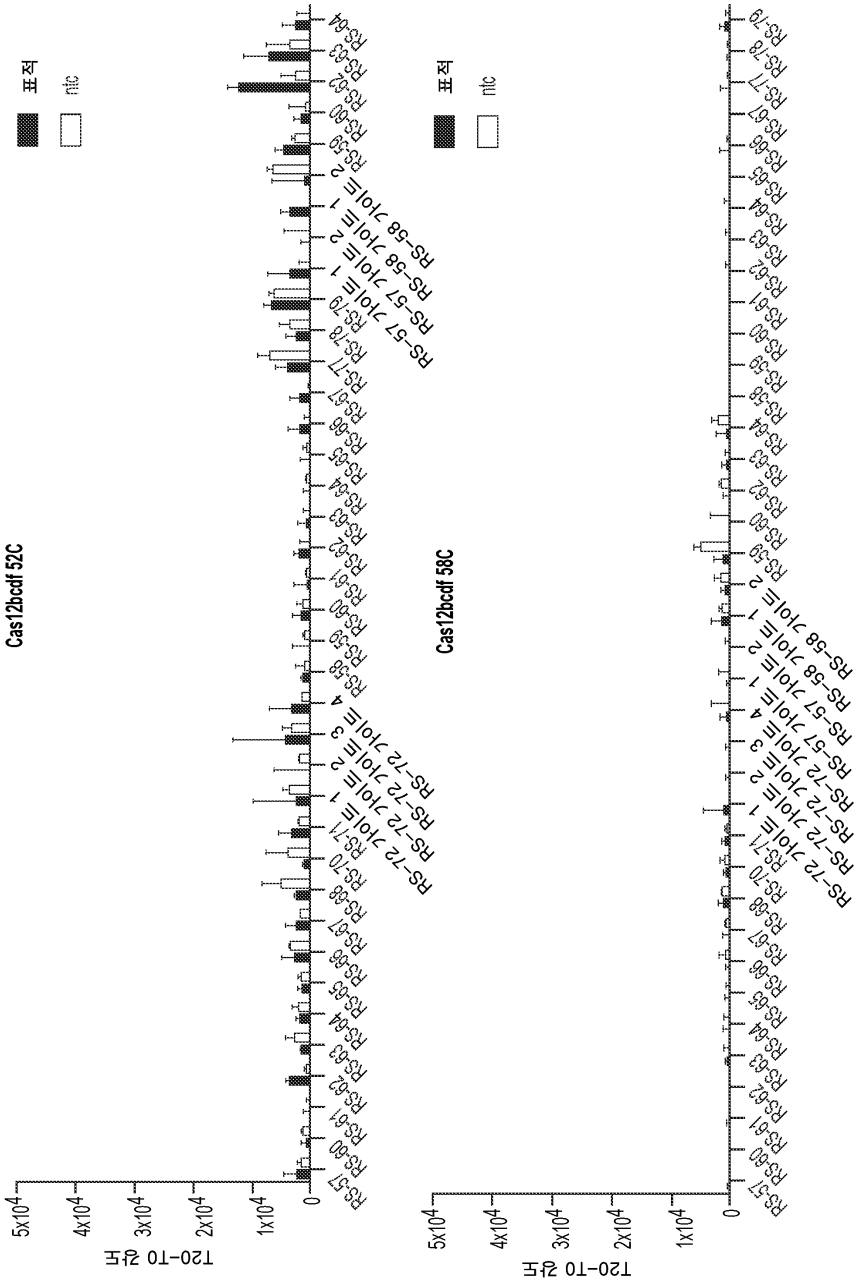
도면10


RS10
RS28
RS54
RS38
T20-T0 강도
온도/℃
정제된 Cas12a 요약
RS54
RS10
RS38
RS28

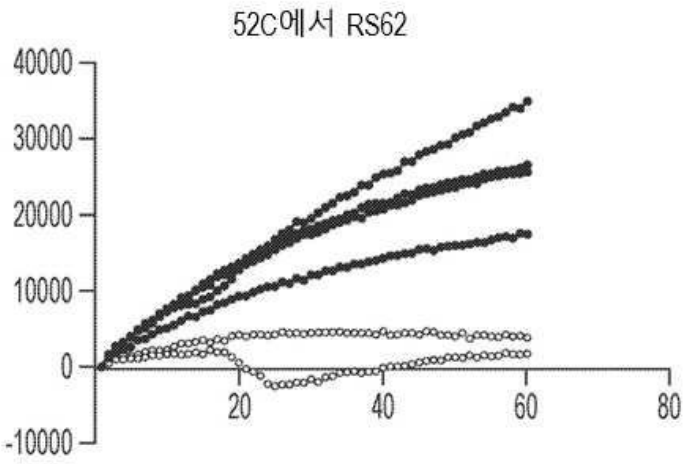
도면11


가이드1 표적
가이드1 ntc
가이드2 표적
가이드2 ntc
가이드3 표적
가이드3 ntc
cas12a 58C
T20-T0 강도
5x10^4
4x10^4
3x10^4
2x10^4
1x10^4
0
RS12
RS28
RS29
RS31
RS38
RS39
RS45
RS47
RS50
RS54
RS56
RS9
가이드1 표적
가이드1 ntc
가이드2 표적
가이드2 ntc
가이드3 표적
가이드3 ntc
cas12a 70C
T20-T0 강도
5x10^4
4x10^4
3x10^4
2x10^4
1x10^4
0
RS12
RS28
RS29
RS31
RS38
RS39
RS45
RS47
RS50
RS54
RS56
RS9

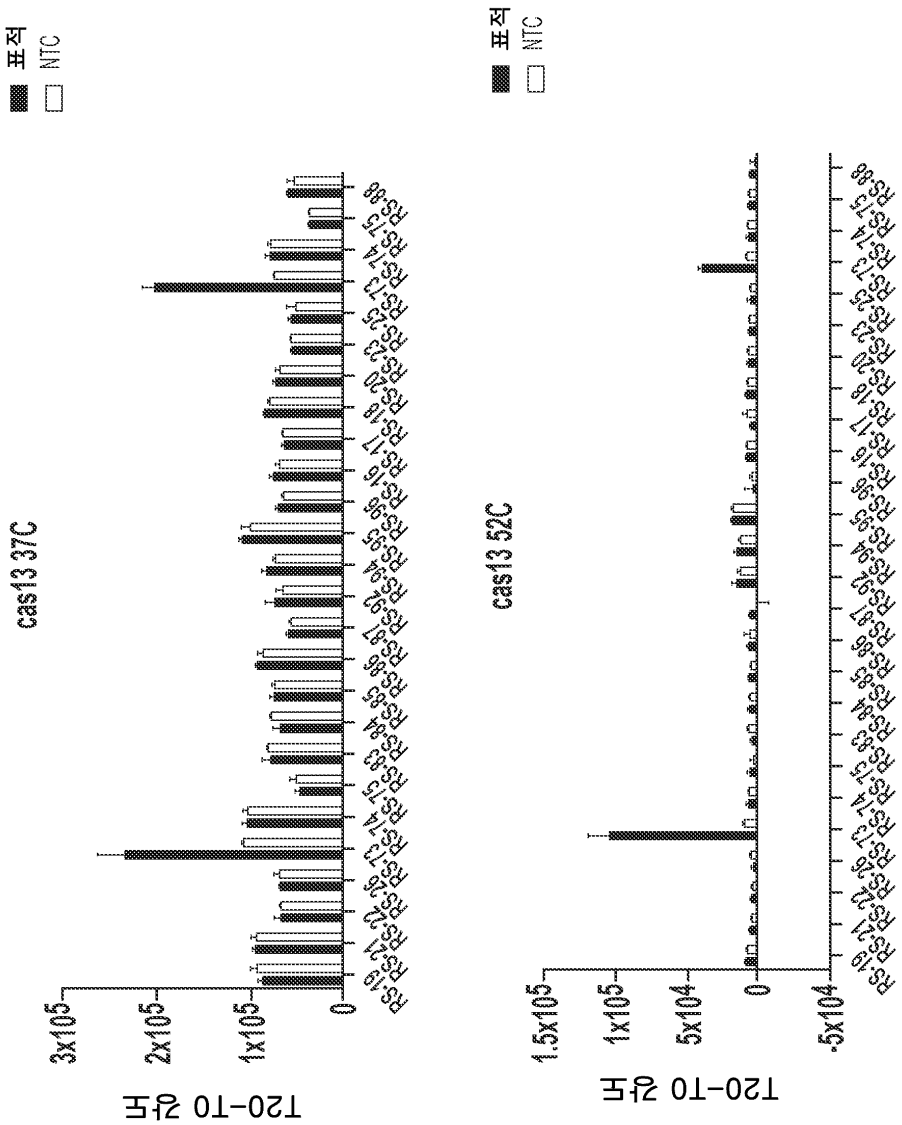
도면12


Cas12bcdf 52C
표적
ntc
T20-T0 값들
5x10^4
4x10^4
3x10^4
2x10^4
1x10^4
0
RS-57
RS-60
RS-61
RS-62
RS-63
RS-64
RS-65
RS-66
RS-67
RS-68
RS-70
RS-71
RS-72 가이드 1
RS-72 가이드 2
RS-72 가이드 3
RS-72 가이드 4
RS-57 가이드 1
RS-57 가이드 2
RS-58 가이드 1
RS-58 가이드 2
RS-59
RS-60
RS-63
RS-64
Cas12bcdf 58C
표적
ntc
T20-T0 값들
5x10^4
4x10^4
3x10^4
2x10^4
1x10^4
0
RS-57
RS-60
RS-61
RS-62
RS-63
RS-64
RS-65
RS-66
RS-67
RS-68
RS-70
RS-71
RS-72 가이드 1
RS-72 가이드 2
RS-72 가이드 3
RS-72 가이드 4
RS-57 가이드 1
RS-57 가이드 2
RS-58 가이드 1
RS-58 가이드 2
RS-59
RS-60
RS-63
RS-64
RS-65
RS-66
RS-67
RS-68
RS-70
RS-71
RS-72 가이드 1
RS-72 가이드 2
RS-72 가이드 3
RS-72 가이드 4
RS-57 가이드 1
RS-57 가이드 2
RS-58 가이드 1
RS-58 가이드 2
RS-59
RS-60
RS-61
RS-62

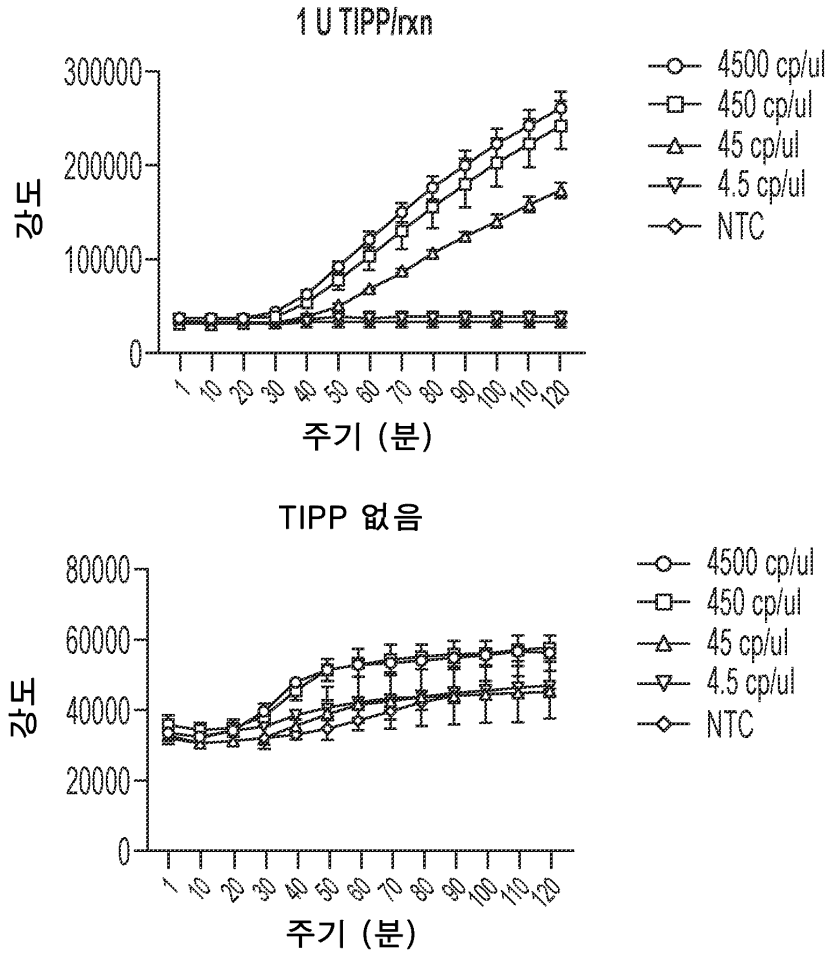
도면13


52C에서 RS62
40000
30000
20000
10000
0
-10000
20
40
60
80

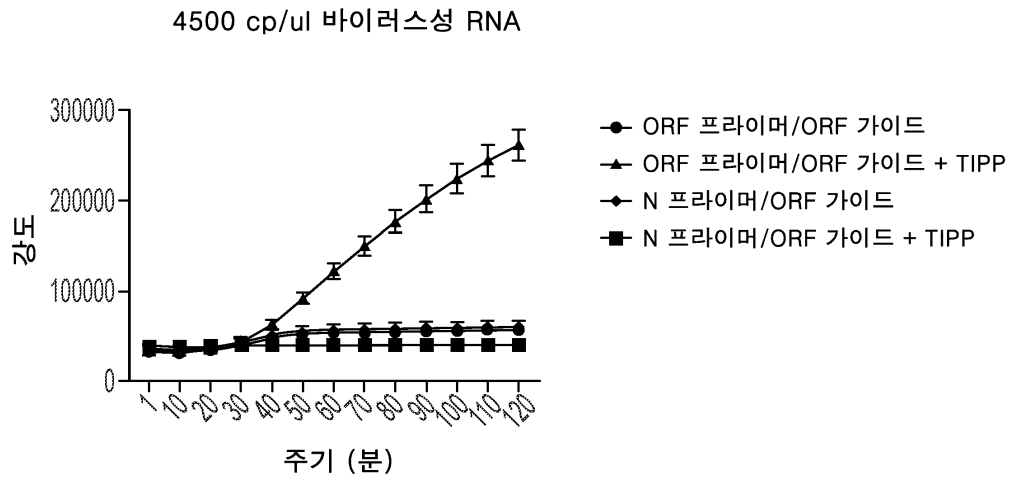
도면14


표적
NTC
cas13 37C
3x10⁵
2x10⁵
1x10⁵
0
T20-T0 강도
표적
NTC
cas13 52C
1.5x10⁵
1x10⁵
5x10⁴
0
-5x10⁴
T20-T0 강도

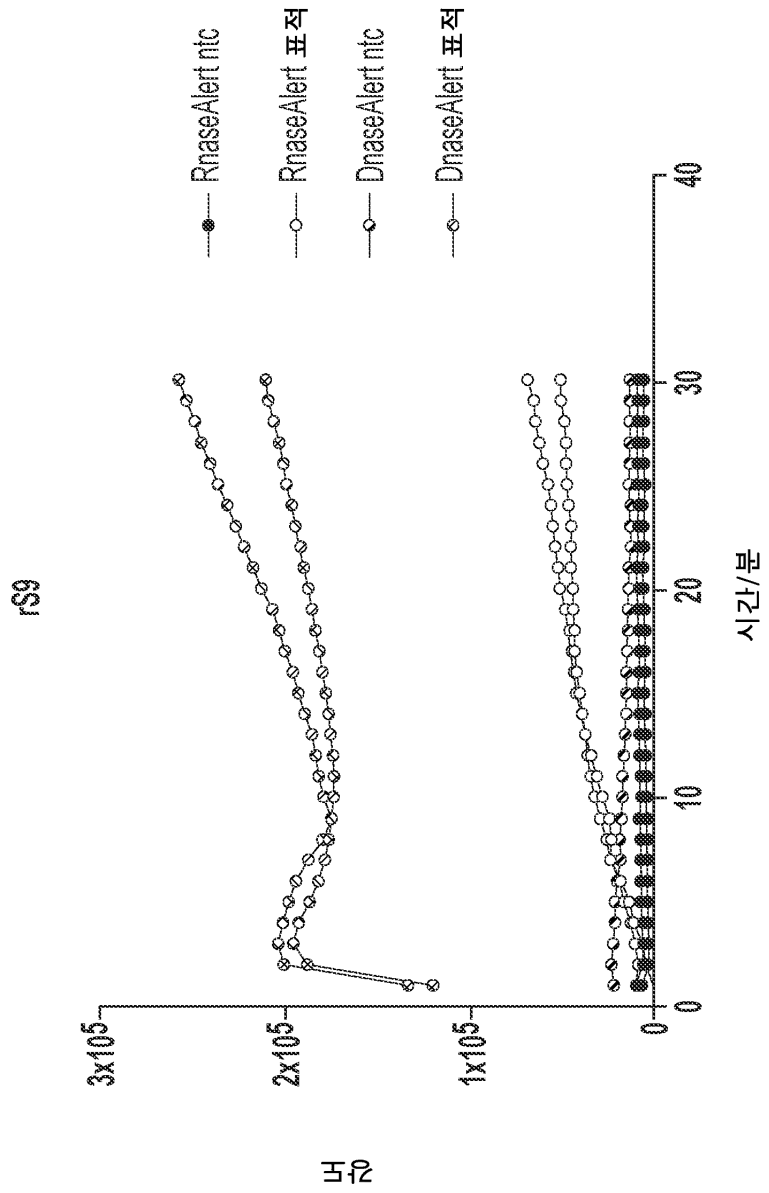
도면15


1 U TIPP/rxn
300000
200000
100000
0
강도
1 10 20 30 40 50 60 70 80 90 100 110 120
주기 (분)
4500 cp/ul
450 cp/ul
45 cp/ul
4.5 cp/ul
NTC
TIPP 없음
80000
60000
40000
20000
0
강도
1 10 20 30 40 50 60 70 80 90 100 110 120
주기 (분)
4500 cp/ul
450 cp/ul
45 cp/ul
4.5 cp/ul
NTC

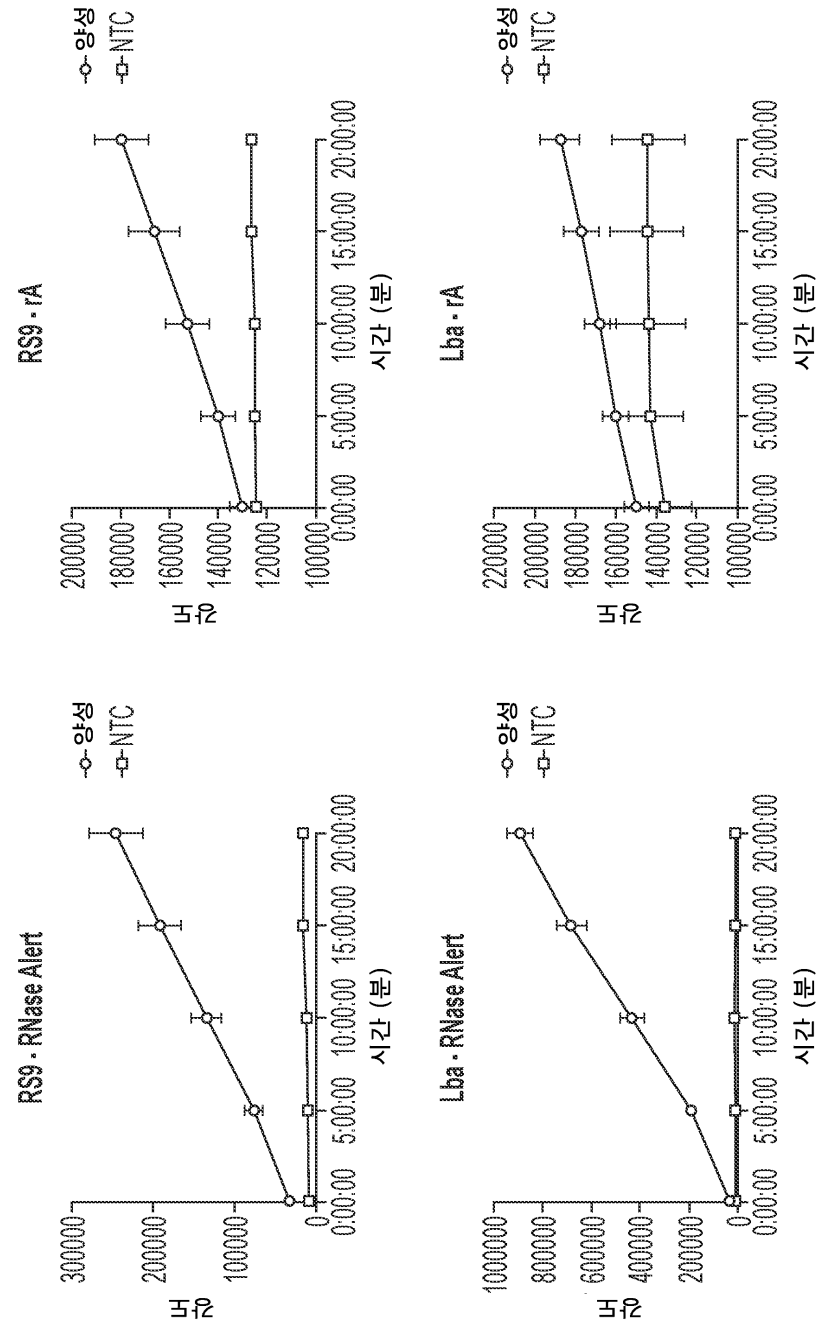
도면16


4500 cp/ul 바이러스성 RNA
300000
200000
100000
0
강도
1 10 20 30 40 50 60 70 80 90 100 110 120
주기 (분)
ORF 프라이머/ORF 가이드
ORF 프라이머/ORF 가이드 + TIPP
N 프라이머/ORF 가이드
N 프라이머/ORF 가이드 + TIPP

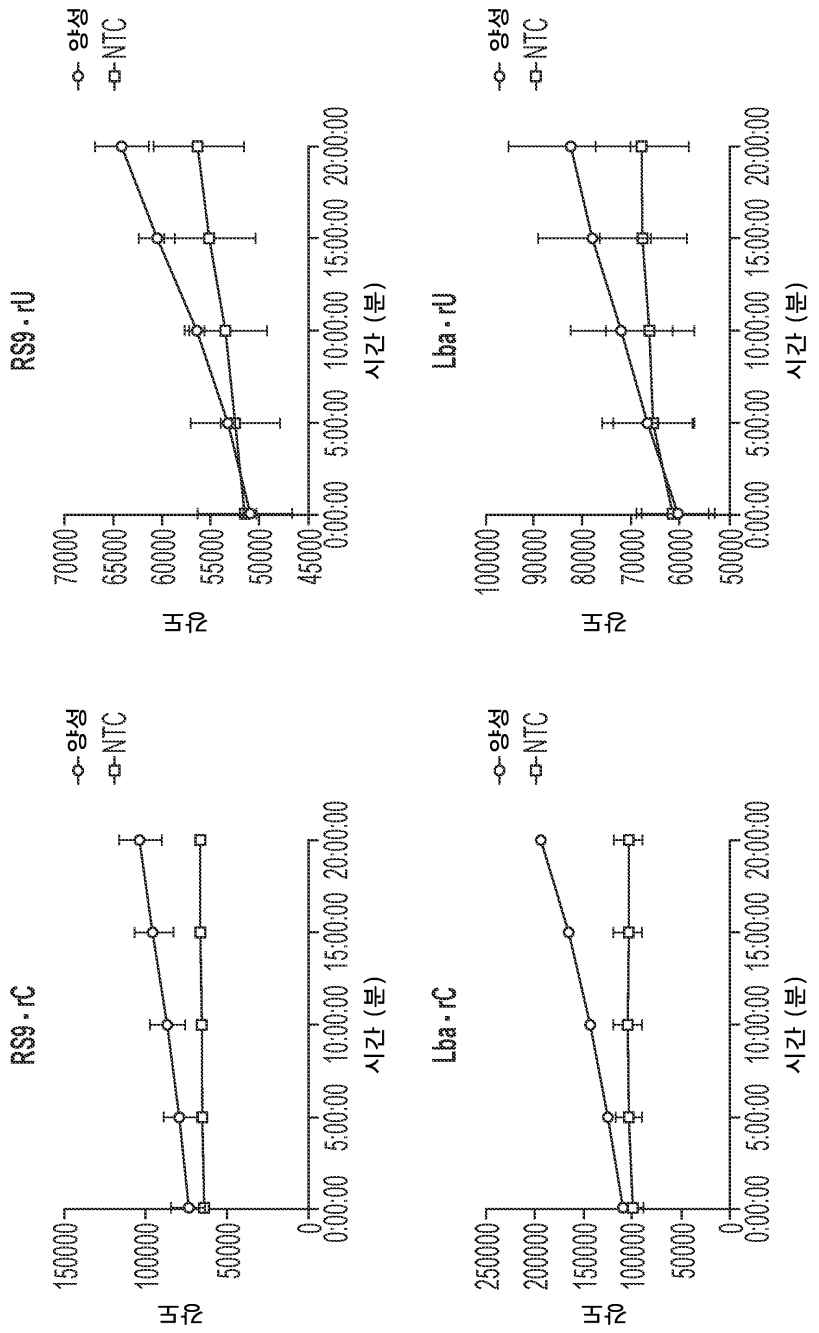
도면17


RnaseAlert ntc
RnaseAlert 표적
DnaseAlert ntc
DnaseAlert 표적
rS9
3x105
2x105
1x105
0
10
20
30
40
시간/분

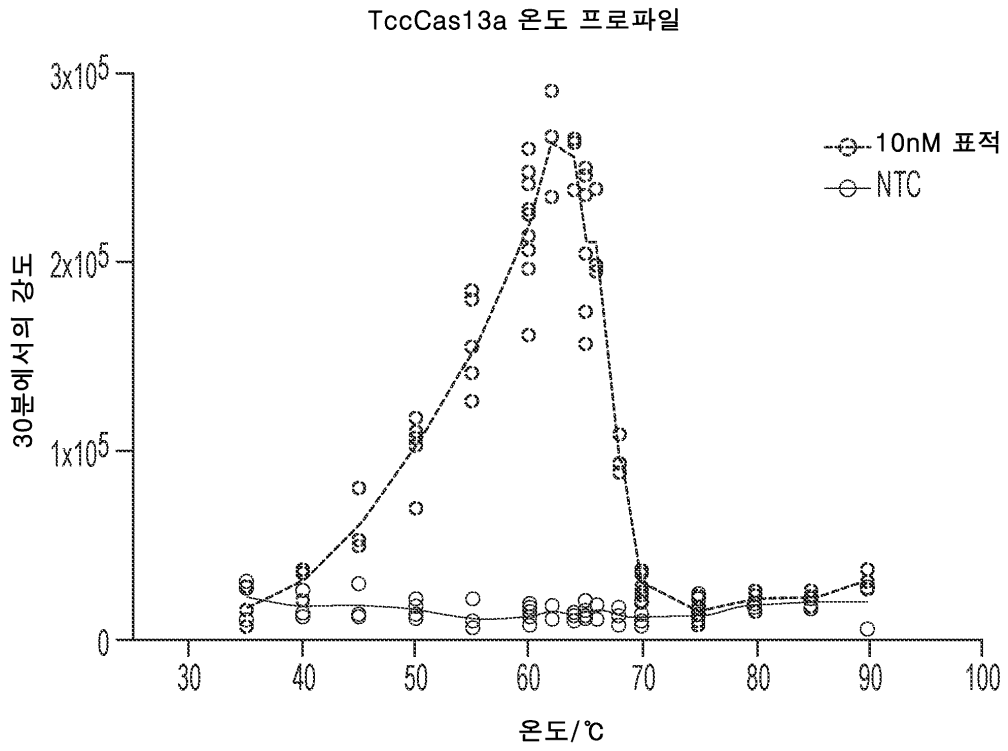
도면18a


RS9 - rA
Lba - rA
RS9 - RNase Alert
Lba - RNase Alert
양성
NTC
강도
시간 (분)
0:00:00
5:00:00
10:00:00
15:00:00
20:00:00

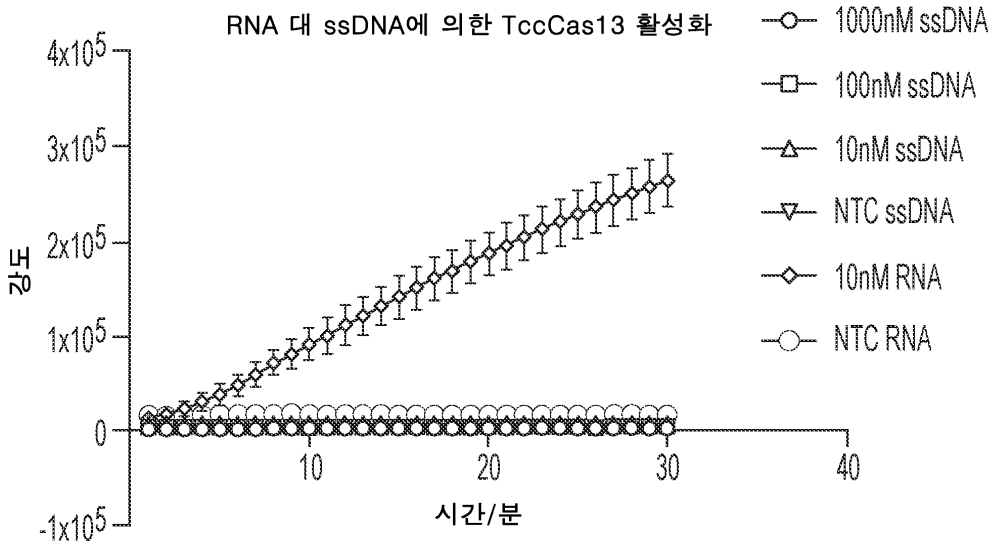
도면18b


RS9·rU
Lba·rU
RS9·rC
Lba·rC
양성
NTC
형광
시간 (분)
0:00:00
5:00:00
10:00:00
15:00:00
20:00:00

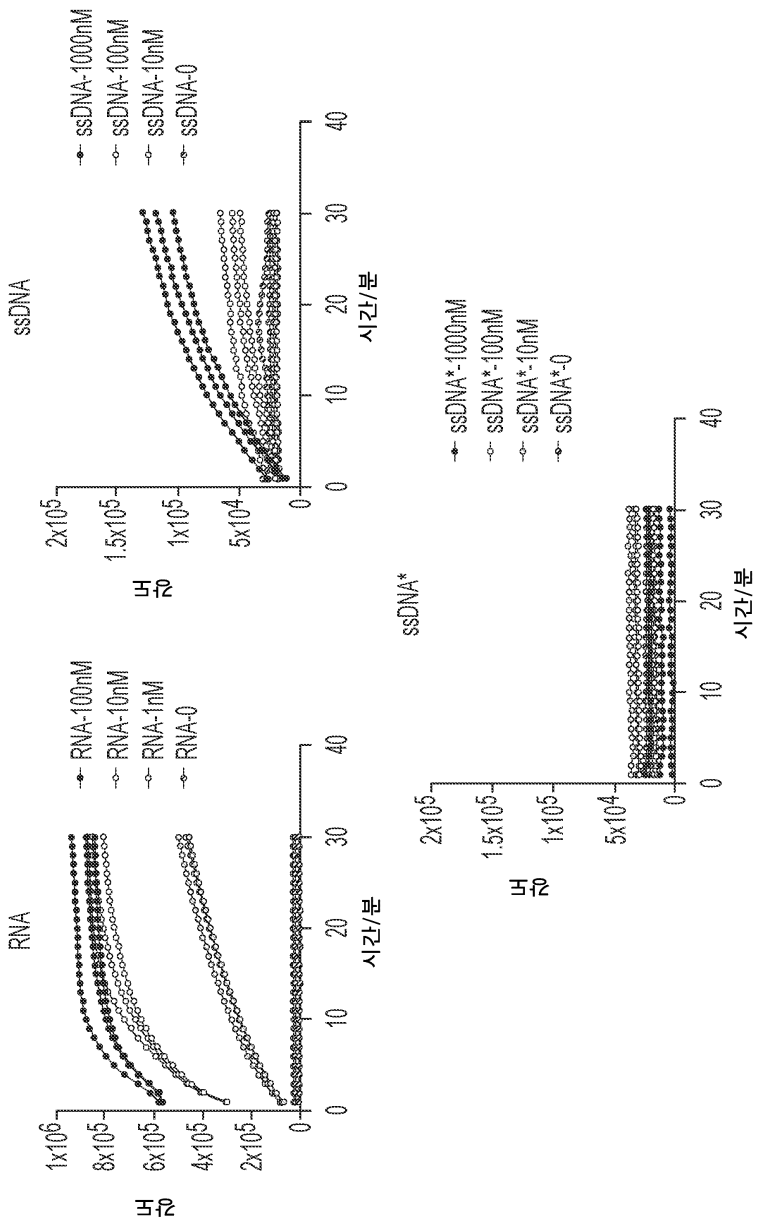
도면19


TccCas13a 온도 프로파일
10nM 표적
NTC
30분에서의 강도
온도/℃
3x10^5
2x10^5
1x10^5
0
30
40
50
60
70
80
90
100

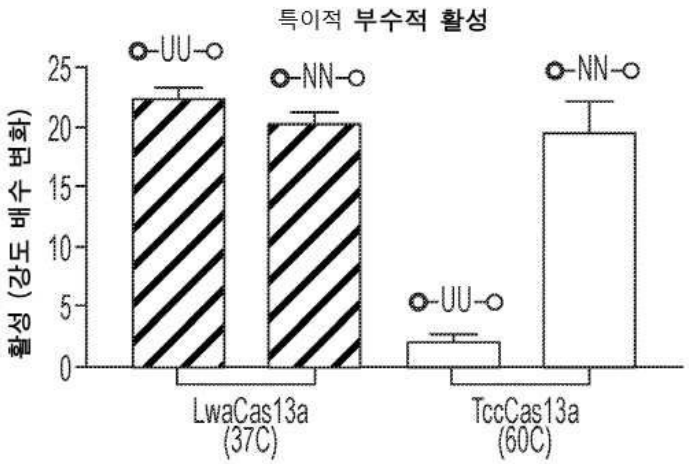
도면20


RNA 대 ssDNA에 의한 TccCas13 활성화
1000nM ssDNA
100nM ssDNA
10nM ssDNA
NTC ssDNA
10nM RNA
NTC RNA
강도
시간/분
4x10^5
3x10^5
2x10^5
1x10^5
0
-1x10^5
10
20
30
40

도면21

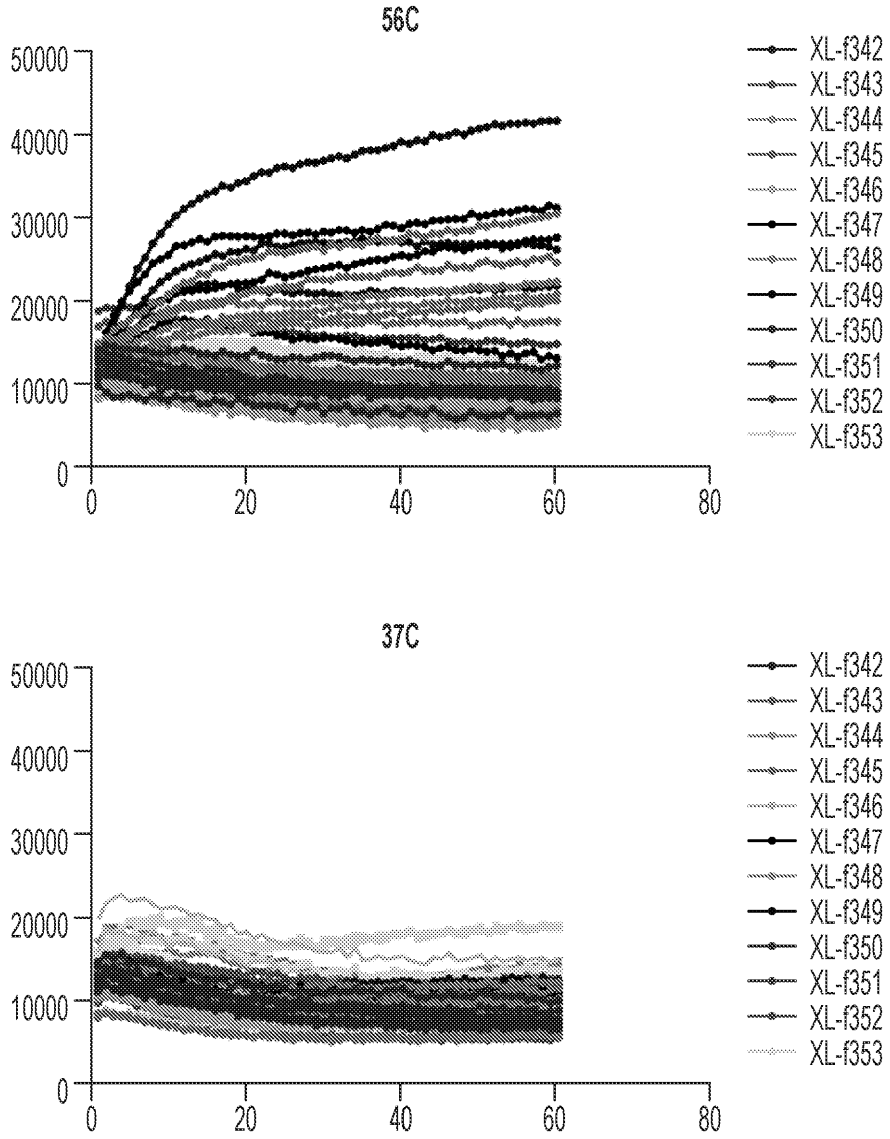

RNA
RNA-100nM
RNA-10nM
RNA-1nM
RNA-0
강도
시간/분
ssDNA
ssDNA-1000nM
ssDNA-100nM
ssDNA-10nM
ssDNA-0
강도
시간/분
ssDNA*
ssDNA*-1000nM
ssDNA*-100nM
ssDNA*-10nM
ssDNA*-0
강도
시간/분

도면22

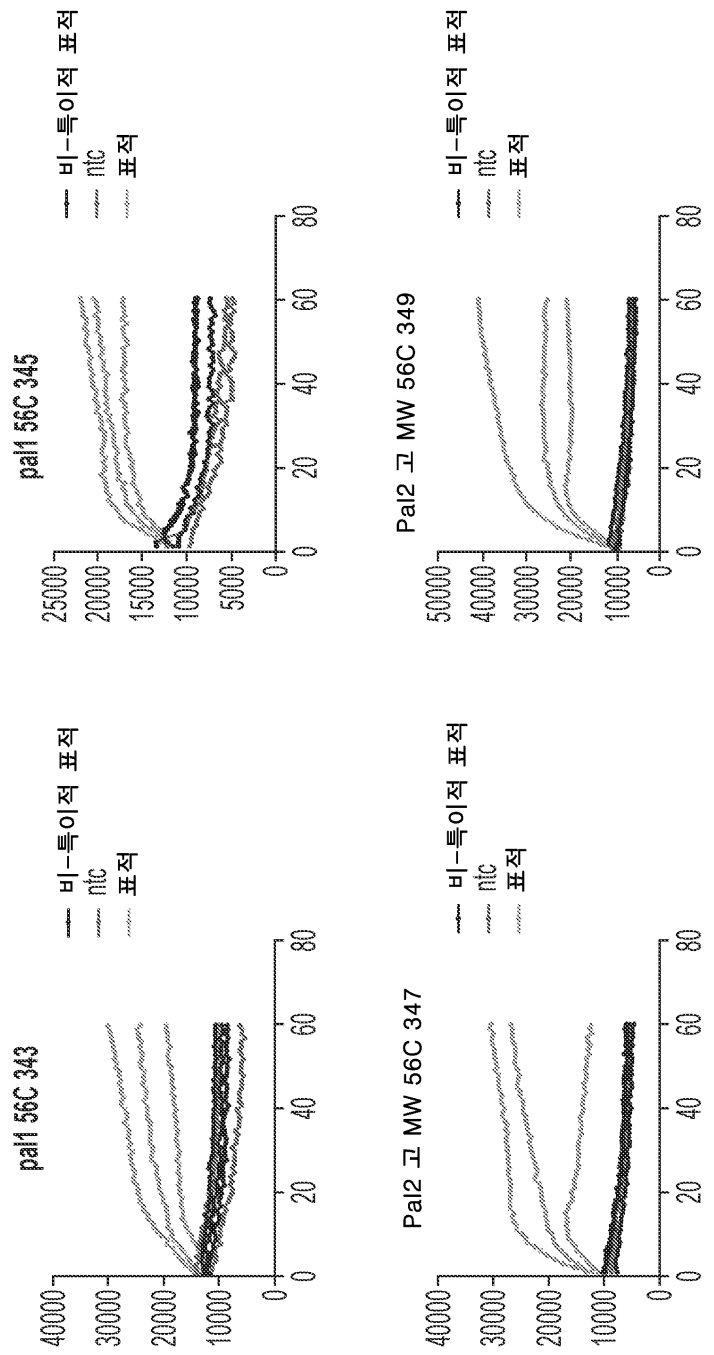


명칭	5'-mod.	링커 서열	L(nt)	3'-mod.
NN		*RnaseAlert*		
UU	6-FAM	TAUUGC	6	IowaBlack

도면23


56C
50000
40000
30000
20000
10000
0
0
20
40
60
80
XL-f342
XL-f343
XL-f344
XL-f345
XL-f346
XL-f347
XL-f348
XL-f349
XL-f350
XL-f351
XL-f352
XL-f353
37C
50000
40000
30000
20000
10000
0
0
20
40
60
80
XL-f342
XL-f343
XL-f344
XL-f345
XL-f346
XL-f347
XL-f348
XL-f349
XL-f350
XL-f351
XL-f352
XL-f353

도면24


pal1 56C 345
비-특이적 표적
ntc
표적
25000
20000
15000
10000
5000
0
0
20
40
60
80
Pal2 고 MW 56C 349
비-특이적 표적
ntc
표적
50000
40000
30000
20000
10000
0
0
20
40
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pal1 56C 343
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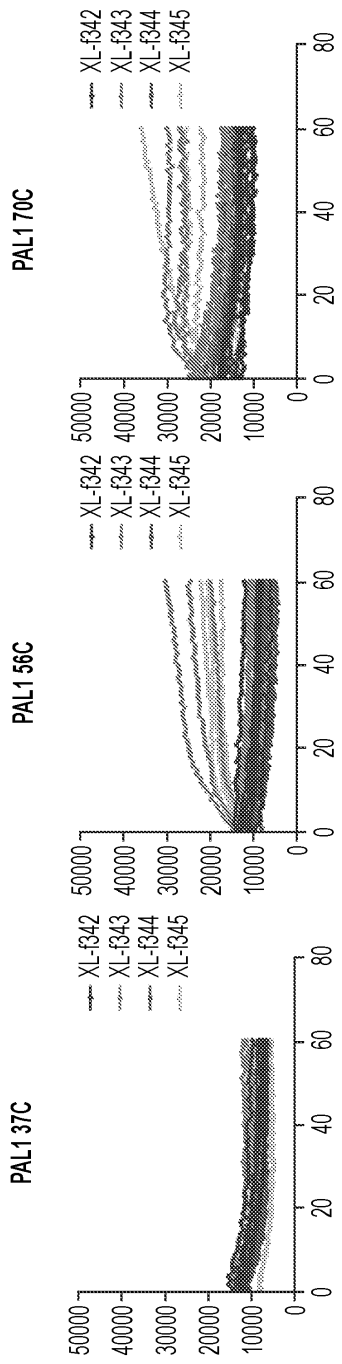
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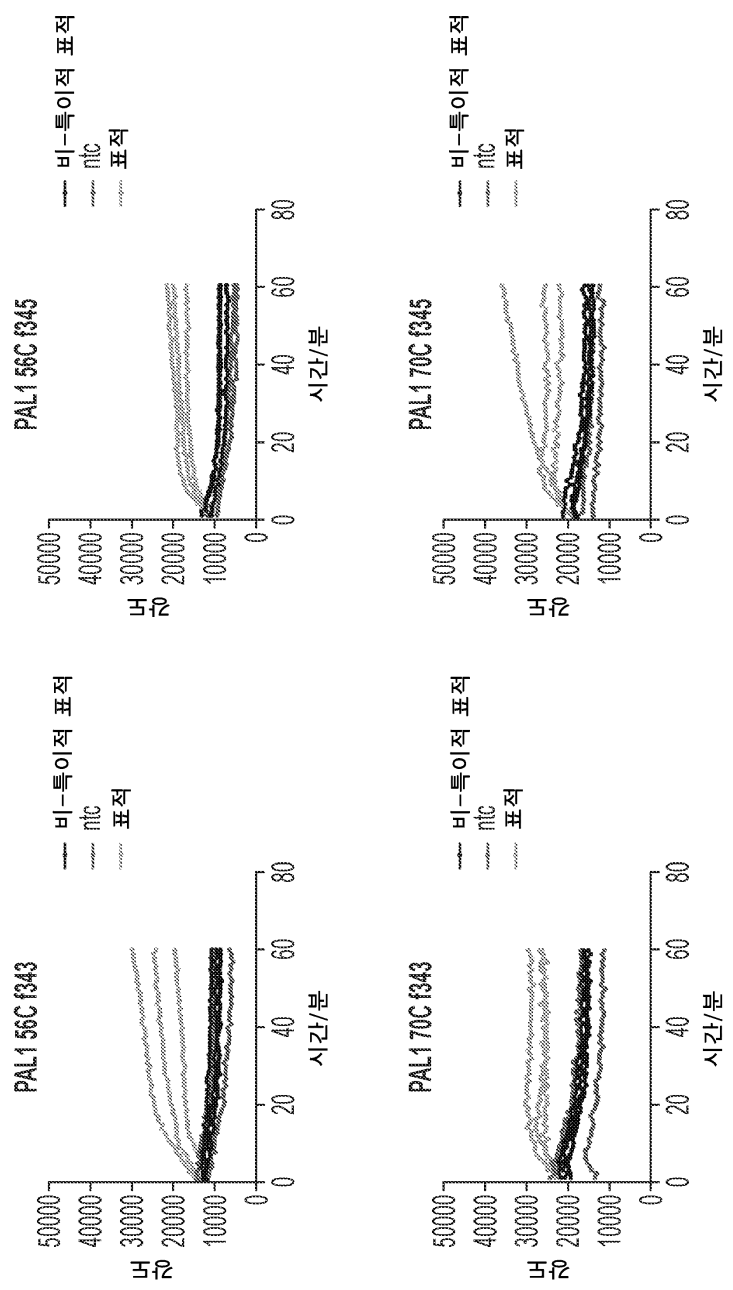
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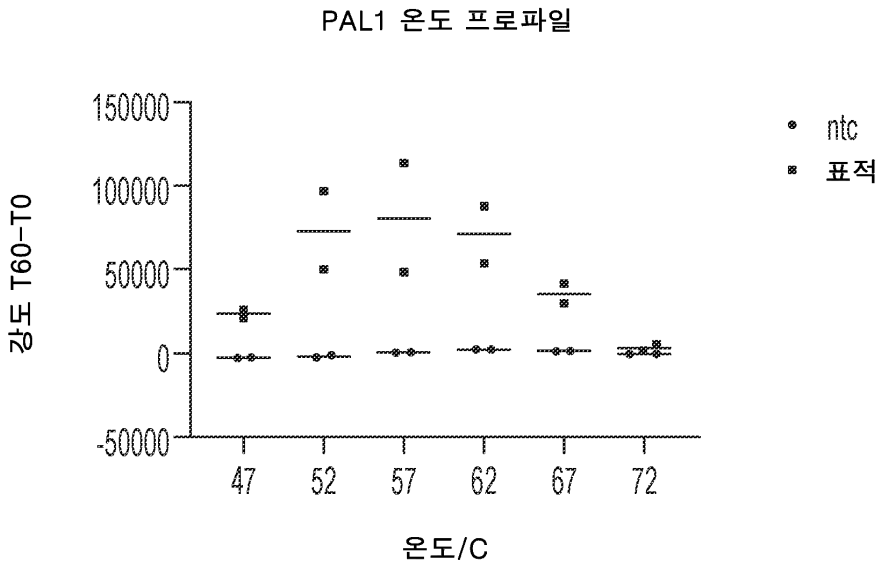
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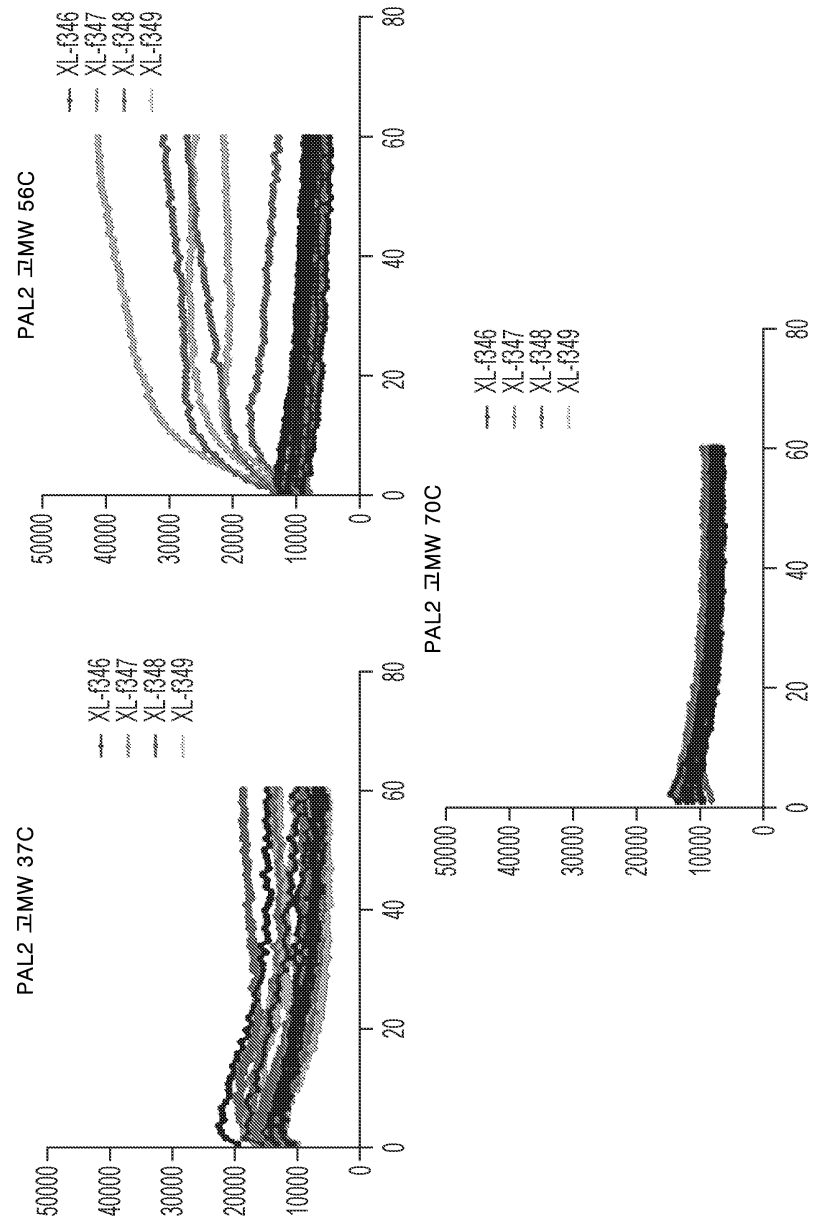
표적

도면28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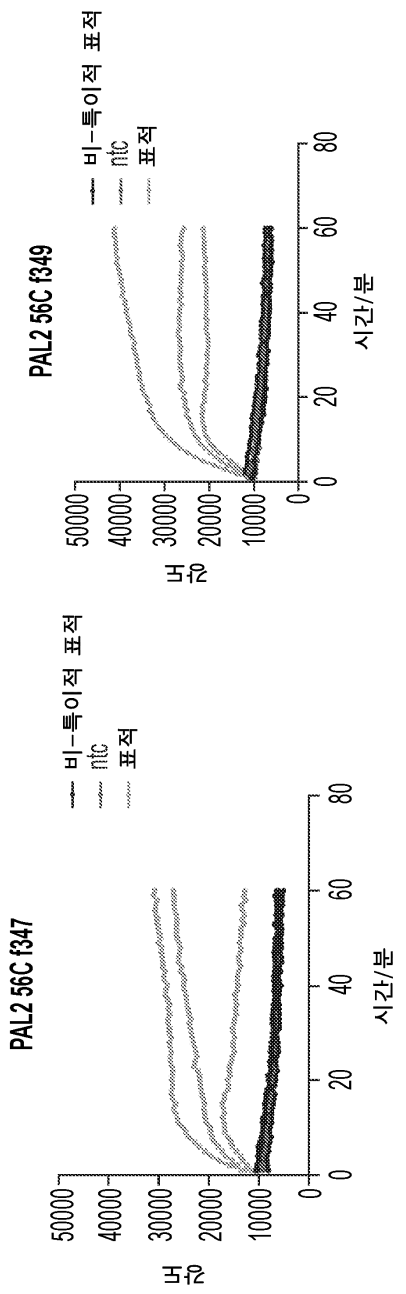
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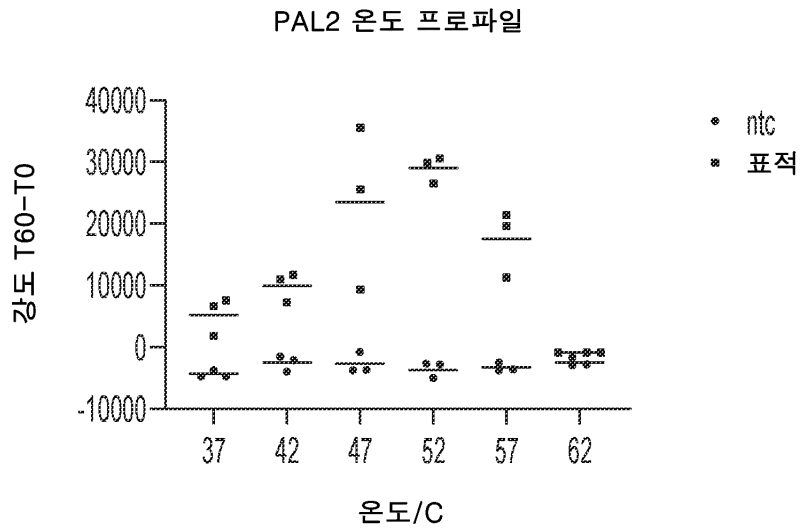

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1160 1165 1170

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980 985 990

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995 1000 1005

Phe Val Leu Leu Ala Leu Leu Tyr His His Gly Val Thr Pro Asp

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485 490 495

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545 550 555 560

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850 855 860

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1040 1045 1050
Glu Lys Leu Ser Glu Glu Glu Ala Glu Leu Leu Val Glu Ala Asp
1055 1060 1065
Glu Ala Arg Glu Lys Ser Val Val Leu Met Arg Asp Pro Ser Gly
1070 1075 1080
Ile Ile Asn Arg Gly Asn Trp Thr Arg Gln Lys Glu Phe Trp Ser
1085 1090 1095

Met Val Asn Gln Arg Ile Glu Gly Tyr Leu Val Lys Gln Ile Arg
1100 1105 1110
Ser Arg Val Pro Leu Gln Asp Ser Ala Cys Glu Asn Thr Gly Asp
1115 1120 1125
Ile

<210> 4

<211> 1147

<212> PRT

<213> Alicyclobacillus kakegawensis

<400> 4

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

20 25 30
Val Arg Tyr Tyr Thr Glu Trp Val Ser Leu Met Arg Gln Glu Ile Leu
35 40 45
Tyr Ser Arg Gly Pro Asp Gly Gly Gln Gln Cys Tyr Met Thr Ala Glu
50 55 60
Asp Cys Gln Arg Glu Leu Leu Arg Arg Leu Arg Asn Arg Gln Leu His
65 70 75 80
Asn Gly Arg Gln Asp Gln Pro Gly Thr Asp Ala Asp Leu Leu Ala Ile

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

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

Gln Gly Val Arg Thr Trp Asp Arg Asp Met Phe Gln Gln Ala Leu Glu

210 215 220

Arg Leu Met Ser Trp Glu Ser Trp Asn Arg Arg Val Gly Glu Glu Tyr

225 230 235 240

Ala Arg Leu Phe Gln Gln Lys Met Lys Phe Glu Gln Glu His Phe Ala

245 250 255

Glu Gln Ser His Leu Val Lys Leu Ala Arg Ala Leu Glu Ala Asp Met

260 265 270

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

275 280 285

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

290 295 300

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

305 310 315 320

Arg Gln Val Gln Ala Glu Lys Arg Arg Asp Phe Gly Ser His Asp Leu

325 330 335

Phe Ala Lys Leu Ala Glu Pro Lys Tyr Gln Pro Leu Trp Arg Ala Asp

340 345 350

Glu Thr Phe Leu Thr Arg Tyr Ala Leu Tyr Asn Gly Val Leu Arg Asp

355 360 365

Leu Glu Lys Ala Arg Gln Phe Ala Thr Phe Thr Leu Pro Asp Ala Cys

370 375 380

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

385 390 395 400

His Lys Tyr Glu Phe Leu Phe Asp His Leu Gly Pro Gly Arg His Ala

405 410 415

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

420 425 430

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

435 440 445

Leu Val Leu Arg Glu Glu Glu Lys Ser Ser Val Ala Leu His Leu His

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    450                 455                 460
Asp Thr Ala Arg Pro Asp Gly Phe Met Ala Glu Trp Ala Gly Ala Lys

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

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

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

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

705 710 715 720

Leu Thr Arg Leu Glu Ala Tyr Cys Gly Arg Val Pro Asp Asp Glu Trp

725 730 735

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

740 745 750

Lys Gln Val Arg Asp Trp Arg Lys Gln Val Lys Ser Gly Ala Lys Val

755 760 765

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

770 775 780

Gln Ile Asp Tyr Leu Glu Gln Gln Tyr Lys Phe Leu Arg Arg Trp Ser

785 790 795 800

Phe Phe Ala Arg Ala Ser Gly Leu Val Val Arg Ala Asp Arg Glu Ser

805 810 815

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

820 825 830

Arg Leu Lys Lys Leu Ala Asp Arg Ile Leu Met Glu Ala Leu Gly Tyr

835 840 845

Val Tyr Glu Ala Ser Gly Pro Arg Glu Gly Gln Trp Thr Ala Gln His

850 855 860

Pro Pro Cys Gln Leu Ile Ile Leu Glu Glu Leu Ser Ala Tyr Arg Phe

865 870 875 880

Ser Asp Asp Arg Pro Pro Ser Glu Asn Ser Lys Leu Met Ala Trp Gly

885 890 895

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

900 905 910

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

915 920 925

Arg Thr Gly Ala Pro Gly Val Arg Cys Arg Arg Val Pro Ala Arg Phe

930 935 940

Val Gly Ala Thr Val Asp Asp Ser Leu Pro Leu Trp Leu Thr Glu Phe

945 950 955 960

Leu Asp Lys His Arg Leu Asp Lys Asn Leu Leu Arg Pro Asp Asp Val

965 970 975

Ile Pro Thr Gly Glu Gly Glu Phe Leu Val Ser Pro Cys Gly Glu Glu

980 985 990

Ala Ala Arg Val Arg Gln Val His Ala Asp Ile Asn Ala Ala Gln Asn

995 1000 1005

Leu Gln Arg Arg Leu Trp Gln Asn Phe Asp Ile Thr Glu Leu Arg

1010 1015 1020

Leu Arg Cys Asp Val Lys Met Gly Gly Glu Gly Thr Val Leu Val

1025 1030 1035

Pro Arg Val Asn Asn Ala Arg Ala Lys Gln Leu Phe Gly Lys Lys

1040 1045 1050

Val Leu Val Ser Gln Asp Gly Val Thr Phe Phe Glu Arg Ser Gln

1055 1060 1065

Thr Gly Gly Lys Pro His Ser Glu Lys Gln Thr Asp Leu Thr Asp

1070 1075 1080

Lys Glu Leu Glu Leu Ile Ala Glu Ala Asp Glu Ala Arg Ala Lys

1085 1090 1095

Ser Val Val Leu Phe Arg Asp Pro Ser Gly His Ile Gly Lys Gly

1100 1105 1110

His Trp Ile Arg Gln Arg Glu Phe Trp Ser Leu Val Lys Gln Arg

1115 1120 1125

Ile Glu Ser His Thr Ala Glu Arg Ile Arg Val Arg Gly Val Gly

1130 1135 1140

Ser Ser Leu Asp

1145

<210> 5

<211> 1108

<212> PRT

<213> Bacillus hisashii

<400> 5

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Met Ala Thr Arg Ser Phe Ile Leu Lys Ile Glu Pro Asn Glu Glu Val
1               5                  10                  15

Lys Lys Gly Leu Trp Lys Thr His Glu Val Leu Asn His Gly Ile Ala
            20                  25                  30
Tyr Tyr Met Asn Ile Leu Lys Leu Ile Arg Gln Glu Ala Ile Tyr Glu
        35                  40                  45
His His Glu Gln Asp Pro Lys Asn Pro Lys Lys Val Ser Lys Ala Glu
    50                  55                  60
Ile Gln Ala Glu Leu Trp Asp Phe Val Leu Lys Met Gln Lys Cys Asn
65                  70                  75                  80

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

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

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

Glu Asp Ile Gln Ala Leu Lys Ala Leu Glu Gln Tyr Glu Lys Glu Arg

260 265 270

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

275 280 285

Ser Lys Arg Gly Leu Arg Gly Trp Arg Glu Ile Ile Gln Lys Trp Leu

290 295 300

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

305 310 315 320

Asp Tyr Gln Arg Lys His Pro Arg Glu Ala Gly Asp Tyr Ser Val Tyr

325 330 335

Glu Phe Leu Ser Lys Lys Glu Asn His Phe Ile Trp Arg Asn His Pro

340 345 350

Glu Tyr Pro Tyr Leu Tyr Ala Thr Phe Cys Glu Ile Asp Lys Lys Lys

355 360 365

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

370 375 380

His Pro Leu Trp Val Arg Phe Glu Glu Arg Ser Gly Ser Asn Leu Asn

385 390 395 400

Lys Tyr Arg Ile Leu Thr Glu Gln Leu His Thr Glu Lys Leu Lys Lys

405 410 415

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

420 425 430

Gly Trp Glu Glu Lys Gly Lys Val Asp Ile Val Leu Leu Pro Ser Arg

435 440 445

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

450 455 460

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

465 470 475 480

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

485 490 495

Pro His Lys Val Glu Ser Gly Asn Val Gly Arg Ile Tyr Phe Asn Met
500 505 510
Thr Val Asn Ile Glu Pro Thr Glu Ser Pro Val Ser Lys Ser Leu Lys
515 520 525

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

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

Gln Gln Phe Glu Asp Ile Thr Glu Arg Glu Lys Arg Val Thr Lys Trp
660 665 670
Ile Ser Arg Gln Glu Asn Ser Asp Val Pro Leu Val Tyr Gln Asp Glu
675 680 685
Leu Ile Gln Ile Arg Glu Leu Met Tyr Lys Pro Tyr Lys Asp Trp Val
690 695 700
Ala Phe Leu Lys Gln Leu His Lys Arg Leu Glu Val Glu Ile Gly Lys
705 710 715 720

Glu Val Lys His Trp Arg Lys Ser Leu Ser Asp Gly Arg Lys Gly Leu
725 730 735
Tyr Gly Ile Ser Leu Lys Asn Ile Asp Glu Ile Asp Arg Thr Arg Lys

740 745 750

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

755 760 765

Arg Leu Glu Pro Gly Gln Arg Phe Ala Ile Asp Gln Leu Asn His Leu

770 775 780

Asn Ala Leu Lys Glu Asp Arg Leu Lys Lys Met Ala Asn Thr Ile Ile

785 790 795 800

Met His Ala Leu Gly Tyr Cys Tyr Asp Val Arg Lys Lys Lys Trp Gln

805 810 815

Ala Lys Asn Pro Ala Cys Gln Ile Ile Leu Phe Glu Asp Leu Ser Asn

820 825 830

Tyr Asn Pro Tyr Glu Glu Arg Ser Arg Phe Glu Asn Ser Lys Leu Met

835 840 845

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

850 855 860

Ile Tyr Gly Leu Gln Val Gly Glu Val Gly Ala Gln Phe Ser Ser Arg

865 870 875 880

Phe His Ala Lys Thr Gly Ser Pro Gly Ile Arg Cys Ser Val Val Thr

885 890 895

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

900 905 910

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

915 920 925

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

930 935 940

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

945 950 955 960

Lys Arg Phe Trp Thr Arg Thr His Gly Phe Tyr Lys Val Tyr Cys Lys

965 970 975

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

980 985 990

Gln Lys Gln Lys Ile Ile Glu Glu Phe Gly Glu Gly Tyr Phe Ile Leu
995 1000 1005

Lys Asp Gly Val Tyr Glu Trp Val Asn Ala Gly Lys Leu Lys Ile
1010 1015 1020

Lys Lys Gly Ser Ser Lys Gln Ser Ser Ser Glu Leu Val Asp Ser
1025 1030 1035

Asp Ile Leu Lys Asp Ser Phe Asp Leu Ala Ser Glu Leu Lys Gly
1040 1045 1050

Glu Lys Leu Met Leu Tyr Arg Asp Pro Ser Gly Asn Val Phe Pro
1055 1060 1065

Ser Asp Lys Trp Met Ala Ala Gly Val Phe Phe Gly Lys Leu Glu
1070 1075 1080

Arg Ile Leu Ile Ser Lys Leu Thr Asn Gln Tyr Ser Ile Ser Thr
1085 1090 1095

Ile Glu Asp Asp Ser Ser Lys Gln Ser Met
1100 1105

<210> 6

<211> 1090

<212> PRT

<213> Laceyella sediminis

<400> 6

Met Ser Ile Arg Ser Phe Lys Leu Lys Ile Lys Thr Lys Ser Gly Val
1 5 10 15

Asn Ala Glu Glu Leu Arg Arg Gly Leu Trp Arg Thr His Gln Leu Ile
20 25 30

Asn Asp Gly Ile Ala Tyr Tyr Met Asn Trp Leu Val Leu Leu Arg Gln
35 40 45

Glu Asp Leu Phe Ile Arg Asn Glu Glu Thr Asn Glu Ile Glu Lys Arg
50 55 60

Ser Lys Glu Glu Ile Gln Gly Glu Leu Leu Glu Arg Val His Lys Gln
65 70 75 80

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

85 90 95

Gln Thr Leu Arg His Leu Tyr Glu Glu Ile Val Pro Ser Val Ile Gly

100 105 110

Lys Ser Gly Asn Ala Ser Leu Lys Ala Arg Phe Phe Leu Gly Pro Leu

115 120 125

Val Asp Pro Asn Asn Lys Thr Thr Lys Asp Val Ser Lys Ser Gly Pro

130 135 140

Thr Pro Lys Trp Lys Lys Met Lys Asp Ala Gly Asp Pro Asn Trp Val

145 150 155 160

Gln Glu Tyr Glu Lys Tyr Met Ala Glu Arg Gln Thr Leu Val Arg Leu

165 170 175

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

180 185 190

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

195 200 205

Asp Arg Asp Met Phe Gln Gln Ala Ile Glu Arg Leu Leu Ser Trp Glu

210 215 220

Ser Trp Asn Arg Arg Val Arg Glu Arg Arg Ala Gln Phe Glu Lys Lys

225 230 235 240

Thr His Asp Phe Ala Ser Arg Phe Ser Glu Ser Asp Val Gln Trp Met

245 250 255

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

260 265 270

Asn Ala Phe Ala Pro Asn Glu Pro Tyr Ala Leu Thr Lys Lys Ala Leu

275 280 285

Arg Gly Trp Glu Arg Val Tyr His Ser Trp Met Arg Leu Asp Ser Ala

290 295 300

Ala Ser Glu Glu Ala Tyr Trp Gln Glu Val Ala Thr Cys Gln Thr Ala

305 310 315 320

Met Arg Gly Glu Phe Gly Asp Pro Ala Ile Tyr Gln Phe Leu Ala Gln

325 330 335

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

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

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

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

Gly Leu Asp Ser Leu Ser Glu Gly Leu Arg Val Met Ser Ile Asp Leu
565 570 575
Gly Gln Arg Thr Ser Ala Thr Val Ser Val Phe Glu Ile Thr Lys Glu

580 585 590

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

595 600 605

Leu Phe Ala Val His Gln Arg Ser Phe Leu Leu Ala Leu Pro Gly Glu

610 615 620

Asn Pro Pro Gln Lys Ile Lys Gln Met Arg Glu Ile Arg Trp Lys Glu

625 630 635 640

Arg Asn Arg Ile Lys Gln Gln Val Asp Gln Leu Ser Ala Ile Leu Arg

645 650 655

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

660 665 670

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

675 680 685

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

690 695 700

Asp Leu Gln Trp Asn Gln Ala Ile Lys Asn Ala His His Gln Leu Glu

705 710 715 720

Pro Val Val Gly Lys Gln Ile Ser Leu Trp Arg Lys Asp Leu Ser Thr

725 730 735

Gly Arg Gln Gly Ile Ala Gly Leu Ser Leu Trp Ser Ile Glu Glu Leu

740 745 750

Glu Ala Thr Lys Lys Leu Leu Thr Arg Trp Ser Lys Arg Ser Arg Glu

755 760 765

Pro Gly Val Val Lys Arg Ile Glu Arg Phe Glu Thr Phe Ala Lys Gln

770 775 780

Ile Gln His His Ile Asn Gln Val Lys Glu Asn Arg Leu Lys Gln Leu

785 790 795 800

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

805 810 815

Gln Lys Lys Trp Ile Glu Val Tyr Pro Ala Cys Gln Val Val Leu Phe

820 825 830

Glu Asn Leu Arg Ser Tyr Arg Phe Ser Tyr Glu Arg Ser Arg Arg Glu
835 840 845
Asn Lys Lys Leu Met Glu Trp Ser His Arg Ser Ile Pro Lys Leu Val
850 855 860
Gln Met Gln Gly Glu Leu Phe Gly Leu Gln Val Ala Asp Val Tyr Ala
865 870 875 880

Ala Tyr Ser Ser Arg Tyr His Gly Arg Thr Gly Ala Pro Gly Ile Arg
885 890 895
Cys His Ala Leu Thr Glu Ala Asp Leu Arg Asn Glu Thr Asn Ile Ile
900 905 910
His Glu Leu Ile Glu Ala Gly Phe Ile Lys Glu Glu His Arg Pro Tyr
915 920 925
Leu Gln Gln Gly Asp Leu Val Pro Trp Ser Gly Gly Glu Leu Phe Ala
930 935 940

Thr Leu Gln Lys Pro Tyr Asp Asn Pro Arg Ile Leu Thr Leu His Ala
945 950 955 960
Asp Ile Asn Ala Ala Gln Asn Ile Gln Lys Arg Phe Trp His Pro Ser
965 970 975
Met Trp Phe Arg Val Asn Cys Glu Ser Val Met Glu Gly Glu Ile Val
980 985 990
Thr Tyr Val Pro Lys Asn Lys Thr Val His Lys Lys Gln Gly Lys Thr
995 1000 1005

Phe Arg Phe Val Lys Val Glu Gly Ser Asp Val Tyr Glu Trp Ala
1010 1015 1020
Lys Trp Ser Lys Asn Arg Asn Lys Asn Thr Phe Ser Ser Ile Thr
1025 1030 1035
Glu Arg Lys Pro Pro Ser Ser Met Ile Leu Phe Arg Asp Pro Ser
1040 1045 1050
Gly Thr Phe Phe Lys Glu Gln Glu Trp Val Glu Gln Lys Thr Phe
1055 1060 1065

Trp Gly Lys Val Gln Ser Met Ile Gln Ala Tyr Met Lys Lys Thr

1070 1075 1080

Ile Val Gln Arg Met Glu Glu

1085 1090

<210> 7

<211> 1133

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 7

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Gln Asn Gln Glu Glu Ser Asn Ala Leu Asn Ala Phe Lys Gly Phe Thr

20 25 30

Thr His Phe Lys Asp Phe Gln Glu Asn Arg Lys Asn Met Tyr Ser Glu

35 40 45

Asp Lys Glu Ser Thr Ala Ile Ala Tyr Arg Ile Ile His Glu Asn Leu

50 55 60

Pro Val Phe Ile Thr Asn Asn Ile Arg Phe Glu Lys Ile Ile Asn Glu

65 70 75 80

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

85 90 95

Leu Ala Asn Asn Lys Leu Lys Asp Ile Phe Asn Ile Glu Tyr Phe Gln

100 105 110

Asn Thr Leu Thr Gln Asn Asp Ile Thr Arg Tyr Asn Thr Ile Ile Gly

115 120 125

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

130 135 140

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

145 150 155 160

Lys Pro Leu Tyr Lys Gln Ile Leu Ser Glu Glu Asn Ser Ala Ser Phe

165 170 175

Ile Val Pro Ala Phe Glu Lys Asp Asn Glu Val Leu Gln Ser Ile Phe
180 185 190
Asp Phe Trp Asn Lys Cys Ile Ile Asp Ala Lys Gly Pro Ile Ser Gly
195 200 205
Lys Lys Tyr Asn Leu Leu Ser Lys Ile Gln Ser Leu Leu Gln Asn Leu

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

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

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

405 410 415
Lys Pro Phe Ser Glu Glu Lys Phe Val Leu Thr Phe Asn Ser Pro Thr

420 425 430

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

435 440 445

Ile Leu Arg Lys Asp Asn Lys Tyr Tyr Leu Gly Ile Met Asn Lys Gly

450 455 460

Asp Asn Lys Ile Phe Lys Lys Tyr Asp Glu Glu Pro Gly Asp Asp Tyr

465 470 475 480

Tyr Glu Lys Met Val Tyr Lys Leu Leu Pro Gly Pro Asn Arg Met Leu

485 490 495

Arg Lys Val Phe Phe Ser Asn Lys Asn Ile Glu Tyr Tyr Lys Pro Asn

500 505 510

Gln Asp Ile Gln Asn Leu Tyr Asn Lys Gly Glu Phe Lys Lys Gly Glu

515 520 525

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

530 535 540

Ser Ile Ser Lys Asn Gly Asp Trp Ser Val Phe Asn Phe Lys Phe Lys

545 550 555 560

Lys Thr Thr Ala Tyr Asp Asp Ile Ser Gln Phe Tyr Lys Asp Val Glu

565 570 575

Asn Gln Gly Tyr Lys Leu Phe Phe Lys Thr Ile Lys Thr Ser Tyr Ile

580 585 590

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

595 600 605

Lys Asp Phe Ser Glu Asn Lys Lys Arg Lys Asp Glu Ser Asn Pro Asn

610 615 620

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

625 630 635 640

Asn Val Val Tyr Lys Leu Asn Gly Lys Ala Glu Val Phe Tyr Arg Lys

645 650 655

Lys Ser Ile Glu Tyr Pro Glu Glu Ile Arg Arg Lys Gly His His Tyr

660 665 670

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

725 730 735
Arg Asn Leu Leu Tyr Leu Ser Leu Ile Asp Ser Asn Gly Asn Ile Val
740 745 750
Lys Gln Gln Ser Leu Asn Ile Ile Glu Leu Pro Lys Tyr Gln Lys Gln
755 760 765
Ile Asp Tyr His Ala Lys Leu Asn Glu Lys Glu Lys Gln Arg Leu Ala
770 775 780
Ala Arg Gln Asn Trp Asp Val Ile Glu Asn Ile Lys Glu Leu Lys Glu

785 790 795 800
Gly Tyr Leu Ser Gln Val Ile His Gln Ile Ala Arg Leu Met Val Asp
805 810 815
Tyr Lys Ala Ile Leu Val Met Glu Asp Leu Asn Phe Gly Phe Lys Arg
820 825 830
Gly Arg Phe Lys Val Glu Lys Gln Val Tyr Gln Lys Phe Glu Lys Met
835 840 845
Leu Ile Asp Lys Leu Ser Tyr Leu Val Phe Lys Glu Lys Asn Leu Cys

850 855 860
Glu Pro Gly Gly Ser Leu Arg Ala Tyr Gln Leu Ser Ala Pro Phe Lys
865 870 875 880
Ser Phe Lys Ala Leu Gly Lys Gln Ser Gly Met Ile Phe Tyr Val Pro
885 890 895
Ala Gln Tyr Thr Ser Lys Ile Asp Pro Thr Thr Gly Phe Tyr Asn Phe
900 905 910
Leu Asn Ile Asp Val Ser Asn Leu Ala Arg Ser Lys Glu Thr Phe Ser

915 920 925

Lys Phe Asp Lys Ile Val Tyr Asn Lys Lys Glu Asp Tyr Phe Glu Phe

930 935 940

Tyr Cys Lys Met Ile Asn Phe Glu Ser Ala Asn Gln Leu Thr Lys Lys

945 950 955 960

Ser Gln Asn Lys Ala Asn Ala Glu Leu Lys Glu Phe Gln Trp Ile Leu

965 970 975

Cys Ser Thr His His Asp Arg Phe Lys Val Glu Arg Lys Asn Asn Gln

980 985 990

Ile Asn Tyr Cys Lys Ile Asn Val Asn Glu Glu Leu Lys Lys Leu Leu

995 1000 1005

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

1010 1015 1020

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

1025 1030 1035

Tyr Leu Leu Lys Ile Leu Val Ser Leu Arg Tyr Asn Asn Gly Lys

1040 1045 1050

Lys Gly Ser Glu Glu Gln Asp Phe Ile Leu Ser Pro Val Lys Asn

1055 1060 1065

Ala Ser Gly Lys Phe Phe Cys Thr Leu Asp Asn Asn Asn Thr Leu

1070 1075 1080

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

1085 1090 1095

Gly Leu Met Ile Val Gln Arg Val Lys Ala Gly Gly Lys Leu Asp

1100 1105 1110

Leu Ser Ile Ser Lys Asp Asp Trp Ile Asn Phe Leu Ile Met Asn

1115 1120 1125

Lys Lys Leu Pro Lys

1130

<210> 8

<211> 1352

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 8

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

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Val Gly Lys Thr Leu Arg

20 25 30

Met Leu Glu Asp Ala Lys Val Phe Lys Thr Asp Glu Leu Ile Gln Lys
35 40 45

Lys Tyr Glu Gln Thr Lys Pro Phe Ile Asn Lys Leu His Gln Glu Phe
50 55 60

Val Lys Glu Ser Leu Glu Gly Arg Ser Leu Glu Gly Leu Glu Ser Tyr
65 70 75 80

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

85 90 95

Gln Lys Asn Leu Gly Ile Lys Glu Lys Glu Leu Tyr Lys Gln Val Thr
100 105 110

Gln Leu Phe Asn Ala Lys Ala Lys Glu Trp Ser Glu Pro Tyr Ala His
115 120 125

Leu Gly Leu Lys Lys Lys Asp Ile Gly Ile Leu Phe Glu Glu Gly Val
130 135 140

Phe Lys Ile Leu Lys Glu Lys Tyr Asn Asn Asp Lys Asp Ala Lys Ile

145 150 155 160

Thr Asn Lys Val Thr Gly Glu Ile Phe Phe Glu Asp Phe Trp Lys Gly
165 170 175

Phe Val Gly Tyr Phe Gln Lys Phe Phe Glu Thr Arg Lys Asn Phe Tyr
180 185 190

Lys Asp Asp Gly Thr Ser Thr Ala Ile Ala Thr Arg Ile Val Ala Gln
195 200 205

Asn Leu Lys Arg Phe Cys Asp Asn Ile Gly Leu Phe Glu Lys Ile Lys

210 215 220

Asp Gln Ile Asp Ser Ser Glu Val Glu Gln Ser Phe Gly Ile Ser Met

225 230 235 240

Glu Lys Val Phe Ser Leu Asp Phe Tyr Asn Gln Cys Leu Leu Gln Gly

245 250 255

Gly Ile Asp Lys Tyr Asn Glu Ile Leu Gly Gly Lys Thr Leu Glu Asn

260 265 270

Gly Glu Lys Phe Lys Gly Ile Asn Glu Leu Ile Asn Lys Tyr Arg Gln

275 280 285

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

290 295 300

Ile Leu Ser Glu Lys Glu Ser Phe Ile Asp Glu Ile Lys Asn Asp Lys

305 310 315 320

Glu Leu Glu Glu Thr Leu Lys Asn Leu His Glu Thr Ala Lys Val Lys

325 330 335

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

340 345 350

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

355 360 365

Ile Ser His Lys Trp Thr Gly Gly Thr Asp Leu Phe Ala Glu Asn Leu

370 375 380

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

385 390 395 400

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

405 410 415

Lys Thr Ala Leu Glu Asn Val Pro Lys Asp Ile Asn Phe Trp Lys Glu

420 425 430

Arg Tyr Tyr Val Asn Lys Glu Gly Glu Asn Lys Glu Phe Phe Leu Gly

435 440 445

Asn Gly Glu Ile Trp Gln Gln Phe Leu Gln Ile Phe Asn Phe Glu Phe

450 455 460

Asn Glu Leu Phe Gln Lys Glu Ile Ile Asp Asn Gln Thr Gly Lys Lys

465 470 475 480

Met His Ile Gly Tyr Lys Val Tyr Lys Glu Glu Ile Ser Lys Leu Leu

485 490 495

Glu Asp Phe Lys Val Asp Lys Asp Ser Thr Val Ile Ile Lys His Phe

500 505 510

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

515 520 525

Glu Lys Lys Arg Thr Trp Arg Asp Glu Tyr Asp Leu Asp Thr Phe Tyr

530 535 540

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

545 550 555 560

Glu Ile Val Gln Ile Tyr Asn Lys Leu Arg Asn Tyr Leu Thr Lys Lys

565 570 575

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

580 585 590

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

595 600 605

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

610 615 620

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

625 630 635 640

Glu Lys Gly Lys Tyr Glu Lys Met Asn Tyr Lys Tyr Phe Pro Ser Pro

645 650 655

Ser Lys Met Ile Pro Lys Thr Ser Thr Gln Val His Glu Val Lys Lys

660 665 670

His Phe Lys Asn Ser Ser Glu Pro Phe Phe Leu Glu Glu Ser Ser Ser

675 680 685

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

690 695 700

Leu Asn Asn Phe Glu Tyr Lys Lys Ser Tyr Leu Ser Thr Leu Asn Gly

705 710 715 720

Glu Ser Pro Asp Glu Ser Gln Arg Val Lys Ala Asp Ser Lys Lys Thr

725 730 735

Gly Gln Val Lys Leu Phe Gln Lys Glu Phe Leu Asn Leu Ser Gln Asn

740 745 750

Glu Leu Leu Tyr Lys Lys Ser Leu Phe Ala Trp Val Asp Phe Cys Lys

755 760 765

Glu Tyr Leu Asp Cys Phe Pro Ser Thr Gly Asp Gly Phe Leu Gln Phe

770 775 780

Lys Lys Tyr Ile Gln Asp Thr Glu Lys Tyr Glu Ser Ile Asp Gln Phe

785 790 795 800

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

805 810 815

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

820 825 830

Phe Lys Ile His Asn Lys Asp Trp Asn Leu Lys Asp Gly Lys Pro Lys

835 840 845

Thr Gly Met Lys Asn Leu His Thr Met Tyr Phe Glu Ser Leu Phe Ser

850 855 860

Ser Glu Asn Ile Ala Gln Asn Phe Pro Met Lys Leu Asn Gly Gln Ala

865 870 875 880

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

885 890 895

Lys Asp Ser Lys Gly Lys Asn Val Val Asp His Lys Arg Tyr Glu Glu

900 905 910

Asp Lys Ile Phe Phe His Leu Pro Met Thr Leu Asn Arg Gly Lys Ser

915 920 925

Leu Phe Asn Phe Asn Val Gln Leu Asn Asn Phe Leu Ala Asp Asn Pro

930 935 940

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

945 950 955 960

Tyr Ser Val Ile Asn Gln Asn Gln Glu Ile Leu Asp Gly Gly Thr Leu
965 970 975
Asn Val Val Lys Gly Gly Asn Gly Lys Asp Ile Asp Tyr His Lys Lys

980 985 990
Leu Glu Asp Lys Ala Glu Lys Arg Glu Gln Ala Arg Lys Asp Trp Gln
995 1000 1005
Asp Val Glu Gly Ile Lys Asp Leu Lys Lys Gly Tyr Ile Ser Gln
1010 1015 1020
Val Val Arg Lys Leu Ala Asp Leu Ala Ile Glu His Asn Ala Ile
1025 1030 1035
Ile Val Phe Glu Asp Leu Asn Met Arg Phe Lys Gln Ile Arg Gly

1040 1045 1050
Gly Ile Glu Lys Ser Val Tyr Gln Gln Leu Glu Lys Ala Leu Ile
1055 1060 1065
Glu Lys Leu Ser Phe Leu Val Arg Lys Asn Glu Lys Asn Pro Glu
1070 1075 1080
Glu Ala Gly Tyr Leu Leu Lys Ala Tyr Gln Leu Ser Ala Pro Phe
1085 1090 1095
Glu Thr Phe Gln Arg Ile Gly Lys Gln Thr Gly Ile Ile Phe Tyr

1100 1105 1110
Thr Gln Ala Ser Tyr Thr Ser Lys Ile Asp Pro Leu Thr Gly Trp
1115 1120 1125
Arg Pro Asn Leu Tyr Leu Lys Tyr Ser Asn Ala Lys Lys Ala Lys
1130 1135 1140
Ala Asp Ile Ser Lys Phe Ser Glu Ile Glu Phe Ile Asn Asn Arg
1145 1150 1155
Phe Glu Phe Thr Tyr Asp Leu Gln Glu Phe Arg Ser Gln Lys Asp

1160 1165 1170
Lys Lys Lys Glu Tyr Pro Lys Lys Thr Leu Trp Thr Leu Cys Ser
1175 1180 1185
Ser Val Glu Arg Tyr Arg Trp Asn Arg Lys Leu Asn Asp Asn Lys

1190 1195 1200

Gly Gly Tyr Glu His Tyr Ser Asp Leu Thr Ser Asp Phe Lys Lys

1205 1210 1215

Leu Phe Lys Lys Tyr Asn Ile Asn Ile Asn Glu Asp Ile Leu Gly

1220 1225 1230

Gln Ile Glu Asn Met Asp Thr Asp Asp Arg Lys Asn Asn Ala Arg

1235 1240 1245

Phe Phe Ser Gly Phe Met Phe Phe Trp Asn Leu Ile Cys Gln Ile

1250 1255 1260

Arg Asn Thr Asn Ser Asp Val Ile Ser Gly Glu Ser Asp Asn Asp

1265 1270 1275

Phe Ile Leu Ser Pro Val Glu Pro Phe Phe Asp Ser Arg Lys Ala

1280 1285 1290

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

1295 1300 1305

Ala Phe Asn Ile Ala Arg Lys Gly Ile Met Ile Leu Lys Lys Ile

1310 1315 1320

Ser Gln Tyr Val Glu Glu Asn Glu Asn Cys Asp Lys Leu Lys Trp

1325 1330 1335

Gly Asp Leu Tyr Ile Ser His Thr Asp Trp Asp Asn Phe Ile

1340 1345 1350

<210> 9

<211> 921

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 9

Met Thr Asn Tyr Thr Asp Phe Ile Gly Leu Tyr Pro Val Gln Lys Thr

1 5 10 15

Leu Arg Phe Glu Leu Arg Pro Gln Gly Lys Thr Ala Glu Lys Met Arg

20 25 30

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

35 40 45

Val Met Lys Ala Leu Ile Asp Asp Tyr His Arg Arg Phe Ile Asn Glu

50 55 60

Leu Leu Glu Lys Ala Ser Phe Asp Trp Gln Pro Leu Phe Glu Ala Leu

65 70 75 80

Asn Asn Val Lys Val Asn Lys Asp Asp Lys Ser Lys Lys Glu Leu Glu

85 90 95

Lys Glu Gln Leu His Met Arg Lys Glu Leu Ile Gly Leu Phe Glu Lys

100 105 110

Asp Glu Arg Phe Lys Tyr Leu Phe Ser Glu Lys Leu Phe Ser Glu Leu

115 120 125

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

130 135 140

Met Arg Ser Phe Asp Arg Phe Ser Gly Tyr Phe Ile Gly Phe His Glu

145 150 155 160

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

165 170 175

Tyr Arg Val Val Ala Glu Asn Phe Pro Lys Phe Ala Asp Asn Cys Arg

180 185 190

Lys Tyr Ser Leu Ile Lys Glu Asn Met Gln Glu Ala Val Val Glu Phe

195 200 205

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

210 215 220

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

225 230 235 240

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

245 250 255

Arg Gly Leu Asn Glu Phe Leu Asn Leu Tyr Tyr Gln Lys Val Thr Asp

260 265 270

Asn Lys Arg Ile Lys Met Ala Pro Leu Tyr Lys Gln Ile Leu Cys Glu

275 280 285

Ser Lys Thr Lys Ser Phe Ile Pro Tyr Met Phe Glu Asn Asp Glu Glu

290 295 300

Val Ile Ser Ser Ile Asn Gln Tyr Tyr Asp Ser Val Lys Tyr Asp Ile

305 310 315 320

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

325 330 335

Ser Lys Ile Phe Ile Asp Gln Lys Ser Ile Ser Ser Ile Ser Ile Val

340 345 350

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

355 360 365

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

370 375 380

Asp Lys Trp Leu Ser Ser Ser Tyr Phe Thr Leu Lys Glu Val Phe Glu

385 390 395 400

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

405 410 415

Leu Val Leu Lys Asn Ile Glu Glu Phe Asp Lys Ser Cys Leu Leu Glu

420 425 430

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

435 440 445

Phe Leu Asp Leu Leu Met Glu Val Gln His Leu Met Lys Pro Phe Asn

450 455 460

Ala Lys Glu Asp Leu Asp Lys Asp Ala Ala Phe Tyr Ser Glu Tyr Asn

465 470 475 480

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

485 490 495

Arg Asn Tyr Ala Thr Lys Lys Lys Tyr Ser Thr Tyr Lys Ile Lys Met

500 505 510

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

515 520 525

Arg Asp Asn Thr Ala Val Ile Leu Leu Arg Gly Asn Asn Tyr Tyr Leu
530 535 540
Gly Ile Met Asn Pro Lys Lys Lys Thr Lys Phe Glu Glu Leu Pro Ser

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

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

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

740 745 750
Leu Val Asn Arg Thr Asp Arg Lys Asp Asn Pro Ile Pro Asn Ser Ile
755 760 765
Tyr Tyr Glu Leu Phe Lys Tyr Lys Thr Gly Gln Ile Lys Ser Val Ser

770 775 780

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

785 790 795 800

Tyr Pro Ile Thr Lys Asp Arg Arg Tyr Thr Glu Asp Arg Met Phe Phe

805 810 815

His Ile Pro Ile Thr Leu Asn Phe Gly Ser Ser Gly Asn Thr Asn Ile

820 825 830

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

835 840 845

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

850 855 860

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

865 870 875 880

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

885 890 895

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

900 905 910

Glu Gly Tyr Leu Ser Tyr Val Ile His

915 920

<210> 10

<211> 1238

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 10

Met Lys Asp Phe Tyr Gln Phe Thr Asn Leu Tyr Ala Leu Ser Lys Thr

1 5 10 15

Leu Arg Phe Ser Leu Ile Pro Thr Pro Ala Thr Lys Gln Met Leu Glu

20 25 30

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

35 40 45

Ala Thr Lys Pro Tyr Phe Asp Arg Leu His Arg Glu Phe Ala Leu Glu
50 55 60

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

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

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

Lys Ile Leu Gly Gly Glu Thr Leu Gln Asn Gly Glu Lys Val Lys Gly
260 265 270
Leu Asn Glu Cys Ile Asn Leu His Lys Gln Lys Thr Gly Glu Lys Leu
275 280 285
Pro Phe Phe Lys Ser Leu Asp Lys Gln Ile Leu Ser Glu Lys Asp Lys

290 295 300

Phe Phe Ile Asp Glu Ile Ser Asn Glu Thr Gln Leu Leu Glu Val Leu
305 310 315 320

Lys Ser Phe Val Ala Ser Ala Glu Ser Lys Thr Asp Thr Ile Lys Thr
325 330 335

Leu Val Asp Asp Phe Val Lys Asp Gln Asp Lys Tyr Asp Leu Asn Tyr
340 345 350

Ile Tyr Phe Ser Asn Asp Gly Leu Asn Thr Ile Thr Arg Lys Trp Thr
355 360 365

Thr Glu Thr Gln Val Phe Glu Glu Ala Leu Tyr Thr Ala Leu Lys Ala
370 375 380

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

Phe Pro Asp Phe Ile Pro Phe Ala His Leu Lys Thr Ala Leu Glu Ser
405 410 415

Ile Lys Ile Asp Gly Thr Ile Trp Arg Asp Asn Phe Asn Ala Ile Glu
420 425 430

Asn Phe Glu Glu Lys Ser Ile Trp Ala Gln Phe Leu Ala Ile Tyr Asn
435 440 445

Phe Glu Leu Ser Asn Leu Phe Glu Thr Glu Ile Lys Asn Pro Glu Ile
450 455 460

Gly Asn Cys Pro Thr Ile Gly Tyr Asn Val Tyr Lys Gln Asp Phe Glu
465 470 475 480

Glu Leu Leu Lys Ser Phe Val Tyr Asp Pro Asn Ala Lys Val Thr Ile
485 490 495

Lys Asn Phe Ala Asp Asn Val Leu Ser Ile Tyr Gln Met Ala Lys Tyr
500 505 510

Phe Ala Val Glu Lys Lys Arg Gly Trp Asn Thr Asp Tyr Glu Leu Asp
515 520 525

Val Phe Tyr Thr Asp Pro Gln Asn Gly Tyr Leu Gln Tyr Tyr Glu Asn
530 535 540

Ala Tyr Glu Glu Ile Val Gln Val Tyr Asn Lys Leu Arg Asn Tyr Leu
545 550 555 560
Thr Lys Lys Pro Tyr Ser Glu Glu Lys Trp Lys Leu Asn Phe Asp Ser
565 570 575

Gly Thr Pro Ile Lys Tyr Thr Thr Arg Ala Ile Ile Phe Asn Asn Thr
580 585 590
Thr Asn Glu Arg Tyr Tyr Leu Gly Leu Leu Lys Lys Gly Val Ala Lys
595 600 605
Pro Arg Glu Phe Glu Pro Ile Asn Asn Asn Ile Ile Ser Ser Gly Glu
610 615 620
Phe Arg Arg Met Ile Ile Gln Gln Leu Lys Phe Gln Thr Leu Ala Gly
625 630 635 640

Lys Gly Tyr Val Arg Asp Phe Gly Val Lys Tyr Ser Glu Asp Lys Asp
645 650 655
Gly Val Lys His Leu Gln Gln Leu Ile Lys Lys Gln Tyr Leu Ser Lys
660 665 670
Tyr Pro Cys Leu Lys Lys Ile Ala Asp Gly Val Tyr Asn Asp Lys Lys
675 680 685
Ala Phe Asp Ala Asp Ile Lys Asp Val Leu Leu Glu Thr Tyr Asn Leu
690 695 700

Asp Phe Gln Pro Ile Ser Glu Glu Phe Ile Leu Asn Lys Asn Arg Leu
705 710 715 720
Gly Glu Ile Tyr Leu Phe Glu Ile His Asn Lys Asp Trp Asn Leu Lys
725 730 735
Asp Gly Lys Asn Lys Ser Gly Ser Lys Asn Leu His Thr Met Tyr Phe
740 745 750
Glu Ser Leu Phe Val Asp Lys Thr Thr Phe Lys Leu Asn Asn Glu Gly
755 760 765

Ala Glu Val Phe Tyr Arg Pro Ala Thr Asn Glu Gly Lys Leu Gly Thr
770 775 780
Lys Lys Asp Arg Asn Gly Lys Ile Ile Ile Asn His Lys Arg Tyr Ala

785 790 795 800

Thr Asp Lys Ile Leu Phe His Cys Pro Ile Gly Leu Asn Lys Asp Ala

805 810 815

Gly Lys Ser Tyr Thr Phe Asn Ala Lys Ile Asn Asn Met Leu Ala Asn

820 825 830

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

835 840 845

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

850 855 860

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

865 870 875 880

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

885 890 895

Trp Gln Ala Val Glu Gly Ile Lys Asp Leu Lys Arg Gly Tyr Ile Ser

900 905 910

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

915 920 925

Ile Val Phe Glu Asp Leu Asn Met Arg Phe Lys Gln Ile Arg Gly Gly

930 935 940

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

945 950 955 960

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

965 970 975

His Leu Leu Lys Ala Tyr Gln Leu Val Ala Pro Phe Glu Ser Phe Gln

980 985 990

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

995 1000 1005

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

1010 1015 1020

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

1025 1030 1035

Phe Ser Lys Ile Glu Phe Val Asn Asn Arg Phe Glu Leu Thr Tyr
1040 1045 1050

Asp Ile Lys Asn Phe Val Leu Asp Lys Lys Val Val Leu Ser Asn
1055 1060 1065

Lys Thr Lys Trp Thr Val Cys Ser Ser Val Glu Arg Phe Arg Trp
1070 1075 1080

Asn Arg Arg Leu Glu Ser Asn Gln Gly Asn Tyr Glu His Tyr Glu
1085 1090 1095

Asn Leu Thr Glu Asn Leu Ser Ser Leu Phe Lys Asp Phe Gly Phe
1100 1105 1110

Glu Ile Glu Gln Asn Ile Ile Arg Gln Val Glu Gln Leu Ala Thr
1115 1120 1125

Lys Gly Asn Glu Gln Phe Phe Arg Ser Phe Ile Phe Tyr Val Asn
1130 1135 1140

Leu Ile Phe Gln Ile Arg Asn Thr Asp Ala Lys Ala Lys Asp Gln
1145 1150 1155

Asn Lys Glu Asp Phe Ile Leu Ser Pro Val Glu Pro Phe Phe Asp
1160 1165 1170

Ser Arg Thr Pro Glu Lys Phe Gly Glu Asn Leu Pro Glu Asn Gly
1175 1180 1185

Asp Asp Asn Gly Ala Phe Asn Ile Ala Arg Lys Gly Ile Ile Met
1190 1195 1200

Leu Asn Lys Ile Ser Ala Tyr Lys Gln Glu Val Gly Asn Val Asp
1205 1210 1215

Lys Ile Ile Trp Lys Asp Leu Phe Ile Ser Ala Ala Glu Trp Asp
1220 1225 1230

Asn Phe Thr Gln Glu
1235

<210> 11

<211> 1301

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 11

Met Asp Ser Tyr Glu Gln Phe Thr Lys Leu Tyr Pro Ile Gln Lys Thr
1 5 10 15

Ile Arg Phe Glu Leu Lys Pro Gln Gly Arg Thr Lys Glu His Phe Asp
20 25 30

Asn Ser Asn Phe Leu Glu Lys Asp Arg Glu Arg Asp Asp Asn Tyr Lys
35 40 45

Ile Leu Lys Glu Val Ile Asp Asp Tyr His Arg Glu Phe Ile Asp Glu
50 55 60

Cys Leu Ser Asn Ile Gln Leu Asn Trp Asp Asp Leu Lys Lys Phe Ser
65 70 75 80

Glu Glu Tyr Arg Arg Ser Lys Glu Lys Lys Asn Asn Arg Asp Ser Glu
85 90 95

Ser Glu Gln Lys Arg Met Ser Thr Thr Ser Glu Thr Arg Ala Ile Asn
100 105 110

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

Ser Ala Phe Lys Lys Asp Asp Arg Phe Lys His Leu Phe Ser Glu Lys
130 135 140

Leu Phe Ser Ile Leu Leu Lys Asn Gln Ile Tyr Glu Lys Gly Thr Leu
145 150 155 160

Glu Glu Ile Glu Ala Phe Asp Cys Phe Asn Lys Phe Ser Gly Tyr Phe
165 170 175

Lys Ser Phe His Glu Asn Arg Lys Asn Met Tyr Ser Asp Glu Asp Lys
180 185 190

Glu Thr Ala Ile Ser Tyr Arg Ile Ile Asn Glu Asn Phe Pro Lys Leu
195 200 205

Leu Asp Asn Phe Glu Lys Tyr Gln Tyr Val Cys Arg Glu Tyr Pro Glu
210 215 220

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

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

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

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

Ala Tyr Val Ser Glu Ile Cys Val Ala Arg Arg Asn Ile Asp Lys Glu

465 470 475 480

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

485 490 495

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

500 505 510

Phe His Leu Leu Ser Pro Phe Gln Leu His Pro Asn Thr Pro His Asp

515 520 525

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

530 535 540

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

545 550 555 560

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

565 570 575

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

580 585 590

Ile Arg Asp Gly Lys Tyr Tyr Leu Gly Ile Met Asn Pro Lys Asn Lys

595 600 605

Arg Lys Ile Lys Phe Asp Glu Gly Ser Gly Ala Gly Pro Phe Tyr Gln

610 615 620

Lys Met Val Tyr Lys Leu Leu Pro Gly Pro Tyr Arg Met Leu Pro Lys

625 630 635 640

Val Phe Phe Ala Lys Lys Asn Ile Asp Tyr Tyr Asn Pro Ser Gln Glu

645 650 655

Ile Arg Glu Gly Tyr Lys Ala Gly Lys His Lys Lys Gly Lys Glu Phe

660 665 670

Asp Lys Gly Phe Cys His Lys Leu Ile Asp Phe Phe Lys Glu Ser Ile

675 680 685

Gln Lys Asn Glu Asn Trp Lys Val Phe Asp Phe Lys Phe Ser Pro Thr

690 695 700

Glu Ser Tyr Asp Asp Ile Ser Glu Phe Tyr Gln Glu Val Glu Lys Gln

705 710 715 720

Gly Tyr Arg Met Tyr Phe Val Asn Ile Pro Ser Asp Thr Ile Asp Arg
725 730 735

Tyr Val Glu Gly Gly Asp Met Phe Leu Phe Gln Ile Tyr Asn Lys Asp
740 745 750

Phe Ala Lys Gly Ala Lys Gly Asn Lys Asp Met His Thr Leu Tyr Trp
755 760 765

Asn Ala Val Phe Ser Glu Glu Asn Leu Gln Lys Gly Val Met Lys Leu
770 775 780

Ser Gly Glu Ala Glu Leu Phe Tyr Arg Lys Lys Ser Asp Ile Lys Asp
785 790 795 800

Pro Pro His Arg Glu Gly Glu Ile Leu Val Asn Arg Thr Tyr Ile Asp
805 810 815

Arg Thr His Val Ser Gly Val Met Gly Glu Gln Asn Thr Val Lys Glu
820 825 830

Ser Arg Ile Pro Val Pro Asp Glu Ile His Lys Asn Leu Phe Asp Tyr
835 840 845

Tyr Asn His Gly Arg Glu Leu Thr Lys Glu Glu Lys Glu Tyr Cys Asp
850 855 860

Lys Val Gly Ser Phe Lys Ala Tyr Tyr Gly Ile Val Lys Asp Arg Arg
865 870 875 880

Tyr Leu Glu Asn Lys Met Tyr Phe His Val Pro Leu Thr Leu Asn Phe
885 890 895

Lys Ala Ile Gly Glu Lys Arg Ile Asn Lys Met Ala Ile Glu Lys Phe
900 905 910

Leu Thr Asp Glu Asn Ala Cys Ile Ile Gly Ile Asp Arg Gly Glu Arg
915 920 925

Asn Leu Leu Tyr Tyr Ser Ile Ile Asp Arg Asn Gly Lys Ile Ile Asp
930 935 940

Gln Lys Ser Leu Asn Val Ile Asp Gly Phe Asp Tyr His Glu Lys Leu
945 950 955 960

Ser Gln Arg Gln Thr Glu Arg Glu Val Ala Arg Gln Ser Trp Asn Ser

965 970 975

Ile Gly Lys Ile Lys Asp Leu Lys Glu Gly Tyr Leu Ala Lys Ala Val
980 985 990
His Glu Ile Ser Lys Met Ala Ile Lys Tyr Asn Ala Ile Val Val Leu
995 1000 1005
Glu Asp Leu His Phe Gly Phe Lys Lys Gly Arg Leu Lys Val Glu
1010 1015 1020
Lys Gln Ile Tyr Gln Lys Phe Glu Glu Met Leu Ile Asn Lys Leu
1025 1030 1035

Asn Tyr Leu Val Phe Lys Asp Val Ser Asp Ser Ser Asp Ala Gly
1040 1045 1050
Gly Val Leu Asn Ala Tyr Gln Leu Thr Ala Pro Leu Glu Ser Phe
1055 1060 1065
Ser Lys Leu Gly Lys Gln Ser Gly Ile Leu Phe Tyr Val Pro Ala
1070 1075 1080
Ala Phe Thr Ser Val Ile Asp Pro Thr Thr Gly Phe Val Asp Leu
1085 1090 1095

Phe Asn Ser Ser Ser Ile Thr Ser Thr Gln Lys Lys Lys Glu Phe
1100 1105 1110
Leu Gln Arg Phe Glu Ser Ile Val Tyr Ser Ala Arg Asp Gly Gly
1115 1120 1125
Ile Phe Ala Phe Thr Phe Asp Tyr Arg Asn Phe Ser Lys Ile Ala
1130 1135 1140
Thr Asp His Arg Asn Met Trp Thr Val Tyr Thr His Gly Glu Arg
1145 1150 1155

Ile Arg Tyr Val Arg Asp Glu Lys Cys Tyr Lys Thr Thr Asp Pro
1160 1165 1170
Thr Lys Arg Ile Lys Glu Ala Leu Ser Gly Ile Glu Tyr Asp Asp
1175 1180 1185
Gly Ser Asp Ile Arg Asp Lys Ile Thr Gln Ser Gly Asp Asn Asn
1190 1195 1200

Leu Ile Asn Thr Val Tyr His Ser Phe Met Asp Thr Ile Lys Met
1205 1210 1215

Arg Asn Lys Asp Gly Arg Ile Asp Tyr Ile Ile Ser Pro Val Lys
1220 1225 1230
Asn Arg Asn Gly Glu Phe Phe Arg Ser Asp Tyr Lys His Arg Asp
1235 1240 1245
Phe Pro Val Asp Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu
1250 1255 1260
Lys Gly Glu Leu Leu Met Arg Met Ile Gly Lys Thr Tyr Asp Ser
1265 1270 1275

Asn Ser Asp Lys Met Pro Lys Leu Glu His Lys Asp Trp Phe Glu
1280 1285 1290
Phe Met Gln Thr Arg Gly Asp Gln
1295 1300

<210> 12
<211> 1368
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
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Tyr Glu Ile Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Val Glu Asn

20 25 30
Thr Gln Thr Met Leu Asp Glu Ala Asp Val Phe Gly Lys Asp Lys Val
35 40 45
Ile Lys Asp Lys Tyr Thr Lys Thr Lys Pro Phe Ile Asp Lys Leu His
50 55 60
Arg Glu Phe Val Asp Glu Ser Leu Lys Asp Val Ser Leu Ser Gly Leu
65 70 75 80

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

85 90 95

Lys Asp Ile Val Lys Glu Leu Lys Lys Glu Glu Glu Arg Leu Arg Lys

100 105 110

Glu Val Val Glu Phe Phe Asp Asn Thr Ala Lys Lys Trp Ala Asn Glu

115 120 125

Lys Tyr Lys Glu Leu Gly Leu Lys Lys Lys Asp Ile Gly Ile Leu Phe

130 135 140

Glu Glu Ser Val Phe Asp Leu Leu Lys Glu Lys Tyr Gly Glu Glu Gln

145 150 155 160

Asp Ser Phe Leu Lys Glu Glu Lys Gly Asp Phe Leu Lys Asn Glu Lys

165 170 175

Gly Glu Lys Val Ser Ile Phe Asp Glu Trp Lys Gly Phe Val Gly Tyr

180 185 190

Phe Thr Lys Phe Gln Glu Thr Arg Lys Asn Phe Tyr Lys Asn Asp Gly

195 200 205

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

210 215 220

Phe Cys Asp Asn Ile Asp Asp Phe Lys Lys Ile Lys Asn Lys Ile Asp

225 230 235 240

Phe Ser Glu Val Glu Lys Asn Phe Asn Lys Thr Ala Asp Val Phe Ser

245 250 255

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

260 265 270

Asn Glu Phe Ile Gly Gly Lys Thr Leu Glu Asn Gly Lys Lys Leu Lys

275 280 285

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

290 295 300

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

305 310 315 320

Glu Lys Leu Ser Phe Gly Ile Glu Asn Asp Glu Gln Leu Leu Val Val

325 330 335

Leu Asn Ser Phe Tyr Glu Thr Ala Glu Glu Lys Thr Lys Ile Leu Arg

340 345 350

Thr Leu Phe Gly Asp Phe Val Glu His Asn Glu Asn Tyr Asp Leu Asp

355 360 365

Lys Thr Tyr Ile Ser Lys Val Ala Phe Asn Thr Ile Ser His Lys Trp

370 375 380

Thr Asn Glu Thr His Lys Phe Glu Glu Leu Leu Tyr Gly Ala Met Lys

385 390 395 400

Glu Asp Lys Pro Ile Gly Leu Asn Tyr Asp Lys Lys Glu Asp Ser Tyr

405 410 415

Lys Phe Pro Asp Phe Ile Ala Leu Gly Tyr Leu Lys Lys Cys Leu Asn

420 425 430

Asn Leu Asp Cys Asp Thr Lys Phe Trp Lys Glu Lys Tyr Tyr Glu Asn

435 440 445

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

450 455 460

Asn Ala Trp Asp Gln Phe Leu Gln Ile Phe Ile Phe Glu Phe Asn Gln

465 470 475 480

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

485 490 495

Gly Tyr Asp Asn Phe Arg Lys Asp Phe Glu Glu Ile Ile Asn Gln Lys

500 505 510

Asp Phe Lys Asn Asp Glu Asn Leu Lys Ile Ala Ile Lys Asn Phe Ala

515 520 525

Asp Ser Val Leu Trp Ile Tyr Gln Met Ala Lys Tyr Phe Ala Ile Glu

530 535 540

Lys Lys Arg Gly Trp Asp Asp Asp Phe Glu Leu Ser Glu Phe Tyr Thr

545 550 555 560

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

565 570 575

Ile Val Gln Lys Tyr Asn Asp Leu Arg Asn Tyr Leu Thr Lys Lys Pro
580 585 590
Tyr Lys Glu Asp Lys Trp Lys Leu Asn Phe Glu Asn Pro Thr Leu Ala

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

660 665 670
Lys Met Ile Pro Lys Cys Ser Thr Gln Leu Asn Glu Ala Lys Asn His
675 680 685
Phe Arg Asn Ser Ala Asp Asp Leu Glu Ile Lys Lys Ser Phe Ser Asn
690 695 700
Pro Leu Lys Ile Thr Lys Arg Ile Phe Asp Leu Asn Asn Ile Gln Tyr
705 710 715 720
Asp Lys Thr Asn Val Ser Lys Lys Ile Ser Gly Asp Asn Lys Gly Ile

725 730 735
Lys Ile Phe Gln Lys Glu Tyr Tyr Lys Ile Ser Gly Asp Phe Asp Val
740 745 750
Tyr Lys Ser Ala Leu Asn Asp Trp Ile Asp Phe Cys Lys Asp Phe Leu
755 760 765
Ser Lys Tyr Asp Ser Thr Lys Asp Phe Asp Phe Ser Ile Leu Arg Lys
770 775 780
Thr Lys Asp Tyr Lys Ser Leu Asp Glu Phe Tyr Val Asp Val Ala Lys

785 790 795 800
Ile Thr Tyr Lys Ile Ser Phe Thr Pro Val Ser Glu Ser Tyr Ile Asp
805 810 815
Gln Lys Asn Lys Asn Gly Glu Leu Tyr Leu Phe Glu Ile Tyr Asn Gln

820 825 830

Asp Phe Ala Lys Gly Lys Met Gly Ala Lys Asn Leu His Thr Leu Tyr

835 840 845

Phe Glu Asn Val Phe Ser Pro Glu Asn Ile Ser Lys Asn Phe Pro Ile

850 855 860

Lys Leu Asn Gly Asn Ala Glu Leu Phe Phe Arg Pro Lys Ser Ile Glu

865 870 875 880

Ser Lys Lys Glu Lys Arg Asn Phe Val Arg Glu Ile Val Asn Lys Lys

885 890 895

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

900 905 910

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

915 920 925

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

930 935 940

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

945 950 955 960

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

965 970 975

Glu Glu Arg Ala Gly Glu Arg Glu Gln Ser Arg Lys Asp Trp Gln Val

980 985 990

Val Glu Gly Ile Lys Asp Leu Lys Lys Gly Tyr Ile Ser Gln Val Val

995 1000 1005

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

1010 1015 1020

Leu Glu Asp Leu Asn Met Arg Phe Lys Gln Ile Arg Gly Gly Ile

1025 1030 1035

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

1040 1045 1050

Leu Ser Phe Leu Val Glu Lys Gly Glu Lys Asp Pro Asn Gln Ala

1055 1060 1065

Gly His Ile Leu Lys Ala Tyr Gln Leu Ala Ala Pro Phe Thr Ser
1070 1075 1080
Phe Lys Asp Met Gly Lys Gln Thr Gly Ile Val Phe Tyr Thr Gln
1085 1090 1095
Ala Ser Tyr Thr Ser Lys Thr Cys Pro Asn Cys Gly Phe Arg Lys

1100 1105 1110
Asn Asn Asn Lys Phe Tyr Phe Glu Asn Asn Ile Gly Lys Ala Gln
1115 1120 1125
Asp Ala Leu Lys Lys Leu Lys Thr Phe Glu Tyr Asp Ser Glu Asn
1130 1135 1140
Lys Cys Phe Gly Leu Ser Tyr Cys Leu Ser Asp Phe Ala Asn Lys
1145 1150 1155
Glu Glu Val Glu Lys Asn Lys Asn Lys Lys Arg Asn Asn Ala Pro

1160 1165 1170
Tyr Ser Asp Ile Glu Lys Lys Asp Cys Phe Glu Leu Ser Thr Lys
1175 1180 1185
Asp Ala Val Arg Tyr Arg Trp His Asp Lys Asn Thr Glu Arg Gly
1190 1195 1200
Lys Thr Phe Phe Glu Gly Glu Ser Val Tyr Glu Glu Lys Glu Glu
1205 1210 1215
Lys Glu Ile Gly Gln Thr Lys Arg Gly Leu Val Lys Glu Tyr Asp

1220 1225 1230
Ile Ser Lys Cys Leu Ile Gly Leu Phe Glu Lys Thr Gly Leu Asp
1235 1240 1245
Tyr Lys Gln Asn Leu Leu Asp Lys Ile Asn Ser Gly Lys Phe Asp
1250 1255 1260
Gly Thr Phe Tyr Lys Asn Leu Phe Asn Tyr Leu Asn Leu Leu Phe
1265 1270 1275
Glu Ile Arg Asn Ser Ile Ser Gly Thr Glu Ile Asp Tyr Ile Ser

1280 1285 1290
Cys Pro Glu Cys Gln Phe His Thr Asp Lys Ser Lys Thr Ile Lys

1295 1300 1305

Asn Gly Asp Asp Asn Gly Ser Tyr Asn Ile Ala Arg Lys Gly Met

1310 1315 1320

Ile Ile Leu Asp Lys Ile Lys Gln Phe Lys Lys Glu Asn Gly Ser

1325 1330 1335

Leu Asp Lys Met Gly Trp Gly Glu Leu Phe Ile Asp Leu Glu Glu

1340 1345 1350

Trp Asp Lys Phe Ala Gln Lys Lys Asn Asn Asn Ile Ile Asp Lys

1355 1360 1365

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<211> 1285

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 13

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

1 5 10 15

Leu Lys Phe Glu Met Arg Pro Val Gly Asn Thr Gln Lys Met Leu Asp

20 25 30

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

35 40 45

Lys Thr Lys Pro Tyr Phe Asp Arg Leu His Arg Glu Phe Ile Glu Glu

50 55 60

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

65 70 75 80

Leu Val Asp Trp Gln Lys Asp Lys Lys Asn Asn Val Ala Met Lys Ala

85 90 95

Tyr Glu Asn Ser Leu Gln Arg Leu Arg Thr Glu Ile Gly Lys Ile Phe

100 105 110

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

115 120 125

Leu Lys Asn Lys Asn Thr Asp Ile Leu Phe Glu Glu Ala Val Phe Gly
130 135 140
Ile Leu Lys Ala Arg Tyr Gly Glu Glu Lys Asp Thr Phe Ile Glu Val

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

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

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

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

370 375 380

Thr Phe Ala Lys Tyr Leu Phe Glu Ala Met Lys Ser Gly Lys Leu Ala

385 390 395 400

Lys Tyr Glu Lys Lys Asp Asn Ser Tyr Lys Phe Pro Asp Phe Ile Ala

405 410 415

Leu Ser Gln Met Lys Ser Ala Leu Leu Ser Ile Ser Leu Glu Gly His

420 425 430

Phe Trp Lys Glu Lys Tyr Tyr Lys Ile Ser Lys Phe Gln Glu Lys Thr

435 440 445

Asn Trp Glu Gln Phe Leu Ala Ile Phe Leu Tyr Glu Phe Asn Ser Leu

450 455 460

Phe Ser Asp Lys Ile Asn Thr Lys Asp Gly Glu Thr Lys Gln Val Gly

465 470 475 480

Tyr Tyr Leu Phe Ala Lys Asp Leu His Asn Leu Ile Leu Ser Glu Gln

485 490 495

Ile Asp Ile Pro Lys Asp Ser Lys Val Thr Ile Lys Asp Phe Ala Asp

500 505 510

Ser Val Leu Thr Ile Tyr Gln Met Ala Lys Tyr Phe Ala Val Glu Lys

515 520 525

Lys Arg Ala Trp Leu Ala Glu Tyr Glu Leu Asp Ser Phe Tyr Thr Gln

530 535 540

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

545 550 555 560

Val Gln Val Tyr Asn Lys Leu Arg Asn Tyr Leu Thr Lys Lys Pro Tyr

565 570 575

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

580 585 590

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

595 600 605

Lys Gly Gly Lys Tyr Tyr Leu Gly Leu Ile Thr Lys Gly His Asn Lys

610 615 620

Ile Phe Asp Asp Arg Phe Gln Glu Lys Phe Ile Val Gly Ile Glu Gly
625 630 635 640
Gly Lys Tyr Glu Lys Ile Val Tyr Lys Phe Phe Pro Asp Gln Ala Lys
645 650 655
Met Phe Pro Lys Val Cys Phe Ser Ala Lys Gly Leu Glu Phe Phe Arg

660 665 670
Pro Ser Glu Glu Ile Leu Arg Ile Tyr Asn Asn Ala Glu Phe Lys Lys
675 680 685
Gly Glu Thr Tyr Ser Ile Asp Ser Met Gln Lys Leu Ile Asp Phe Tyr
690 695 700
Lys Asp Cys Leu Thr Lys Tyr Glu Gly Trp Ala Cys Tyr Thr Phe Arg
705 710 715 720
His Leu Lys Pro Thr Glu Glu Tyr Gln Asn Asn Ile Gly Glu Phe Phe

725 730 735
Arg Asp Val Ala Glu Asp Gly Tyr Arg Ile Asp Phe Gln Gly Ile Ser
740 745 750
Asp Gln Tyr Ile His Glu Lys Asn Glu Lys Gly Glu Leu His Leu Phe
755 760 765
Glu Ile His Asn Lys Asp Trp Asn Leu Asp Lys Ala Arg Asp Gly Lys
770 775 780
Ser Lys Thr Thr Gln Lys Asn Leu His Thr Leu Tyr Phe Glu Ser Leu

785 790 795 800
Phe Ser Asn Asp Asn Val Val Gln Asn Phe Pro Ile Lys Leu Asn Gly
805 810 815
Gln Ala Glu Ile Phe Tyr Arg Pro Lys Thr Glu Lys Asp Lys Leu Glu
820 825 830
Ser Lys Lys Asp Lys Lys Gly Asn Lys Val Ile Asp His Lys Arg Tyr
835 840 845
Ser Glu Asn Lys Ile Phe Phe His Val Pro Leu Thr Leu Asn Arg Thr

850 855 860
Lys Asn Asp Ser Tyr Arg Phe Asn Ala Gln Ile Asn Asn Phe Leu Ala

865 870 875 880

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

885 890 895

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

900 905 910

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

915 920 925

Lys Lys Ala Glu Asn Arg Glu Gln Ala Arg Arg Asp Trp Gln Asp Val

930 935 940

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

945 950 955 960

Lys Leu Ala Asp Leu Ala Ile Lys His Asn Ala Ile Ile Ile Leu Glu

965 970 975

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

980 985 990

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

995 1000 1005

Val Asp Lys Gly Glu Lys Asn Pro Glu Gln Ala Gly His Leu Leu

1010 1015 1020

Lys Ala Tyr Gln Leu Ser Ala Pro Phe Glu Thr Phe Gln Lys Met

1025 1030 1035

Gly Lys Gln Thr Gly Ile Ile Phe Tyr Thr Gln Ala Ser Tyr Thr

1040 1045 1050

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

1055 1060 1065

Lys Tyr Phe Ser Ala Lys Lys Ala Lys Asp Asp Ile Ala Lys Phe

1070 1075 1080

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

1085 1090 1095

Ile Lys Asp Phe Gln Gln Ala Lys Glu Tyr Pro Asn Lys Thr Val

1100 1105 1110

Trp Lys Val Cys Ser Asn Val Glu Arg Phe Arg Trp Asp Lys Asn

1115 1120 1125

Leu Asn Gln Asn Lys Gly Gly Tyr Thr His Tyr Thr Asn Ile Thr

1130 1135 1140

Glu Asn Ile Gln Glu Leu Phe Thr Lys Tyr Gly Ile Asp Ile Thr

1145 1150 1155

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

1160 1165 1170

Thr Ser Phe Phe Arg Asp Phe Ile Phe Tyr Phe Asn Leu Ile Cys

1175 1180 1185

Gln Ile Arg Asn Thr Asp Asp Ser Glu Ile Ala Lys Lys Asn Gly

1190 1195 1200

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

1205 1210 1215

Arg Lys Asp Asn Gly Asn Lys Leu Pro Glu Asn Gly Asp Asp Asn

1220 1225 1230

Gly Ala Tyr Asn Ile Ala Arg Lys Gly Ile Val Ile Leu Asn Lys

1235 1240 1245

Ile Ser Gln Tyr Ser Glu Lys Asn Glu Asn Cys Glu Lys Met Lys

1250 1255 1260

Trp Gly Asp Leu Tyr Val Ser Asn Ile Asp Trp Asp Asn Phe Val

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Thr Gln Ala Asn Ala Arg His

1280 1285

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<211> 1366

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 14

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Thr Asn Leu Tyr Ser Leu Asn Lys Thr Leu Arg Phe Ser Leu Thr Pro

20 25 30

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

35 40 45

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

50 55 60

Lys Lys Tyr Leu Asn Lys Leu His Gln Glu Phe Ile Gln Glu Ala Met

65 70 75 80

Lys Phe Phe Ala Phe Ser Glu Glu Glu Leu Lys Gly Phe Glu Lys Glu

85 90 95

Tyr Leu Asn Leu Leu Asn Phe Thr Asp Lys Asp Asn Phe Lys Lys Lys

100 105 110

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

115 120 125

Lys Ile Ala Thr Tyr Phe Ser Lys Phe Lys Ser Glu Lys Tyr Gln Ser

130 135 140

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

145 150 155 160

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

165 170 175

Lys Tyr Lys Pro Thr Lys Asp Glu Lys Lys Glu Gly Glu Ala Val Asn

180 185 190

Phe Ser Thr Tyr Leu Thr Gly Phe Asn Glu Asn Arg Lys Asn Phe Tyr

195 200 205

Lys Ser Glu Asp Lys Ala Gly Gln Phe Ala Thr Arg Thr Ile Asp Asn

210 215 220

Leu Ala Gln Phe Ile Lys Asn Lys Lys Leu Phe Glu Asp Lys Tyr Gln

225 230 235 240

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

245 250 255

Asn Leu Asp Tyr Phe Asn Asn Leu Phe Leu Gln Glu Gly Leu Asp Glu
260 265 270
Tyr Asn Gly Ile Leu Gly Asn Asn Lys Gly Glu Glu Asn Lys Ser Asn
275 280 285
Glu Gly Ile Asn Gln Lys Ile Asn Ile Phe Lys Gln Lys Glu Lys Ala
290 295 300

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

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

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

Lys Glu Lys Asn Glu Tyr Glu Ile Leu Pro Phe Gly Ser Leu Lys Glu

500 505 510

Leu Lys Glu Lys Tyr Phe Glu Ala Val Lys Lys Tyr Lys Glu Lys Met

515 520 525

Val Asp Thr Glu Ser Gly Leu Thr Asp Asp Glu Glu Lys Glu Ile Lys

530 535 540

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

545 550 555 560

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

565 570 575

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

580 585 590

Thr Asn Glu Leu Lys Ile Tyr Gln Tyr Tyr Ser Glu Phe Arg Asn Tyr

595 600 605

Leu Thr Gln Asn Asn Ser Val Glu Glu Lys Ile Lys Leu Asn Phe Asn

610 615 620

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

625 630 635 640

Phe Ser Ile Ile Phe Gln Glu Asn Gly Lys Tyr Tyr Leu Gly Ile Ile

645 650 655

Asn Lys Glu Lys Asp Lys Thr Ile Leu Asp Lys Asp Lys His Pro Glu

660 665 670

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

675 680 685

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

690 695 700

Lys Lys Gly Asp Glu Asp Val Gly Trp Ser Glu Glu Ile Gln Lys Ile

705 710 715 720

Lys Asp Glu Phe Ala Glu Phe Gln Glu Tyr Lys Lys Lys Ser Lys Asp

725 730 735

Asn Trp Lys Asp Glu Phe Asn Arg Gly Lys Leu Asn Lys Leu Ile Asp

740 745 750

Tyr Tyr Lys Gln Val Leu Glu Lys His Ser Glu Gly Tyr Met Asn Thr
755 760 765

Tyr Asn Phe Glu Leu Lys Asp Ser Ser Lys Tyr Lys Asn Leu Gly Glu
770 775 780

Phe Asn Asp Asp Ile Ala Arg Gln Asn Tyr Lys Val Lys Phe Val Gly
785 790 795 800

Ile Asp Lys Asn Tyr Ile Asp Glu Lys Val Ala Asn Gly Glu Leu Phe
805 810 815

Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Glu Asp Lys Lys Glu Gly
820 825 830

Ser Thr Asn Asn Leu Glu Thr Ile Tyr Phe Lys Glu Leu Phe Ser Lys
835 840 845

Glu Asn Leu Glu Asn Pro Val Phe Lys Leu Ser Gly Gly Ala Glu Met
850 855 860

Phe Phe Arg Asn Lys Ile Glu Lys Lys Lys Glu Lys Lys Lys Leu Asp
865 870 875 880

Lys Asp Gly Lys Pro Met Ile Ser Lys Lys Gly Glu Lys Val Val Asp
885 890 895

Lys Arg Arg Phe Ser Glu Asn Lys Ile Leu Phe His Leu Pro Ile Glu
900 905 910

Ile Asn Tyr Gly Lys Gly Lys Met Pro Asn Phe Asn Lys Lys Ile Asn
915 920 925

Glu Tyr Ile Ser Lys Asn Pro Glu Asn Ile Lys Ile Ile Gly Ile Asp
930 935 940

Arg Gly Glu Lys His Leu Leu Tyr Tyr Ser Ile Ile Asp Gln Asn Gly
945 950 955 960

Asn Asn Ile Glu Ser Met Ser Leu Asn Ala Val Asp Glu Phe Gly Asn
965 970 975

Phe Val Asn Pro Glu Lys Leu Glu Glu Tyr Glu Ile Asp Asn Asn Gly
980 985 990

Lys Lys Glu Arg Arg Trp Lys Tyr Ile Val Asn Asp Lys Glu Ile Lys

995 1000 1005

Val Thr Asn Tyr Gln Arg Lys Leu Asp Glu Leu Glu Lys Glu Arg
1010 1015 1020
Gln Lys Ser Arg Gln Ser Trp Gln Asn Ile Asn Lys Ile Lys Asn
1025 1030 1035
Leu Lys Lys Gly Tyr Ile Ser Phe Val Val Lys Lys Ile Val Asp
1040 1045 1050
Leu Ala Ile Glu Asn Asn Ala Ile Ile Ile Leu Glu Asp Leu Asn
1055 1060 1065

Phe Gly Phe Lys Ser Phe Arg Gln Lys Ile Glu Lys Asn Val Tyr
1070 1075 1080
Gln Gln Phe Glu Lys Ala Leu Ile Asp Lys Leu Gly Phe Val Val
1085 1090 1095
Asp Lys Gln Lys Gln Asn Gln Arg Phe Ala Pro Gln Leu Ser Ala
1100 1105 1110
Pro Phe Glu Ser Phe Gln Lys Ile Gly Lys Gln Thr Gly Ile Val
1115 1120 1125

Tyr Tyr Val Leu Ala Asn Asn Thr Ser Lys Val Cys Pro Ser Cys
1130 1135 1140
Gln Trp Ile Lys Asn Phe Tyr Leu Lys Tyr Glu Lys Lys Asn Thr
1145 1150 1155
Ile Phe Asn Leu Gln Lys Asn Gln Lys Leu Lys Val Phe Phe Glu
1160 1165 1170
Gln Glu Lys Asn Arg Phe Arg Phe Glu Tyr Gln Met Ser Lys Glu
1175 1180 1185

Tyr Ile Ser Val Tyr Ser Asp Val Asp Arg Gln Arg Tyr Asp Lys
1190 1195 1200
Thr Lys Asn Gln Asn Lys Gly Gly Tyr Leu Glu Tyr Lys Asn Ser
1205 1210 1215
Asn Gln Lys Glu Ile Ile Asp Lys Asp Gly Val Ile Gln Lys Gln
1220 1225 1230

Ser Ile Thr Leu Gln Leu Lys Glu Leu Phe Lys Glu Asn His Ile
1235 1240 1245

Asp Leu Glu Lys Glu Ile Leu Lys Gln Leu Asp Asn Lys Lys Glu
1250 1255 1260
Lys Asn Ser Gly Tyr Thr Gly Val Tyr Asn Lys Phe Ile Tyr Leu
1265 1270 1275
Phe Asn Leu Ile Leu Gln Ile Arg Asn Ala Ile Ser Phe Arg Glu
1280 1285 1290
Lys Asp Tyr Ile Gln Cys Pro Ser Cys His Phe Asp Thr Arg Lys
1295 1300 1305

Glu Asn Tyr Leu Lys Ile Asn Asp Gly Asp Gly Asn Gly Ala Tyr
1310 1315 1320
Asn Ile Ala Leu Arg Gly Leu Tyr Leu Leu Lys Gly Lys Asn Gly
1325 1330 1335
Ile Ile Asn Asn Leu Glu Lys Ile Lys Leu Ile Phe Ser Asn Asn
1340 1345 1350
Asp Tyr Phe Gln Trp Ala Lys Lys Leu Lys Asn Lys Lys
1355 1360 1365

<210>
15

<211> 1285

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas12 sequence

<400> 15

Met Glu Glu Lys Met Leu Lys Ser Tyr Asp Tyr Phe Thr Lys Leu Tyr
1 5 10 15
Ser Leu Gln Lys Thr Leu Arg Phe Glu Leu Lys Pro Ile Gly Lys Thr
20 25 30
Leu Glu His Ile Lys Asn Ser Gly Ile Ile Glu Ser Asp Glu Thr Leu
35 40 45

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

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

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

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

290 295 300

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

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

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

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

Tyr Tyr Glu Ala Leu Leu Pro Leu Asn Ser Leu Tyr Asn Lys Val Arg
545 550 555 560

Asn Tyr Met Thr Arg Lys Pro Tyr Ser Val Glu Lys Phe Lys Leu Asn
565 570 575

Phe Asn Ser Pro Thr Leu Leu Asp Gly Trp Asp Lys Asn Lys Glu Thr
580 585 590

Ala Asn Leu Ser Ile Ile Leu Arg Lys Asn Gly Lys Tyr Tyr Leu Gly
595 600 605

Ile Met Asn Lys Glu Asn Asn Thr Ile Phe Glu Tyr Tyr Pro Gly Thr
610 615 620

Lys Ser Asn Asp Tyr Tyr Glu Lys Met Ile Tyr Lys Leu Leu Pro Gly
625 630 635 640

Pro Asn Lys Met Leu Pro Lys Val Phe Phe Ser Lys Lys Gly Leu Glu
645 650 655

Tyr Tyr Asn Pro Pro Lys Glu Ile Leu Asn Ile Tyr Glu Lys Gly Glu
660 665 670

Phe Lys Lys Asp Lys Ser Gly Asn Phe Lys Lys Glu Ser Leu His Thr
675 680 685

Leu Ile Asp Phe Tyr Lys Glu Ala Ile Ala Lys Asn Glu Asp Trp Glu
690 695 700

Val Phe Asn Phe Lys Phe Lys Asn Thr Lys Glu Tyr Glu Asp Ile Ser
705 710 715 720

Gln Phe Tyr Arg Asp Val Glu Glu Gln Gly Tyr Leu Ile Thr Phe Glu
725 730 735

Lys Val Asp Ala Asn Tyr Val Asp Lys Leu Val Lys Glu Gly Lys Leu
740 745 750

Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Glu Asn Lys Lys Ser
755 760 765

Lys Gly Asn Pro Asn Leu His Thr Ile Tyr Trp Lys Gly Leu Tyr Asp
770 775 780

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

785 790 795 800

Val Phe Tyr Arg Lys Lys Ser Ile Asp Tyr Pro Glu Glu Ile Tyr Asn

805 810 815

His Gly His His Lys Glu Glu Leu Leu Gly Lys Phe Asn Tyr Pro Ile

820 825 830

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

835 840 845

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

850 855 860

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

865 870 875 880

Ile Asp Arg Gly Glu Arg His Leu Leu Tyr Leu Ser Leu Ile Asp Lys

885 890 895

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

900 905 910

Asn Tyr Asp Lys Glu Ile Asp Tyr Arg Val Lys Leu Asp Glu Lys Glu

915 920 925

Lys Lys Arg Asp Glu Ala Arg Lys Asn Trp Asp Val Ile Glu Asn Ile

930 935 940

Lys Glu Leu Lys Glu Gly Tyr Met Ser Gln Val Ile His Ile Ile Ala

945 950 955 960

Lys Met Met Val Glu Glu Lys Ala Ile Leu Ile Met Glu Asp Leu Asn

965 970 975

Ile Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Lys Gln Val Tyr Gln

980 985 990

Lys Phe Glu Lys Met Leu Ile Asp Lys Leu Asn Tyr Leu Val Phe Lys

995 1000 1005

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

1010 1015 1020

Leu Thr Ser Lys Phe Asp Ser Phe Lys Lys Leu Gly Lys Gln Ser

1025 1030 1035

Gly Phe Ile Phe Tyr Val Pro Ser Ala Tyr Thr Ser Lys Ile Asp
1040 1045 1050
Pro Thr Thr Gly Phe Tyr Asn Phe Ile Gln Val Asp Val Pro Asn
1055 1060 1065

Leu Glu Lys Gly Lys Glu Phe Phe Ser Lys Phe Glu Lys Ile Ile
1070 1075 1080
Tyr Asn Thr Lys Glu Asp Tyr Phe Glu Phe His Cys Lys Tyr Gly
1085 1090 1095
Lys Phe Val Ser Glu Pro Lys Asn Lys Asp Asn Asp Arg Lys Thr
1100 1105 1110
Lys Glu Ser Leu Thr Tyr Tyr Asn Ala Ile Lys Asp Thr Val Trp
1115 1120 1125

Val Val Cys Ser Thr Asn His Glu Arg Tyr Lys Ile Val Arg Asn
1130 1135 1140
Lys Ala Gly Tyr Tyr Glu Ser His Pro Val Asp Val Thr Lys Asn
1145 1150 1155
Leu Lys Asp Ile Phe Ser Gln Ala Asn Ile Asn Tyr Asn Glu Gly
1160 1165 1170
Lys Asp Ile Lys Pro Ile Ile Ile Glu Ser Asn Asn Ala Lys Leu
1175 1180 1185

Leu Lys Ser Ile Ala Glu Gln Leu Lys Leu Ile Leu Ala Met Arg
1190 1195 1200
Tyr Asn Asn Gly Lys His Gly Asp Asp Glu Lys Asp Tyr Ile Leu
1205 1210 1215
Ser Pro Val Lys Asn Lys Gln Gly Lys Phe Phe Cys Thr Leu Asp
1220 1225 1230
Gly Asn Gln Thr Leu Pro Ile Asn Ala Asp Ala Asn Gly Ala Tyr
1235 1240 1245

Asn Ile Ala Leu Lys Gly Leu Leu Leu Ile Glu Lys Ile Lys Lys
1250 1255 1260
Gln Gln Gly Lys Ile Lys Asp Leu Tyr Ile Ser Asn Leu Glu Trp

1265 1270 1275

Phe Met Phe Met Met Ser Arg

1280 1285

<210> 16

<211> 1238

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 16

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

1 5 10 15

Ile Arg Phe Glu Leu Lys Pro Gln Gly Arg Thr Met Glu His Leu Glu

20 25 30

Thr Phe Asn Phe Phe Glu Glu Asp Arg Asp Arg Ala Glu Lys Tyr Lys

35 40 45

Ile Leu Lys Glu Ala Ile Asp Glu Tyr His Lys Lys Phe Ile Asp Glu

50 55 60

His Leu Thr Asn Met Ser Leu Asp Trp Asn Ser Leu Lys Gln Ile Ser

65 70 75 80

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

85 90 95

Ser Glu Gln Lys Arg Met Arg Gln Glu Ile Val Ser Glu Phe Lys Lys

100 105 110

Asp Asp Arg Phe Lys Asp Leu Phe Ser Lys Lys Leu Phe Ser Glu Leu

115 120 125

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

130 135 140

Leu Lys Ser Phe Asp Lys Phe Ser Gly Tyr Phe Ile Gly Leu His Glu

145 150 155 160

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

165 170 175

Asn Arg Ile Val Asn Glu Asn Phe Pro Lys Phe Leu Asp Asn Leu Gln
180 185 190
Lys Tyr Gln Glu Ala Arg Lys Lys Tyr Pro Glu Trp Ile Ile Lys Ala

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

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

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

385 390 395 400
Asp Val Leu Glu Ala Ile Lys Arg Thr Gly Asn Asn Asp Ala Phe Asn
405 410 415
Glu Tyr Ile Ser Lys Met Arg Thr Ala Arg Glu Lys Ile Asp Ala Ala

420 425 430

Arg Lys Glu Met Lys Phe Ile Ser Glu Lys Ile Ser Gly Asp Glu Glu

435 440 445

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

450 455 460

His Phe Phe Asn Leu Phe Lys Ala Arg Gln Asp Ile Pro Leu Asp Gly

465 470 475 480

Ala Phe Tyr Ala Glu Phe Asp Glu Val His Ser Lys Leu Phe Ala Ile

485 490 495

Val Pro Leu Tyr Asn Lys Val Arg Asn Tyr Leu Thr Lys Asn Asn Leu

500 505 510

Asn Thr Lys Lys Ile Lys Leu Asn Phe Lys Asn Pro Thr Leu Ala Asn

515 520 525

Gly Trp Asp Gln Asn Lys Val Tyr Asp Tyr Ala Ser Leu Ile Phe Leu

530 535 540

Arg Asp Gly Asn Tyr Tyr Leu Gly Ile Ile Asn Pro Lys Arg Lys Lys

545 550 555 560

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

565 570 575

Met Val Tyr Lys Gln Ile Pro Gly Pro Asn Lys Asn Leu Pro Arg Val

580 585 590

Phe Leu Thr Ser Thr Lys Gly Lys Lys Glu Tyr Lys Pro Ser Lys Glu

595 600 605

Ile Ile Glu Gly Tyr Glu Ala Asp Lys His Ile Arg Gly Asp Lys Phe

610 615 620

Asp Leu Asp Phe Cys His Lys Leu Ile Asp Phe Phe Lys Glu Ser Ile

625 630 635 640

Glu Lys His Lys Asp Trp Ser Lys Phe Asn Phe Tyr Phe Ser Pro Thr

645 650 655

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

660 665 670

Gly Tyr Arg Met His Phe Glu Asn Ile Ser Ala Glu Thr Ile Asp Glu

675 680 685

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

690 695 700

Phe Val Lys Ala Ala Thr Gly Lys Lys Asp Met His Thr Ile Tyr Trp

705 710 715 720

Asn Ala Ala Phe Ser Pro Glu Asn Leu Gln Asp Val Val Val Lys Leu

725 730 735

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

740 745 750

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

755 760 765

Arg Thr Pro Val Pro Asp Lys Ile His Lys Lys Leu Thr Asp Tyr His

770 775 780

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

785 790 795 800

Val Arg Tyr Phe Lys Ala His Tyr Asp Ile Thr Lys Asp Arg Arg Tyr

805 810 815

Leu Asn Asp Lys Ile Tyr Phe His Val Pro Leu Thr Leu Asn Phe Lys

820 825 830

Ala Asn Gly Lys Lys Asn Leu Asn Lys Met Val Ile Glu Lys Phe Leu

835 840 845

Ser Asp Glu Lys Ala His Ile Ile Gly Ile Asp Arg Gly Glu Arg Asn

850 855 860

Leu Leu Tyr Tyr Ser Ile Ile Asp Arg Ser Gly Lys Ile Ile Asp Gln

865 870 875 880

Gln Ser Leu Asn Val Ile Asp Gly Phe Asp Tyr Arg Glu Lys Leu Asn

885 890 895

Gln Arg Glu Ile Glu Met Lys Asp Ala Arg Gln Ser Trp Asn Ala Ile

900 905 910

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

915 920 925

Glu Ile Thr Lys Met Ala Ile Gln Tyr Asn Ala Ile Val Val Met Glu

930 935 940

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

945 950 955 960

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

965 970 975

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

980 985 990

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

995 1000 1005

Thr Gly Ile Leu Phe Tyr Val Pro Ala Ala Tyr Thr Ser Lys Ile

1010 1015 1020

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

1025 1030 1035

Thr Asn Ala Gln Glu Arg Lys Glu Phe Leu Gln Lys Phe Glu Ser

1040 1045 1050

Ile Ser Tyr Ser Ala Lys Asp Gly Gly Ile Phe Ala Phe Ala Phe

1055 1060 1065

Asp Tyr Arg Lys Phe Gly Thr Ser Lys Thr Asp His Lys Asn Val

1070 1075 1080

Trp Thr Ala Tyr Thr Asn Gly Glu Arg Met Arg Tyr Ile Lys Glu

1085 1090 1095

Lys Lys Arg Asn Glu Leu Phe Asp Pro Ser Lys Glu Ile Lys Glu

1100 1105 1110

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

1115 1120 1125

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

1130 1135 1140

Met Tyr Ser Ser Phe Ile Ala Ala Ile Gln Met Arg Val Tyr Asp

1145 1150 1155

Gly Lys Glu Asp Tyr Ile Ile Ser Pro Ile Lys Asn Ser Lys Gly

1160 1165 1170

Glu Phe Phe Arg Thr Asp Pro Lys Arg Arg Glu Leu Pro Ile Asp

1175 1180 1185

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

1190 1195 1200

Thr Met Arg Ala Ile Ala Glu Lys Phe Asp Pro Asp Ser Glu Lys

1205 1210 1215

Met Ala Lys Leu Glu Leu Lys His Lys Asp Trp Phe Glu Phe Met

1220 1225 1230

Gln Thr Arg Gly Asp

1235

<210> 17

<211> 1347

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 17

Met Ala Ser Ser His Phe Ile Ser Leu Asp Asn Ser Phe Ser Lys Phe

1 5 10 15

Thr Asn Leu Tyr Ser Leu Ser Lys Thr Leu Arg Phe Glu Leu Val Pro

20 25 30

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

35 40 45

Asp Gln Ile Ile Gln Val Lys Tyr Glu Lys Thr Lys Pro Phe Ile Asp

50 55 60

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

65 70 75 80

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

85 90 95

Ala Asn Leu Asp Ser Ala Lys Lys Gln Leu Arg Lys His Val Val Asp

100 105 110

Gln Phe Asn Ala Thr Ala Ser Leu Trp Val Ser Arg His Lys Asp Val

115 120 125

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

130 135 140

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

145 150 155 160

Asp Asn His Gly Lys Gln Ile Ser Ile Phe Asp Ser Trp Lys Gly Phe

165 170 175

Thr Gly Tyr Phe Asp Lys Phe Gln Gln Thr Arg Arg Asn Leu Tyr Lys

180 185 190

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

195 200 205

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

210 215 220

Lys Val Ser Phe Ile Asp Val Glu Lys Ser Phe Gly Lys Thr Cys Ser

225 230 235 240

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

245 250 255

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

260 265 270

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

275 280 285

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

290 295 300

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

305 310 315 320

Val Pro Arg Val Leu Ala Phe Tyr Arg Thr Val Asp Ala Lys Tyr Lys

325 330 335

Leu Phe Leu Lys Leu Leu Asp Asp Phe Val Thr Asn Gln Asp Val Tyr

340 345 350

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

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

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

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

595 600 605

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

610 615 620

Ile Leu Arg Gln Gly Asp Lys Tyr Phe Leu Gly Val Met Lys Lys Gly

625 630 635 640

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

645 650 655

Pro Glu Ala Tyr Phe Glu Lys Met Val Tyr Lys Tyr Thr Lys Asp Val

660 665 670

Val Thr Gly Ile Pro Lys Ser Ser Thr Gln Val Lys Glu Val Gln Glu

675 680 685

His Phe Arg Asn Ser Asp Glu Asp Phe Phe Leu Glu Glu Cys Ser Ser

690 695 700

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

705 710 715 720

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

725 730 735

Arg Trp Ala Leu Asn Thr Asp Glu Glu Lys Asn Tyr Val Lys Ser Phe

740 745 750

Gln Lys Ser Tyr Leu Ser Leu Gly Gly Ser Pro Glu Leu Tyr Cys Lys

755 760 765

Ser Val Thr Leu Trp Ile Gly Phe Cys Leu Asn Phe Leu Lys Ser Tyr

770 775 780

Pro Ser Ala Ala Tyr Phe Asp Tyr Ser Gln Leu Arg Gln Ala Ser Asp

785 790 795 800

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

805 810 815

Thr Ile Leu Phe Gln Asn Val Ser Glu Lys Tyr Val Arg Val Lys Asn

820 825 830

Lys Asn Gly Glu Leu Tyr Leu Phe Gln Ile Lys Asn Lys Asp Trp Asn

835 840 845

Glu Gly Ser Thr Gly Lys Lys Asn Leu His Thr Leu Tyr Phe Glu Ser

850 855 860

Leu Phe Ser Lys Glu Asn Ala Lys Gln Gly Phe Pro Phe Lys Leu Ser
865 870 875 880
Gly Asn Ala Glu Leu Phe Phe Arg Pro Gly Ser Ile Glu Gln Thr Tyr
885 890 895
Glu Arg Arg Asn Phe Pro Arg Glu Ile Pro Leu Lys Arg Arg Tyr Ser
900 905 910
Lys Asp Gly Ile Phe Phe His Ile Pro Val Gln Val Asn Arg Thr Lys

915 920 925

Val Gly Ser Pro Asn Gln Phe Asn Lys Glu Val Asn Asp Phe Leu Ala
930 935 940
Gly Asn Pro Asn Ile Asn Ile Ile Gly Val Asp Arg Gly Glu Lys His
945 950 955 960
Leu Val Tyr Tyr Ser Val Ile Ser Gln Asn Gly Glu Lys Ile Asp Gly
965 970 975
Gly Ser Phe Asn Glu Ile Asn Gly Gln Asp Tyr His Asp Lys Leu Glu

980 985 990

Lys Arg Ala Lys Glu Arg Glu Gln Gln Arg Arg Asp Trp Glu Thr Val
995 1000 1005
Glu Gly Ile Lys Asp Leu Lys Lys Gly Tyr Ile Ser Gln Val Val
1010 1015 1020
Lys Lys Leu Ala Asp Leu Ala Ile Glu His Asn Ala Ile Ile Val
1025 1030 1035
Met Glu Asp Leu Asn Met Arg Phe Lys Gln Ile Arg Gly Gly Ile

1040 1045 1050
Glu Lys Ser Val Tyr Gln Gln Leu Glu Lys Ala Leu Ile Asp Lys
1055 1060 1065
Leu Ser Phe Leu Val Asn Lys Gly Glu Val Asp Pro Gln Lys Ala
1070 1075 1080
Gly His Leu Leu Lys Ala Tyr Gln Leu Thr Ala Pro Ile Asp Ala

1085 1090 1095

Phe Lys Asp Met Gly Lys Gln Thr Gly Ile Met Phe Tyr Thr Gln

1100 1105 1110

Ala Ala Tyr Thr Ser Lys Ile Asp Pro Val Thr Gly Trp Arg Pro

1115 1120 1125

His Leu Tyr Leu Lys Tyr Ser Ser Val Glu Lys Ala Lys Asp Asp

1130 1135 1140

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

1145 1150 1155

Phe Thr Tyr Asn Ile Thr Asp Phe Arg Thr Gln Lys Glu Trp Pro

1160 1165 1170

Leu Lys Thr Glu Trp Thr Val Cys Ser Cys Val Glu Arg Phe Arg

1175 1180 1185

Trp Asn Lys Lys Leu Ala Asn Gly Lys Gly Asp Tyr Glu His Tyr

1190 1195 1200

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

1205 1210 1215

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

1220 1225 1230

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

1235 1240 1245

Phe Ala Leu Val Cys Gln Ile Arg Asn Thr Asn Ser Glu Glu Ala

1250 1255 1260

Gly Asn Leu Asn Asp Phe Ile Leu Ser Pro Val Glu Pro Phe Phe

1265 1270 1275

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

1280 1285 1290

Gly Asp Glu Asn Gly Ala Tyr Asn Ile Ala Arg Lys Gly Met Ile

1295 1300 1305

Ile Leu Asn Thr Leu Ser Thr Phe Lys Asn Asp His Gly Ser Cys

1310 1315 1320

Glu Gly Leu Ser Trp Gly Asp Leu Tyr Ile Ser Asp Thr Gln Trp
1325 1330 1335
Asp Asp Phe Ala Gln Ser Phe His Gly
1340 1345

<210> 18
<211> 1227
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 18
Met Asp Ala Lys Glu Phe Thr Gly Gln Tyr Pro Leu Ser Lys Thr Leu
1 5 10 15
Arg Phe Glu Leu Arg Pro Ile Gly Arg Thr Trp Asp Asn Leu Glu Ala
20 25 30
Ser Gly Tyr Leu Ala Glu Asp Arg His Arg Ala Glu Cys Tyr Pro Arg
35 40 45

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

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

165 170 175

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

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

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

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

Ile Asn Asp Leu Arg Ala Val Asp Leu Asp Ser Leu Asn Asp Asp Gly
420 425 430

Tyr Glu Ala Ala Val Ser Lys Ile Arg Glu Ser Leu Glu Pro Tyr Met
435 440 445

Asp Leu Phe His Glu Leu Glu Ile Phe Ser Val Gly Asp Glu Phe Pro
450 455 460

Lys Cys Ala Ala Phe Tyr Ser Glu Leu Glu Glu Val Ser Glu Gln Leu
465 470 475 480

Ile Glu Ile Ile Pro Leu Phe Asn Lys Ala Arg Ser Phe Cys Thr Arg
485 490 495

Lys Arg Tyr Ser Thr Asp Lys Ile Lys Val Asn Leu Lys Phe Pro Thr
500 505 510

Leu Ala Asp Gly Trp Asp Leu Asn Lys Glu Arg Asp Asn Lys Ala Ala
515 520 525

Ile Leu Arg Lys Asp Gly Lys Tyr Tyr Leu Ala Ile Leu Asp Met Lys
530 535 540

Lys Asp Leu Ser Ser Ile Arg Thr Ser Asp Glu Asp Glu Ser Ser Phe
545 550 555 560

Glu Lys Met Glu Tyr Lys Leu Leu Pro Ser Pro Val Lys Met Leu Pro
565 570 575

Lys Ile Phe Val Lys Ser Lys Ala Ala Lys Glu Lys Tyr Gly Leu Thr
580 585 590

Asp Arg Met Leu Glu Cys Tyr Asp Lys Gly Met His Lys Ser Gly Ser
595 600 605

Ala Phe Asp Leu Gly Phe Cys His Glu Leu Ile Asp Tyr Tyr Lys Arg
610 615 620

Cys Ile Ala Glu Tyr Pro Gly Trp Asp Val Phe Asp Phe Lys Phe Arg
625 630 635 640

Glu Thr Ser Asp Tyr Gly Ser Met Lys Glu Phe Asn Glu Asp Val Ala
645 650 655

Gly Ala Gly Tyr Tyr Met Ser Leu Arg Lys Ile Pro Cys Ser Glu Val

660 665 670

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

675 680 685

Lys Asp Tyr Ser Glu Asn Ala His Gly Asn Lys Asn Met His Thr Met

690 695 700

Tyr Trp Glu Gly Leu Phe Ser Pro Gln Asn Leu Glu Ser Pro Val Phe

705 710 715 720

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

725 730 735

Asn Asp Ala Lys Thr Val His Pro Lys Gly Ser Val Leu Val Pro Arg

740 745 750

Asn Asp Val Asn Gly Arg Arg Ile Pro Asp Ser Ile Tyr Arg Glu Leu

755 760 765

Thr Arg Tyr Phe Asn Arg Gly Asp Cys Arg Ile Ser Asp Glu Ala Lys

770 775 780

Ser Tyr Leu Asp Lys Val Lys Thr Lys Lys Ala Asp His Asp Ile Val

785 790 795 800

Lys Asp Arg Arg Phe Thr Val Asp Lys Met Met Phe His Val Pro Ile

805 810 815

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

820 825 830

Ile Asp Gly Ile Ile Asp Asp Gln Asp Leu Lys Ile Ile Gly Ile Asp

835 840 845

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

850 855 860

Asn Ile Leu Tyr Gln Asp Ser Leu Asn Ile Leu Asn Gly Tyr Asp Tyr

865 870 875 880

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

885 890 895

Asn Trp Thr Lys Val Glu Gly Ile Arg Lys Met Lys Glu Gly Tyr Leu

900 905 910

Ser Leu Ala Val Ser Lys Leu Ala Asp Met Ile Ile Glu Asn Asn Ala
915 920 925
Ile Ile Val Met Glu Asp Leu Asn His Gly Phe Lys Ala Gly Arg Ser
930 935 940

Lys Ile Glu Lys Gln Val Tyr Gln Lys Phe Glu Ser Met Leu Ile Asn
945 950 955 960
Lys Leu Gly Tyr Met Val Leu Lys Asp Lys Ser Ile Asp Gln Ser Gly
965 970 975
Gly Ala Leu His Gly Tyr Gln Leu Ala Asn His Val Thr Thr Leu Ala
980 985 990
Ser Val Gly Lys Gln Cys Gly Val Ile Phe Tyr Ile Pro Ala Ala Phe
995 1000 1005

Thr Ser Lys Ile Asp Pro Thr Thr Gly Phe Ala Asp Leu Phe Ala
1010 1015 1020
Leu Ser Asn Val Lys Asn Val Ala Ser Met Arg Glu Phe Phe Ser
1025 1030 1035
Lys Met Lys Ser Val Ile Tyr Asp Lys Ala Glu Gly Lys Phe Ala
1040 1045 1050
Phe Thr Phe Asp Tyr Leu Asp Tyr Asn Val Lys Ser Glu Cys Gly
1055 1060 1065

Arg Thr Leu Trp Thr Val Tyr Thr Val Gly Glu Arg Phe Thr Tyr
1070 1075 1080
Ser Arg Val Asn Arg Glu Tyr Val Arg Lys Val Pro Thr Asp Ile
1085 1090 1095
Ile Tyr Asp Ala Leu Gln Lys Ala Gly Ile Ser Val Glu Gly Asp
1100 1105 1110
Leu Arg Asp Arg Ile Ala Glu Ser Asp Gly Asp Thr Leu Lys Ser
1115 1120 1125

Ile Phe Tyr Ala Phe Lys Tyr Ala Leu Asp Met Arg Val Glu Asn
1130 1135 1140
Arg Glu Glu Asp Tyr Ile Gln Ser Pro Val Lys Asn Ala Ser Gly

1145 1150 1155

Glu Phe Phe Cys Ser Lys Asn Ala Gly Lys Ser Leu Pro Gln Asp

1160 1165 1170

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

1175 1180 1185

Gln Leu Arg Met Leu Ser Glu Gln Tyr Asp Pro Asn Ala Glu Ser

1190 1195 1200

Ile Arg Leu Pro Leu Ile Thr Asn Lys Ala Trp Leu Thr Phe Met

1205 1210 1215

Gln Ser Gly Met Lys Thr Trp Lys Asn

1220 1225

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<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 19

Met Val Asn Lys Gln Asn Glu Arg Gly Asp Phe Asp Asp Leu Thr Asn

1 5 10 15

Leu Tyr Glu Ile Ser Lys Thr Leu Arg Phe Glu Leu Val Pro Val Gly

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Glu Leu Glu Glu Tyr Leu Ala Ile Phe Ile Glu Trp Arg Lys Asp Lys

85 90 95

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

100 105 110

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

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

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

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

325 330 335
Thr Lys Lys Ile Lys Val Ile Lys Ser Leu Phe Gly Asp Phe Val Glu
340 345 350
Asn Asn Glu Asn Tyr Asp Leu Glu Lys Ile Tyr Ile Ser Lys Lys Ala

355 360 365

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

370 375 380

Lys Leu Leu Phe Glu Ser Met Lys Ser Asp Lys Pro Ala Gly Leu Lys

385 390 395 400

Tyr Asp Lys Lys Glu Asn Asn Tyr Lys Phe Pro Asp Phe Ile Ala Val

405 410 415

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

420 425 430

Trp Lys Asp Arg Tyr Tyr Ile Glu Leu Glu Leu Asp Asn Gln Val Val

435 440 445

Trp Lys Gln Phe Leu Asp Ile Phe Tyr Trp Glu Phe Ser Ser Leu Phe

450 455 460

Lys Arg Ser Phe Val Asn Lys Glu Thr Gly Glu Ile Ser Glu Val Gly

465 470 475 480

Cys Asp Ile Phe Glu Lys Lys Phe Ile Asn Leu Ile Asp Asp Phe Glu

485 490 495

Tyr Asn Gln Lys Ser Lys Ile Leu Ile Lys Asp Phe Ala Asp Ser Val

500 505 510

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

515 520 525

Lys Trp Ser Thr Glu Phe Glu Thr Asp Ser Lys Phe Tyr Asp Asp Ser

530 535 540

Glu Ile Gly Phe Arg Asn Cys Phe Tyr Glu Asp Val Phe Glu Gly Ile

545 550 555 560

Val Gln Val Tyr Asn Lys Leu Arg Asn Tyr Leu Thr Lys Lys Pro Phe

565 570 575

Ser Glu Glu Lys Trp Lys Leu Asn Phe Glu Asn Pro Thr Leu Ala Ala

580 585 590

Gly Trp Asp Lys Asn Lys Glu Lys Asp Asn Ser Thr Val Ile Leu Arg

595 600 605

Lys Asp Glu Lys Tyr Phe Leu Ala Ile Met Lys Lys Gly Asn Asn Val
610 615 620
Ile Phe Asp Asp Arg Asn Lys Ala Leu Phe Ser Gln Asn Leu Glu His
625 630 635 640
Gly Lys Tyr Glu Lys Val Val Tyr Lys Phe Ala Lys Asp Val Thr Leu

645 650 655
Gly Ile Pro Lys Ser Thr Thr Gln Thr Lys Ser Val Ile Ala His Phe
660 665 670
Lys Asn Ser Asp Glu Asp Tyr Gln Ile Thr Asn Gly Ser Ala Val Gly
675 680 685
Asp Phe Leu Glu Pro Leu Val Val Thr Lys Arg Ile Phe Glu Leu Asn
690 695 700
Asn Lys Ile Tyr Ser Lys Asn Asn Leu Gly Lys Val Leu Tyr Arg Ser

705 710 715 720
Glu Val Ser Lys Asp Lys Gln Lys Glu Tyr Ile Lys Leu Phe Gln Lys
725 730 735
Lys Tyr Leu Val Leu Gly Gly Asn Lys Asn Leu Tyr Arg Asp Ala Val
740 745 750
Lys Glu Trp Ile Asp Phe Cys Lys Ser Phe Ile Lys Val Tyr Pro Ser
755 760 765
Tyr Lys Tyr Phe Asp Phe Ser Leu Leu Lys Glu Ala Val Glu Tyr Asn

770 775 780
Ser Val Asp Glu Phe Tyr Lys Glu Leu Asn Ser Tyr Gly Tyr Ala Ile
785 790 795 800
Ser Phe Gln Asp Ile Ser Cys Asp Tyr Ile Glu Glu Lys Asn Lys Asn
805 810 815
Gly Glu Leu Tyr Leu Phe Gln Ile Lys Asn Lys Asp Trp Asn Lys Gly
820 825 830
Ser Thr Gly Met Lys Asn Leu His Thr Leu Tyr Phe Glu Ser Leu Phe

835 840 845
Ser Glu Glu Asn Ile Lys Asn Asn Phe Val Thr Lys Leu Asn Gly Gly

850 855 860

Ala Glu Ile Phe Tyr Arg Pro Lys Thr Ser Lys Glu Lys Leu Gly Arg

865 870 875 880

Lys Lys Ile Val Arg Asn Gly Gln Glu Val Phe Val Val Asn His Lys

885 890 895

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

900 905 910

Arg Gly Lys Gly Lys Leu Leu Lys Phe Asn Ala Arg Ile Asn Asp Leu

915 920 925

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

930 935 940

Lys His Leu Ala Tyr Tyr Ser Ile Ile Asp Gln Lys Cys Lys Ile Leu

945 950 955 960

Asp Ser Gly Thr Leu Asn Glu Val Gly Ala Lys Val Asp Tyr His Glu

965 970 975

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

980 985 990

Gly Trp Gly Gln Ile Glu Asp Ile Lys Asn Leu Lys Lys Gly Tyr Val

995 1000 1005

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

1010 1015 1020

Ala Ile Leu Val Phe Glu Asp Leu Asn Met Arg Phe Lys Gln Ile

1025 1030 1035

Arg Gly Gly Ile Glu Lys Ser Ile Tyr Gln Gln Leu Glu Lys Ala

1040 1045 1050

Leu Ile Asp Lys Leu Asn Phe Leu Val Lys Lys Gly Glu Lys Asp

1055 1060 1065

Ser Lys Ser Ala Gly His Leu Leu Lys Ala Tyr Gln Leu Ala Ala

1070 1075 1080

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

1085 1090 1095

Phe Tyr Thr Gln Ala Ser Tyr Thr Ser Lys Ile Asp Pro Ile Thr

1100 1105 1110

Gly Trp Arg Pro Asn Leu Tyr Leu Lys His Ser Asn Ala Asn Asp

1115 1120 1125

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

1130 1135 1140

Asp Arg Phe Glu Phe Glu Tyr Asp Leu Lys Lys Phe Ile Glu Met

1145 1150 1155

Lys Glu Val Pro Glu Asn Thr Lys Trp Thr Leu Cys Ser Cys Val

1160 1165 1170

Gln Arg Tyr Arg Trp Asn Arg Lys Leu Asn Ala Asn Lys Gly Gly

1175 1180 1185

Tyr Asp Ser Tyr Asn Asp Leu Thr Lys Asn Phe Lys Ala Leu Phe

1190 1195 1200

Glu Ser Val Gly Ile Asp Ile Lys Lys Asn Ile Lys Glu Gln Ile

1205 1210 1215

Val Lys Met Glu Ile Lys Gly Asn Glu Lys Phe Phe Lys Ser Phe

1220 1225 1230

Ile Phe Tyr Trp Gln Leu Leu Cys Gln Ile Arg Asn Thr Asp Glu

1235 1240 1245

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

1250 1255 1260

Pro Phe Phe Asp Ser Arg Lys Lys Asn Gly Asp Asp Leu Pro Lys

1265 1270 1275

Asn Gly Asp Asp Asn Gly Ala Tyr Asn Ile Ala Arg Lys Gly Val

1280 1285 1290

Ile Val Leu Asn Lys Ile Ser Glu Phe Ser Lys Gln Asn Gly Asn

1295 1300 1305

Cys Glu Lys Cys Gly Trp Lys Glu Leu Tyr Val Ser Ala Lys Asp

1310 1315 1320

Trp Asp Asp Phe Val Gln Ala Lys

1325 1330

<210> 20

<211> 1275

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 20

Met Gln Asn Lys Gln Ser Phe Ala Asp Phe Thr Asn Leu Tyr Ser Leu
1 5 10 15

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Ile Gly Gln Thr Gln Ala
20 25 30

Met Leu Asp Glu Asn Lys Ile Phe Glu Val Asp Glu Asn Arg Lys Lys
35 40 45

Ala Tyr Asp Lys Thr Lys Pro Tyr Phe Asp Arg Leu His Arg Glu Phe
50 55 60

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

Phe Glu Thr Phe Lys Gln Phe Arg Ser Asn Gln Asn Asn Lys Asp Leu
85 90 95

Lys Glu Leu Ile Asn Lys Gln Gln Lys Phe Leu Arg His Gln Ile Val
100 105 110

Thr Leu Phe Asp Glu Asn Gly Lys His Trp Ala Thr Thr Lys Tyr Ala
115 120 125

His Leu Lys Ile Lys Lys Lys Asn Leu Asp Ile Leu Phe Asp Glu Gln
130 135 140

Val Phe Tyr Ile Leu Lys Glu Arg Tyr Gly Ser Glu Lys Glu Thr Gln
145 150 155 160

Leu Val Asp Lys Glu Thr Gly Ala Val Thr Ser Ile Phe Asp Asn Trp
165 170 175

Lys Gly Phe Thr Gly Tyr Phe Thr Lys Phe Phe Glu Thr Arg Lys Asn

180 185 190

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

195 200 205

Asp Gln Asn Leu Asn Arg Phe Phe Asp Asn Leu Glu Thr Phe His Lys

210 215 220

Ile Lys Asp Lys Ile Asp Val Lys Glu Val Glu Ile Phe Phe Lys Leu

225 230 235 240

Lys Ala Asp Asn Val Phe Ser Ile Asp Phe Tyr Asn Gln Cys Leu Leu

245 250 255

Gln Asn Gly Ile Asp Lys Tyr Asn Asp Phe Leu Gly Gly Gln Thr Leu

260 265 270

Glu Asn Gly Glu Lys Gln Lys Gly Ile Asn Glu Ile Ile Asn Lys Tyr

275 280 285

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

290 295 300

Lys Gln Ile Leu Ser Glu Lys Asp Arg Phe Ile Asn Glu Ile Glu Ser

305 310 315 320

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

325 330 335

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

340 345 350

Thr Asp Lys Tyr Lys Leu Glu Lys Ile Tyr Leu Thr Lys Glu Ala Phe

355 360 365

Asn Thr Ile Ala Asn Lys Trp Thr Asp Glu Thr Gln Ile Phe Glu Asp

370 375 380

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

385 390 395 400

Phe Ile Pro Leu Ala Tyr Ile Lys Glu Ala Leu Glu Val Ile Glu Lys

405 410 415

Asp Arg Lys Phe Phe Lys Asp Arg Tyr Tyr Asn Asp Pro Gln Ile Gly

420 425 430

Phe Phe Pro Asp Gln Ser Tyr Trp Glu Gln Phe Leu Ala Ile Leu Asn
435 440 445

Phe Glu Phe Met Thr His Phe Gln Arg Val Ala Lys Asp Lys Ile Thr
450 455 460

Gly Lys Lys Ile Glu Leu Gly Tyr Phe Val Phe Glu Lys Arg Ile Lys
465 470 475 480

Glu Leu Leu Asp Ser Asp Pro Ser Leu Asn Ser Gln Ser Lys Ile Ile
485 490 495

Ile Lys Glu Phe Ala Asp Glu Val Leu His Ile Phe Gln Met Ala Lys
500 505 510

Tyr Phe Ala Leu Glu Lys Lys Arg Glu Trp Lys Gly Asp Tyr Tyr Gln
515 520 525

Leu Asp Asp Gln Phe Tyr Asn His Ile Asp Tyr Gly Phe Lys Asp Gln
530 535 540

Phe Tyr Glu Asn Ala Tyr Glu Lys Ile Val Gln Pro Tyr Asn Lys Ile
545 550 555 560

Arg Asn Tyr Leu Thr Lys Lys Pro Tyr Ser Asp Val Lys Trp Lys Leu
565 570 575

Asn Phe Gly Asn Pro Thr Leu Ala Asn Gly Trp Asp Lys Asn Lys Glu
580 585 590

Ala Asp Asn Thr Ala Val Ile Leu Lys Lys Asp Gly Asn Tyr Tyr Leu
595 600 605

Gly Val Met Lys Lys Gly Lys Asn Lys Ile Phe Ser Asp Gln Asn Lys
610 615 620

Glu Lys Tyr Lys Ala Tyr Asn Ser Ala Tyr Tyr Glu Lys Leu Val Tyr
625 630 635 640

Lys Leu Phe Pro Asp Pro Ser Lys Met Phe Pro Lys Val Cys Phe Ser
645 650 655

Lys Lys Gly Leu Asn Phe Phe Gln Pro Ser Glu Glu Ile Leu Arg Ile
660 665 670

Tyr Lys Asn Asn Glu Phe Lys Lys Gly Asn Thr Phe Ser Ile Ser Ser

675 680 685

Met Gln Lys Leu Ile Ala Phe Tyr Ile Asp Cys Leu Gly Leu Tyr Glu
690 695 700
Gly Trp Lys His Tyr Glu Phe Lys Asn Ile Lys Asp Val Arg Gln Tyr
705 710 715 720
Lys Glu Asn Ile Gly Glu Phe Tyr Ala Asp Val Ala Glu Ser Gly Tyr
725 730 735
Lys Leu Trp Phe Glu Lys Ile Ser Glu Glu Tyr Ile Thr Gln Lys Asn
740 745 750

Gln Leu Gly Glu Leu Phe Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ala
755 760 765
Lys Lys Thr Thr Gly Arg Lys Asn Leu His Thr Ile Tyr Phe Glu Glu
770 775 780
Leu Phe Ser Gln Thr Asn Ile Asp Asn Asn Phe Pro Phe Lys Leu Asn
785 790 795 800
Gly Gln Ala Glu Leu Phe Tyr Arg Pro Lys Ser Leu Glu Lys Ile Glu
805 810 815

Glu Lys Arg Asn Phe Lys Arg Ser Ile Val Asn Lys Lys Arg Tyr Thr
820 825 830
Gln Asn Lys Ile Phe Phe His Val Pro Ile Thr Leu Asn Arg Thr Ser
835 840 845
Glu Asn Ile Gly Arg Phe Asn Val Arg Val Asn Asn Phe Leu Ala Asn
850 855 860
Asn Ser Asn Val Asn Ile Val Gly Val Asp Arg Gly Glu Lys Asn Leu
865 870 875 880

Ala Tyr Tyr Ser Ile Ile Lys Gln Asn Gly Glu Val Leu Lys Ser Gly
885 890 895
Ser Leu Asn Ile Ile Asn Gly Val Asp Tyr His Ala Leu Leu Thr Asp
900 905 910
Arg Ala Gln Arg Arg Glu Gln Glu Arg Arg Asn Trp Gln Asp Val Glu
915 920 925

Ser Ile Lys Asp Leu Lys Arg Gly Tyr Ile Ser Gln Val Val His Glu
930 935 940

Leu Val Ser Leu Ala Ile Lys Tyr Asn Ala Ile Ile Val Met Glu Asp
945 950 955 960
Leu Asn Met Arg Phe Lys Gln Ile Arg Gly Gly Ile Glu Lys Ser Thr
965 970 975
Tyr Gln Gln Leu Glu Lys Ala Leu Ile Glu Lys Leu Asn Phe Leu Val
980 985 990
Asn Lys Glu Glu Thr Asp Ser Asn Gln Ala Gly Asn Leu Leu Asn Ala
995 1000 1005

Tyr Gln Leu Thr Ala Pro Phe Lys Thr Phe Lys Asp Met Gly Lys
1010 1015 1020
Gln Thr Gly Ile Ile Phe Tyr Thr Gln Ala Ser Tyr Thr Ser Lys
1025 1030 1035
Ile Asp Pro Leu Thr Gly Trp Arg Pro Asn Ile Tyr Leu Arg Tyr
1040 1045 1050
Ser Asn Ala Lys Gln Ala Lys Ala Asp Ile Leu Met Phe Thr Asn
1055 1060 1065

Ile Tyr Phe Ser Glu Lys Lys Asp Arg Phe Glu Phe Thr Tyr Asp
1070 1075 1080
Leu Glu Lys Ile Asp Asp Lys Arg Lys Asp Leu Pro Ile Lys Thr
1085 1090 1095
Glu Trp Thr Val Cys Ser Asn Val Glu Arg Phe Ser Trp Glu Lys
1100 1105 1110
Ser Leu Asn Asn Asn Lys Gly Gly Tyr Val His Tyr Pro Ile Gln
1115 1120 1125

Asp Ser Asn Gly Glu Glu Ser Ile Thr Ser Lys Leu Lys Lys Leu
1130 1135 1140
Phe Met Asp Phe Gly Ile Asp Leu Thr Asp Ile Lys Thr Gln Ile
1145 1150 1155
Glu Ser Leu Asp Thr Asn Lys Lys Asp Asn Ala Asn Phe Phe Arg

1160 1165 1170

Lys Phe Ile Phe Tyr Phe Gln Leu Ile Cys Gln Ile Arg Asn Thr

1175 1180 1185

Gln Val Asn Lys Ser Asp Asp Gly Asn Asp Phe Ile Phe Ser Pro

1190 1195 1200

Val Glu Pro Phe Phe Asp Ser Arg Phe Ala Asp Lys Phe Arg Lys

1205 1210 1215

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

1220 1225 1230

Arg Lys Gly Leu Ile Ile Leu His Lys Ile Ser Asp Tyr Phe Val

1235 1240 1245

Lys Glu Gly Ser Thr Asp Lys Ile Ser Trp Lys Asp Leu Ser Ile

1250 1255 1260

Ser Gln Thr Glu Trp Asp Asn Phe Thr Thr Asp Lys

1265 1270 1275

<210> 21

<211> 1313

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 21

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

1 5 10 15

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

20 25 30

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

35 40 45

Lys Lys Tyr Glu Ala Thr Lys Pro Phe Phe Asp Arg Leu His Arg Lys

50 55 60

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

65 70 75 80

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

85 90 95

Asn Gln Lys Glu Leu Glu Lys Gln Glu Lys Leu Leu Arg Lys Gln Ile

100 105 110

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

115 120 125

Lys Ile Asn Phe Lys Lys Ser Gly Leu Asn Ile Leu Phe Glu Glu Ser

130 135 140

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

145 150 155 160

Leu Lys Asn Asp Asp Asn Glu Phe Ile Phe Asp Lys Asp Gly Asn Lys

165 170 175

Ile Ser Ile Phe Asp Ser Trp Lys Gly Phe Thr Gly Tyr Phe Lys Lys

180 185 190

Phe Phe Glu Thr Arg Lys Asn Phe Tyr Lys Asp Asp Gly Thr Ser Thr

195 200 205

Ala Ile Ala Thr Arg Ile Ile Asp Gln Asn Leu Arg Arg Phe Cys Asp

210 215 220

Asn Ile Phe Ile Tyr Asn Lys Ile Lys Asn Lys Leu Asp Phe Ser Ser

225 230 235 240

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

245 250 255

Tyr Tyr Met Asp Cys Ile Leu Gln Asp Asp Ile Asp Leu Tyr Asn Gly

260 265 270

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

275 280 285

Asn Glu Ile Ile Asn Lys Tyr Arg Gln Asp Asn Lys Gly Asp Lys Ile

290 295 300

Pro Phe Phe Lys Lys Leu Asp Lys Gln Ile Leu Ser Glu Lys Asp Arg

305 310 315 320

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

325 330 335

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

340 345 350

Leu Val Asn Gln Leu Cys Val Asn Asp Ser Asp Phe Glu Leu Asp Lys

355 360 365

Ile Tyr Ile Ser Lys Glu Ala Phe Asn Thr Ile Ser His Lys Trp Thr

370 375 380

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

385 390 395 400

Asp Lys Ile Thr Gly Leu Asp Tyr Lys Lys Ala Glu Asp Lys Tyr Lys

405 410 415

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

420 425 430

Leu Asp Lys Asp Ser Glu Phe Trp Lys Ser His Tyr Tyr Lys Thr Glu

435 440 445

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

450 455 460

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

465 470 475 480

Val Asn Val Glu Asn Lys Asp Gly Lys Met Lys Glu Lys Glu Ile Gly

485 490 495

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

500 505 510

Leu Thr Asp Lys Ser Lys Ile Ile Ile Lys Asp Phe Ala Asp Asn Val

515 520 525

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

530 535 540

Glu Trp Asn Tyr Thr Lys Leu Glu Leu Ala Asp Phe Tyr Ile Asn Pro

545 550 555 560

Asp Phe Gly Tyr Glu Ile Phe Tyr Gly Asn Ala Tyr Glu Glu Ile Ile

565 570 575

Gln Ile Tyr Asn Lys Leu Arg Asn Tyr Leu Thr Lys Lys Pro Phe Ser
580 585 590
Glu Glu Lys Trp Lys Leu Asn Phe Glu Asn Pro Thr Leu Ala Gly Gly

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

660 665 670
Cys Phe Ser Lys Lys Gly Leu Asp Phe Phe Glu Pro Ser Glu Lys Ile
675 680 685
Ile Asp Ile Tyr Lys Asp Gly Lys Phe Lys Gln Gly Asp Thr Phe Ser
690 695 700
Ile Asp Ser Met Gln Gln Leu Ile Asp Phe Tyr Lys Arg Ala Leu Arg
705 710 715 720
Glu Tyr Asn Gly Trp Lys Met Tyr Asp Phe Ser Lys Leu Lys Asp Thr

725 730 735
Asn Asp Tyr Thr Thr Asn Ile Gly Glu Phe Tyr Asn Asp Val Ala Cys
740 745 750
Ala Gly Tyr Lys Val Trp Phe Asp Asn Ile Ser Glu Glu Tyr Ile Gln
755 760 765
Glu Lys Asn Glu Asn Gly Glu Leu Tyr Leu Phe Glu Ile His Asn Lys
770 775 780
Asp Trp Asn Leu Lys Asp Glu Lys Lys Lys Thr Gly Thr Lys Asn Leu

785 790 795 800
His Thr Leu Tyr Phe Glu Ser Leu Phe Ser Asp Glu Asn Ala Leu Arg
805 810 815
Asp Phe Val Met Lys Leu Ser Gly Glu Ala Glu Leu Phe Phe Arg Pro

820 825 830

Lys Thr Asn Ala Asp Lys Leu Gly Tyr Arg Lys Asp Lys Lys Gly Asn

835 840 845

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

850 855 860

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

865 870 875 880

Arg Asn Ile Asn Asn Phe Leu Ala Asn Asn Ser Asp Ile Asn Val Ile

885 890 895

Gly Ile Asp Arg Gly Glu Lys His Leu Ala Tyr Tyr Ser Val Ile Ser

900 905 910

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

915 920 925

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

930 935 940

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

945 950 955 960

Gly Tyr Ile Ser Gln Val Val Arg Lys Leu Ala Asp Leu Ala Ile Glu

965 970 975

His Asn Ala Ile Ile Val Leu Glu Asp Leu Asn Met Arg Phe Lys Gln

980 985 990

Ile Arg Gly Gly Ile Glu Lys Ser Ile Tyr Gln Gln Leu Glu Lys Ala

995 1000 1005

Leu Ile Glu Lys Leu Asn Phe Leu Val Asn Lys Lys Glu Ile Asp

1010 1015 1020

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

1025 1030 1035

Pro Phe Glu Thr Phe Gln Lys Met Gly Lys Gln Thr Gly Ile Ile

1040 1045 1050

Phe Tyr Thr Gln Ala Ser Tyr Thr Ser Lys Ile Asp Pro Leu Thr

1055 1060 1065

Gly Trp Arg Pro Asn Leu Tyr Leu Lys Lys Gly Asn Ala Lys Ile

1070 1075 1080

Asn Lys Glu Gln Ile Glu Lys Phe Ser Lys Ile Glu Phe Thr Asn

1085 1090 1095

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

1100 1105 1110

Lys Lys Lys Tyr Pro Gln Lys Thr Lys Trp Thr Leu Cys Ser Ser

1115 1120 1125

Val Glu Arg Trp Arg Trp Asp Arg Lys Leu Asn Asn Asn Lys Gly

1130 1135 1140

Gly Tyr Ile His Tyr Glu Asp Leu Thr Thr Glu Phe Lys Ser Leu

1145 1150 1155

Phe Glu Lys Phe Glu Ile Asp Ile Glu Gly Asp Ile Leu Glu Gln

1160 1165 1170

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

1175 1180 1185

Ser Gly Phe Ile Tyr Leu Trp Gly Leu Leu Ser Gln Ile Arg Asn

1190 1195 1200

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

1205 1210 1215

Asp Lys Asn Glu Glu Ile Ser Glu Lys Glu Lys Phe Asp Val Asp

1220 1225 1230

Phe Ile Leu Ser Pro Val Glu Pro Phe Phe Asp Ser Arg Thr Pro

1235 1240 1245

Glu Lys Phe Gly Glu Asn Leu Pro Lys Asn Gly Asp Asp Asn Gly

1250 1255 1260

Ala Tyr Asn Ile Ala Arg Lys Gly Ile Ile Thr Leu Glu Arg Ile

1265 1270 1275

Lys Lys Phe Tyr Glu Leu Ser Asp Lys Glu Arg Glu Lys Leu Lys

1280 1285 1290

Tyr Pro Asp Leu Phe Ile Thr Asn Ala Glu Trp Asp Asp Phe Ala

1295 1300 1305

Thr Lys Arg Asp Ser

1310

<210> 22

<211> 1155

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 22

Met Asp Asn Asn Thr Thr Leu Glu Lys Thr Glu Leu Gly Leu Gly Ile

1 5 10 15

Thr Tyr Asn His Asp Lys Val Glu Asp Lys His Tyr Phe Gly Gly Phe

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Asn Asn Lys Ser Lys Ser Ile Arg Gln His Ile Ile Leu Leu Leu Asp

100 105 110

Thr Ile Asn Asn Leu Arg Asn Tyr Tyr Thr His Tyr Tyr His Lys Lys

115 120 125

Val Ile Ile Asp Asp Ala Leu Tyr Pro Leu Leu Asp Thr Ile Leu Leu

130 135 140

Lys Val Val Leu Glu Ile Lys Lys Lys Lys Leu Lys Glu Asp Lys Thr

145 150 155 160

Lys Gln Leu Leu Lys Lys Gly Leu Glu Lys Glu Met Ala Ile Leu Phe

165 170 175

Asn Leu Met Lys Lys Glu Gln Lys Glu Lys Lys Ile Lys Gly Trp Asn
180 185 190
Ile Asp Lys Asn Ile Lys Gly Ala Val Leu Asn Arg Ala Phe Ser His
195 200 205
Leu Leu Tyr Asn Asp Gly Ile Ser Asp Tyr Arg Lys Ser Lys Ser Asn

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

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

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

405 410 415
Asn Arg Thr Ile Lys Gln Gln Ile Asn Val Phe Gly Asn Leu Thr Glu

420 425 430

Ile His Lys Lys Lys Asn Asp Tyr Phe Glu Lys Glu Glu Asn Lys Glu

435 440 445

Lys Ile Leu Glu Trp Glu Leu Phe Pro Asn Pro Ser Tyr His Phe Gln

450 455 460

Lys Glu Asn Ile Pro Ile Phe Ile Asp Leu Glu Lys Ser Lys Glu Thr

465 470 475 480

Asn Glu Leu Ala Lys Glu Tyr Ala Lys Glu Lys Lys Lys Ile Phe Gly

485 490 495

Ser Ser Arg Lys Lys Gln Gln Asn Thr Ala Lys Lys Asn Arg Glu Ala

500 505 510

Ile Ile Asn Leu Val Phe Asp Lys Tyr Lys Thr Ser Asp Arg Lys Thr

515 520 525

Val Thr Phe Glu Gln Pro Thr Ala Leu Leu Ser Phe Asn Glu Leu Asn

530 535 540

Ala Phe Leu Tyr Ala Phe Leu Val Glu Asn Lys Thr Gly Lys Glu Leu

545 550 555 560

Glu Lys Ile Ile Ile Glu Lys Ile Ala Asn Gln Tyr Gln Ile Leu Lys

565 570 575

Asn Cys Ser Ser Thr Val Asp Lys Thr Asn Asp Ser Ile Pro Lys Ser

580 585 590

Ile Lys Lys Ile Ala His Pro Thr Thr Asp Ser Phe Tyr Ser Glu Gly

595 600 605

Lys Lys Ile Asp Ile Glu Lys Leu Glu Arg Asp Ile Lys Ile Glu Ile

610 615 620

Glu Lys Thr Asn Glu Lys Leu Glu Thr Ile Lys Glu Asn Glu Thr Ser

625 630 635 640

Ala Lys Asn Tyr Lys Arg Asn Glu Arg Asp Ile Gln Lys Arg Lys Leu

645 650 655

Tyr Arg Lys Tyr Val Phe Phe Thr Asn Glu Ile Gly Ile Glu Ala Thr

660 665 670

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

725 730 735
Asn Phe Thr Phe Glu Thr Phe Tyr Lys Lys Tyr Leu Asp Asn Arg Lys
740 745 750
Asp Thr Leu Glu Thr Tyr Leu Ser Ala Ile Glu Asn Leu Lys Thr Met
755 760 765
Thr Asp Val Pro Pro Lys Ile Leu Lys Lys Ser Trp Ala Glu Leu Phe
770 775 780
Arg Phe Phe Asp Lys Lys Ile Tyr Leu Leu Ser Thr Ile Glu Thr Lys

785 790 795 800
Ile Asn Glu Leu Ile Thr Lys Pro Ile Asn Leu Ser Arg Gly Val Phe
805 810 815
Asp Glu Lys Pro Thr Phe Ile Asn Gly Lys Ser Pro Asn Lys Glu Asn
820 825 830
Asp Gln His Leu Phe Ala Asn Trp Phe Ile His Ala Lys Glu Gln Thr
835 840 845
Ile Phe Gln Asp Phe Tyr Asn Leu Ala Leu Glu Thr Pro Lys Glu Ile

850 855 860
Asn Asn Leu Lys Lys Gln Asn Tyr Lys Leu Glu Arg Ser Ile Asn Asn
865 870 875 880
Leu Lys Ile Glu Asp Ile Tyr Ile Lys Gln Met Val Asp Phe Leu Tyr
885 890 895
Gln Lys Leu Phe Glu Gln Ser Phe Lys Gly Ser Leu Gln Asp Leu Tyr
900 905 910
Thr Ser Lys Glu Lys Arg Glu Val Glu Lys Ser Lys Ala Lys Asn Glu

915 920 925

Gln Thr Pro Asp Glu Ser Phe Ile Trp Lys Lys Gln Val Glu Ile Asn

930 935 940

Ala Leu Asn Gly Arg Ile Ile Ala Lys Thr Lys Ile Lys Asp Ile Gly

945 950 955 960

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

965 970 975

Tyr Asp Asn Arg Ile Trp Asn Phe Ser Leu Asp Asn Asp Gly Asp Thr

980 985 990

Thr Lys Lys Leu Tyr Ser Leu Asn Thr Glu Leu Glu Ser Tyr Glu Arg

995 1000 1005

Ile Arg Arg Glu Lys Leu Leu Lys Gln Ile Gln Glu Phe Glu Gln

1010 1015 1020

Phe Leu Leu Lys Gln Glu Thr Glu Tyr Ser Ala Glu Arg Lys His

1025 1030 1035

Pro Glu Lys Phe Glu Lys Asp Gly Asn Pro Asn Phe Lys Lys Tyr

1040 1045 1050

Ile Ile Glu Gly Met Leu Asn Lys Ile Thr Pro Val Asn Glu Ile

1055 1060 1065

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

1070 1075 1080

Asp Phe Asn Glu Ile Val Lys Leu Asn Asn Glu Ser Ile Lys Lys

1085 1090 1095

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

1100 1105 1110

Leu Ile Asp Lys Asn Leu Phe Thr Phe Ser Leu Gln Leu Tyr Ser

1115 1120 1125

Lys Asn Glu Asn Glu Asn Phe Ser Glu Tyr Leu Asp Lys Val Cys

1130 1135 1140

Gln Lys Ile Ile Gln Glu Phe Ile Glu Lys Leu Lys

1145 1150 1155

<210> 23

<211> 1134

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 23

Met Asn Glu Thr Asp Tyr Leu Ala Lys Arg Leu Glu Tyr Asn Tyr Ala
1 5 10 15

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

Asn Asn Ile Asn Asp Leu Ser Lys Ala Phe Lys Glu Lys Phe Gly Met
35 40 45

Lys Pro Lys Ser Cys Ile Leu Asp Phe Phe Thr Gln Asp Lys Ala Ile
50 55 60

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

Ile Arg Tyr Leu Tyr Leu Pro Thr Ser His Lys Arg Phe Glu Asn Val
85 90 95

Pro Lys Asn Gln Leu Ile Ser Glu Gln Arg Asn Tyr Phe Lys Asn Ser
100 105 110

Leu Lys Val Leu Lys Asn Leu Ile Arg Asp Tyr Arg Asn Phe Tyr Thr
115 120 125

His His Phe His Lys Pro Ile Pro Val Phe Pro Glu Thr Tyr Lys Leu
130 135 140

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

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

Glu Leu Ala Gln Leu Glu Lys Leu Lys Leu Glu Asp Leu Lys Lys Leu
180 185 190

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

195 200 205

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

210 215 220

Thr Ile Ser Lys Tyr Tyr Ser Ala Val Pro Thr Glu Asp Ile Asp Thr

225 230 235 240

Glu Asn Gly Val Thr Ile Ser Glu Ser Gly Ile Ile Phe Leu Leu Gly

245 250 255

Leu Phe Leu Thr Lys Lys Gln Ser Glu Asp Leu Arg Ser Arg Val Lys

260 265 270

Gly Phe Lys Ala Lys Leu Ile Val Asn Pro Glu Asn Pro Ile Asn Lys

275 280 285

Lys Asn Asn Ser Leu Lys Tyr Met Ala Thr His Trp Val Phe Gly Tyr

290 295 300

Leu Gly Phe Lys Gly Leu Lys Asn Arg Phe Thr Thr Thr Phe Thr Lys

305 310 315 320

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

325 330 335

Glu Leu Tyr Gln Val Leu Pro Glu Glu Leu Lys Asn Glu Phe Leu Glu

340 345 350

Asp Met Asn Glu Tyr Leu Lys Glu Glu Asn Ser Glu Ser Leu Asp Lys

355 360 365

Ala Thr Val Ile His Pro Val Ile Arg Lys Arg Tyr Glu Asn Lys Phe

370 375 380

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

385 390 395 400

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

405 410 415

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

420 425 430

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

435 440 445

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

Glu Tyr Lys Val Arg Thr Asp Asn Lys Ile Lys Pro Asp Ala Ile Leu
515 520 525
Gln Asp Leu Gly Lys Pro Glu Lys Leu Ala Pro Val Ala Met Leu Ser
530 535 540
Leu Asn Glu Leu Pro Ala Leu Leu His Leu Val Leu Thr Lys Lys Thr
545 550 555 560
Pro Glu Glu Ile Glu Ile Ile Ile Ala Gln Lys Ile Ala Glu Arg Tyr
565 570 575

Asn Val Leu Thr Asn Tyr Lys Ala Gly Asp Asp Ile Ser Lys Gly Gln
580 585 590
Ile Thr Lys Asn Leu Leu Lys Ala Lys Gln Lys Lys Glu Val Asn Leu
595 600 605
Asp Lys Leu Gln Leu Ala Ile Glu Lys Glu Ile Ala Val Thr Asn Asp
610 615 620
Lys Leu Gln Thr Ile Ala Leu His Ile Lys Glu Arg Asn Asp Pro Lys
625 630 635 640

Gln Lys Arg Lys Tyr Val Phe Thr Asn Lys Glu Ile Gly Leu Gln Val
645 650 655
Thr Trp Leu Ala Asn Asp Leu Lys Arg Phe Met Pro Lys Gly Ser Arg
660 665 670
Gln Asn Trp Arg Gly Gln His His Ser Gln Leu Gln Lys Ser Leu Ala
675 680 685
Phe Tyr Asp Ile Gln Pro Lys Glu Pro Leu Ser Leu Leu Glu Glu Val

690 695 700

Trp Asp Phe Lys Asn Glu Ala Tyr Leu Trp Asn Asn Gly Ile Arg Arg
705 710 715 720
Ser Phe Asp Lys Arg Asp Phe Ile Ser Phe Tyr Thr Ser Tyr Leu Asn
725 730 735
Asn Arg Lys Glu Thr Phe Gln Arg Phe Lys Asp Gln Leu Asn Gly Ile
740 745 750
Arg Ser Asn Lys Lys Ile Leu Asp Lys Phe Ile Lys Gln Gln His Leu
755 760 765

Trp Asn Leu Phe His Lys Arg Leu Tyr Val Ile Asp Thr Ile Glu Glu
770 775 780
Gln Val Glu Lys Leu Leu Val Lys Pro Met Gln Phe Pro Lys Gly Val
785 790 795 800
Phe Asp His Lys Pro Thr Tyr Ile Lys Gly Lys Ser Ile Gln Glu Asn
805 810 815
Pro Glu Cys Phe Ala Asp Trp Tyr Val Ala Trp Asn Gln His Thr Asp
820 825 830

Tyr Gln Lys Phe Tyr Ser Trp Asp Arg Asp Tyr Lys Ser Ala Tyr Leu
835 840 845
Ser Gly Glu Gln Glu Lys Thr Glu Lys Arg Phe Ile Arg Val Gln Gly
850 855 860
Ser Lys Ile Asn Lys Val Lys Gln Gln Asp Val Leu Leu Ala Lys Met
865 870 875 880
Ala Ser Ile Ile Phe Asn Glu Leu Tyr Leu Pro Glu Asp Ala Glu His
885 890 895

Leu Asp Leu Asn Leu Ser Asp Ile Tyr Lys Thr Gln Thr Glu Arg Lys
900 905 910
Ala Glu Ile Glu Ala Ala Leu Ile Gln Ser His Lys Thr Thr Gly Asp
915 920 925
Asn Ser Ala Asn Ile Ile Lys Ser Thr Ser Ala Trp Thr Leu Thr Val
930 935 940

Pro Tyr Cys Ser Lys Asn Ile Tyr Glu Pro Gln Val Lys Leu Lys Glu
945 950 955 960

Leu Gly Lys Phe Lys Lys Phe Ile Ala Ser Gln Lys Val Gln Thr Leu
965 970 975
Phe Glu Tyr Lys Pro Gln Lys Ile Trp Asn Lys Thr Glu Leu Glu Glu
980 985 990
Val Leu Glu Leu Lys Ala Asn Ser Tyr Glu Val Ile Arg Arg Asp Tyr
995 1000 1005
Leu Leu Lys Ser Ile Gln Glu Phe Glu Lys Tyr Met Ile Lys Lys
1010 1015 1020

Leu Pro Thr Leu Ile Asp Thr Asn Glu His Pro Asn Phe Asn Lys
1025 1030 1035
Tyr Leu Thr Thr Phe Leu Lys Ser Leu Glu Leu Val Ser Glu Glu
1040 1045 1050
Asp Ala Lys Trp Leu Ile Ser Lys Lys Asp Phe Asp Thr Thr Pro
1055 1060 1065
Ile Asp Glu Leu Lys Lys Gln Ser Lys Ile Met Glu Lys Ala Phe
1070 1075 1080

Leu Leu Val Met Ile Arg Asn Lys Phe Ser His Asn Gln Leu Pro
1085 1090 1095
Arg Lys Ile Tyr Tyr Asp Glu Ile Tyr Lys Asn Val Pro Asn Ala
1100 1105 1110
Val Ser Ile Asn Phe Asn Glu Leu Phe Leu Glu Tyr Thr Asn Gln
1115 1120 1125
Thr Ile Leu Glu Phe Lys
1130

<210> 24
<211> 1145
<212> PRT
<213> Unknown
<220><223> Description of Unknown:

Cas13 sequence

<400> 24

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

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

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

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

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

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

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

Asn Leu Lys Lys His Phe Phe Ser Gln Leu Ser Asp Asp Glu Asn Thr
450 455 460
Asp Trp Glu Phe Phe Pro Asn Pro Ser Tyr Asn Phe Leu Thr Gln Ala
465 470 475 480
Asp Asn Ser Pro Ala Asn Asn Ile Pro Ile Tyr Leu Glu Leu Lys Asn

485 490 495

Gln Gln Ile Ile Lys Glu Lys Asp Ala Ile Lys Ala Glu Val Asn Gln

500 505 510

Thr Gln Asn Arg Asn Pro Asn Lys Pro Ser Lys Arg Asp Leu Leu Asn

515 520 525

Lys Ile Leu Lys Thr Tyr Glu Asp Phe His Gln Gly Asp Pro Thr Ala

530 535 540

Ile Leu Ser Leu Asn Glu Ile Pro Ala Leu Leu His Leu Phe Leu Val

545 550 555 560

Lys Pro Asn Asn Lys Thr Gly Gln Gln Ile Glu Asn Ile Ile Arg Ile

565 570 575

Lys Ile Glu Lys Gln Phe Lys Ala Ile Asn His Pro Ser Lys Asn Asn

580 585 590

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

595 600 605

Ala Ile Lys Leu Lys Lys Asp Leu Glu Ala Glu Leu Asp Met Leu Asn

610 615 620

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

625 630 635 640

Asp Lys Leu Leu Lys Glu His Gln Phe Thr Pro Lys Asn Lys Arg Pro

645 650 655

Glu Leu Arg Lys Tyr Val Phe Tyr Lys Ser Glu Lys Gly Glu Glu Ala

660 665 670

Thr Trp Leu Ala Asn Asp Ile Lys Arg Phe Met Pro Lys Asp Phe Lys

675 680 685

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

690 695 700

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

705 710 715 720

Cys Glu Phe Asp His Ser Leu Leu Asp Ile Asn Ala Tyr Phe Gln Lys

725 730 735

Asp Asn Phe Glu Asp Phe Phe Ser Lys Tyr Leu Glu Asn Arg Ile Glu
740 745 750

Thr Leu Glu Gly Val Leu Lys Lys Leu His Asp Phe Lys Asn Glu Pro
755 760 765

Thr Pro Leu Lys Gly Val Phe Lys Asn Cys Phe Lys Phe Leu Lys Arg
770 775 780

Gln Asn Tyr Val Thr Glu Ser Pro Glu Ile Ile Lys Lys Arg Ile Leu
785 790 795 800

Ala Lys Pro Thr Phe Leu Pro Arg Gly Val Phe Asp Glu Arg Pro Thr
805 810 815

Met Lys Lys Gly Lys Asn Pro Leu Lys Asp Lys Asn Glu Phe Ala Glu
820 825 830

Trp Phe Val Glu Tyr Leu Glu Asn Lys Asp Tyr Gln Lys Phe Tyr Asn
835 840 845

Ala Glu Glu Tyr Arg Met Arg Asp Ala Asp Phe Lys Lys Asn Ala Val
850 855 860

Ile Lys Lys Gln Lys Leu Lys Asp Phe Tyr Thr Leu Gln Met Val Asn
865 870 875 880

Tyr Leu Leu Lys Glu Val Phe Gly Lys Asp Glu Met Asn Leu Gln Leu
885 890 895

Ser Glu Leu Phe Gln Thr Arg Gln Glu Arg Leu Lys Leu Gln Gly Ile
900 905 910

Ala Lys Lys Gln Met Asn Lys Glu Thr Gly Asp Ser Ser Glu Asn Thr
915 920 925

Arg Asn Gln Thr Tyr Ile Trp Asn Lys Asp Val Pro Val Ser Phe Phe
930 935 940

Asn Gly Lys Val Thr Ile Asp Lys Val Lys Leu Lys Asn Ile Gly Lys
945 950 955 960

Tyr Lys Arg Tyr Glu Arg Asp Glu Arg Val Lys Thr Phe Ile Gly Tyr
965 970 975

Glu Val Asp Glu Lys Trp Met Met Tyr Leu Pro His Asn Trp Lys Asp

980 985 990

Arg Tyr Ser Val Lys Pro Ile Asn Val Ile Asp Leu Gln Ile Gln Glu

995 1000 1005

Tyr Glu Glu Ile Arg Ser His Glu Leu Leu Lys Glu Ile Gln Asn

1010 1015 1020

Leu Glu Gln Tyr Ile Tyr Asp His Thr Thr Asp Lys Asn Ile Leu

1025 1030 1035

Leu Gln Asp Gly Asn Pro Asn Phe Lys Met Tyr Val Leu Asn Gly

1040 1045 1050

Leu Leu Ile Gly Ile Lys Gln Val Asn Ile Pro Asp Phe Ile Val

1055 1060 1065

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

1070 1075 1080

Ala Ser Cys Ser Glu Leu Glu Lys Lys Thr Ile Ile Leu Ile Ala

1085 1090 1095

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

1100 1105 1110

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

1115 1120 1125

Tyr Ala Asn Tyr Tyr Leu Lys Val Leu Lys Lys Met Ile Ser Asp

1130 1135 1140

Leu Ala

1145

<210> 25

<211> 1147

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 25

Met Glu Asp Lys Thr Thr Gly Ala Gly Ile Ser Tyr Asp His Thr Leu

1 5 10 15

Met Glu Asp Lys His Phe Phe Gly Gly Phe Leu Asn Leu Ala Gln Asn
20 25 30
Asn Ile Asp Ala Leu Leu Lys Ala Phe Lys Glu Arg Phe Asn Val Arg
35 40 45

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

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

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

Leu Leu Phe Leu Leu Ser Met Phe Leu Asn Lys Lys Asp Ile Glu Ala
245 250 255
Leu Lys Ser Arg Val Lys Gly Phe Lys Ala Lys Ile Ile Arg Asp Gly

260 265 270

Glu Glu Asn Ile Ser Gly Leu Lys Phe Met Ala Thr His Trp Val Phe

275 280 285

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

290 295 300

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

305 310 315 320

Pro Asp Glu Val Tyr Lys Thr Phe Asp Lys Gln Thr Gln Glu Glu Phe

325 330 335

Ile Glu Asp Ile Asn Glu Tyr Met Lys Val Gly Asn Lys Asp Leu Ser

340 345 350

Leu Glu Glu Ser Thr Val Ile His Pro Val Ile Arg Lys Arg Tyr Asp

355 360 365

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

370 375 380

Phe Pro Thr Leu Arg Phe Gln Val His Ile Gly Asn Tyr Ile His Asp

385 390 395 400

Arg Arg Ile Lys Asn Ile Asp Gly Thr Ala Phe Gln Thr Glu Arg Ser

405 410 415

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

420 425 430

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

435 440 445

Gly Trp Glu Ile Phe Pro Asn Pro Ser Tyr Asn Ile Ile Glu Asn Asn

450 455 460

Ile Pro Ile Tyr Ile Glu Met Gly Asp His Phe Asn Asp Glu Val Leu

465 470 475 480

Gln Ser Lys Met Ala Arg Lys Lys Gln Lys Pro Glu Glu Leu Lys Asp

485 490 495

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

500 505 510

Asn Asp Lys Gly Leu Met Asp Val Ile Thr Val Ser Pro Thr Ala Gln
515 520 525

Leu Ser Leu Asn Glu Leu Pro Ala Ile Leu Tyr Glu Leu Leu Val Lys
530 535 540

Lys Thr Pro Ala Lys Thr Ile Glu Lys Lys Leu Val Gly Lys Leu Asn
545 550 555 560

Gln Arg Leu Lys Glu Ile Lys Asn Tyr Asn Pro Glu Lys Pro Leu Pro
565 570 575

Ala Ser Gln Ile Ser Lys Arg Leu Arg Leu Asn Arg Glu Glu Gly Ser
580 585 590

Ile Asn Thr Lys Lys Ile Ile Ala Leu Leu Gln Lys Glu Leu Asn Tyr
595 600 605

Thr Gln Glu Lys Leu Asp Leu Leu Glu Lys Asn Arg Lys Glu Tyr Gly
610 615 620

Lys Lys Val Asp Gly Lys Ile Leu Arg Lys Tyr Val Phe Gly Leu Lys
625 630 635 640

Glu Ile Gly Asn Leu Ala Thr Asp Met Ala Met Asp Ile Lys Arg Phe
645 650 655

Met Pro Ala Asn Val Arg Lys Glu Trp Lys Gly Tyr Gln His Ser Gln
660 665 670

Leu Gln Gln Ser Leu Ala Phe Tyr Asp Lys Arg Pro Glu Glu Ala Phe
675 680 685

Asn Ile Leu Gln Glu Val Trp Asp Ile Asn Arg Glu Lys Ser Leu Trp
690 695 700

Asp Thr Trp Ile Leu Asn Ala Phe Gln Thr Ser Gly Asn Phe Glu Arg
705 710 715 720

Phe Phe Glu Leu Tyr His Glu Gly Arg Lys Lys Tyr Ile Gln Gln Gln
725 730 735

Leu Glu Asn Ile Asp Arg Tyr Thr Asp Asn Lys Lys Phe Leu Gln Lys
740 745 750

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

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        755                 760                 765
Thr Leu Glu Ser Leu Glu Ile Glu Lys Leu Lys Ile Leu Ser Lys Pro
    770                 775                 780
Phe Ile Leu Pro Arg Gly Thr Phe Asp Glu Lys Pro Thr Phe Ile Met
785                 790                 795                 800
Gly Glu Lys Val Thr Glu Asn Pro Glu Leu Phe Ala Asp Trp Tyr Thr
                805                 810                 815

Tyr Gly Tyr Gln Gln His Glu Phe Gln Lys Phe Tyr Ser Trp Pro Arg
            820                 825                 830
Asp Tyr Lys Asp Leu Leu Gln Asn Glu Gln Lys Arg Asp Pro Asp Phe
        835                 840                 845
Ala Glu Asn Lys Lys Gly Leu Ser Asp Leu Lys Gln Leu Glu Leu Leu
    850                 855                 860
Gln Leu Lys Gln Asp Ile Ile Ile Lys Lys Ile Lys Thr Gln Asp Leu
865                 870                 875                 880

Tyr Leu Lys Leu Ile Met Asp Ala Leu Phe Ile Glu Val Phe Gly Gln
                885                 890                 895
Glu Ala Asp Ile Ser Leu Asn Asp Leu Tyr Leu Thr Gln Glu Glu Arg
            900                 905                 910
Leu Glu Lys Glu Lys Leu Ala Leu Lys Gln His Gln Arg Val Glu Gly
        915                 920                 925
Asp Asp Ser Pro Asn Val Ile Lys Asp Asn Phe Ile Trp Ser Lys Thr
    930                 935                 940

Met Pro Tyr Lys His Asp Lys Ile Tyr Glu Pro Gln Val Arg Leu Lys
945                 950                 955                 960
Asp Phe Gly Lys Phe Lys His Phe Leu Leu Asp Asp Lys Val Ala Lys
                965                 970                 975
Ile Leu Ser Tyr Asp Leu Gln Glu Thr Trp Asn Lys Asn Glu Leu Glu
            980                 985                 990
Ile Gln Ile Asn Thr Gly Gln Asp  Ser Tyr Glu Val Ile  Arg Arg Glu
        995                 1000                1005
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Glu Leu Leu Lys Glu Ile Gln Leu Leu Glu Lys Gln Ile Leu Glu
1010 1015 1020
Thr Phe Ser His Thr Leu Asp Glu His Pro Lys Glu Phe Glu Asp
1025 1030 1035
Glu Lys Gly Asn Pro Asn Phe Lys Met Tyr Met Ala Asn Gly Val
1040 1045 1050
Ile Arg Lys Gly Ser Ser Thr Thr Ala Lys Asp Glu Ala Asp Trp
1055 1060 1065

Leu Glu His Glu Lys Asp Phe Asp Asn Leu Ser Leu Glu Ile Phe
1070 1075 1080
Asn Ser Lys Ser Glu Ile Thr Gln Leu Thr Phe Leu Ile Val Leu
1085 1090 1095
Ile Arg Asn Lys Phe Gly His Asn Gln Leu Pro Ile Lys Gln Phe
1100 1105 1110
Tyr Glu Ile Ile Gln Asn Glu Tyr Ser Ile Thr Gly Glu Thr Ile
1115 1120 1125

Ser Arg Leu Tyr Leu Asn Phe Ile Ile Tyr Ala Lys Ala Arg Leu
1130 1135 1140
Lys Asp Leu Met
1145
<210> 26
<211> 1133
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 26
Met Glu Glu Lys Leu Gly Lys Gly Val Glu Tyr Asn Pro Phe Lys Lys
1 5 10 15
Glu Asp Lys Tyr Tyr Phe Gly Gly Tyr Phe Asn Leu Ala Glu Asn Asn
20 25 30

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

35 40 45

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

50 55 60

Ser Leu Val Asp Tyr Glu Lys Trp Val Asn Ala Phe Ala Asp Tyr Phe

65 70 75 80

Pro Ile Val Asn Tyr Leu Asp Arg Glu Thr Ile Lys Lys Gly Glu Lys

85 90 95

Val Val Glu Val Pro Arg Glu Lys Arg Ile Glu Cys Phe Arg Asp Met

100 105 110

Phe Lys Gly Leu Ile Asn Thr Ile Ser Gln Leu Arg His Tyr Tyr Thr

115 120 125

His Tyr His His Glu Pro Ile Glu Ile Asp Asp Lys Ile Leu Ser Phe

130 135 140

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

145 150 155 160

Leu Lys Thr Asp Lys Thr Lys Glu Leu Ile Lys Asp Ser Leu Gln Glu

165 170 175

Glu Leu Asp Ile Leu Cys Lys Leu Lys Val Lys Tyr Leu Glu Ser Lys

180 185 190

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

195 200 205

Tyr Asn Asp Val Phe Arg Arg Phe Ile Tyr Lys Asp Glu Lys Gly Asn

210 215 220

Glu Ser Leu Lys Asp Ile Ile Arg Thr Lys Gln Ile Lys Val His Gln

225 230 235 240

Asn Ser Ser Tyr Leu Glu Leu Pro Ile Ser Ser Ser Gly Ile Ile Phe

245 250 255

Leu Leu Ser Leu Phe Leu Asn Lys Lys Glu Val Glu Ser Leu Lys Ser

260 265 270

Asn Ile Arg Gly Tyr Lys Gly Lys Ser Lys Ser Glu Glu Thr Thr Pro

275 280 285

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

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

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

Asn Asn Asp Lys Asp Ala Gly Lys Ile Gly Ile Gln Val Lys Leu Leu
485 490 495
Asn Lys Asp Ile Glu Ala Val Leu Asn Glu Ser Lys Asn Thr Leu Asn
500 505 510
Asn Lys Thr Arg Lys Ser Asp Lys Ile Ser Lys Lys Glu Ile Ile Asn
515 520 525
Lys Ile Val Gln Ile Asn Asp Asp Thr Lys Tyr Asn Asn Lys Asn Ile

530 535 540

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

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

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

Asp Phe Tyr Asn Arg Tyr Leu Ser Leu Arg Ile Ser Tyr Leu Glu Asn
740 745 750
Val Ile Asp Arg Val Glu Cys Phe Ser Asn Glu Pro Lys Ala Phe Lys
755 760 765
Ser Val Leu Lys Glu Cys Phe Val Phe Leu Lys Lys Gln Asn Tyr Thr
770 775 780

Asn His Ser Leu Asp Glu Gln Val Lys Lys Ile Leu Ala Asn Pro Ile
785 790 795 800

Phe Ile Glu Arg Gly Phe Leu Asp Thr Lys Pro Thr Met Ile Gln Gly
805 810 815
Val Lys Phe Ser Glu Asn Lys Gly Cys Phe Ala Asp Trp Phe Val His
820 825 830
Tyr Lys Glu Tyr Glu His Tyr Gln Lys Phe Tyr Asp Thr Asn Leu Tyr
835 840 845
Pro Val Glu Ser Ile Glu Asp Lys Glu Arg Gln Lys Leu Glu Ala Thr
850 855 860

Ile Lys Lys Gln Gln Lys Asn Asp Val Phe Thr Leu Leu Met Ile Lys
865 870 875 880
Lys Ile Phe Asn Asp Leu Phe Asn Gln Asp Phe Glu Ala Asn Leu Tyr
885 890 895
Glu Met Tyr Gln Ser Lys Glu Glu Arg Glu Lys Asn Gln Leu Val Ala
900 905 910
Lys Glu Thr Gln Asn Arg Asn Leu Asn Phe Ile Trp Asn Lys Pro Ile
915 920 925

Ala Ile Asp Leu Phe Asp Gly Lys Val Lys Ile Asp Glu Val Lys Leu
930 935 940
Lys Asp Val Gly Ser Phe Arg Lys Tyr Glu Asn Asp Lys Arg Val Gln
945 950 955 960
Thr Phe Ile Thr Tyr Ile Pro Glu Ile Gln Trp Ile Pro Tyr Leu Pro
965 970 975
Asn Thr Trp Glu Gly Ile Asn Leu Pro Val Asn Val Ile Glu Arg Gln
980 985 990

Ile Asp Arg Tyr Glu Lys Val Arg Ser Glu Glu Leu Leu Lys Glu Val
995 1000 1005
Gln Ala Ile Glu Lys Tyr Ile Tyr Glu Gln Val Asn Asp Lys Thr
1010 1015 1020
Glu Leu Leu Gln Asn Gly Asn Gln Asn Phe Lys Asn Tyr Leu Val

1025 1030 1035

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

1040 1045 1050

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

1055 1060 1065

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

1070 1075 1080

Ile Asn Ile Arg Asn Gln Phe Ser His Asn Gln Phe Pro Lys Ser

1085 1090 1095

Ala Phe Tyr Gln Phe Cys Gln Lys Ile Leu Ser Ile Glu Glu Asp

1100 1105 1110

Glu Leu Phe Ala Asp Tyr Tyr Leu Arg Leu Phe Lys Leu Leu Arg

1115 1120 1125

Asn Glu Leu Leu Asp

1130

<210> 27

<211> 1156

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 27

Met Asn Thr Arg Val Thr Gly Met Gly Val Ser Tyr Asp His Thr Lys

1 5 10 15

Lys Glu Asp Lys His Phe Phe Gly Gly Phe Leu Asn Leu Ala Gln Asp

20 25 30

Asn Ile Thr Ala Val Ile Lys Ala Phe Cys Ile Lys Phe Asp Lys Asn

35 40 45

Pro Met Ser Ser Val Gln Phe Ala Glu Ser Cys Phe Thr Asp Lys Asp

50 55 60

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

65 70 75 80

Pro Val Ile Gly Tyr Leu Asn Tyr Gly Gly Asp Arg Asn Thr Phe Arg
85 90 95

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

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

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

Tyr Leu Ser Phe Lys Gly Met Lys Gln Arg Leu Ser Thr Asp Phe His
290 295 300
Glu Glu Thr Leu Leu Ile Gln Ile Ile Asp Glu Leu Ser Lys Val Pro
305 310 315 320
Asp Glu Val Tyr His Asp Phe Asp Thr Ala Thr Arg Glu Lys Phe Val

325 330 335

Glu Asp Ile Asn Glu Tyr Ile Arg Glu Gly Asn Glu Asp Phe Ser Leu

340 345 350

Gly Asp Ser Thr Ile Ile His Pro Val Ile Arg Lys Arg Tyr Glu Asn

355 360 365

Lys Phe Asn Tyr Phe Ala Val Arg Phe Leu Asp Glu Phe Ile Lys Phe

370 375 380

Pro Ser Leu Arg Phe Gln Val His Leu Gly Asn Phe Val His Asp Arg

385 390 395 400

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

405 410 415

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

420 425 430

Lys Thr Glu Tyr Ile Glu Lys Glu Leu Asp Leu Asp Ser Asp Thr Gly

435 440 445

Trp Glu Ile Phe Pro Asn Pro Ser Tyr Val Phe Ile Asp Asn Asn Ile

450 455 460

Pro Ile Tyr Ile Ser Thr Asn Lys Thr Phe Lys Asn Gly Ser Ser Glu

465 470 475 480

Phe Ile Lys Leu Arg Arg Lys Glu Lys Pro Glu Glu Met Lys Met Arg

485 490 495

Gly Glu Asp Lys Lys Glu Lys Arg Asp Ile Ala Ser Met Ile Gly Asn

500 505 510

Ala Gly Ser Leu Asn Ser Lys Thr Pro Leu Ala Met Leu Ser Leu Asn

515 520 525

Glu Met Pro Ala Leu Leu Tyr Glu Ile Leu Val Lys Lys Thr Thr Pro

530 535 540

Glu Glu Ile Glu Leu Ile Ile Lys Glu Lys Leu Asp Ser His Phe Glu

545 550 555 560

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

565 570 575

Ser Lys Arg Leu Arg Asn Asn Thr Thr Asp Lys Gly Lys Lys Val Ile
580 585 590
Asn Pro Glu Lys Leu Ile His Leu Ile Asn Lys Glu Ile Asp Ala Thr
595 600 605

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

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

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

Ile Lys Val Asp Glu Gln Pro Glu Leu Phe Ala Glu Trp Tyr Gln Tyr
805 810 815
Gly Tyr Ser Thr Glu His Val Phe Gln Asn Phe Tyr Gly Trp Glu Arg

820 825 830

Asp Tyr Asn Asp Leu Leu Glu Ser Glu Leu Glu Lys Asp Asn Asp Phe

835 840 845

Ser Lys Asn Ser Ile His Tyr Ser Arg Thr Ser Gln Leu Glu Leu Ile

850 855 860

Lys Leu Lys Gln Asp Leu Lys Ile Lys Lys Ile Lys Ile Gln Asp Leu

865 870 875 880

Phe Leu Lys Leu Ile Ala Gly His Ile Phe Glu Asn Ile Phe Lys Tyr

885 890 895

Pro Ala Ser Phe Ser Leu Asp Glu Leu Tyr Leu Thr Gln Glu Glu Arg

900 905 910

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

915 920 925

Asp His Ser Asp Asn Ile Ile Lys Asp Asn Phe Ile Gly Ser Lys Thr

930 935 940

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

945 950 955 960

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

965 970 975

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

980 985 990

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

995 1000 1005

Lys Leu Phe Lys Lys Ile Gln Asn Phe Glu Leu Gln Thr Leu Thr

1010 1015 1020

Asp Trp Pro Trp Asn Gly Thr Asp His Pro Glu Glu Phe Gly Thr

1025 1030 1035

Thr Asp Asn Lys Gly Val Asn His Pro Asn Phe Lys Met Tyr Val

1040 1045 1050

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

1055 1060 1065

Glu Asp Asn Trp Leu Glu Asn Leu Asn Glu Thr His Phe Lys Asn
1070 1075 1080
Leu Ser Phe Gln Glu Leu Glu Thr Lys Ser Lys Ser Ile Gln Thr
1085 1090 1095
Ala Phe Leu Ile Ile Met Ile Arg Asn Gln Phe Ala His Asn Gln
1100 1105 1110

Leu Pro Ala Val Gln Phe Phe Glu Phe Ile Gln Lys Lys Tyr Pro
1115 1120 1125
Glu Ile Gln Gly Ser Thr Thr Ser Glu Leu Tyr Leu Asn Phe Ile
1130 1135 1140
Asn Leu Ala Val Val Glu Leu Leu Glu Leu Leu Glu Lys
1145 1150 1155

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<211> 1036
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
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Met Glu Thr Gln Ile Leu Gly Asn Gly Ile Ser Tyr Asp His Thr Lys
1 5 10 15
Thr Glu Asp Lys His Phe Phe Gly Gly Phe Leu Asn Thr Ala Gln Asn
20 25 30
Asn Ile Asp Leu Leu Ile Lys Ala Tyr Ile Ser Lys Phe Glu Ser Ser
35 40 45
Pro Arg Lys Leu Asn Ser Val Gln Phe Pro Asp Val Cys Phe Lys Lys
50 55 60
Asn Asp Ser Asp Ala Asp Phe Gln His Lys Leu Gln Phe Ile Arg Lys
65 70 75 80
His Leu Pro Val Ile Gln Tyr Leu Lys Tyr Gly Gly Asn Arg Glu Val
85 90 95
Leu Lys Glu Lys Phe Arg Leu Leu Leu Gln Ala Val Asp Ser Leu Arg

100 105 110

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

115 120 125

Leu Leu Thr Leu Leu Asp Thr Ile Phe Gly Glu Ile Gly Asn Glu Val

130 135 140

Arg Gln Asn Lys Met Lys Asp Asp Lys Thr Arg His Leu Leu Lys Lys

145 150 155 160

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

165 170 175

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

180 185 190

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

195 200 205

Phe Lys Asp Ala Glu Asp Phe Lys Pro Thr Val Ser Tyr Ser Ser Tyr

210 215 220

Tyr Tyr Asp Ser Asp Thr Ala Glu Asn Gly Ile Ser Ile Ser Gln Ser

225 230 235 240

Gly Leu Leu Phe Leu Leu Ser Met Phe Leu Gly Arg Arg Glu Met Glu

245 250 255

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

260 265 270

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

275 280 285

Phe Ser Glu Phe Cys Phe Lys Gly Ile Lys Thr Arg Leu Asn Ala Asp

290 295 300

Tyr His Glu Glu Thr Leu Leu Ile Gln Leu Ile Asp Glu Leu Ser Lys

305 310 315 320

Val Pro Asp Glu Leu Tyr Arg Ser Phe Asp Val Ala Thr Arg Glu Arg

325 330 335

Phe Ile Glu Asp Ile Asn Glu Tyr Ile Arg Asp Gly Lys Glu Asp Lys

340 345 350

Ser Leu Ile Glu Ser Lys Ile Val His Pro Val Ile Arg Lys Arg Tyr

355 360 365

Glu Ser Lys Phe Asn Tyr Phe Ala Ile Arg Phe Leu Asp Glu Phe Val

370 375 380

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

385 390 395 400

Asp Arg Arg Ile Lys Ser Ile Glu Gly Thr Gly Phe Lys Thr Glu Arg

405 410 415

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

420 425 430

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

435 440 445

Thr Gly Trp Glu Leu Leu Pro His Pro Ser Tyr Val Phe Ile Asp Asn

450 455 460

Asn Ile Pro Ile His Leu Thr Val Asp Pro Ser Phe Lys Asn Gly Val

465 470 475 480

Lys Glu Tyr Gln Glu Lys Arg Lys Leu Gln Lys Pro Glu Glu Met Lys

485 490 495

Asn Arg Gln Gly Gly Asp Lys Met His Lys Pro Ala Ile Ser Ser Lys

500 505 510

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

515 520 525

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

530 535 540

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

545 550 555 560

Val Phe Glu Arg Ile Arg Asp Tyr Asp Pro Lys Val Pro Leu Pro Ala

565 570 575

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

580 585 590

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

595 600 605

Glu Arg Lys Leu Ala Leu Ile Thr Lys Asn Arg Arg Glu Cys Arg Glu

610 615 620

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

625 630 635 640

Leu Gly Thr Glu Ala Thr Trp Leu Ala Asn Asp Ile Lys Arg Phe Met

645 650 655

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

660 665 670

Gln Gln Ser Leu Ala Phe Phe Glu Ser Arg Pro Gly Glu Ala Arg Ser

675 680 685

Leu Leu Gln Ala Gly Trp Asp Phe Ser Asp Gly Ser Ser Phe Trp Asn

690 695 700

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

705 710 715 720

Tyr Glu Ser Tyr Leu Asn Gly Arg Met Lys Tyr Phe Leu Arg Leu Ala

725 730 735

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

740 745 750

Ile Lys Gln Gln Met Pro Lys Gly Leu Phe Asp Arg Arg Leu Tyr Met

755 760 765

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

770 775 780

Ile Phe Pro Arg Gly Ile Phe Asp Asp Lys Pro Thr Phe Lys Lys Gly

785 790 795 800

Val Gln Val Ser Glu Glu Pro Glu Ala Phe Ala Asp Trp Tyr Ser Tyr

805 810 815

Gly Tyr Asp Val Lys His Lys Phe Gln Glu Phe Tyr Ala Trp Asp Arg

820 825 830

Asp Tyr Glu Glu Leu Leu Arg Glu Glu Leu Glu Lys Asp Thr Ala Phe

835 840 845

Thr Lys Asn Ser Ile His Tyr Ser Arg Glu Ser Gln Ile Glu Leu Leu
850 855 860
Ala Lys Lys Gln Asp Leu Lys Val Lys Lys Val Arg Ile Gln Asp Leu
865 870 875 880
Tyr Leu Lys Leu Met Ala Glu Phe Leu Phe Glu Asn Val Phe Gly His
885 890 895
Glu Leu Ala Leu Pro Leu Asp Gln Phe Tyr Leu Thr Gln Glu Glu Arg

900 905 910
Leu Lys Gln Glu Gln Glu Ala Ile Val Gln Ser Gln Arg Pro Lys Gly
915 920 925
Asp Asp Ser Pro Asn Ile Val Lys Glu Asn Phe Ile Trp Ser Lys Thr
930 935 940
Ile Pro Phe Lys Ser Gly Arg Val Phe Glu Pro Asn Val Lys Leu Lys
945 950 955 960
Asp Ile Gly Lys Phe Arg Asn Leu Leu Thr Asp Glu Lys Val Asp Ile

965 970 975
Leu Leu Ser Tyr Asn Asn Thr Glu Ile Gly Lys Gln Val Ile Glu Asn
980 985 990
Glu Leu Ile Ile Gly Ala Gly Ser Tyr Glu Phe Ile Arg Arg Glu Gln
995 1000 1005
Leu Phe Lys Glu Ile Gln Gln Met Lys Arg Leu Ser Leu Arg Ser
1010 1015 1020
Val Arg Gly Met Gly Val Pro Ile Arg Leu Asn Leu Lys

1025 1030 1035
<210> 29
<211> 1161
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
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Lys Asn Glu Asp Lys His Tyr Phe Gly Ser Phe Leu Asn Leu Ala Asn

20 25 30

Asn Asn Ile Glu Gln Ile Ile Glu Glu Phe Arg Ile Arg Leu Ser Leu

35 40 45

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

50 55 60

Lys Lys Ser Tyr Thr Asp Trp Glu Arg Gly Ile Asn Ile Leu Lys Glu

65 70 75 80

Tyr Leu Pro Val Ile Asp Tyr Leu Asp Leu Ala Ile Thr Asp Lys Glu

85 90 95

Phe Glu Lys Ile Asp Leu Lys Gln Lys Glu Thr Ala Lys Arg Lys Tyr

100 105 110

Phe Arg Thr Asn Phe Ser Leu Leu Ile Asp Thr Ile Ile Asp Leu Arg

115 120 125

Asn Phe Tyr Thr His Tyr Phe His Lys Pro Ile Ser Ile Asn Pro Asp

130 135 140

Val Ala Lys Phe Leu Asp Lys Asn Leu Leu Asn Val Cys Leu Asp Ile

145 150 155 160

Lys Lys Gln Lys Met Lys Thr Asp Lys Thr Lys Gln Ala Leu Lys Asp

165 170 175

Gly Leu Asp Lys Glu Leu Lys Lys Leu Ile Glu Leu Lys Lys Ala Glu

180 185 190

Leu Lys Glu Lys Lys Ile Lys Thr Trp Asn Ile Thr Glu Asn Val Glu

195 200 205

Gly Ala Val Tyr Asn Asp Ala Phe Asn His Met Val Tyr Lys Asn Asn

210 215 220

Ala Gly Val Thr Ile Leu Lys Asp Tyr His Lys Ser Ile Leu Pro Asp

225 230 235 240

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

245 250 255

Val Phe Leu Leu Ser Met Phe Leu Ser Lys Lys Glu Ile Glu Gln Phe
260 265 270
Lys Ser Asn Leu Glu Gly Phe Lys Gly Lys Val Ile Gly Glu Asn Gly
275 280 285
Glu Tyr Glu Ile Ser Lys Phe Asn Asn Ser Leu Lys Tyr Met Ala Thr

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

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

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

485 490 495
Glu Ala Lys Gln Cys Gln Ile Ala Ile Asp Arg Ile Lys Cys Thr Thr

500 505 510

Asn Pro Ala Lys Lys Arg Asn Thr Arg Lys Ser Lys Glu Glu Ile Ile

515 520 525

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

530 535 540

Ala Leu Leu Ser Ser Asn Glu Leu Pro Ala Leu Ile Tyr Glu Leu Leu

545 550 555 560

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

565 570 575

Ile Val Asn Gln Tyr Lys Thr Ile Ala Gly Phe Glu Lys Gly Gln Asn

580 585 590

Leu Ser Asn Ser Leu Ile Thr Lys Lys Leu Lys Lys Ser Glu Pro Asn

595 600 605

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

610 615 620

Leu Glu Ile Thr Glu Asn Lys Leu Asn Ile Ile Lys Asn Asn Arg Ala

625 630 635 640

Glu Phe Arg Thr Gly Ala Lys Arg Lys His Ile Phe Tyr Ser Lys Glu

645 650 655

Leu Gly Gln Glu Ala Thr Trp Ile Ala Tyr Asp Leu Lys Arg Phe Met

660 665 670

Pro Glu Ala Ser Arg Lys Glu Trp Lys Gly Phe His His Ser Glu Leu

675 680 685

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

690 695 700

Leu Leu Asn Met Phe Trp Asn Phe Asp Asn Asp Gln Leu Ile Gly Asn

705 710 715 720

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

725 730 735

Lys Tyr Leu Ile Lys Arg Asp Glu Ile Leu Glu Gly Phe Lys Ser Phe

740 745 750

Ile Ser Asn Phe Lys Asp Glu Pro Lys Leu Leu Lys Lys Gly Ile Lys
755 760 765
Asp Ile Tyr Arg Val Phe Asp Lys Arg Tyr Tyr Ile Ile Lys Ser Thr
770 775 780
Asn Ala Gln Lys Glu Gln Leu Leu Ser Lys Pro Ile Cys Leu Pro Arg
785 790 795 800
Gly Ile Phe Asp Asn Lys Pro Thr Tyr Ile Glu Gly Val Lys Val Glu

805 810 815
Ser Asn Ser Ala Leu Phe Ala Asp Trp Tyr Gln Tyr Thr Tyr Ser Asp
820 825 830
Lys His Glu Phe Gln Ser Phe Tyr Asp Met Pro Arg Asp Tyr Lys Glu
835 840 845
Gln Phe Glu Lys Phe Glu Leu Asn Asn Ile Lys Ser Ile Gln Asn Lys
850 855 860
Lys Asn Leu Asn Lys Ser Asp Lys Phe Ile Tyr Phe Arg Tyr Lys Gln

865 870 875 880
Asp Leu Lys Ile Lys Gln Ile Lys Ser Gln Asp Leu Phe Ile Lys Leu
885 890 895
Met Val Asp Glu Leu Phe Asn Val Val Phe Lys Asn Asn Ile Glu Leu
900 905 910
Asn Leu Lys Lys Leu Tyr Gln Thr Ser Asp Glu Arg Phe Lys Asn Gln
915 920 925
Leu Ile Ala Asp Val Gln Lys Asn Arg Glu Lys Gly Asp Thr Ser Asp

930 935 940
Asn Lys Met Asn Glu Asn Phe Ile Trp Asn Met Thr Ile Pro Leu Ser
945 950 955 960
Leu Cys Asn Gly Gln Ile Glu Glu Pro Lys Val Lys Leu Lys Asp Ile
965 970 975
Gly Lys Phe Arg Lys Leu Glu Thr Asp Asp Lys Val Ile Gln Leu Leu
980 985 990
Glu Tyr Asp Lys Ser Lys Val Trp Lys Lys Leu Glu Ile Glu Asp Glu

995 1000 1005

Leu Glu Asn Met Pro Asn Ser Tyr Glu Arg Ile Arg Arg Glu Lys

1010 1015 1020

Leu Leu Lys Gly Ile Gln Glu Phe Glu His Phe Leu Leu Glu Lys

1025 1030 1035

Glu Lys Phe Asp Gly Ile Asn His Pro Lys His Phe Glu Gln Asp

1040 1045 1050

Leu Asn Pro Asn Phe Lys Thr Tyr Val Ile Asn Gly Val Leu Arg

1055 1060 1065

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

1070 1075 1080

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

1085 1090 1095

Ile His Leu Ala Tyr Phe Leu Ile His Val Arg Asn Lys Phe Gly

1100 1105 1110

His Asn Gln Leu Pro Lys Leu Glu Ala Phe Glu Leu Met Lys Lys

1115 1120 1125

Tyr Tyr Lys Lys Asn Asn Glu Glu Thr Tyr Ala Glu Tyr Phe His

1130 1135 1140

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

1145 1150 1155

Lys His Ser

1160

<210> 30

<211> 848

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<220><221> MOD_RES

<222> (821)..(822)

<

223> Any amino acid

<400> 30

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

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

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

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

245 250 255

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

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

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

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

Glu Leu Gln Lys Arg Lys Gly Lys Leu Ser Lys His Asn Ile Val Glu
500 505 510

Ile Ile Phe Lys Glu Thr Lys Gly Lys Asp Lys Pro Arg Val Asp Glu
515 520 525

Pro Leu Ala Leu Leu Ser Leu Asn Glu Ile Pro Ala Leu Leu Tyr Gln
530 535 540

Ile Leu Glu Lys Gly Ala Thr Pro Glu Asp Ile Glu Leu Ile Ile Lys
545 550 555 560

Asn Lys Leu Ala Glu Arg Phe Glu Lys Ile Lys Asn Tyr Asp Pro Glu
565 570 575

Thr Pro Ala Pro Ala Ser Gln Ile Ser Lys Arg Leu Arg Asn Asn Thr
580 585 590

Thr Ala Lys Gly Gln Glu Thr Leu Asn Ala Glu Lys Leu Ser Ile Leu
595 600 605

Ile Glu Arg Glu Ile Glu Asp Thr Glu Thr Lys Leu Asp Ala Ile Glu
610 615 620

Glu Lys Arg Arg Lys Ala Lys Lys Glu Tyr Arg Arg Asn Ser Pro Gln
625 630 635 640

Lys Ser Ile Phe Ser Asn Ser Glu Leu Gly Arg Ile Ala Ala Trp Leu
645 650 655

Ala Asp Asp Ile Lys Arg Phe Met Pro Ala Glu Leu Arg Lys Asn Trp
660 665 670

Lys Gly Tyr Gln His Ser Gln Leu Gln Gln Ser Leu Ala Tyr Phe Glu
675 680 685

Lys Arg Pro Gln Glu Ala Phe Leu Leu Leu Lys Glu Gly Trp Asp Thr
690 695 700

Ser Asp Gly Ser Ser Tyr Trp Asn Ile Trp Val Ile Asn Ser Phe Ser
705 710 715 720

Glu Thr Glu Asp Phe Glu Lys Phe Tyr Glu Asn Tyr Leu Arg Lys Arg
725 730 735

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

740 745 750

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

755 760 765

Leu Phe Pro Lys Arg His Tyr Ile Leu Lys Asp Leu Glu Thr Glu Lys

770 775 780

Asn Lys Val Leu Ser Lys Pro Leu Val Phe Ser Arg Gly Leu Phe Asp

785 790 795 800

Ser Asn Pro Thr Phe Ile Lys Gly Val Lys Val Thr Glu Asn Pro Glu

805 810 815

Leu Phe Ala Glu Xaa Xaa Asn Gly Ile Ala Thr Gly Thr Lys Arg Asn

820 825 830

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

835 840 845

<210> 31

<211> 1241

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<220><221> MOD_RES

<222> (644)..(727)

<223> Any amino acid

<400> 31

Met Glu Gln Asn Lys Leu Gly Lys Gly Ile Asp Tyr Asn Pro Phe Lys

1 5 10 15

Thr Val Asp Lys His Tyr Phe Gly Gly Phe Phe Asn Leu Ala Asp Asn

20 25 30

Asn Ile Gln Glu Val Phe Asp Glu Ile Asn Ile Arg Tyr Lys Asn Gly

35 40 45

Asn Leu Lys Pro Lys Val Ala Ile Glu Arg Tyr Thr Thr Glu Asn Thr

50 55 60

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

65 70 75 80

Pro Ile Val Lys Glu Ile Asp Gln Lys Asn Lys Lys Asp Ser Asn Asp

85 90 95

Lys Val Ile Glu Lys Thr Arg Ile Glu Arg Ile Thr Asp Phe Arg Asp

100 105 110

Ala Phe Ile Leu Phe Ile Glu Thr Ile Glu Lys Leu Arg Ser Tyr Tyr

115 120 125

Thr His Tyr Gln His Asp Asp Ile Thr Ile Asp Asn Gln Leu Phe Ile

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

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

195 200 205

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

210 215 220

Ile Asn Ser Ile Tyr Asn Asp Ala Ile Arg Pro Phe Leu Tyr Glu Asn

225 230 235 240

Ala Asn Lys Val Glu Leu Ser Asp Lys Lys Lys Thr Ala Phe Asn Glu

245 250 255

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

260 265 270

Ser Gly Ile Ile Phe Leu Leu Ser Cys Phe Leu Asn Arg Lys Glu Ile

275 280 285

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

290 295 300

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

305 310 315 320

His Arg Ile Tyr Ser Val Met Cys Tyr Lys Gly Leu Lys Asn Lys Ile
325 330 335
Arg Thr Ser Glu Ser Ala Thr Lys Glu Thr Leu Leu Met Gln Met Ile

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

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

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

530 535 540
Val His Gln Ile Ile Asp Lys Asn Leu Asp Met His Ile Gly Gln Pro
545 550 555 560
Val Ala Tyr Leu Ser Met Asn Asp Ile His Ala Ile Ile Phe Ser Ile

565 570 575

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

580 585 590

Ile Glu Lys Lys Ile Lys Asp Gln Ile Asn Asn Gln Ile Thr Glu Ile

595 600 605

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

610 615 620

Asn Ser Asn Tyr Pro Asn Thr His Lys Leu Tyr Asp Asp Ile Ser Asn

625 630 635 640

Glu Ile Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

645 650 655

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

660 665 670

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

675 680 685

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

690 695 700

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

705 710 715 720

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Glu Ile Glu Val Leu Asp Lys Leu

725 730 735

Met Gln Lys His Glu Lys Arg Val Lys Glu Tyr Ile Asn Thr Gln Glu

740 745 750

Asp Lys Lys Tyr Lys Pro Ala Arg Lys His Ile Leu Tyr Asn Ser Glu

755 760 765

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

770 775 780

Pro Lys Glu Phe Lys Glu Asn Trp Lys Gly His Tyr His Ser Glu Phe

785 790 795 800

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

805 810 815

Ile Leu Asn Asp Leu Asp Tyr Arg Lys Glu Ile Pro Phe Ile Asp Phe
820 825 830
Ser Lys Asn Thr Leu Ala Asp Phe Tyr Phe Glu Tyr Leu Lys Lys Arg
835 840 845
Lys Ile Tyr His Lys Asn Leu Trp Val Glu Val Asn Lys Leu Ile Lys

850 855 860
Gly Glu Asn Ile Asn Lys Glu Lys Leu Phe Asp Asn Cys Phe Arg Ile
865 870 875 880
Tyr Lys Arg Lys Asn Tyr Val Ser Asn Val Ile Asp Glu Lys Val Asn
885 890 895
Thr Ile Leu Ser Asn Pro Ile Phe Ile Glu Arg Gly Phe Ile Asp Glu
900 905 910
Lys Pro Thr Ile Ile Pro Lys Met Pro Leu Glu Gly Asn Glu Glu His

915 920 925
Phe Ala Ala Trp Phe Val Ala Phe Lys Ser Phe Lys Asn Asn Glu Phe
930 935 940
Gln Asn Phe Tyr Asp Thr Asn Lys Tyr Pro Leu Glu Thr Lys Asp Lys
945 950 955 960
Thr Asn Ser Glu Leu Lys Lys Ile Gln Thr Lys Thr Tyr Asn Gln Lys
965 970 975
Lys Asn Asp Trp Ala Thr Trp Leu Ile Val Gln Tyr Ile Phe Lys Asp

980 985 990
Ile Phe Ser Thr Asp Leu Gln Asn Val Lys Leu Ser Glu Leu Phe Gln
995 1000 1005
Thr Arg Glu Gln Arg Ile Gln Asn Gln Val Lys Ala Leu Asp Gly
1010 1015 1020
Glu Arg Asn Gln Asn Phe Ile Trp Asn Arg Thr Ile Asp Leu Gln
1025 1030 1035
Leu Asn Glu Lys Ile Lys Ile Pro Asn Val Lys Leu Lys Asp Ile

1040 1045 1050
Gly Asn Phe Arg Lys Tyr Val Asn Asp Ser Arg Val Glu Ala Phe

1055 1060 1065

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

1070 1075 1080

Asn Trp Gln Lys Glu Asp Glu Ser Lys Pro Lys Pro Val Asn Val

1085 1090 1095

Ile Gln Leu Gln Leu Asp Asp Tyr Glu Lys Ile Arg Arg Glu Glu

1100 1105 1110

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

1115 1120 1125

Thr Asn Val Lys Thr Val Leu Leu Gln Asp Gly Asn Pro Asn Phe

1130 1135 1140

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

1145 1150 1155

Asn Ile Ser Ala Phe Thr Val Leu His Glu Lys Thr Asn Phe Asp

1160 1165 1170

Lys Ile Asp Phe Asn Val Leu Glu Asn Cys Ser Glu Ile Glu Gln

1175 1180 1185

Ser Ala Thr Leu Ile Ile Leu Ile Arg Asn Lys Phe Ala His Asn

1190 1195 1200

Gln Leu Pro Ser Ser Asp Cys Tyr Gln Phe Cys Ser Lys Ile Leu

1205 1210 1215

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

1220 1225 1230

Phe Met Ile Leu Lys Asp Lys Leu

1235 1240

<210> 32

<211> 1147

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 32

Met Glu Glu Thr Thr Thr Met Gly Lys Gly Val Ala Tyr Asp His Thr
1 5 10 15
Leu Phe Lys Asp Lys His Tyr Phe Ala Gly Tyr Leu Asn Leu Ala Val
20 25 30

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

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

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

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

245 250 255

Phe Phe Leu Gly Ile Phe Leu Ser Arg Lys Glu Ser Asn Asp Leu Arg

260 265 270

Gly Arg Ile Lys Gly Phe Lys Gly Thr Val Ile Lys Asp Leu Pro Asp

275 280 285

Phe Pro Asn Glu Lys Asn Asn Ser Leu Lys Phe Met Ala Thr His Trp

290 295 300

Val Phe Thr Tyr Leu Asn Ile Lys Pro Ile Lys Gln Lys Leu Asn Thr

305 310 315 320

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

325 330 335

Lys Ile Pro Asn Glu Ile Tyr Arg Asn Leu Cys Phe Lys Lys Gln Gln

340 345 350

Glu Phe Val Glu Asp Ile Asn Glu Tyr Ile Lys Glu Gly Asp Asp Ile

355 360 365

Asp Thr Leu Asn Ser Ser Thr Val Ile His Pro Val Ile Arg Lys Arg

370 375 380

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

385 390 395 400

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

405 410 415

His His Ile Gln Arg Lys Lys Leu Ser Gly Thr Glu Tyr Glu Thr Glu

420 425 430

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

435 440 445

Ser Asn Ile Lys Gly Asp Tyr Phe Ile Gln Asn Asn Pro Asp Asn Glu

450 455 460

Ala Leu Gly Trp Glu Ile Tyr Pro Asn Pro Ser Tyr Asn Phe Thr Gly

465 470 475 480

Asn Asn Ile Pro Ile Tyr Phe Asp Ile Asn Asp Gln Asp Lys Glu Lys

485 490 495

Ile Asn Glu Tyr Lys Ser Ile Arg Asn Phe Ser Glu Lys Arg Ile Leu
500 505 510

Arg Lys Lys Asn Lys Lys Asn Lys Gln Glu Ile Phe Asp Leu Ile Asn
515 520 525

Asn Thr Leu Thr Thr Arg Val Phe Thr Ala Glu Pro Thr Ala Ile Leu
530 535 540

Ser Leu Asn Glu Leu Pro Ala Leu Leu Tyr Thr Ile Leu Cys Glu Asn
545 550 555 560

Lys Thr Ala Ser Glu Ile Glu Asn Leu Leu Arg Arg Thr Tyr Leu Lys
565 570 575

Arg Leu Asn Thr Ile Lys Asn Tyr Gln Pro Gly Thr Leu Pro Gln Ser
580 585 590

Lys Ile Thr Lys Asn Leu Asn Lys Ser Thr Asn Gln Glu Ser Leu Asp
595 600 605

Val Ser Lys Leu Ile Lys Ala Met Lys His Glu Ile Ser Ile Ser Asn
610 615 620

Glu Lys Leu Thr Leu Ile Lys Lys Asn Gln Asn Glu Val Lys Asp Thr
625 630 635 640

Ser His Arg Arg Lys Tyr Val Phe Asn Ser Lys Glu Leu Gly Ile Glu
645 650 655

Ala Thr Trp Leu Ala Asn Asp Leu Lys Arg Phe Met Pro Lys Lys Val
660 665 670

Arg Glu Asn Trp Lys Gly Tyr Met His Ser Gln Leu Gln Asn Ser Ile
675 680 685

Ala Tyr Tyr Ser Gln Lys Pro Lys Glu Ala Leu Ser Ile Leu Ser Ser
690 695 700

Val Trp Asn Phe Asn Asp Asp Asn Tyr Ile Trp Asn Glu Gly Ile Lys
705 710 715 720

Lys Ala Phe Asn Glu Lys Glu Phe Glu Lys Phe Tyr Cys Lys Tyr Leu
725 730 735

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

740 745 750

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

755 760 765

Gln Asn Leu Asp Cys Leu Phe His Ile Arg Thr Tyr Thr Ile Asp Ser

770 775 780

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

785 790 795 800

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

805 810 815

Thr Glu Lys Pro Glu Leu Phe Ala Asp Trp Tyr Thr Tyr Thr Tyr Lys

820 825 830

Glu His Pro Leu Gln Glu Phe Tyr Ser Phe Thr Lys Asp Tyr Glu Cys

835 840 845

Asn Phe Lys Lys Glu Lys Leu Thr Val Lys Glu Phe Val Lys Asn Gln

850 855 860

Glu Gln Leu Asn Pro Glu Glu Gln Leu Asn Leu Phe Lys Leu Lys Glu

865 870 875 880

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

885 890 895

Val Val Asp Asn Ile Tyr Asn Lys Ile Phe Glu Tyr Asn Ile Asp Ile

900 905 910

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

915 920 925

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

930 935 940

Lys Thr Ile Leu Tyr Gln Asp Lys Gln Ile Arg Glu Thr Lys Val Gln

945 950 955 960

Leu Lys Asp Ile Asn Lys Ile Lys Arg Phe Leu Glu Glu Asp Lys Val

965 970 975

Lys Gln Ile Leu Ser Tyr Asp Ile Asn Lys Gln Trp Glu Ile Glu Glu

980 985 990

Leu Lys Tyr Glu Leu Tyr Ile Lys Pro Asn Ser Tyr Glu Val Ile Arg
995 1000 1005

Arg Glu Lys Leu Phe Lys Ala Ile Gln Glu Phe Glu Ser Tyr Ile
1010 1015 1020

Leu Thr Ile Asn Asn Phe Asp Gly Ser Asn His Pro Ser Ile Leu
1025 1030 1035

Glu Tyr Asn Ser Asn Pro Arg Phe Lys His Tyr Val Val Asn Gly
1040 1045 1050

Leu Leu Leu Lys Lys Gly Leu Ala Thr Asn Glu Glu Ile Glu Trp
1055 1060 1065

Leu Leu Ala Lys Gly Gln Lys Glu Phe Asn Thr Phe Asp Lys Ser
1070 1075 1080

Ile Val Glu Lys Pro Glu Ile Ile Gln Lys Ala Phe Leu Leu Val
1085 1090 1095

Leu Ile Arg Asn Lys Phe Ala His Ser Gln Leu Pro Ile Lys Glu
1100 1105 1110

Tyr Tyr Glu Met Ile Arg Ser Tyr Thr Lys Asn Ile Glu Asn Leu
1115 1120 1125

Asn Thr Thr Glu Ile Ile Phe Gln Phe Thr Thr Asn Thr Ile Asn
1130 1135 1140

Glu Leu Lys Arg
1145

<210> 33

<211> 1108

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
cas12b sequence

<400> 33

Met Ala Thr Arg Ser Phe Ile Leu Lys Ile Glu Pro Asn Glu Glu Val
1 5 10 15

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

```
            20                  25                  30
Tyr Tyr Met Asn Ile Leu Lys Leu Ile Arg Gln Glu Ala Ile Tyr Glu
        35                  40                  45
His His Glu Gln Asp Pro Lys Asn Pro Lys Lys Val Ser Lys Ala Glu
    50                  55                  60
Ile Gln Ala Glu Leu Trp Asp Phe Val Leu Lys Met Gln Lys Cys Asn
65                  70                  75                  80

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

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

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

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

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

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

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

515 520 525

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

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

Gln Gln Phe Glu Asp Ile Thr Glu Arg Glu Lys Arg Val Thr Lys Trp
660 665 670
Ile Ser Arg Gln Glu Asn Ser Asp Val Pro Leu Val Tyr Gln Asp Glu
675 680 685
Leu Ile Gln Ile Arg Glu Leu Met Tyr Lys Pro Tyr Lys Asp Trp Val
690 695 700
Ala Phe Leu Lys Gln Leu His Lys Arg Leu Glu Val Glu Ile Gly Lys
705 710 715 720

Glu Val Lys His Trp Arg Lys Ser Leu Ser Asp Gly Arg Lys Gly Leu
725 730 735
Tyr Gly Ile Ser Leu Lys Asn Ile Asp Glu Ile Asp Arg Thr Arg Lys
740 745 750
Phe Leu Leu Arg Trp Ser Leu Arg Pro Thr Glu Pro Gly Glu Val Arg
755 760 765

Arg Leu Glu Pro Gly Gln Arg Phe Ala Ile Asp Gln Leu Asn His Leu
770 775 780

Asn Ala Leu Lys Glu Asp Arg Leu Lys Lys Met Ala Asn Thr Ile Ile
785 790 795 800
Met His Ala Leu Gly Tyr Cys Tyr Asp Val Arg Lys Lys Lys Trp Gln
805 810 815
Ala Lys Asn Pro Ala Cys Gln Ile Ile Leu Phe Glu Asp Leu Ser Asn
820 825 830
Tyr Asn Pro Tyr Glu Glu Arg Ser Arg Phe Glu Asn Ser Lys Leu Met
835 840 845

Lys Trp Ser Arg Arg Glu Ile Pro Arg Gln Val Ala Leu Gln Gly Glu
850 855 860
Ile Tyr Gly Leu Gln Val Gly Glu Val Gly Ala Gln Phe Ser Ser Arg
865 870 875 880
Phe His Ala Lys Thr Gly Ser Pro Gly Ile Arg Cys Ser Val Val Thr
885 890 895
Lys Glu Lys Leu Gln Asp Asn Arg Phe Phe Lys Asn Leu Gln Arg Glu
900 905 910

Gly Arg Leu Thr Leu Asp Lys Ile Ala Val Leu Lys Glu Gly Asp Leu
915 920 925
Tyr Pro Asp Lys Gly Gly Glu Lys Phe Ile Ser Leu Ser Lys Asp Arg
930 935 940
Lys Leu Val Thr Thr His Ala Asp Ile Asn Ala Ala Gln Asn Leu Gln
945 950 955 960
Lys Arg Phe Trp Thr Arg Thr His Gly Phe Tyr Lys Val Tyr Cys Lys
965 970 975

Ala Tyr Gln Val Asp Gly Gln Thr Val Tyr Ile Pro Glu Ser Lys Asp
980 985 990
Gln Lys Gln Lys Ile Ile Glu Glu Phe Gly Glu Gly Tyr Phe Ile Leu
995 1000 1005
Lys Asp Gly Val Tyr Glu Trp Gly Asn Ala Gly Lys Leu Lys Ile

1010 1015 1020

Lys Lys Gly Ser Ser Lys Gln Ser Ser Ser Glu Leu Val Asp Ser

1025 1030 1035

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

1040 1045 1050

Glu Lys Leu Met Leu Tyr Arg Asp Pro Ser Gly Asn Val Phe Pro

1055 1060 1065

Ser Asp Lys Trp Met Ala Ala Gly Val Phe Phe Gly Lys Leu Glu

1070 1075 1080

Arg Ile Leu Ile Ser Lys Leu Thr Asn Gln Tyr Ser Ile Ser Thr

1085 1090 1095

Ile Glu Asp Asp Ser Ser Lys Gln Ser Met

1100 1105

<210> 34

<211> 1468

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12b sequence

<400> 34

Met Ala Thr Ala Val Asp Thr Ser Thr Thr Arg Ala Tyr Thr Leu Arg

1 5 10 15

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

20 25 30

Ala Val Asn Arg Gly Ala Trp Val Trp Gly Asp Trp Leu Leu Thr Leu

35 40 45

Arg Gly Gly Leu Pro Ala Ser Leu Ala Asp Gly Asp Ala Glu Arg Arg

50 55 60

Val Val Leu Ala Leu Ser Trp Leu Ser Val Glu Ser Pro Ala Ser Leu

65 70 75 80

Ala Pro Gln Ala His Ile Val Ala Tyr Gly Ser Asp Ala Arg Asp Glu

85 90 95

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

100 105 110

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

115 120 125

Ala Leu Met Ala Ser Ile Arg Glu Asp Ala Val Trp Val Asp Arg Ser

130 135 140

Ala Cys Phe Ala Glu Ala Gln Gln Cys Tyr Arg Gly Leu Ser Ser Glu

145 150 155 160

Trp Ala Arg Lys Thr Leu Phe Asp Phe Leu Gly Gly Glu Asp Asp Tyr

165 170 175

Phe Lys Pro Ser Ala Lys Glu Gly Ala Ser Ser Lys Ala Lys Asp Phe

180 185 190

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

195 200 205

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

210 215 220

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

225 230 235 240

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

245 250 255

Glu Lys Leu Tyr Arg Gln Leu Lys Arg Ala Val Gly Trp Lys Gly Arg

260 265 270

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

275 280 285

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

290 295 300

Ala Ala Val Gln Ser Ser Gln Thr Ser Asp His Ala Ala Val Pro Asp

305 310 315 320

Trp Arg Ser His Trp Pro Ala Glu Ile Thr Gly Leu Pro Met Pro Tyr

325 330 335

Arg Val Asp Arg Asp Tyr Ile Trp Glu His Gly Val Met Leu Asp His

340 345 350

Ala Leu Arg Arg Val Ser Ser Ala His Thr Trp Ile Lys Arg Ala Glu

355 360 365

Ala Glu Arg Arg Arg Phe Gln Gln Asp Ala Ala Lys Met Gly Ser Ile

370 375 380

Pro Glu Glu Ala Arg Asn Trp Leu Asp Ala Phe Arg Glu Arg Arg Ser

385 390 395 400

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

405 410 415

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

420 425 430

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

435 440 445

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

450 455 460

Gly Asp Glu His Val Asp Asp Pro Glu Arg Cys Leu Ala Asp Asp Arg

465 470 475 480

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

485 490 495

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

500 505 510

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

515 520 525

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

530 535 540

Thr Ala Ala Gln Gln Arg Arg Lys Thr Thr Gln Lys Leu Ala Gln Ala

545 550 555 560

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

565 570 575

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

580 585 590

Val Lys Ile Ser Gln Arg Trp Arg Ser Lys Arg Phe Trp Arg Asp Leu
595 600 605
Asp Leu Asp His Phe Gly Ser His Pro Ser Ala Ala Val Ser Arg Ala

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

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

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

805 810 815
Lys Gly Arg Pro Val Thr Lys Thr Thr Ile Tyr Arg Arg Ile Gly Pro
820 825 830
Asp Lys Leu Pro Asp Gly Thr Asp His Pro Ala Pro Trp Ala Arg Leu

835 840 845

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

850 855 860

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

865 870 875 880

Val Gly Leu Glu Pro Ile Val Asp Arg Pro Arg Val Asp Asp Leu His

885 890 895

Ser Asp Ala Val Arg Val Ala Arg Leu Gly Leu Arg Arg Leu Ala Asp

900 905 910

Ala Ala Arg Ile Ala Phe Ala Met Thr Ala Ala Lys Lys Pro Ile Ser

915 920 925

Gly Gly His Glu Val Glu Leu Thr Thr Ala Gln Arg Ile Glu Phe Leu

930 935 940

Gln Asp Ala Leu Leu Leu Trp Gln Ser Leu Ala Ala Ser Arg Arg Tyr

945 950 955 960

Arg Asp Asp Trp Ala Glu Lys Leu Trp Gln Ser Trp Val Val Glu Lys

965 970 975

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

980 985 990

Gln Arg Ala Ala Ser Leu Lys Thr Ala Arg Gln Ser Leu Arg Lys Val

995 1000 1005

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

1010 1015 1020

His Arg Leu Trp Ala Glu Arg Trp Gln Gln Arg Gln Thr Glu Trp

1025 1030 1035

Arg Arg His Leu Arg Trp Leu Arg Arg Leu Ile Leu Pro Arg Arg

1040 1045 1050

Lys Asp His Gln Gln Glu Asp Arg Pro Leu Gln Arg Val Gly Gly

1055 1060 1065

Leu Ser Val Lys Arg Ile Gln Thr Ile Arg Gln Leu Tyr Gln Val

1070 1075 1080

Leu Lys Ala Phe Arg Met Arg Pro Glu Pro Ser Asp Leu Arg Lys

1085 1090 1095

Asn Ile Pro Ala Pro Gly Asp Arg Ser Leu Ala Ser Phe Gly Arg

1100 1105 1110

Arg Ile Leu Asn His Leu Glu Arg Leu Arg Glu Gln Arg Ile Lys

1115 1120 1125

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

1130 1135 1140

Ile Ser Lys Pro Pro Gly Arg Asp Arg Arg Arg Pro Gln Gln Pro

1145 1150 1155

Val Asp Arg Pro Cys His Ala Val Val Ile Glu Asn Leu Gln His

1160 1165 1170

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

1175 1180 1185

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

1190 1195 1200

Cys Glu Leu His Gly Leu Leu Phe Val Glu Val Ser Pro Ala Tyr

1205 1210 1215

Thr Ser Arg Gln Asp Ser Arg Thr Gly Ala Pro Gly Leu Arg Cys

1220 1225 1230

Glu Asp Val Ser Arg Thr Ala Leu Gln Glu Ala Ala Arg Arg Met

1235 1240 1245

His Ala Ser His Ser Arg Pro Ser Asn Ser Ser Pro Gly Gly Ser

1250 1255 1260

Gln Thr Gln Phe Glu Arg Glu Val Cys Arg Trp Ile Asn Glu Phe

1265 1270 1275

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

1280 1285 1290

Val Leu Lys Ala Phe Leu His His Gln Ala Ser Ile Pro Thr Ser

1295 1300 1305

Leu Ser Thr Ile Leu Leu Pro Arg Arg Gly Gly Glu Leu Phe Val

1310 1315 1320

Ser Ala Asp Pro Asp Ser Pro Leu Ala Cys Gly Leu Gln Ala Asp

1325 1330 1335

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

1340 1345 1350

Asp Trp Met Gly Ala Trp Trp Phe Val Leu Val Asp Arg Ala Ser

1355 1360 1365

Gly Gln Pro Val Glu Glu Gln Val Gln Gly Cys Pro Ile Trp Leu

1370 1375 1380

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

1385 1390 1395

Ser Asp Ser Pro Thr Ala Ala Arg Arg Ser Asn Gly Thr Gly Ala

1400 1405 1410

Lys Gly Arg Ala Arg Ala Asn Glu Tyr Trp Trp Ser Ser Leu Ser

1415 1420 1425

Ala Thr Thr Leu Pro Asp His Lys Ala Trp Gln Pro Thr Gln Asp

1430 1435 1440

Tyr Trp Arg Asp Ile Glu Gln Arg Val Val Lys Arg Leu Leu Arg

1445 1450 1455

Leu Leu Asp Gly Ser Glu Trp Ser Glu Asp

1460 1465

<210> 35

<211> 1375

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12b sequence

<400> 35

Met Asn Arg Ile Tyr Gln Gly Arg Val Ser Lys Ile Glu Ile Lys Asp

1 5 10 15

Ser Glu Gly Asn Phe Arg Asn Val Pro Val Gly Ser Pro Asp Thr Cys

20 25 30

Pro Leu Trp Arg His His Arg Ile Phe Gln Asp Ala Val Asn Tyr Tyr
35 40 45
Leu Val Ala Leu Gly Ala Leu Ala Gly Thr Gly Ser Glu Asn Ala Phe
50 55 60

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

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

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

Glu Thr Asp Ile Arg Ile Pro Arg Tyr Phe Phe Gly Gly Ala Gly Ala
260 265 270
Glu Leu Arg Lys Phe Arg Leu Asp Leu Phe Leu Ile Ala Ala Tyr Val

275 280 285

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

290 295 300

Pro Ser Ala Ser Lys Ser Ser Lys Lys Lys Asp Glu Thr Glu Glu Val

305 310 315 320

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

325 330 335

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

340 345 350

Val Gly Ala Asn Ala Gln Lys Pro Ile Trp Arg Asp Phe Asp Ile Ala

355 360 365

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

370 375 380

Glu Glu Arg Glu Glu Lys Leu Lys Lys Ala Glu Glu Thr Leu His Tyr

385 390 395 400

Met Leu Gly Ile Ser Asp Ala Ile Pro Arg Ser Ser Asp Ser Glu Thr

405 410 415

Glu Glu Gln Ala Pro Ser Arg Pro Gly Lys Asp Pro Arg Trp Pro Leu

420 425 430

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

435 440 445

Trp Gln Leu Ser Arg Ser Ala Met Arg Gly Leu Arg Asp Ile Ile Gly

450 455 460

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

465 470 475 480

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

485 490 495

Val Gln Leu Phe Leu Leu Leu Cys Glu Glu Arg Tyr His Ala Leu Trp

500 505 510

Gln Thr Glu Thr Asp Asp Glu Arg Gly Asp Glu Ser Glu Glu Asn Asp

515 520 525

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

Leu Ala Lys Val Lys Phe Gly Glu Thr Thr Glu Glu Asn Ser Glu Val
580 585 590
Lys Ser Gln Phe Val Glu Ala Ala Ile Ala Leu Lys Glu Gly Glu Asn
595 600 605
Leu Lys Glu Ala Arg Val Arg Ile Thr Phe Ser Ala Pro Arg Leu His
610 615 620
Arg Asp Glu Leu Leu Gly Gly Ala Glu Ser Arg Trp Leu Gln Pro Ile
625 630 635 640

Thr Ala Ala Leu Gly Phe Ser Asn Pro Ala Pro Ser Val Lys Phe Asp
645 650 655
Ser Ala Val Ala Leu Met Pro Asp His Met Asp Asp Gly Arg Ile Arg
660 665 670
His Leu Leu Asn Phe Pro Val Asn Phe Asp Ser Ala Trp Leu His Gln
675 680 685
Ser Ile Gly Lys Ala Asp Leu Trp Lys Ser Gln Phe Asn Gly Thr Lys
690 695 700

Asp Lys Asn Leu His Leu His Trp Ala Gly Thr Ala Arg Asp Thr Thr
705 710 715 720
Arg Lys Asn Thr Trp Trp Glu Asn Arg Thr Ile Ile Glu Asn Gly Phe
725 730 735
Thr Val Leu Ser Asn Asp Leu Gly Gln Arg Ser Ala Gly Ala Trp Ala
740 745 750
Leu Leu Lys Val Thr Cys Ser Arg Pro Asp Thr Lys His Pro Val Arg
755 760 765

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

770 775 780

Thr Gly Ile His Arg Leu Pro Gly Glu Asp Gln Arg Ile Leu Lys Asn
785 790 795 800

Gly Lys Trp Ala Thr Glu Gln Ser Gly Lys Lys Gly Arg Asn Ala Thr
805 810 815

Phe Ser Glu Tyr Glu Ala Ala Cys Val Leu Ala Lys Asn Leu Gly Cys
820 825 830

Glu Ser Val Glu Asn Trp Leu Gly Met Ser Gly Glu Lys Ser Tyr Pro
835 840 845

Ala Leu Asn Asp Gln Leu Val Lys Ile Ala Asn Arg Arg Ile Thr Arg
850 855 860

Leu Gly Thr Tyr His Arg Trp Ser Cys Phe Ser Pro Glu Lys Phe Glu
865 870 875 880

Asp Pro Ala Arg Arg Ala Asn Val Ile Gly Gly Gln Leu Ala Glu Leu
885 890 895

Ser Ala Tyr Gln Asp Glu Asn Val Thr Val Ser Ala Asp Ile Leu Lys
900 905 910

Ser Gly Asp Phe Glu Gly Phe Arg His Arg Ala Gly Ala Ala Phe Glu
915 920 925

Ala Leu Arg Thr Glu Leu Glu Val His Leu Val Asn Leu Ala Asn Leu
930 935 940

Thr Ala Pro Leu Arg Gln Lys Val Trp Ser Trp Gln Lys Arg Pro Asp
945 950 955 960

Ser Ser Gly Tyr Gly Asp Leu Leu Met Val Asp Leu Asp Asp Cys His
965 970 975

Pro Lys Ile Arg Gly Gln Arg Gly Leu Ser Met Ala Arg Leu Glu Gln
980 985 990

Leu Glu Gly Leu Arg Arg Leu Phe Leu Arg Tyr Asn Arg Ser Leu Asp
995 1000 1005

Arg Ser Pro Gly Ile Pro Ala Lys Phe Gly Arg Glu Asp Val Gly
1010 1015 1020

Arg Thr Ser Gly Glu Pro Cys Gln Ala Leu Leu Val Lys Ile Asp
1025 1030 1035
Arg Met Lys Glu Gln Arg Val Asn Gln Thr Ala His Leu Ile Leu
1040 1045 1050
Ala Gln Ala Leu Gly Val Arg Leu Cys Pro His Arg Ile Glu Glu
1055 1060 1065
Asn Glu Arg Lys Ser Arg Asp Leu His Gly Glu Tyr Glu Lys Ile
1070 1075 1080

Pro Gly Arg Glu Pro Val Asp Phe Ile Val Ile Glu Asp Leu Ser
1085 1090 1095
Arg Tyr Leu Ser Ser Gln Gly Arg Ala Pro Ser Glu Asn Ser Arg
1100 1105 1110
Leu Met Lys Trp Ala His Arg Ala Val Arg Asp Lys Leu Lys Met
1115 1120 1125
Leu Ala Glu Glu Pro Phe Gly Ile Pro Val Val Glu Thr Val Pro
1130 1135 1140

Ala Tyr Ser Ser Arg Phe His Ala Leu Asn Gly Gln Ala Gly Ser
1145 1150 1155
Arg Leu His Glu Leu His Glu Leu Glu Ala Tyr Gln Gln Gln Ser
1160 1165 1170
Leu Ile Asn Leu Ala Ala Lys Thr Asp Phe Gln Asn Arg Asp Arg
1175 1180 1185
Ser Lys Ala Ala Gly Glu Leu Phe Glu Gln Phe Gln Ala Leu Ala
1190 1195 1200

Lys Leu Asn Glu Arg Arg Arg Ala Glu Gly Lys Lys Val Pro Arg
1205 1210 1215
Thr Leu Tyr Tyr Pro Lys Ser Gly Gly Pro Leu Phe Leu Ala Ser
1220 1225 1230
Arg Asp Gly Asp Thr Ile His Ala Asp Val Asn Ala Ala Ile Asn
1235 1240 1245
Leu Gly Leu Arg Ala Ile Ala Ala Pro Ala Cys Ile Asp Ile His

1250 1255 1260

Arg Arg Leu Arg Ala Thr Lys Glu Lys Glu Val Tyr Arg Pro Arg
1265 1270 1275
Val Gly Asn Ala Arg Glu Lys Ser Ala Phe Ser Lys Asp Asp Ile
1280 1285 1290
Ile Gln Pro Ser Gly Ala Pro Ser Lys Lys Phe Ala Ser Ser Ser
1295 1300 1305
Ser Pro Asn Phe Phe Tyr Glu Pro Glu Asp Leu Lys Gln Ala Asn
1310 1315 1320

Gly Glu Pro Leu Phe Asp Arg Ala Met Phe Gly Glu Tyr Ser Leu
1325 1330 1335
Val Ser Gly Val Ser Leu Trp Ser Met Val Asn Asn Ala Ile Tyr
1340 1345 1350
Ile Arg Cys Val Glu Leu Asn Arg Thr Arg Leu His Gly Lys Asp
1355 1360 1365
Pro Asp Asp Gln Ile Pro Met
1370 1375

<210> 36
<211> 1254
<212> PRT
<213> Unknown
<220
><223> Description of Unknown:
cas12b sequence
<400> 36
Met Ser Ile Thr Arg Ser Ile Lys Val Lys Leu Ile Val Pro Arg Asp
1 5 10 15
Ala Ser Leu Glu Ala Arg Gln Leu Arg Glu Gly Leu Trp Ala Thr His
20 25 30
Leu Phe Val Asn Asp Gly Cys His Tyr Tyr Glu Arg Leu Leu Leu Glu
35 40 45
Phe Arg Gln Arg Asp Val Cys Val Gly Lys Asp Asp Ala Gly Lys Asp

50 55 60

Val Ile Val Pro Ala Ala Glu Trp Ala Asp Arg Leu Arg Ala Arg Leu

65 70 75 80

Gly Arg Asn Gly Met Val Pro Ser His Ile Glu Ala Ala Leu Pro Ile

85 90 95

Phe Arg Glu Leu Tyr Glu Asn Met Val Pro Ser Ala Leu Lys Ala Lys

100 105 110

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

115 120 125

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

130 135 140

Arg Pro Leu Leu Pro Val Ser Gly Asp Asp Pro Ala Phe Glu Pro Ala

145 150 155 160

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

165 170 175

Gly Arg Cys Pro Ala Trp Val Thr Ala Tyr Arg Lys Gly Pro Glu Gly

180 185 190

Ser Ala Trp Val Glu Lys Leu Arg Ile Gln Leu Arg Glu Ala Val Glu

195 200 205

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

210 215 220

Ala Val Pro Ala Ala Pro Pro Leu Gly Ala Gly Ile Asp Ala Leu Arg

225 230 235 240

Pro Leu Leu Pro Leu Leu Gly Gly Asp Pro Ala Phe Glu Pro Ala Ala

245 250 255

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

260 265 270

Arg Pro Pro Thr Trp Val Thr Ala His Pro Thr Trp Val Arg Ala His

275 280 285

Arg Lys Asp Ala Glu Cys Leu Glu Ala Ala Asp Asp Phe Lys Trp Val

290 295 300

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

305 310 315 320

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

325 330 335

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

340 345 350

Val Phe Glu Arg Gly Ala Met Glu Leu Ala Ile Glu His Leu Ile Gly

355 360 365

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

370 375 380

Lys Arg His Asp Asp Leu Leu Gln Trp Ile Glu Ala Glu Ala Pro Asp

385 390 395 400

Ala Leu Leu Ala Val Arg Ala Tyr Glu Ala Ala Arg Thr Ile His Leu

405 410 415

Ala Thr Leu Gly Glu Leu Gly Ala Ala Pro Gln Tyr Thr Leu Arg Leu

420 425 430

Arg Glu Ile Arg Pro Trp Arg Lys Leu Arg Glu Trp Leu Leu Gln Asn

435 440 445

Pro Asp Ala Thr Ile Asp Glu Arg Arg Arg Arg Leu Ala Thr Met Gln

450 455 460

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

465 470 475 480

Ala Pro Glu Arg Arg Ala Leu Val Glu His Pro Ala Gly Asp Val Val

485 490 495

Thr Arg Ile Ala Val Leu Asn Ile Arg Lys Ser Ile Leu Asp Arg Ser

500 505 510

Arg Leu Phe Pro Thr Cys Thr Leu Ala Asp Pro Val Glu His Pro Arg

515 520 525

Phe Ala Lys Phe Gly Lys Pro Gly Asp Lys Asn Ser Ala Gly Tyr Ala

530 535 540

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

545 550 555 560

Pro Arg Gln Asp Gly Leu Leu Val Pro Thr Asp Leu Arg Val Pro Phe

565 570 575

Ala Pro Ser Gly Gln Met Arg Asp Leu Arg Ala Ser Gly Leu Asp Ile

580 585 590

Ser Tyr Glu Arg Gln Asp Gly Arg Gly Arg Gln Ala Ala Lys Leu Gln

595 600 605

Gly Gly Asn Leu Met Phe Asp Arg Thr His Phe Ala Arg Cys Gly Ala

610 615 620

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

625 630 635 640

Leu Ser Ser Pro Ala Ala Ser Leu Ala Met Lys Thr Ala Thr Pro Val

645 650 655

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

660 665 670

Tyr Glu Lys Ala Ala Pro Pro Glu Gly Phe Arg Val Leu Ser Val His

675 680 685

Met Gly Leu Arg Thr Ala Ala Thr Ala Ser Met Leu Arg Phe Gly Ala

690 695 700

Pro Glu Glu Gly Gly His Glu Val Pro Val Ser Gly Leu Ala Gly Glu

705 710 715 720

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

725 730 735

Glu Asp Pro Asp Thr Arg Thr Glu Ala Asn Arg Gly Val Ala Lys Arg

740 745 750

Glu Leu Arg Gly Leu Gly Arg Gly Ile Gly Cys Leu Lys Ala Ile Arg

755 760 765

Arg Ala Ser Ala Ser Ala Thr Pro Glu Asp Arg Ala Glu Ala Leu Val

770 775 780

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

785 790 795 800

Ala Glu Ala Val Gly Arg Leu Asp Pro His Gly Asp Pro Asp Asp Trp

805 810 815

Lys Thr Ala Cys Ala Ala Leu Tyr Ala Ala Val Glu Ala Asp Leu Gly

820 825 830

Val Ala Ile Ser Ser Trp Arg Lys Ala Ala Arg Ala Gly Gly Ala Thr

835 840 845

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

850 855 860

Ser Phe Arg Phe Leu Arg Ser Trp Asp Leu Arg Ala Arg Pro His Asp

865 870 875 880

Gly Asp Pro Arg Arg Pro Arg Pro Gly Tyr Ala Ser Lys Leu Leu His

885 890 895

His Ile Asp Gly Val Lys Asp Asp Arg Val Lys Thr Thr Ala Asp Arg

900 905 910

Ile Val Gln Ala Ala Cys Gly Arg Ala Trp Ile Gly Gly Pro Thr Val

915 920 925

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

930 935 940

Gly Pro Arg Ala Asp Leu Ile Leu Leu Pro Asp Leu Thr His Phe Arg

945 950 955 960

Phe Arg Ser Asp Arg Pro Arg Ala Glu Asn Ser Arg Leu Met Arg Trp

965 970 975

Ala His Arg Gln Leu Ala Ile Tyr Val Arg Met Gln Ala Glu Val Glu

980 985 990

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

995 1000 1005

Ala Trp Thr Gly Ala Pro Gly Val Arg Cys Glu Pro Val Thr Ala

1010 1015 1020

Asp His Leu Arg Gly Ile Ala Lys Arg Glu Asp Tyr Trp Leu Ala

1025 1030 1035

Arg Leu Leu Arg Glu Gly Ala Leu Lys His Leu Arg Ile Asp Pro

1040 1045 1050

Ala Ser Leu Arg Val Asp Asp Leu Val Pro Met Asp His Gly Lys

1055 1060 1065

Ile Leu Val Ala Leu Asp Gly Val Asp Leu Pro Gly Leu Arg Ile

1070 1075 1080

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

1085 1090 1095

Ile Glu Gly His Gly Leu Ala Tyr Arg Leu Pro Gly Ala Arg Val

1100 1105 1110

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

1115 1120 1125

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

1130 1135 1140

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

1145 1150 1155

Tyr Asp Arg Pro Gln Gly Ala Arg Lys Ala Leu Gly Leu Ser Leu

1160 1165 1170

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

1175 1180 1185

Pro Ala Pro Glu Asn Asp Asp Glu Ala Leu Glu Glu Glu Ala Glu

1190 1195 1200

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

1205 1210 1215

Asp Pro Ser Gly Ala Val Ala Gly Gly Gly Trp Leu Glu Ala Ser

1220 1225 1230

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

1235 1240 1245

Glu Leu Gly Arg Leu Gly

1250

<210> 37

<211> 1388

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12b sequence

<400> 37

Met Ser Leu Asn Arg Ile Tyr Gln Gly Arg Val Ala Ala Val Glu Thr
1 5 10 15

Gly Thr Ala Leu Ala Lys Gly Asn Val Glu Trp Met Pro Ala Ala Gly
20 25 30

Gly Asp Glu Val Leu Trp Gln His His Glu Leu Phe Gln Ala Ala Ile
35 40 45

Asn Tyr Tyr Leu Val Ala Leu Leu Ala Leu Ala Asp Lys Asn Asn Pro
50 55 60

Val Leu Gly Pro Leu Ile Ser Gln Met Asp Asn Pro Gln Ser Pro Tyr
65 70 75 80

His Val Trp Gly Ser Phe Arg Arg Gln Gly Arg Gln Arg Thr Gly Leu
85 90 95

Ser Gln Ala Val Ala Pro Tyr Ile Thr Pro Gly Asn Asn Ala Pro Thr
100 105 110

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

Ala Thr Leu Asp Ala Ala Leu Met Gln Leu Leu Lys Ala Cys Asp Gly
130 135 140

Ala Gly Ala Ile Gln Gln Glu Gly Arg Ser Tyr Trp Pro Lys Phe Cys
145 150 155 160

Asp Pro Asp Ser Thr Ala Asn Phe Ala Gly Asp Pro Ala Met Leu Arg
165 170 175

Arg Glu Gln His Arg Leu Leu Leu Pro Gln Val Leu His Asp Pro Ala
180 185 190

Ile Thr His Asp Ser Pro Ala Leu Gly Ser Phe Asp Thr Tyr Ser Ile
195 200 205

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

210 215 220

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

Ser Ala Ala Asp Phe Asp Arg Leu Ala Ser Ser Leu Lys Lys Ile Pro
245 250 255

Asp Asp Asp Ser Arg Leu Asn Leu Gln Gly Tyr Val Gly Ser Ser Ala
260 265 270

Lys Gly Glu Val Gln Ala Arg Leu Phe Ala Leu Leu Leu Phe Arg His
275 280 285

Leu Glu Arg Ser Ser Phe Thr Leu Gly Leu Leu Arg Ser Ala Thr Pro
290 295 300

Pro Pro Lys Asn Ala Glu Thr Pro Pro Pro Ala Gly Val Pro Leu Pro
305 310 315 320

Ala Ala Ser Ala Ala Asp Pro Val Arg Ile Ala Arg Gly Lys Arg Ser
325 330 335

Phe Val Phe Arg Ala Phe Thr Ser Leu Pro Cys Trp His Gly Gly Asp
340 345 350

Asn Ile His Pro Thr Trp Lys Ser Phe Asp Ile Ala Ala Phe Lys Tyr
355 360 365

Ala Leu Thr Val Ile Asn Gln Ile Glu Glu Lys Thr Lys Glu Arg Gln
370 375 380

Lys Glu Cys Ala Glu Leu Glu Thr Asp Phe Asp Tyr Met His Gly Arg
385 390 395 400

Leu Ala Lys Ile Pro Val Lys Tyr Thr Thr Gly Glu Ala Glu Pro Pro
405 410 415

Pro Ile Leu Ala Asn Asp Leu Arg Ile Pro Leu Leu Arg Glu Leu Leu
420 425 430

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

Tyr Gly Leu Gln Arg Arg Thr Ile Arg Gly Phe Arg Glu Leu Arg Arg
450 455 460

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

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

Leu Thr Pro Ala Asp Pro Glu Tyr Ser Arg Arg Gln Tyr Asp Phe Asn
565 570 575
Ala Val Ser Lys Phe Gly Ala Gly Ser Arg Ser Ala Asn Arg His Glu
580 585 590
Pro Gly Gln Thr Glu Arg Gly His Asn Thr Phe Thr Thr Glu Ile Ala
595 600 605
Ala Arg Asn Ala Ala Asp Gly Asn Arg Trp Arg Ala Thr His Val Arg
610 615 620

Ile His Tyr Ser Ala Pro Arg Leu Leu Arg Asp Gly Leu Arg Arg Pro
625 630 635 640
Asp Thr Asp Gly Asn Glu Ala Leu Glu Ala Val Pro Trp Leu Gln Pro
645 650 655
Met Met Glu Ala Leu Ala Pro Leu Pro Thr Leu Pro Gln Asp Leu Thr
660 665 670
Gly Met Pro Val Phe Leu Met Pro Asp Val Thr Leu Ser Gly Glu Arg
675 680 685

Arg Ile Leu Leu Asn Leu Pro Val Thr Leu Glu Pro Ala Ala Leu Val
690 695 700
Glu Gln Leu Gly Asn Ala Gly Arg Trp Gln Asn Gln Phe Phe Gly Ser

705 710 715 720

Arg Glu Asp Pro Phe Ala Leu Arg Trp Pro Ala Asp Gly Ala Val Lys

725 730 735

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

740 745 750

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

755 760 765

Ala Leu Leu Asn Val Thr Ala Gln Lys Pro Ala Lys Pro Val His Arg

770 775 780

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

785 790 795 800

Ala Arg Met Ile Arg Leu Pro Gly Glu Asp Ala Arg Leu Phe Val Arg

805 810 815

Gly Lys Leu Val Gln Glu Pro Tyr Gly Glu Arg Gly Arg Asn Ala Ser

820 825 830

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

835 840 845

Asn Pro Asp Glu Leu Leu Gly Ala Asp Pro Arg Arg His Ser Tyr Pro

850 855 860

Glu Ile Asn Asp Lys Leu Leu Val Ala Leu Arg Arg Ala Gln Ala Arg

865 870 875 880

Leu Ala Arg Leu Gln Asn Arg Ser Trp Arg Leu Arg Asp Leu Ala Glu

885 890 895

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

900 905 910

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

915 920 925

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

930 935 940

Gln Ile Ala Asn Leu Ile Leu Pro Leu Arg Gly Arg Arg Trp Glu Trp

945 950 955 960

Arg Pro His Val Glu Val Pro Asp Cys His Ile Leu Ala Gln Ser Asp
965 970 975
Pro Gly Thr Asp Asp Thr Lys Arg Leu Val Ala Gly Gln Arg Gly Ile
980 985 990
Ser His Glu Arg Ile Glu Gln Ile Glu Glu Leu Arg Arg Arg Cys Gln
995 1000 1005

Ser Leu Asn Arg Ala Leu Arg His Lys Pro Gly Glu Arg Pro Val
1010 1015 1020
Leu Gly Arg Pro Ala Lys Gly Glu Glu Ile Ala Asp Pro Cys Pro
1025 1030 1035
Ala Leu Leu Glu Lys Ile Asn Arg Leu Arg Asp Gln Arg Val Asp
1040 1045 1050
Gln Thr Ala His Ala Ile Leu Ala Ala Ala Leu Gly Val Arg Leu
1055 1060 1065

Arg Ala Pro Ser Lys Asp Arg Ala Glu Arg Arg His Arg Asp Ile
1070 1075 1080
His Gly Glu Tyr Glu Arg Phe Arg Ala Pro Ala Asp Phe Val Val
1085 1090 1095
Ile Glu Asn Leu Ser Arg Tyr Leu Ser Ser Gln Asp Arg Ala Arg
1100 1105 1110
Ser Glu Asn Thr Arg Leu Met Gln Trp Cys His Arg Gln Ile Val
1115 1120 1125

Gln Lys Leu Arg Gln Leu Cys Glu Thr Tyr Gly Ile Pro Val Leu
1130 1135 1140
Ala Val Pro Ala Ala Tyr Ser Ser Arg Phe Ser Ser Arg Asp Gly
1145 1150 1155
Ser Ala Gly Phe Arg Ala Val His Leu Thr Pro Asp His Arg His
1160 1165 1170
Arg Met Pro Trp Ser Arg Ile Leu Ala Arg Leu Lys Ala His Glu
1175 1180 1185

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

1190 1195 1200

Ala Val Arg Gly Leu Phe Asp Arg Leu Asp Arg Phe Asn Ala Gly

1205 1210 1215

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

1220 1225 1230

Gly Gly Pro Val Phe Val Pro Leu Gly Asp Ala Thr Pro Met Gln

1235 1240 1245

Ala Asp Leu Asn Ala Ala Ile Asn Ile Ala Leu Arg Gly Ile Ala

1250 1255 1260

Ala Pro Asp Arg His Asp Ile His His Arg Leu Arg Ala Glu Asn

1265 1270 1275

Lys Lys Arg Ile Leu Ser Leu Arg Leu Gly Thr Gln Arg Glu Lys

1280 1285 1290

Ala Arg Trp Pro Gly Gly Ala Pro Ala Val Thr Leu Ser Thr Pro

1295 1300 1305

Asn Asn Gly Ala Ser Pro Glu Asp Ser Asp Ala Leu Pro Glu Arg

1310 1315 1320

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

1325 1330 1335

Arg Val Thr Ile Glu Gly Val Ser Gln Lys Phe Ala Thr Gly Arg

1340 1345 1350

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

1355 1360 1365

Arg Leu Asn Glu Thr Val Thr Asp Asn Asn Arg Asn Glu Glu Glu

1370 1375 1380

Asp Asp Ile Pro Met

1385

<210> 38

<211> 1172

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12b sequence

<400> 38

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

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

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

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

Lys Asp Lys Trp Trp Lys Asn Lys Arg Asp Gly Val Asp Thr Trp Ala
```

225 230 235 240

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

245 250 255

Ser Ile Arg Glu Glu Leu Trp Asp Arg Leu Gly Leu Leu Pro Leu Gly

260 265 270

Ser Leu Tyr Phe Lys Lys Pro Val Gly Asn Lys Trp Asn Arg Met Ala

275 280 285

Phe Arg Leu Ala Ile Ala His Leu Leu Ser Trp Glu Ser Trp Asn His

290 295 300

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

305 310 315 320

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

325 330 335

Leu Arg Gln Tyr Gln Lys Glu Arg His Glu Glu Leu Ser Arg Thr Ser

340 345 350

Phe Val Asp Asp Asp Arg Pro Phe Thr Ile Gly Ala Arg Met Ile Arg

355 360 365

Ala Trp Gly Arg Val Arg Glu Ala Trp Arg Asn Lys Gly Asp Gly Ile

370 375 380

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

385 390 395 400

Lys Phe Gly Asp Pro His Leu Phe Leu Trp Leu Ala Glu Ala Gly Arg

405 410 415

Glu Ser Leu Trp Arg Asp Glu Asp Val Leu Thr Thr Phe Val Glu Ile

420 425 430

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

435 440 445

Thr Phe Ala Asp Ala Arg Leu His Pro Arg Trp Ala Met Tyr Glu Ala

450 455 460

Leu Gly Gly Thr Asn Leu Arg Asn Tyr Glu Leu Thr Pro Glu Gly Lys

465 470 475 480

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

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

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

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

725 730 735

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

Met Ile Glu Tyr Leu Glu Ala Val Arg Lys Leu Leu Ile Gly Trp Ser
805 810 815
Thr His Gly Arg Asp Tyr Gly Glu Ile Asn Arg Gln Asn Lys Lys Arg
820 825 830
Tyr Gly Thr Val Ala Ser Lys Leu Leu Lys His Ile Asn Lys Leu Lys
835 840 845
Glu Asp Arg Thr Lys Ala Gly Thr Asp Leu Ile Ile Gln Ala Ala Arg
850 855 860

Gly Tyr Ile Pro Leu Pro Gly Lys Gly Trp Met Glu Lys Tyr Arg Pro
865 870 875 880
Cys Arg Val Ile Leu Phe Glu Asp Leu Ala Arg Tyr Arg Phe Lys Val
885 890 895
Asp Arg Pro Arg Arg Glu Asn Ser Gln Leu Met Lys Trp Gly His Arg
900 905 910
Glu Ile Ile Asn Glu Ala Thr Leu Gln Gly Glu Ile Tyr Gly Met Val
915 920 925

Val Glu Thr Ala Gly Ala Gly Phe Ser Ser Arg Phe His Ala Lys Thr
930 935 940
Gly Ala Pro Gly Val Arg Cys Arg Tyr Leu Lys Glu Asp Asp Phe Glu
945 950 955 960
Asn Gly Ala Pro Lys Glu Phe Leu Val Arg Gln Met Lys Asn Leu Met
965 970 975

Lys Gly Asp Arg Leu Glu Pro Gly Leu Leu Val Pro Trp Asp Gly Gly
980 985 990

Glu Leu Phe Ala Thr Val Asp Asn Gly Lys Pro Ile Val Ile His Ala
995 1000 1005

Asp Ile Asn Ala Ala Gln Asn Leu Gln Arg Arg Phe Trp Thr Arg
1010 1015 1020

Phe Ala Asp Ala Tyr Arg Val Asn Ala Val Glu Glu Asn Asp Asn
1025 1030 1035

Trp Val Val Thr Asp Thr Gly Val Arg Val Leu Gly Ala Leu Glu
1040 1045 1050

Met Ala Val His Gly Glu Ala Asp Arg Lys Pro Arg Thr Gly Phe
1055 1060 1065

Thr Leu His Gly Thr Leu Gln Ser Gly Ala Glu Leu Lys Ala Glu
1070 1075 1080

Gly Lys Lys Thr Asp Ile Lys Asp Val Glu Glu Asp Lys Asp Asp
1085 1090 1095

Ser Ile Ser Ser Glu Ile Ile Glu Leu Gln Asp Glu Lys Glu Arg
1100 1105 1110

Lys Gly Arg Glu Thr Phe Phe Arg Asp Pro Ser Gly Gly Ile Leu
1115 1120 1125

Asp Pro Gly Lys Trp Tyr Gly Ser Lys Arg Phe Trp Gly Arg Ala
1130 1135 1140

Lys Gly Ala Val Thr Glu Ala Leu Leu Asp Asn Gln Gly Ala Asn
1145 1150 1155

Asn Ala Leu Glu Glu Lys Pro Gly Asn Asp Glu Leu Pro Phe
1160 1165 1170

<210> 39

<211> 1108

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12b sequence

<400> 39

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Met Ala Thr Arg Ser Phe Ile Leu Lys Ile Glu Pro Asn Glu Glu Val
1               5                  10                  15
Lys Lys Gly Leu Trp Lys Thr His Glu Val Leu Asn His Gly Ile Ala
            20                  25                  30
Tyr Tyr Met Asn Ile Leu Lys Leu Ile Arg Gln Glu Ala Ile Tyr Glu
        35                  40                  45

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

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

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

225 230 235 240

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

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

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

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

Leu Gly Gly Ala Arg Val Gln Phe Asp Arg Asp His Leu Arg Arg Tyr
485 490 495

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

Ile Glu Ser Leu Glu Ile Gly Leu Arg Val Met Ser Ile Asp Leu Gly
565 570 575
Gln Arg Gln Ala Ala Ala Ala Ser Ile Phe Glu Val Val Asp Gln Lys
580 585 590
Pro Asp Ile Glu Gly Lys Leu Phe Phe Pro Ile Lys Gly Thr Glu Leu
595 600 605
Tyr Ala Val His Arg Ala Ser Phe Asn Ile Lys Leu Pro Gly Glu Thr
610 615 620

Leu Val Lys Ser Arg Glu Val Leu Arg Lys Ala Arg Glu Asp Asn Leu
625 630 635 640
Lys Leu Met Asn Gln Lys Leu Asn Phe Leu Arg Asn Val Leu His Phe
645 650 655
Gln Gln Phe Glu Asp Ile Thr Glu Arg Glu Lys Arg Val Thr Lys Trp
660 665 670
Ile Ser Arg Gln Glu Asn Ser Asp Val Pro Leu Val Tyr Gln Asp Glu
675 680 685

Leu Ile Gln Ile Arg Glu Leu Met Tyr Lys Pro Tyr Lys Asp Trp Val
690 695 700
Ala Phe Leu Lys Gln Leu His Lys Arg Leu Glu Val Glu Ile Gly Lys
705 710 715 720
Glu Val Lys His Trp Arg Lys Ser Leu Ser Asp Gly Arg Lys Gly Leu

725 730 735

Tyr Gly Ile Ser Leu Lys Asn Ile Asp Glu Ile Asp Arg Thr Arg Lys

740 745 750

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

755 760 765

Arg Leu Glu Pro Gly Gln Arg Phe Ala Ile Asp Gln Leu Asn His Leu

770 775 780

Asn Ala Leu Lys Glu Asp Arg Leu Lys Lys Met Ala Asn Thr Ile Ile

785 790 795 800

Met His Ala Leu Gly Tyr Cys Tyr Asp Val Arg Lys Lys Lys Trp Gln

805 810 815

Ala Lys Asn Pro Ala Cys Gln Ile Ile Leu Phe Glu Asp Leu Ser Asn

820 825 830

Tyr Asn Pro Tyr Glu Glu Arg Ser Arg Phe Glu Asn Ser Lys Leu Met

835 840 845

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

850 855 860

Ile Tyr Gly Leu Gln Val Gly Glu Val Gly Ala Gln Phe Ser Ser Arg

865 870 875 880

Phe His Ala Lys Thr Gly Ser Pro Gly Ile Arg Cys Ser Val Val Thr

885 890 895

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

900 905 910

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

915 920 925

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

930 935 940

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

945 950 955 960

Lys Arg Phe Trp Thr Arg Thr His Gly Phe Tyr Lys Val Tyr Cys Lys

965 970 975

Ala Tyr Gln Val Asp Gly Gln Thr Val Tyr Ile Pro Glu Ser Lys Asp
980 985 990
Gln Lys Gln Lys Ile Ile Glu Glu Phe Gly Glu Gly Tyr Phe Ile Leu
995 1000 1005

Lys Asp Gly Val Tyr Glu Trp Val Asn Ala Gly Lys Leu Lys Ile
1010 1015 1020
Lys Lys Gly Ser Ser Lys Gln Ser Ser Ser Glu Leu Val Asp Ser
1025 1030 1035
Asp Ile Leu Lys Asp Ser Phe Asp Leu Ala Ser Glu Leu Lys Gly
1040 1045 1050
Glu Lys Leu Met Leu Tyr Arg Asp Pro Ser Gly Asn Val Phe Pro
1055 1060 1065

Ser Asp Lys Trp Met Ala Ala Gly Val Phe Phe Gly Lys Leu Glu
1070 1075 1080
Arg Ile Leu Ile Ser Lys Leu Thr Asn Gln Tyr Ser Ile Ser Thr
1085 1090 1095
Ile Glu Asp Asp Ser Ser Lys Gln Ser Met
1100 1105

<210> 40
<211> 1450
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
cas12b sequence
<400> 40
Met Tyr Arg Gly Phe Cys Thr Val Thr Ala Thr Ser Gly Gly Trp Gln

1 5 10 15
Ser Thr Thr Phe Leu Ala Gly Ala Gln Met Ala Asp Thr Thr Thr Arg
20 25 30
Ala Tyr Thr Leu Lys Leu Gln Gly Asp Arg Leu Ala Leu Trp Arg Asn
35 40 45
His Val Ile Phe Asn Asn Gly Val Lys Ala Trp Gly Glu Trp Leu Leu

50 55 60

Cys Leu Arg Gly Gly Leu Pro Ala Ser Leu Ala Asp His Arg Asp Ser

65 70 75 80

Leu Asp Val Ser Lys Gly Glu Ile Ser Arg Thr Phe Lys Glu Arg Thr

85 90 95

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

100 105 110

Ala Thr Glu Lys Lys Val Arg Glu Glu Val Ala Ser Arg Arg Lys Lys

115 120 125

Val Thr Glu Thr Ala Val Ala Lys Glu Leu Leu Ala Ala Arg Arg Ser

130 135 140

Glu Leu Arg Arg Ile Leu Ala Leu Ser Trp Leu Cys Pro Glu Thr Pro

145 150 155 160

Val Gln Leu Val Pro Gln Ala Ala Ile Val Ala Ala Ala Asp Asp Ser

165 170 175

Asp Arg Glu Gln Lys Val Leu Asp Gly Phe Arg Gln Ile Leu Lys Arg

180 185 190

Lys Gly Val Ser Asp Val Ala Gly Trp Val Gln Asp Cys Asp Ala Thr

195 200 205

Leu Arg Ala Thr Ile Arg Ser Asp Ala Val Trp Val Asp Arg Thr Ala

210 215 220

Cys Phe Cys Ser Met Pro Arg Ala Val Arg Pro Ser Glu Val Asp Ala

225 230 235 240

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

245 250 255

Thr Ala Ser Ala Ser Ser Gly Pro Ala Glu Pro Lys Asp Phe Ala Asn

260 265 270

Thr Cys Arg Asp Trp Val Ser Ser Phe Trp Gly Gly Gly Glu Lys Ser

275 280 285

Asn Lys Ala Ser Ile Leu Ala Ala Leu Ser Ala Ile Ala Gln Ile Lys

290 295 300

Pro Thr Arg Val Val Gly Lys Arg Gly Pro Ala Ala Leu Ala Val Ile
305 310 315 320
Ala Gly Val Leu Glu Gln Lys Pro Val Asp Asp Ser Val Glu Ala Leu

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

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

450 455 460
Arg Lys Trp Leu Glu Asp Tyr Val Glu Ala Arg Thr Ala Ala Ser Gly
465 470 475 480
Ala Val Asp Gly Tyr Gln Leu Arg Lys Arg Ala Leu Gly Gly Trp Ala
485 490 495
Asp Val Val Ala Ala Trp Ser Arg Cys Glu Thr Ser Glu Asp Arg Ile
500 505 510
Ala Ala Val Arg Glu Leu Gln Ala Asp Trp Glu Lys Ala Gly Asp Val

515 520 525
Gln Leu Phe Glu Ala Leu Ala Ala Asp Asp Ala Ile Cys Val Trp Gln
530 535 540
Ser Ala Asn Gly Lys Thr Ala Ala Ser Ile Leu Thr Asp Tyr Val Arg

545 550 555 560

Ala Ala Val Ala Asp Gln Asn Ala Thr Arg Phe Lys Val Pro Ala Tyr

565 570 575

Arg His Pro Asp Pro Leu Arg Ser Pro Thr Phe Val Gly Phe Gly Asn

580 585 590

Ser Gln Trp Ser Ile Ala Tyr Ser Ala Gln Gly Glu Ala Arg Glu Arg

595 600 605

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

610 615 620

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

625 630 635 640

Asp Leu Trp Ala Gly Asp Lys Met Val Pro Thr Gln Phe Arg Trp Gln

645 650 655

Ser Arg Arg Leu Leu Ser Asp Leu Ala Leu His Ser Val Pro Ala Met

660 665 670

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

675 680 685

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

690 695 700

Asn Gly Arg Leu Gln Ala Pro Arg Arg Gln Leu Glu Asp Leu Ala Arg

705 710 715 720

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

725 730 735

Pro Lys Val Arg Ser Arg Leu Lys His Leu Gly Trp Phe Leu Thr His

740 745 750

Ser Ala Lys Leu Thr Pro Ser Gly Pro Trp Leu Asp Tyr Val Ala Gly

755 760 765

Gly Leu Ala Asn Gly Trp Lys Trp Ala Glu Gly Arg Glu Gly Ala Cys

770 775 780

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

785 790 795 800

Leu Ser Arg Leu Pro Gly Leu Arg Leu Leu Ser Val Asp Leu Gly Leu
805 810 815
Arg Thr Ser Ala Ala Ala Ala Val Trp Gln Val Val Ser Lys Arg Gln
820 825 830
Leu Thr Ala Ala Lys Asp Gly Ala Lys Ser Val Ser Asp Thr Asp Leu

835 840 845
Phe Cys Leu Val Arg Thr Gly Asp Arg Thr Gln Val Tyr Arg Arg Ile
850 855 860
Gly Leu Ser Ala Trp Ala Arg Leu Glu Arg Gln Phe Leu Ile Arg Leu
865 870 875 880
Asp Gly Glu Lys Ala Ala Ala Arg Pro Ala Thr Thr Asn Glu Trp Glu
885 890 895
Ser Leu Gln Ser Phe Arg Ala Trp Leu Gly Cys Gly Ile Glu Arg Arg

900 905 910
Pro Glu Lys Leu Pro Pro Val Asp Ser Leu Gln Gln Ser Ala Glu Arg
915 920 925
Leu Cys Arg Leu Gly Leu Arg Arg Leu Ser Asp Leu Ala Arg Val Ala
930 935 940
Tyr Leu Leu Thr Ala Lys Glu Arg Pro Ile Met Gly Gly Arg Thr Ala
945 950 955 960
Pro Leu Asp Glu Glu Gly Thr Val Gln Ala Ala Gln Asp Ala Leu Ser

965 970 975
Ile Leu His Ala Leu Gly Ser Ser Glu Asp Phe Ser Asp Ala Arg Leu
980 985 990
Gln Gly Ile Trp Arg Thr Ala Ile Gly Asp Thr Pro Pro Leu Ala Ala
995 1000 1005
Arg Leu Thr Lys Lys Gln Arg Gln Glu Leu Arg Glu Ala Leu Arg
1010 1015 1020
Pro Ala Ala Glu Lys Leu Arg Gly Lys Ala Ala Leu Gly Lys Glu

1025 1030 1035
Leu Ala Asp Leu Trp Lys Glu Arg Ser Ala Ala Trp Ala Lys His

1040 1045 1050

Leu Arg Trp Leu Arg Asp Trp Val Ile Pro Arg Phe Asp Lys Arg

1055 1060 1065

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

1070 1075 1080

Ser Leu Asp Arg Ile Ala Thr Ile Arg Gly Val Tyr Gln Ile Met

1085 1090 1095

Arg Ala Tyr Ala Ser Arg Ala Glu Pro Thr Asn Leu Arg Ala Gly

1100 1105 1110

Val Glu Arg Leu Glu Lys Ala Ala Ala Lys Lys Leu Arg Pro Glu

1115 1120 1125

Phe Gly Arg Arg Met Leu Ala Lys Met Glu Arg Leu Arg Glu Asn

1130 1135 1140

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

1145 1150 1155

Val Gly Ser Glu Asp Arg Leu His Trp Glu Arg Gly Arg Arg Arg

1160 1165 1170

Pro Thr Ala Ala Ile Ser Asp Pro Arg Phe Ala Pro Cys His Ala

1175 1180 1185

Val Val Ile Glu Asn Leu Glu Asn Tyr Arg Pro Asp Glu Lys Arg

1190 1195 1200

Thr Arg Arg Glu Asn Arg Gly Leu Met Ser Trp Ala Ala Arg Ala

1205 1210 1215

Val Gly Lys Tyr Leu Ala Glu Gly Cys Gln Leu His Gly Leu Tyr

1220 1225 1230

Leu Arg Gln Val Ser Pro Ala Tyr Thr Ser Arg Gln Asp Ser Arg

1235 1240 1245

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

1250 1255 1260

Leu Leu Asn Pro Glu Gly Trp Ile Gly Arg Leu Val Ala Arg Ala

1265 1270 1275

Ala Glu Ala Val Lys Glu Gly Lys Ala Thr Pro Arg Gln Arg Leu
1280 1285 1290
Leu Val Thr Leu Ala Glu Ser Ala Arg Ala Gly Ile Ala Glu Ser
1295 1300 1305
Ala Ala Val Arg Ile Ile Ala Pro Gly Gly Gln Leu Phe Ile Ala
1310 1315 1320
Ala Asp Pro Gln Ser Pro Ala Ser Asn Gly Ile His Ala Asp Met

1325 1330 1335
Asn Ala Ala Ala Asn Ile Gly Leu Val Ala Leu Leu Asp Pro Asp
1340 1345 1350
Trp Pro Ala Ala Trp Trp Arg Leu Pro Cys Lys Ala Ala Thr Gly
1355 1360 1365
Tyr Val Asp Glu Ser Lys Val Gly Gly Ser Glu Ala Val Pro Leu
1370 1375 1380
Gly Arg Ala Ile Leu Glu Val Gly Ala Glu Ala Gly Lys Val Tyr

1385 1390 1395
Val Asn Ala Trp Ser Asp Pro Gln Asp Ser Ala Val Ser Arg Arg
1400 1405 1410
Glu Trp Thr Asp Thr Lys Arg Tyr Trp Arg Asp Val Glu Glu Arg
1415 1420 1425
Val Val Glu Ile Leu Leu Ala Ser Asn Arg Gly Gly Arg Arg Gly
1430 1435 1440
Lys Pro Gly Ala Val Pro Phe
1445 1450

<210> 41
<211> 792
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
cas12b sequence
<400> 41
Met Ala Thr Lys Ser Phe Glu Ala Lys Ile Val Cys Lys Pro Asp Glu

1 5 10 15

Lys Tyr Thr Ala Glu Gln Lys Lys Gln Phe Leu Trp Phe Thr His Gln

20 25 30

Val Phe Asn Asp Gly Val Arg Lys Val Ile Pro Tyr Val Phe Lys Met

35 40 45

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

50 55 60

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

65 70 75 80

Asp Trp Thr Ser Gly Lys Ile Gly Lys Ser Asp Pro Asn Lys Trp Lys

85 90 95

Glu Leu Leu Lys Tyr Gln Glu Leu Glu Lys Gly Phe Arg Gln Arg Leu

100 105 110

Lys Glu Glu Gly Ile Lys Ser Thr Lys Lys Phe Arg Lys Glu Leu Glu

115 120 125

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

130 135 140

Ala Asp Ala Ala Ala Ile Leu Arg Asn Lys Asn Leu Leu Leu Phe Asn

145 150 155 160

Arg Asp Glu Leu Leu Pro Asn Leu Pro Ser Glu Phe Arg Arg Lys Ile

165 170 175

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

180 185 190

Asn Trp Glu Asp Glu His Ala Glu Trp Leu Ile Glu Lys Asp Lys Trp

195 200 205

Glu Glu Glu His Pro Glu Tyr Met Asn Val Arg Pro Ile Phe Glu Lys

210 215 220

Phe Glu Lys Glu Gln Gly Lys Val Lys Gly Ser Arg Ile Arg Trp Leu

225 230 235 240

Ala Tyr Leu Asp Phe Leu Ser Ser Lys Pro Glu Leu Ala Asn Trp Arg

245 250 255

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

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

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

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

Ile Cys Lys Asn Asn Asn Gly Arg Pro Glu Pro Ile Arg Phe Ile Pro

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

Ser Ile Arg Gln Ala Gly Glu Lys Glu Gly Arg Lys Ser Lys Gly Gln
                565                 570                 575
His Ile Pro Glu Thr Glu Thr Pro Trp Ala His Leu Arg Glu His Ile
            580                 585                 590
Ala Asn Met Lys Glu Asp His Tyr Lys Lys Ala Ala Asn Leu Ile Ile
        595                 600                 605
Arg Thr Ala Leu Gln Asn Gly Ala Gln Val Ile Leu Ile Glu Asn Leu
    610                 615                 620

Arg Asn Tyr Arg Pro Met Leu Glu Arg Thr Asn Leu Glu Asn Arg Arg
625                 630                 635                 640
Arg Met Gln Trp Ala Val Arg Gln Thr Ala Lys Phe Leu Glu Asp Thr
                645                 650                 655
Ala Arg Pro Leu Gly Leu Ile Val Arg Gln Val Ser Ser Ala Tyr Thr
            660                 665                 670
Ser Arg Phe Cys Ser Ser Cys Gly His Pro Gly Ala Arg Val Ser Leu
        675                 680                 685

Pro Gly Gln Lys Asn Trp Glu Lys Phe Tyr Ala Glu Lys Tyr Gly Lys
    690                 695                 700
Glu Arg Lys Met Ile Ala Val Ala Gly Gly Gln Phe Phe Cys Cys Pro
705                 710                 715                 720
Ala Cys Lys Lys Ile Ile Asn Ala Asp Ile Asn Ala Ser Leu Asn Met
                725                 730                 735
His Lys Val Phe Tyr Gln Asn Phe Ile Trp Pro Gly Lys Ile Asp Lys
            740                 745                 750
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Lys Asp Thr Lys Asn Phe Ile Trp Gln Gly Lys Asn Tyr Asn Trp Asp

755 760 765

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

770 775 780

Lys Lys Glu Asp Asp Ile Pro Tyr

785 790

<210> 42

<211> 1382

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12b sequence

<400> 42

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

1 5 10 15

Glu Arg Phe Arg Ile Ile Leu Ser Arg Met Gly Ile Asn Gln Gln Gln

20 25 30

Glu Gln Glu Trp Leu Asp Ala Cys Arg Pro Ala Leu Thr Ala Ser Ile

35 40 45

Arg Glu Asp Ala Val Trp Ile Asp Arg Ser Ala Cys Phe Ala Glu Ala

50 55 60

Gln Gln His Tyr Pro Gly Leu Ser Ser Glu Trp Ala Arg Glu Thr Leu

65 70 75 80

Phe Asp Phe Leu Gly Gly Glu Asn Asp Tyr Phe Ala Leu Pro Asp Pro

85 90 95

Glu Ala Ala Pro Ser Ser Glu Ala Lys Asp Phe Val Gln Lys Ala Gly

100 105 110

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

115 120 125

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

130 135 140

Ile Val Gly Arg Cys Gly Cys Asp Ala Leu Ala Val Leu Leu Thr Thr

145 150 155 160

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

165 170 175

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

180 185 190

Lys Ala Leu Glu Lys Val Arg Asp Ala Pro Glu Val Thr Asp Ala Leu

195 200 205

Trp Arg Gln Thr Ala Asp Thr Leu Arg Gln Glu Ala Val Ala Gln Ser

210 215 220

Ser Arg Ala Ala Gly Gly Ser Gly Val Pro Ala Trp Met Pro Ala Trp

225 230 235 240

Arg Glu Asp Met Glu Ala Arg Leu Gly Met Pro Tyr Arg Gly Ala Arg

245 250 255

Asp Tyr Ile Trp Glu His Ser Val Met Leu Asp His Ala Leu Arg Arg

260 265 270

Val Ser Ser Ala His Thr Trp Ile Lys Arg Ala Glu Ala Lys Arg Arg

275 280 285

Arg Phe Gln Gln Asp Ala Asp Lys Ile Gly Ser Ile Pro Ala Lys Ala

290 295 300

Arg Glu Trp Leu Asp Ala Phe Arg Glu Arg Arg Phe Ser Ala Ser Gly

305 310 315 320

Ala Leu Arg Gly Tyr Leu Ile Arg Glu Arg Ala Ile Asp Gly Trp Asp

325 330 335

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

340 345 350

Gln Arg Ile Ala Ala Ala Arg Asp Val Gln Ala Asn Leu Asp Glu Asp

355 360 365

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

370 375 380

Glu Gly Asp Pro Gln Pro Cys Leu Ala Asp Asp Asp Ala Ile Cys Val

385 390 395 400

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

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

515 520 525
Phe Gly Arg Asp Pro Ser Ala Thr Val Ser Arg Ala Asp Arg Leu Gly
530 535 540
Arg Val Ala Ala Ser Gln His Pro Glu Ala Ala Val His Val Ala Lys
545 550 555 560
Val Phe Glu Gln Gln Asp Trp Asn Gly Arg Leu Gln Val Pro Arg His
565 570 575
Glu Leu Gln Arg Leu Ala Asp Leu Val Tyr Gly Lys Gly Gly Asp Pro

580 585 590
Asp Phe Ala Lys Leu Gly Ser Leu Asp Glu Arg Arg Thr Arg Arg Gln
595 600 605
Trp Glu His Leu Ser Trp Phe Leu Thr Thr Ser Thr Thr Ile Gln Pro
610 615 620
Arg Gly Pro Trp Leu Asp Tyr Val Ala Gln Gly Leu Pro Gln Gly Ile
625 630 635 640
Gln Tyr Lys Lys Gly Arg Asn Gly Tyr Tyr Leu Glu Tyr Ala Ala Asn

645 650 655

Gln Gly Arg Lys Arg Arg Ala Arg Leu Cys Leu Ala Arg Leu Pro Gly

660 665 670

Leu Arg Val Leu Ser Leu Asp Leu Gly Asp Arg Tyr Ala Ala Ala Cys

675 680 685

Ala Val Trp Glu Thr Leu Thr Arg Glu Gln Ile Thr Gln Glu Cys His

690 695 700

Gln Ala Gly His Pro Gly Pro Ser Gln Asp Asp Leu Phe Ile His Leu

705 710 715 720

Arg His Arg Thr Gly Lys Pro Gln Lys Ser Gly Arg Asn Lys Gly Lys

725 730 735

Pro Val Thr Lys Thr Thr Ile Tyr Arg Arg Ile Gly Pro Asp Leu Leu

740 745 750

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

755 760 765

Phe Leu Ile Arg Leu Gln Gly Glu Asp Arg Pro Ala Arg Phe Ala Ser

770 775 780

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

785 790 795 800

Pro Pro Leu Ala Asp Arg Pro Arg Val Asp Asp Leu His Arg Asp Met

805 810 815

Val Arg Leu Ala Arg Leu Gly Leu Arg Arg Leu Ala Asp Ala Ala Arg

820 825 830

Ile Ala Phe Ala Met Thr Ala Thr Lys Lys Pro Ile Ser Gly Gly Arg

835 840 845

Glu Glu Thr Leu Ala Thr Glu Gln Arg Ile Glu Phe Leu Gln Asp Ala

850 855 860

Leu Val Arg Trp Gln Ala Leu Ala Ala Ser Ser Arg Tyr Arg Asp Asp

865 870 875 880

Trp Ala Arg Gln Ala Trp Gln Glu Trp Ile Val Glu Lys Leu Gly Gly

885 890 895

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

900 905 910

Thr Arg Val Glu Thr Ala Arg Arg Ser Leu Arg Glu Val Ala Ala Lys

915 920 925

Leu Ser Asn Pro Gln Ser Ser Ser Ala Thr Glu Leu His Gly Leu Trp

930 935 940

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

945 950 955 960

Trp Leu Arg Arg Leu Ile Leu Pro Arg Arg Lys Asp Tyr Gln Gln Ala

965 970 975

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

980 985 990

Thr Ile Arg Gln Leu Tyr Gln Val Leu Lys Ala Phe Arg Met Arg Pro

995 1000 1005

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

1010 1015 1020

Ser Leu Ala Ser Phe Gly Arg Arg Ile Leu His His Arg Glu Arg

1025 1030 1035

Leu Arg Gln Gln Arg Ile Lys Gln Leu Ala Ser Arg Leu Val Glu

1040 1045 1050

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

1055 1060 1065

Arg Arg Arg Pro Arg Gln Ser Val Asp Ala Pro Cys His Ala Val

1070 1075 1080

Val Ile Glu Asn Leu Glu Arg Tyr Lys Pro Glu Asp Ser Arg Leu

1085 1090 1095

Arg Arg Glu Asn Arg Gln Leu Met Asn Trp Gln Ala Arg Asn Leu

1100 1105 1110

Arg Lys Tyr Ile Val Glu Gly Cys Glu Leu His Gly Leu Leu Phe

1115 1120 1125

Val Glu Val Trp Pro Ala Tyr Thr Ser Arg Gln Asp Thr Arg Thr

1130 1135 1140

Gly Ala Pro Gly Val Arg Cys Glu Asp Val Pro Arg Ser Val Leu

1145 1150 1155

Glu Glu Ala Thr Arg Arg Ile Arg Ala Leu Gly Ser Ala Pro Ser

1160 1165 1170

Gly Ser Ser Arg Gly Arg Ser Glu Thr Arg Phe Glu Arg Glu Val

1175 1180 1185

Cys Arg Trp Ile His Glu Phe Asn Arg Val Val Gly Ser Ser Ser

1190 1195 1200

Gly Leu Ser Pro Arg Gln Ser Val Leu Lys Ala Phe Leu Asp His

1205 1210 1215

Gln Ala Ala Ile Pro Thr Trp Arg Ser Thr Val Arg Leu Pro Arg

1220 1225 1230

Arg Gly Gly Glu Leu Phe Val Ser Ala Asp Ala Asn Ser Pro Leu

1235 1240 1245

Ala Asn Gly Leu Gln Ala Asp Leu Asn Ala Ala Ala Asn Ile Gly

1250 1255 1260

Leu Lys Ala Leu Thr Asp Pro Asp Trp Met Gly Ala Trp Trp Phe

1265 1270 1275

Val Leu Val Lys Arg Asp Ser Gly Gln Pro Val Pro Gln Gln Val

1280 1285 1290

Gln Gly Ser Pro Ile Trp Glu Ser Cys Thr Arg Leu Ser Ser Pro

1295 1300 1305

Ala Thr Val Asp Ser Ser Asp Ser Pro Ala Gly Ala Arg Arg Ser

1310 1315 1320

Lys Gly Arg Gly Ala Arg Gly Arg Ala Arg Ala Thr Glu Tyr Arg

1325 1330 1335

Trp Ser Pro Leu Ser Ala Met Thr Met Pro Asp Asn Lys Thr Trp

1340 1345 1350

Trp Pro Thr Arg Asp Tyr Trp Pro Glu Ile Glu Arg Gln Ile Ala

1355 1360 1365

Asp Arg Leu Leu Arg Glu Gln Ile Asp Pro Glu Asn Arg Phe

1370 1375 1380

<210> 43

<211> 1272

<212> PRT

<213> Unknown

<220><223>

Description of Unknown:

cas12c sequence

<400> 43

Met Lys Lys Thr Ser Pro Leu Lys Arg Ser Ala Leu Arg Thr Ala Arg

1 5 10 15

Arg Gln Ile Ala Arg Gly Cys Leu Pro Ile Gly Asn Arg Asp Ile Ser

20 25 30

Thr Thr Arg Thr Arg Val Leu Pro Leu Ala Asp Ser Val Ala Asp Ala

35 40 45

Val Trp Asn Gln Ala Arg Thr Ala Ala Leu Thr Leu Arg Gly Phe Gly

50 55 60

Ser Gly Ser Leu Phe Asp Leu Leu Leu Asp Leu His Ala Ser Gly Leu

65 70 75 80

Arg Leu Phe Ser Ser Asn Gly Glu Arg Glu Gly Phe Leu Leu Lys Gln

85 90 95

Lys Phe Asp Ala Gly Lys Phe Asp Arg Ala Ala Ala Lys Asp Val Gly

100 105 110

Glu Asp Met Pro Lys Phe Thr Ala Ala Asn Leu Arg Ala Ala Leu Val

115 120 125

Ala Ile Pro Arg Gly Gly Gly Pro Asp Thr Asp Ala Lys Ala Leu Ala

130 135 140

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

145 150 155 160

Pro Pro Lys Leu Leu Lys Asp Met Ala Lys Glu Leu Ala Met Ala Phe

165 170 175

Pro Thr Trp Lys Glu Leu Ser Thr Ala Asn Gly Glu Val Gly Ala Val

180 185 190

Ile Asp Asp Val Ala Arg Met Tyr Gly Leu Arg Trp Pro Ser Leu Arg

195 200 205

Arg Gly Trp Ala Phe Arg Leu Pro Glu Val Thr Arg Glu Leu Gly Ser

210 215 220

Pro Thr Leu Ala Phe Asp Pro Asp Ala Pro Val Ile Asp Glu Thr Ser

225 230 235 240

Ala Thr Ala Arg Phe Ala Ala Ile Val Ala Arg Tyr Leu Pro Glu Cys

245 250 255

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

260 265 270

Thr Thr Thr Asn Ala Asn Gly Leu Ser Trp Leu Phe Gly Val Gly Leu

275 280 285

Arg Gly Met Arg Asp Leu Pro Val Asp Thr Val Ala Asp Thr Leu Ala

290 295 300

Ile Asp Val Thr Arg Gly Arg Asp Ala Leu Arg Ala Leu Val Asn Asp

305 310 315 320

Ile Lys Ala Leu Pro Arg Leu Gly Glu Phe Gly Asp Arg Val Tyr Val

325 330 335

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

340 345 350

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

355 360 365

His Asp Gln Pro Arg Pro Pro Val Leu Asp Asp Ala Asp Trp Lys Pro

370 375 380

Ala Ile Phe Asp Gly Met Gly Phe Thr Pro Trp Glu Val Glu Asp Met

385 390 395 400

Leu Asp Ala Arg Pro Val Glu Val Ala Arg Leu Arg Leu Ala Leu Gly

405 410 415

Val Leu Ala Gly Thr Thr Pro Ala Val Ala Gly Asp Phe Ala Arg Ala

420 425 430

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

435 440 445

Val Ala Ala Leu Ile Asn Ala Arg Val Lys Val Leu Lys Ala Pro Glu

450 455 460

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

465 470 475 480

Val Ser Ile His Pro Asp Glu Gly Glu Pro Ala Gln Val Ile Pro Gln

485 490 495

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

500 505 510

Asp Val Leu Val Ala Asp Tyr Thr Pro Thr Phe Ala Ala Ala Leu Glu

515 520 525

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

530 535 540

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

545 550 555 560

Asp Met Val Ala Arg Val Thr Arg Arg Gly Ser Pro Ser Leu Gly His

565 570 575

Ala Phe Leu Ala Ala Cys Ala Val Gln Gly Leu Thr Arg Pro Gly Thr

580 585 590

Ala Thr Glu Arg Ser Leu Arg Gly His Ile Leu Ser Gly Glu Gln Ala

595 600 605

Leu Phe Val His Pro Tyr Ala Arg Ala Arg Ser Ile Val Arg Leu Glu

610 615 620

His Ala Gly Leu Leu Arg Leu Asp Leu Asp Ala Leu Leu Thr Ala Met

625 630 635 640

Glu Arg Asp Ala Glu Gln Arg Ala Asp Val Arg Glu Gln Ile Val Leu

645 650 655

Arg Phe Thr Arg Gln Ser Leu Leu Leu Gly Gly Leu Pro Gly Arg Ile

660 665 670

Arg Leu Ala Lys Val Pro Trp Thr Gln Glu Ala Ala Ala Ala Ser Gly
675 680 685
Val Arg Gly Ala Pro Trp Leu Lys Leu His Pro Asp Asp Ala Gly Thr

690 695 700
Val Ala Arg Ser Glu Val Ile Lys Ala Phe Thr Ala Arg Phe His Leu
705 710 715 720
Ser Ala Asn Gly Leu Leu Tyr Arg Leu Asn Arg Met Arg Phe Leu Glu
725 730 735
Arg Tyr Asp Ile Arg Cys Phe Ile Gly Asp Thr Leu Leu Phe Ala Pro
740 745 750
Lys Ala Gly Ala Trp Thr Pro Pro Glu Gln Tyr Arg His Gly Lys Tyr

755 760 765
Ala His Trp Leu Ser His Pro Asp Leu Pro Arg Thr Glu Gly Gly Ala
770 775 780
Val Asp Val Val Pro Ala Ala Arg Trp Leu Thr Glu Ala Ser Arg Arg
785 790 795 800
Ala Asp Glu Asp Gly Arg Ala Ser Ala Val Ala Leu Leu Ala Gln Phe
805 810 815
Pro His Glu Trp Val Ala Ala Cys Glu Phe Glu Gly Ala Pro Val Tyr

820 825 830
Glu Gly Val Phe Pro Cys Glu Gly Lys Ile Gly Gly Trp Met Lys Arg
835 840 845
Arg Gly Tyr Arg Leu Ala Pro Pro Arg His Phe Ala Gly Glu Leu Leu
850 855 860
Ala Ala Phe Lys Asp Ala Ser Val Ser Pro His Gly Leu Thr Phe Glu
865 870 875 880
Arg Glu Met Leu Arg Glu Gly Thr Thr Val Arg Glu Leu Ser Arg Arg

885 890 895
Val Val Ala Ala Tyr Pro Ile Ala Val Pro Thr His Pro Asp Ala Glu
900 905 910
Arg Pro Trp Ser Pro Leu His Leu Met Gly Leu Asp Leu Gly Glu Ala

915 920 925

Gly Leu Gly Val Cys Leu Arg His Ile Gly Thr Gly Ala Glu Thr Thr

930 935 940

Leu Leu Leu Pro Val Arg Lys Thr Arg Leu Leu Ala His Arg Glu Glu

945 950 955 960

His Tyr Arg Arg Lys Val Gln Pro Arg Gln Ala Phe Arg Lys Gly Tyr

965 970 975

Gly Asp Ala Met Glu Leu Ala Val Lys Ala Ala Ile Gly Glu Val Cys

980 985 990

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

995 1000 1005

Glu Ser Ala Val Ala Gln Ala Arg Gly Ser Asn Lys Met Ile Gln

1010 1015 1020

Arg Val Phe Ala Gly Val Val Gln His Tyr Thr Phe Val Ala Asn

1025 1030 1035

Asn Gly Ala Ala Gln Thr Val Arg Gln Ser His Trp Phe Gly Ala

1040 1045 1050

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

1055 1060 1065

Arg Gln Met Thr Glu Lys Gln Leu Leu Lys Ala Lys Ala Glu Ala

1070 1075 1080

Val Phe Arg Pro Ala Met Gly Phe Pro Gly Val Met Ala Ser Gly

1085 1090 1095

Tyr Arg Thr Ser Leu Val Cys Ala Cys Cys Gly Glu Asp Val Leu

1100 1105 1110

Asp Ala Val Asp Ala Ala Ala Glu Gly Gly Gln Val Ala Leu Thr

1115 1120 1125

Thr Asp Ala Glu Gly Ser Gly Val Leu Asp Leu Gly Gly Arg Ser

1130 1135 1140

Leu Arg Ile Lys Leu Glu Ala Pro Ser Pro Asn Pro Ile Val Gln

1145 1150 1155

Lys Ala Ala Arg Arg Lys Arg Arg Arg Thr Pro Trp Glu Ala Leu
1160 1165 1170
Ala Asp Arg Thr Trp Thr Leu Thr His Lys Thr Asp Arg Ala Asp
1175 1180 1185
Leu Val Ala Thr Leu Arg Arg Gly Leu Arg Arg Pro Pro Ala Ser

1190 1195 1200
Val Gln Gly His Ala Thr Ser Gly Trp Glu Phe His Cys Ala Ala
1205 1210 1215
Cys Gly His Ile Ala Gln Ala Asp Val Asn Ala Ala Thr Asn Leu
1220 1225 1230
Val Arg Arg Tyr Asp Asp Arg Val Arg Lys Met Glu Gln Ala Arg
1235 1240 1245
Ala His Trp Asp Asp Pro Ser Val Arg Ala Lys Leu Ala Ser Glu

1250 1255 1260
Leu Ala Glu Arg Ala Ala Ala Arg Ser
1265 1270

<210> 44
<211> 1262
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
cas12c sequence
<400> 44
Met Leu Thr Thr Lys Phe Lys Leu Glu Leu Pro Ala Gly Cys Pro Leu
1 5 10 15
Arg Glu Asp Ala Ala Thr Phe Asp Glu Cys Arg Lys Leu Tyr Asp Val
20 25 30

Val Glu Gly Cys Gly Asn Gly Thr Leu Thr Gly Phe Leu Phe Ser Val
35 40 45
Ile Leu Ser Gly Phe Arg Ile Phe Pro Asp Gly Lys Thr Ala Glu Ile
50 55 60
Phe Ala Asn Arg Ser Val Tyr Asp Glu Asp Glu Phe Arg Ser Ala Leu

65 70 75 80

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

85 90 95

Ile Lys Arg Leu Gln Met Glu Val Arg Ala Arg Gly Asn Lys Asp Asn

100 105 110

Arg Phe Val Ala Glu Val Met Met Lys Glu Tyr Arg Gln Thr Leu Cys

115 120 125

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

130 135 140

Phe Glu Glu Met Ala Arg Glu Leu Thr Ser Arg Tyr Arg Ser Trp Asn

145 150 155 160

Glu Leu Lys Gly Asp Leu Leu Gly Ala Cys Lys Ala Val Asp Ala Ala

165 170 175

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

180 185 190

Ala Ala Ala Arg Arg Leu Pro Lys Asp Ser Thr Ile Val Phe Asp Pro

195 200 205

Gln Ser Pro Cys Ile Asp Val Gln Thr Ile Gly Val Asp Ala Met Pro

210 215 220

Tyr Ala Ala Val Ser Thr Ile Leu Ser Tyr Pro Glu Ser Val Gly Glu

225 230 235 240

Lys Arg Arg Asp Phe Val Gln Asn His Leu Thr Thr Pro Ser Ala Ala

245 250 255

Gly Leu Ser Trp Leu Phe Asn Arg Gly Leu Glu Leu Phe Ser Glu Glu

260 265 270

Ser Val Glu Glu Leu Cys Arg Leu Phe His Val Pro Glu Asp Gln Arg

275 280 285

Thr Arg Ile Val Gln Ile Gln Asn Ala Ala Arg Ala Thr Pro Arg Gln

290 295 300

Ser Phe Phe Leu Lys Lys Gly Gly Ala Pro Leu Gly Tyr His Asp Phe

305 310 315 320

Arg Ser Ala Phe Ala Gly Arg Ile Asn Ser Trp Thr Ala Asn Tyr Leu
325 330 335
Asn Arg Leu Glu Glu Leu Gln Gly Leu Leu His Asp Leu Thr Asp Glu
340 345 350

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

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

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

Val Leu Gln Arg Val Ala Arg Val Val Arg Asp Arg Ser Asp Ala Cys
545 550 555 560
Ala Glu Asn Val Arg Gln Trp Phe Leu Lys Glu Asn Val Phe Ala Glu

565 570 575

Arg Lys Asp Phe Asn Lys Phe Phe Phe Asn Arg Leu Gly Asn Leu Tyr

580 585 590

Val Ser Pro Phe Ser Asn Arg Arg His Ala Gly Tyr Lys Leu Ser Asp

595 600 605

Gly Leu Val Glu Arg Ser Gly Ala Val Trp Arg Glu Leu Leu Ala Leu

610 615 620

Val Lys Glu Met Arg Gly Ala Tyr Ala Ser Phe Ser Glu Ala Gly Glu

625 630 635 640

Thr Phe Leu Arg Leu Glu Ser Leu Leu Met Gly Met Arg Ile Gly Ala

645 650 655

Leu Thr Lys Asn Ile Pro Ala Glu Val Ala Ala Leu Arg Leu Asp Asp

660 665 670

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

675 680 685

Gln Ala Glu Val Pro Pro Ser Val Leu Ala Lys Ala Phe Asn Val Tyr

690 695 700

Val Ser Leu Leu Ser Gly Cys Leu Ile Ala Leu Arg Arg Glu Arg Phe

705 710 715 720

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

725 730 735

Val Pro Lys Glu Lys Ser Trp Pro Met Pro Ser Arg Tyr Glu Ala Ser

740 745 750

Pro Ser Trp Thr Pro Ile Phe Glu Asn Asp Val Leu Val Arg Leu Ser

755 760 765

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

770 775 780

Trp Gly Arg Thr Thr Asp Pro Val Leu Lys Lys Ala Leu Arg Glu Leu

785 790 795 800

Phe His Gln Leu Pro His Asp Trp Cys Cys Gln Val Ser Val Arg Ser

805 810 815

Ser Gly Asp Met Thr Pro Ala Lys Arg Lys Glu Asp Asp Arg Asp Val
820 825 830
Leu Ile Val Glu Lys Lys Gly Lys Tyr Asp Ser Thr Ile Ile Ser Lys
835 840 845
Lys Ile Ala Ala Thr Ala Leu Val Arg Leu Val Gly Pro Ser Thr His
850 855 860

Lys Glu Arg Leu Asn Arg Leu Leu Leu Asp Val Gly Glu Val Ala Cys
865 870 875 880
Asp Met Thr Leu Leu Ala Asp Gln Glu Ile Leu Gln Lys Val Glu Asp
885 890 895
Asp Arg Val His Leu Ser Pro Gly Lys Leu Gln Phe Ser Leu Ser Val
900 905 910
Pro Ile Ser Thr Pro Ala Glu Gln Cys Glu Asp Glu Val Lys Ser Glu
915 920 925

Arg Lys Ser Thr His Phe Arg Arg Ile Val Ala Ile Asp Gln Gly Glu
930 935 940
Arg Gly Phe Ala Phe Ala Val Phe Arg Leu Glu Asp Ala Gly Lys Lys
945 950 955 960
Gly Ala Gln Pro Ile Ala Gln Gly Phe Val Asn Ile Pro Ser Ile Arg
965 970 975
Arg Leu Ile Ala Arg Val His Ser Tyr Arg Lys Gly Lys Gln Ser Val
980 985 990

Gln Lys Phe Ser Gln Arg Phe Asp Ser Thr Met Phe Thr Leu Arg Glu
995 1000 1005
Asn Val Ala Gly Asp Val Cys Gly Ala Ile Ala Gly Leu Met Ser
1010 1015 1020
Arg Tyr Arg Ala Phe Pro Val Leu Glu Arg Gln Val Ser Asn Leu
1025 1030 1035
Ala Ser Gly Gly Lys Gln Leu Glu Leu Val Tyr Lys Met Val Asn
1040 1045 1050

Ala Arg Phe Leu Asp Asp Arg Ile Pro Met His Ser Leu Glu Arg

1055 1060 1065

Thr Ser Trp Trp Cys Gly Thr Ser Asp Trp Val Ile Pro Asp Leu

1070 1075 1080

Trp Val Glu Val Pro Glu Ser Tyr Ala Val Lys Ala Lys Lys Asp

1085 1090 1095

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

1100 1105 1110

Thr Pro Gly Ala Gly Val Asn Ala Lys Trp Thr Ser Arg Ile Cys

1115 1120 1125

Ser Gln Cys Gly Gly Asn Ala Met Glu Leu Ile Glu Lys Ala Arg

1130 1135 1140

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

1145 1150 1155

Thr Leu Phe Gly Arg Thr Leu Arg Leu Tyr Lys Arg Pro Ser Glu

1160 1165 1170

Glu Arg Ser Arg Glu Ala Arg Arg Arg Asn Glu Arg Ala Pro Trp

1175 1180 1185

Thr Glu Pro Arg Ala Asp Val Arg Leu Ser Leu Asp Asp Phe Arg

1190 1195 1200

Arg Ala Val Ala Glu Asn Met Arg Arg Gln Pro Lys Ser Leu Gln

1205 1210 1215

Ser Arg Asp Thr Ser Gln Ser Arg Tyr Phe Cys Val Phe Thr Asp

1220 1225 1230

Cys Arg Cys His Asn Lys Glu Gln His Ala Asp Ile Asn Ala Ala

1235 1240 1245

Val Asn Ile Gly Arg Arg Phe Leu Glu Ser Leu Leu Arg Glu

1250 1255 1260

<210> 45

<211> 1262

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12c sequence

<400> 45

Met Arg Arg Gln His His Gly Gly Gln Asn Ala Arg Asp Trp Arg Arg
1 5 10 15
Lys Val Ala Ala Ala Ala Leu Arg Gln Lys Glu Ser Val Phe Thr Tyr

20 25 30
Lys Phe Gly Leu Ser Val Asn Asp Gly Asp Phe Asp Phe Asp Ala Ala
35 40 45
Ala Arg Thr Tyr Asp Ile Thr Glu Gly Ile Glu Arg Gly Ser Leu Ile
50 55 60
Gly Leu Val Cys Ala Val His Leu Ser Gly Phe Arg Leu Phe Ser Lys
65 70 75 80
Val Ala Glu Thr Arg Gln Phe Leu Asn Arg Ser Arg Tyr Pro Glu Asn

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

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

210 215 220
Leu Ala Phe Asp Pro Glu Ser Pro Phe Leu Asn Met Thr Gly Asn Glu

225 230 235 240

Asp Ile Trp Leu His Gln Val Val Ala Val Cys Ala Gly Arg Leu Lys

245 250 255

Arg Tyr Met Pro Glu Ile Asp Pro Ser Ser Arg Lys Phe Ala Ser Arg

260 265 270

Leu Thr Asp Ser Ile Val Ser Ser Gln Asn Asn Gly Leu Ser Trp Leu

275 280 285

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

290 295 300

Ala Glu Thr Leu Ser Val Ser Gln Asn Glu His Arg Arg Val Glu Gln

305 310 315 320

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

325 330 335

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

340 345 350

Trp Val Ser Asn Tyr Trp Lys Arg Ile Cys Glu Leu Thr Val Leu His

355 360 365

Ser Gln Pro Pro Asp Ile Thr Ile Pro Glu Gly Leu Leu Ala Ser Glu

370 375 380

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

385 390 395 400

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

405 410 415

Leu Phe Val Leu Ser Gly Asp Gly Val Pro Arg Ala Asp Asp Ile Ala

420 425 430

Thr Val Glu Asp Val Ala Gly Glu Leu Ala Glu Leu Thr Gly Gln Leu

435 440 445

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

450 455 460

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

465 470 475 480

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

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

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

660 665 670
Thr Phe Val Phe Thr Thr Arg Leu Ser Gly Leu Pro Ala Gln Val Pro
675 680 685
Gly Tyr Leu Ala Lys Pro Lys Ser Asp Leu Thr Asn Ile Pro Pro Leu
690 695 700
Leu Ala Ala Gln Leu Asp Val Asp Glu Val Ser Arg Asp Val Ala Leu
705 710 715 720
Arg Ala Phe Asn Leu Phe Asn Ser Ala Ile Asn Gly Leu Ser Phe Arg

725 730 735

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

740 745 750

His Asp Glu Leu Phe Tyr Val Pro Lys Ala Arg Ala Trp Lys Pro Pro

755 760 765

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

770 775 780

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

785 790 795 800

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

805 810 815

Leu Ser Gln Ala Pro His Asp Trp Phe Val Glu Leu Asp Leu Arg His

820 825 830

Asp Lys Met Pro Gln Leu Ala Gly Leu Pro Val Lys Met Asn Ala Asp

835 840 845

Gly Leu Lys Gly Trp Arg Ala Arg Arg Arg Pro Thr Phe Arg Leu Ala

850 855 860

Gly Pro Pro Ser Phe Lys Thr Trp Leu Asp Arg Ala Leu Thr Ser Thr

865 870 875 880

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

885 890 895

Gln Ser Leu Arg Val Glu Asp Gly Glu Val Arg Leu Ser Ala Glu Pro

900 905 910

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

915 920 925

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

930 935 940

Asp Leu Gly Glu Arg Arg Ile Gly Tyr Ala Val Phe Ser Leu Pro Ala

945 950 955 960

Leu Leu Lys Ser Gly Asn Pro Thr Arg Val Lys Pro Thr Val Val Gly

965 970 975

Ser Val Ala Ile Pro Ala Phe Arg Arg Leu Met Ala Ala Val Arg Arg

980 985 990

His Arg Gly Ser Arg Gln Pro Asn Gln Lys Val Ser Gln Thr Tyr Ser

995 1000 1005

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

1010 1015 1020

Asn Arg Ile Asp Thr Leu Cys Glu Arg Tyr Arg Ala Phe Pro Val

1025 1030 1035

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

1040 1045 1050

Lys Leu Ile Tyr Gly Thr Val Leu Arg Arg Tyr Thr Phe Ser Asn

1055 1060 1065

Val Asp Ala His Lys Ser Ala Arg Ser Ala Tyr Trp Tyr Ser Ala

1070 1075 1080

Asn Arg Trp Gln His Pro Tyr Leu Phe Val Arg Glu Trp Asn Lys

1085 1090 1095

Ala Gln Arg Thr Phe Thr Gly Ser Ala Lys Pro Leu Ala Ile Tyr

1100 1105 1110

Pro Gly Val Thr Ile His Pro Ala Gly Thr Ser Gln Ile Cys His

1115 1120 1125

Arg Cys Gly Arg Asn Ala Leu Arg Ala Leu Arg Asn Met Pro Asp

1130 1135 1140

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

1145 1150 1155

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

1160 1165 1170

Leu Lys Thr Phe Lys Arg Arg Lys Gln Arg Pro Pro Leu Asn Met

1175 1180 1185

Pro Val Pro Glu Gly Ala Arg Pro Arg Asp Gln Leu Glu Arg Val

1190 1195 1200

Leu Arg Arg Asn Met Arg Gln Gln Pro Gln Ser Glu Met Ser Pro

1205 1210 1215

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

1220 1225 1230

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

1235 1240 1245

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

1250 1255 1260

<210> 46

<211> 1283

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12c sequence

<400> 46

Met Thr His Ala Lys Lys Ile Pro Phe Pro Val Leu Lys Arg Ser Thr

1 5 10 15

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

20 25 30

Glu Arg Pro Phe Asn Ser Thr Val Thr Arg Val Val Pro Val Lys Asp

35 40 45

Pro Val Ser Asp Gln Val Trp Ala Val Ala Arg Glu Ala Ala Met Thr

50 55 60

Leu Arg Gly Phe Gly Gln Gly Ser Leu Phe Asp Met Leu Ile His Leu

65 70 75 80

His Ala Asp Gly Phe Arg Leu Phe Pro Ser Gly Arg Glu Arg Glu Ala

85 90 95

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

100 105 110

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

115 120 125

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

130 135 140

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

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

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

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

Ile Gln Gly Asp Thr Ala Val Phe Asp Gly Met Pro Phe Ser Ala Glu
385 390 395 400

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

Glu His Ala Val Lys Val Leu Val Gly Lys Glu Arg Thr Ser Thr Leu
420 425 430

Gly Tyr Gln Lys Ala Val Asp Asp Val Asp Glu Phe Gly Val Trp Ala
435 440 445

Ser Ser Val Asp Ala Val Ile Gly Gln Ile Asn Ala Arg Leu Lys Thr
450 455 460

Leu Glu Arg Ala Gln Glu Pro Leu Gly Lys Leu Met Gly Asp Gly Lys
465 470 475 480

Leu Lys Arg Leu Val Asn Ile His Glu Pro Glu Gly Pro Ala Val Glu
485 490 495

Ile Ile Pro Val Leu Asp Gln Glu Leu Gln Asp Val Leu Thr Ser Cys
500 505 510

Arg Thr Ala Phe Ala Asp Leu Glu Ala Arg Tyr Pro Met Thr Val Ala
515 520 525

Lys Ala Gln Arg His Ala Glu Ala Glu Val Arg Asn Ala Leu Glu Leu
530 535 540

Ala Ser Arg Lys Glu Gly Gly Leu Ser Leu Ala Ser Ala Asp Val Pro
545 550 555 560

Ala Leu Ala Lys Arg Lys Ile Leu Glu Pro Ile Ile Ser Ile Ala Arg
565 570 575

Arg Ser Ser Pro Ala Met Ala Thr Ala Val Leu Thr Glu Cys Leu Arg
580 585 590

Gln Lys Leu Ile Val Lys Gly Thr Gly Ser Glu Arg Ser Leu Arg Gly
595 600 605

Tyr Val Leu Ser Gly Glu Gln Val Ile Tyr Ala His Pro Leu Ser Arg
610 615 620

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

625 630 635 640

Ala Leu Glu Phe Leu Asp Ala Leu Gln Lys Asp Ala Thr Gln Arg Thr

645 650 655

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

660 665 670

Leu Ser Ala Leu Pro Asp Arg Ile Glu Ile Gly Ala Ile Ser Trp Gln

675 680 685

Thr Pro Ser Gln Asn Gln His Ala Pro Trp Ala Asn Leu Arg Pro Val

690 695 700

Asn Gly Thr Val Gly Arg Ser Glu Thr Ile Lys Ser Phe Thr Ala Val

705 710 715 720

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

725 730 735

Phe Met Glu Lys Tyr Asp Leu Arg Cys Phe Ile Gly Ser Thr Leu Leu

740 745 750

Phe Ser Pro Lys Asn Ala Asp Trp Ala Pro Pro Pro Gln Tyr Arg His

755 760 765

Gly Arg Phe Ser Ala Leu Leu Ala Arg Ser Asp Phe Pro Trp Glu Gly

770 775 780

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

785 790 795 800

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

805 810 815

Ala Leu Leu Ala Gln Leu Pro His Asp Trp Val Val Cys Cys Asp Phe

820 825 830

Asp Gly Ala Pro Ser Tyr Glu Gly Ala Phe Val Ser Ala Gly Glu Val

835 840 845

Ser Ala Trp Ala Lys Arg Ser Gly Tyr Leu Leu Thr Pro Pro Arg His

850 855 860

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

865 870 875 880

His Gly Leu Thr Phe Glu Arg Met Leu Glu Arg Asp Gly Asp Ser Val
885 890 895
Ile Glu Thr Gly Arg Arg Val Thr Ala Ala Phe Pro Ile Thr Gln Glu
900 905 910

Val Ala Pro Ala Ala Gln Pro Trp Lys Pro Arg His Leu Ala Gly Leu
915 920 925
Asp Leu Gly Glu Ala Gly Leu Gly Val Cys Leu Lys Asn Leu Asp Asn
930 935 940
Gly His Glu Gln Thr Leu Leu Leu Lys Thr Arg Lys Thr Arg Leu Leu
945 950 955 960
Ala His Ser Ala Glu His Tyr Arg Arg Lys Asp Gln Pro Arg Gln Val
965 970 975

Phe Arg Lys Gln Tyr Asn Gln Ser Ser Glu Asn Ala Ile Lys Ala Ala
980 985 990
Ile Gly Glu Val Cys Gly Leu Ile Asp Asn Leu Ile Ala Arg Tyr Asp
995 1000 1005
Ala Val Pro Val Phe Glu Ser Gln Ala Ala Ala Ala Arg Gly Ser
1010 1015 1020
Asn Arg Met Val Ala Arg Val Tyr Ala Gly Val Leu Gln Arg Tyr
1025 1030 1035

Thr Tyr Val Val Gly Asn Gly Ala Ala Asp Ala Thr Arg Thr Ser
1040 1045 1050
His Trp Leu Gly Ala Asn Arg Trp Ser Tyr Ser Phe Gly Ala Asp
1055 1060 1065
Val Ile Pro Lys Val Arg Asp Leu Ser Pro Glu Val Leu Arg Ser
1070 1075 1080
Ile Lys Lys Pro Glu Asn Val Phe Arg Asp Ala Leu Gly Phe Pro
1085 1090 1095

Gly Val Leu Ala Asn Ala Trp Arg Thr Ser Met Ile Cys Ser Val
1100 1105 1110
Cys Gly Thr Asp Pro Ile Gly Ala Leu Glu Glu Ala Ile Ala Ala

1115 1120 1125

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

1130 1135 1140

Asp Leu Gly Asp Gly Arg Lys Val Thr Leu Arg Val Glu Val Pro

1145 1150 1155

Thr Ser Ser Ala Leu Thr Lys Arg Glu Ala Ser Arg Arg Lys Arg

1160 1165 1170

Arg Ala Pro Trp Glu Ala Lys Val Gly Thr Val Trp Thr Leu Thr

1175 1180 1185

Arg Lys Ser His Arg Asp Asp Leu Leu Thr Thr Ile Arg Arg Ser

1190 1195 1200

Leu Arg Arg Pro Ser Ser Thr Phe Gln Gly Ser Thr Thr Lys Gln

1205 1210 1215

Trp Glu Phe His Cys Pro Cys Cys Gly Gln Ile Gln Gln Ala Asp

1220 1225 1230

Val Asn Ala Ala Ser Asn Leu Val Arg Arg Tyr Phe Val Arg Ala

1235 1240 1245

Ser Asp Asn Ala Arg Ala Arg Gln His Trp Ala Asp Asp Ser Lys

1250 1255 1260

Arg Leu Ala Phe Ile Ala Ser Met Gly Pro Asp Arg Ser Ala Arg

1265 1270 1275

Glu Glu Lys Val Ser

1280

<210> 47

<211> 1125

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12d sequence

<400> 47

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

1 5 10 15

Val Tyr Thr Gly Lys Ala Ala Ile Arg Ser Ile Lys Tyr Pro Leu Val
20 25 30
Ala Pro Asn Lys Thr Ala Leu Asn Asn Leu Ser Glu Lys Ile Ile Tyr
35 40 45

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

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

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

Arg Glu Ser Leu Leu Gly Leu Asp Asn Asn Phe Ser Ala Phe Ser Asn
245 250 255
Tyr Phe Asn Glu Leu Phe Asn Leu Leu Ser Arg Gly Glu Ile Lys Lys

260 265 270

Ile Val Thr Ala Val Leu Ala Val Ser Lys Ser Trp Glu Asn Glu Pro

275 280 285

Glu Leu Glu Lys Arg Leu His Phe Leu Ser Glu Lys Ala Lys Leu Leu

290 295 300

Gly Tyr Pro Lys Leu Thr Ser Ser Trp Ala Asp Tyr Arg Met Ile Ile

305 310 315 320

Gly Gly Lys Ile Lys Ser Trp His Ser Asn Tyr Thr Glu Gln Leu Ile

325 330 335

Lys Val Arg Glu Asp Leu Lys Lys His Gln Ile Ala Leu Asp Lys Leu

340 345 350

Gln Glu Asp Leu Lys Lys Val Val Asp Ser Ser Leu Arg Glu Gln Ile

355 360 365

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

370 375 380

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

385 390 395 400

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

405 410 415

Glu Glu Glu Arg Lys Glu Asp Arg Asp Val Thr Lys Lys Tyr Lys Asp

420 425 430

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

435 440 445

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

450 455 460

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

465 470 475 480

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

485 490 495

Leu Glu Lys Leu Ser Arg Lys Tyr Lys Ile Asn Ala Phe Asn Ser Asn

500 505 510

Arg Phe Lys Gln Ile Thr Glu Gln Val Leu Arg Lys Tyr Asn Asn Gly
515 520 525
Glu Leu Pro Lys Ile Ser Glu Val Phe Tyr Arg Tyr Pro Arg Glu Ser
530 535 540
His Val Ala Ile Arg Ile Leu Pro Val Lys Ile Ser Asn Pro Arg Lys
545 550 555 560

Asp Ile Ser Tyr Leu Leu Asp Lys Tyr Gln Ile Ser Pro Asp Trp Lys
565 570 575
Asn Ser Asn Pro Gly Glu Val Val Asp Leu Ile Glu Ile Tyr Lys Leu
580 585 590
Thr Leu Gly Trp Leu Leu Ser Cys Asn Lys Asp Phe Ser Met Asp Phe
595 600 605
Ser Ser Tyr Asp Leu Lys Leu Phe Pro Glu Ala Ala Ser Leu Ile Lys
610 615 620

Asn Phe Gly Ser Cys Leu Ser Gly Tyr Tyr Leu Ser Lys Met Ile Phe
625 630 635 640
Asn Cys Ile Thr Ser Glu Ile Lys Gly Met Ile Thr Leu Tyr Thr Arg
645 650 655
Asp Lys Phe Val Val Arg Tyr Val Thr Gln Met Ile Gly Ser Asn Gln
660 665 670
Lys Phe Pro Leu Leu Cys Leu Val Gly Glu Lys Gln Thr Lys Asn Phe
675 680 685

Ser Arg Asn Trp Gly Val Leu Ile Glu Glu Lys Gly Asp Leu Gly Glu
690 695 700
Glu Lys Asn Gln Glu Lys Cys Leu Ile Phe Lys Asp Lys Thr Asp Phe
705 710 715 720
Ala Lys Ala Lys Glu Val Glu Ile Phe Lys Asn Asn Ile Trp Arg Ile
725 730 735
Arg Thr Ser Lys Tyr Gln Ile Gln Phe Leu Asn Arg Leu Phe Lys Lys
740 745 750

Thr Lys Glu Trp Asp Leu Met Asn Leu Val Leu Ser Glu Pro Ser Leu

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        755                 760                 765
Val Leu Glu Glu Glu Trp Gly Val Ser Trp Asp Lys Asp Lys Leu Leu
    770                 775                 780
Pro Leu Leu Lys Lys Glu Lys Ser Cys Glu Glu Arg Leu Tyr Tyr Ser
785                 790                 795                 800
Leu Pro Leu Asn Leu Val Pro Ala Thr Asp Tyr Lys Glu Gln Ser Ala
                805                 810                 815

Glu Ile Glu Gln Arg Asn Thr Tyr Leu Gly Leu Asp Val Gly Glu Phe
            820                 825                 830
Gly Val Ala Tyr Ala Val Val Arg Ile Val Arg Asp Arg Ile Glu Leu
        835                 840                 845
Leu Ser Trp Gly Phe Leu Lys Asp Pro Ala Leu Arg Lys Ile Arg Glu
    850                 855                 860
Arg Val Gln Asp Met Lys Lys Lys Gln Val Met Ala Val Phe Ser Ser
865                 870                 875                 880

Ser Ser Thr Ala Val Ala Arg Val Arg Glu Met Ala Ile His Ser Leu
                885                 890                 895
Arg Asn Gln Ile His Ser Ile Ala Leu Ala Tyr Lys Ala Lys Ile Ile
            900                 905                 910
Tyr Glu Ile Ser Ile Ser Asn Phe Glu Thr Gly Gly Asn Arg Met Ala
        915                 920                 925
Lys Ile Tyr Arg Ser Ile Lys Val Ser Asp Val Tyr Arg Glu Ser Gly
    930                 935                 940

Ala Asp Thr Leu Val Ser Glu Met Ile Trp Gly Lys Lys Asn Lys Gln
945                 950                 955                 960
Met Gly Asn His Ile Ser Ser Tyr Ala Thr Ser Tyr Thr Cys Cys Asn
                965                 970                 975
Cys Ala Arg Thr Pro Phe Glu Leu Val Ile Asp Asn Asp Lys Glu Tyr
            980                 985                 990
Glu Lys Gly Gly Asp Glu Phe Ile  Phe Asn Val Gly Asp  Glu Lys Lys
        995                 1000                1005
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Val Arg Gly Phe Leu Gln Lys Ser Leu Leu Gly Lys Thr Ile Lys
1010 1015 1020
Gly Lys Glu Val Leu Lys Ser Ile Lys Glu Tyr Ala Arg Pro Pro
1025 1030 1035
Ile Arg Glu Val Leu Leu Glu Gly Glu Asp Val Glu Gln Leu Leu
1040 1045 1050
Lys Arg Arg Gly Asn Ser Tyr Ile Tyr Arg Cys Pro Phe Cys Gly
1055 1060 1065

Tyr Lys Thr Asp Ala Asp Ile Gln Ala Ala Leu Asn Ile Ala Cys
1070 1075 1080
Arg Gly Tyr Ile Ser Asp Asn Ala Lys Asp Ala Val Lys Glu Gly
1085 1090 1095
Glu Arg Lys Leu Asp Tyr Ile Leu Glu Val Arg Lys Leu Trp Glu
1100 1105 1110
Lys Asn Gly Ala Val Leu Arg Ser Ala Lys Phe Leu
1115 1120 1125

<210> 48

<211

> 1183

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13a sequence

<400> 48

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

50 55 60
Tyr Gln Arg Lys Phe Arg Glu Arg Leu Gly Lys Ala Ile Trp Ala Asp

65 70 75 80

Leu Thr Gly Pro Glu Gly Pro Leu Arg Asp Val Pro Ala Ala Glu Leu

85 90 95

Glu Asp Leu Arg Lys Arg Trp Asp Arg Arg Val His Pro Tyr Pro Asp

100 105 110

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

115 120 125

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

130 135 140

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

145 150 155 160

Gly Gly Gly Thr Arg Asp Ala Gly Arg Ala Val Arg Arg Ala Ser Ser

165 170 175

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

180 185 190

Pro Pro Gln Glu Ala Ala Trp Ser Lys Glu Asp Glu Asp Arg Tyr Phe

195 200 205

Ile Pro His Asp Val Ala Arg Lys Ile Val Leu Ala Ala Lys Ala Gln

210 215 220

Glu Lys Glu Asp His Arg Val Ala Trp Arg Thr Ala Ala Ala Val Leu

225 230 235 240

Phe Glu His Phe Gly Arg Ile Phe Gln Gln Asp Gly Arg Ala Leu Ser

245 250 255

Phe Ala Glu Ala Glu Lys Gln Met Pro Gly Leu Leu Ala Leu His Arg

260 265 270

Ala Val Glu Gly Tyr Tyr Arg Gln Ala Leu Lys Arg His Arg Lys Asp

275 280 285

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

290 295 300

Arg Lys Val Ser Ala Ile Leu Pro Lys Asp Lys Thr Ala Leu Leu Ala

305 310 315 320

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

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

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

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

565 570 575

Leu Pro Lys Ser Val Asn Arg Glu Ser Met Lys Val Pro Ala Ile His

580 585 590

Cys Arg Tyr Ile Leu Thr Arg Leu Leu Tyr Gln Ser Gly Phe Arg Thr

595 600 605

Trp Ile Ala Glu Ala Pro Ala Ala Gln Leu Asn Arg Trp Ile Glu Thr

610 615 620

Ala Thr Glu Arg Ala Gln Lys Ala Thr Val Gly Ile Thr Lys Asn Glu

625 630 635 640

Ala Asp Arg Ala Arg Met Val Gly Gln Ile Lys Val Pro Glu Gly Gln

645 650 655

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

660 665 670

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

675 680 685

Gln Ala Ala Phe Leu Glu Asn Leu Asn Cys Asp Val Met Ala Leu Ala

690 695 700

Phe Asp Lys Tyr Leu Ser Asp His Lys Leu Gly Trp Leu Ala Gly Ile

705 710 715 720

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

725 730 735

Leu Pro Ser Ser Gly Ser Leu Gly Thr Pro Glu Arg Trp Glu Ala Ala

740 745 750

Leu Tyr Ala Val Cys His Leu Ile Pro Val Ser Glu Val Gly Arg Leu

755 760 765

Leu His Gln Leu Arg Arg Trp Ser Asn Gly Gln Lys Ala Thr Pro Asp

770 775 780

Gly Gly Arg Leu Glu Arg Leu Phe Glu Leu Tyr Leu Asp Met His Asp

785 790 795 800

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

805 810 815

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

820 825 830

Leu Gln His Gly Glu His Glu Arg Leu Pro Leu Arg Gly Leu Arg Glu

835 840 845

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

850 855 860

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

865 870 875 880

Arg Ile Gly Asp Ala Pro Ser Gln Val Asp Arg Ala Gln Ala Leu Arg

885 890 895

Thr Glu Met His Ala Ala Leu Cys Lys Lys Arg Lys Leu Ala His Asp

900 905 910

Asp Lys Lys Ser Val Lys Asp Tyr Leu Thr Ser Leu Gln Thr Val Ile

915 920 925

Arg His Arg Arg Leu Ala Asn His Val Arg Leu Thr Asn His Val Arg

930 935 940

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

945 950 955 960

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

965 970 975

Gln Ala Gly Leu Thr Pro Cys Asp Val Phe Ser Lys Glu Pro Pro Lys

980 985 990

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

995 1000 1005

Phe Ala Leu Arg Lys Met Gln Ala Gln Cys Asp Thr His Ala Gly

1010 1015 1020

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

1025 1030 1035

Ala Glu Gly Ala Pro Gly Asn Asp Pro Arg Ile Gln Asn Arg Asn

1040 1045 1050

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

1055 1060 1065

Leu Asp Leu Thr Ala Asp Met Asn Arg Ala Arg Asp Leu Met Ala

1070 1075 1080

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

1085 1090 1095

Leu Leu Glu Arg Glu Asn Ile Val Ile Ala Trp Thr Met Lys Asp

1100 1105 1110

His Gln Leu Thr Asp Ala Val Leu Ala Ala Lys Ser Ile Glu His

1115 1120 1125

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

1130 1135 1140

Leu Gly Tyr Val Ala Ala Leu Phe Gly Gly Arg Val Ala Glu Glu

1145 1150 1155

Ala Pro Asp Ile Met His Asp Arg Thr Val Phe His Leu Val Gly

1160 1165 1170

Ala Leu Thr Glu Glu Met Glu Pro Ala Glu

1175 1180

<210> 49

<211> 1276

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13a sequence

<400> 49

Met Arg Ile Val Arg Pro Tyr Gly Glu Ser Arg Thr Asp Leu Gly Gly

1 5 10 15

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

20 25 30

Arg His Glu Ile Pro Asp Phe Ala Gln Ser His Asp Ala Leu Val Ile

35 40 45

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

50 55 60

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

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

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

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

Lys Thr Leu Lys Lys Gly Val Lys Pro Pro Gln Gln Ala Pro Val Thr
305 310 315 320

Thr Val Leu Pro Lys Asn Ala Gly Glu Leu Leu Arg Leu Val Gln His
325 330 335

Arg Ser Arg Asn Arg Asp Leu Ser Ala Leu Ile Arg Arg Gly Lys Leu
340 345 350

Ile His Tyr Thr Ala Phe Asp Ile Ala Ala Ala Ala Ala Glu Ala Glu
355 360 365

Ser Lys Thr Pro Asp Val Pro Asp Ala Asp Arg Leu Ala Tyr Val Leu
370 375 380

Thr His Trp Pro Asp Asp Leu Ser Ala Ser Arg Tyr Leu Thr Ser Asp
385 390 395 400

Gly Gln Ser Ala Ile Lys Arg Ser Glu Ala Phe Val Arg Val Trp Arg
405 410 415

His Thr Ile Ala Met Ala Ser Leu Thr Leu Arg Asp Trp Ala Ser Met
420 425 430

Asn Asn Asp Leu Gly Asp Val Leu Gly Ser Ala Asn Lys Val Asp Gln
435 440 445

Ala Ile Gly Arg Ala Asn Phe Asp Pro Ala Trp His Asp Lys Lys Val
450 455 460

Arg Leu Leu Phe Gly Ala Arg Ala Ala Leu Phe Pro Ser Asp Asp Asp
465 470 475 480

Gly Arg Lys Ala Leu Leu Ala Ser Val Ile Arg Ala Gly Leu Ala Leu
485 490 495

Arg Asn Ser Ser Phe His Phe Thr Gly Arg Gly Gly Phe Leu Ala Ala
500 505 510

Leu Lys Lys Leu Gly Ser Glu Glu Val Met Val Pro Ser Ile Leu Ala
515 520 525

Ala Ala His Ala Leu Trp Arg Glu Asp Ala Thr Ala Arg Ala Gly Arg
530 535 540

Leu Arg Ala Ala Leu Thr Gly Ala His Ala Ala His Tyr Phe Glu Glu

545 550 555 560

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

565 570 575

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

580 585 590

Asn Thr Trp Lys Gly Lys Glu Ala Leu Val Leu Pro Pro Thr Ala Asn

595 600 605

Arg Arg Gln Leu Glu Asp Pro Ala Arg Arg Cys Arg Tyr Thr Ile Leu

610 615 620

Lys Ala Leu Tyr Glu Arg Pro Phe Arg Ser Trp Leu Ile Ala Arg Ala

625 630 635 640

Pro Glu Glu Val Asn Ala Trp Ile Asp Arg Ala Ile Glu Arg Thr Thr

645 650 655

Arg Ala Ala Lys Asp Met Asn Ala Lys Arg Gly Glu Asp Asp Lys Arg

660 665 670

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

675 680 685

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

690 695 700

Glu Met Arg Val Gln Arg Gly Tyr Gly His Asp Gly Glu Ala Ala Lys

705 710 715 720

Glu Gln Ala Gly Tyr Ile Asp Asp Leu Leu Cys Asp Val Val Ala Leu

725 730 735

Ala Phe Asp Ala Trp Leu Arg Asn Pro Gln Ala Asn Gly Arg Pro Leu

740 745 750

Thr Phe Ile Cys Asp Leu Lys Pro Glu Thr Pro Leu Pro Ala Ala Pro

755 760 765

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

770 775 780

Glu Asp Trp Gln Ala Ala Leu Tyr Leu Leu Leu His Leu Val Pro Val

785 790 795 800

Gly Glu Ala Gly Arg Leu Leu His Gln Leu Ala Lys Trp Thr Val Thr
805 810 815
Ser Arg Leu Ala Asp Asp Leu Leu Asn Ala Asn Val Thr Asp Asp Pro
820 825 830

Ser Lys Ala Glu Arg Thr Ala Asp Glu Glu Asp Leu Lys Arg Leu Val
835 840 845
His Thr Leu Ile Gln His Leu Asp Met His Asp Ala Lys Phe Glu Gly
850 855 860
Gly Asp Ala Leu Thr Gly Cys Glu Pro Phe Ala Ala Leu Phe Ala Ser
865 870 875 880
Arg Pro Gly Phe Ala Arg Ile Phe Pro Ala Glu Ala Asp Glu Arg Leu
885 890 895

Asp Arg Arg Val Pro Lys Arg Gly Leu Arg Glu Ile Met Arg Phe Gly
900 905 910
His His Gly Leu Val Ala Ser Phe Ala Glu Asp Thr Arg Ile Thr Asp
915 920 925
Lys Glu Val Gly Asp Tyr Leu Arg Leu Glu Ile Glu Glu Arg Pro Asp
930 935 940
Asn Val Ala Ala Leu Gln Ala Arg Lys Glu Glu Ala His Glu Arg Trp
945 950 955 960

Val Lys Ala Lys Glu Lys Arg Lys Thr Val Asp Pro Lys His Leu Glu
965 970 975
Asp Tyr Val Thr Ala Leu Cys Gly Ile Ala Arg His Arg Arg Leu Ala
980 985 990
Ser Arg Val Thr Leu Thr Asp Gln Val Gln Val His Arg Leu Leu Met
995 1000 1005
Thr Val Leu Gly Arg Leu Val Asp Phe Ser Gly Met Phe Glu Arg
1010 1015 1020

Asp Leu Tyr Phe Ala Met Leu Gly Leu Leu Asp Glu Lys Gly Ala
1025 1030 1035
Arg Pro Asp Glu Val Phe Ser Gly Pro Ile Asp Glu Pro Lys Ser

1040 1045 1050

Arg Leu Ala Leu Leu Ala Asn Gly Arg Val Leu Ala Ala Leu Arg

1055 1060 1065

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

1070 1075 1080

Asp Leu Glu Arg Leu Phe Gly Met Asp Cys Ser Gly Ile Arg Leu

1085 1090 1095

Leu Glu Ala Asp Glu Arg Gly Asp Thr Cys Leu Arg Asp Ile Arg

1100 1105 1110

Asn Asp Leu Ser His Phe Asn Leu Leu His Asp Asp Ser Phe Ala

1115 1120 1125

Leu Asp Leu Thr Thr Leu Val Asn Arg Thr Arg Gly Leu Met Ser

1130 1135 1140

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

1145 1150 1155

Leu Leu Ala Arg Glu Gly Leu Thr Leu Ser Trp Asp Met Thr Asp

1160 1165 1170

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

1175 1180 1185

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

1190 1195 1200

Pro Glu Pro Val Arg Glu Asn Leu His Ser Pro Thr His Leu Glu

1205 1210 1215

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

1220 1225 1230

Val Thr Asn Leu Asp Leu Ser Ser Ile Asp Trp Ala Ala Glu Pro

1235 1240 1245

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

1250 1255 1260

Lys Ser Pro Pro Lys Arg Arg Ala Tyr His Ala Pro Arg

1265 1270 1275

<210> 50

<211> 1225

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13a sequence

<400> 50

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

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

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

165 170 175
Ala Ala Arg Ala Arg Ser Ile Ala Val Asn Val Leu Arg Pro Ala Asp
180 185 190
Ser Ser Ala Cys Gly Gln Pro Glu Trp Ser Asp Arg Asp Leu Gln Ala

195 200 205

Tyr Arg Val Ala Asp Val Ala Lys Gln Ile Trp Asp Ala Ala Leu Ser

210 215 220

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

225 230 235 240

Val Ala Gly Gly Val Leu Phe Glu His Trp Ala Arg Ile Phe Pro Gly

245 250 255

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

260 265 270

Gly Leu Phe Ala Leu His Met Ala Val Lys Asp Cys Tyr Ala Arg Ile

275 280 285

Leu Lys His His Lys Lys Lys Ala Pro Gly Arg Arg Glu Arg Glu Asn

290 295 300

Gly Asp Val Ser Pro Ile Arg Lys Val Leu Pro Arg Asp Met Asp Glu

305 310 315 320

Leu Phe Ala Arg Ile Ile Ser Gly Arg Gly Asn Arg Asp Leu Asn Ala

325 330 335

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

340 345 350

Ala Asp His Pro Glu Ser Ile Thr Glu Asn Trp Pro Gly Asp Leu Ala

355 360 365

Gly Ser His Tyr Trp Thr Ser Ala Gly Gln Ala Glu Ile Lys Arg Asn

370 375 380

Glu Ala Phe Val Arg Val Trp Arg His Val Val Val Leu Ala Ala Arg

385 390 395 400

Thr Leu Thr Asp Trp Gly Asp Pro His Gly Glu Ile Gly Ser Asp Ile

405 410 415

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

420 425 430

Phe Asn Arg Lys Cys Ala Leu Leu Phe Gly Lys Arg Ala Ser His Phe

435 440 445

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

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

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

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

675 680 685
Gly Glu Arg Ala Arg Gln Gln Ala Glu Tyr Ile Glu Asp Leu Lys Cys

690 695 700

Asp Val Val Gly Leu Ala Tyr Arg Ser Phe Leu Glu Thr Glu Gly Phe

705 710 715 720

Asp Phe Leu Arg Thr Leu Asp Pro Glu Ala Ala Ile Ala Glu Ala His

725 730 735

Arg Phe Asp Pro Ala Glu Leu Pro Asp Pro Ala Val Asp Thr Asp Ala

740 745 750

Glu Asp Trp Glu Ala Val Leu Tyr Phe Leu Val His Leu Val Pro Val

755 760 765

Asp Glu Ile Gly Arg Leu Leu His Gln Met Arg Lys Trp Asp Leu Leu

770 775 780

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

785 790 795 800

Val Asp Lys Val Gln Arg Val Phe Thr Leu Tyr Leu Asp Leu His Asp

805 810 815

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

820 825 830

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

835 840 845

Gln Gly Tyr Glu Glu Asp Arg Arg Val Pro Leu Arg Gly Leu Arg Glu

850 855 860

Ile Met Arg Phe Gly Asp Leu Pro Pro Leu Leu Ser Ile Tyr Gly Arg

865 870 875 880

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

885 890 895

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

900 905 910

Glu Glu Leu His Ala Lys Trp Val Glu Ala Lys Lys Glu Gly Leu Gly

915 920 925

Pro Glu Asp Arg Arg Ala Tyr Val Glu Ala Leu Ala Glu Ile Val Arg

930 935 940

His Arg His Leu Ala Ala His Val Thr Leu Thr Asn His Val Arg Leu
945 950 955 960
His Arg Leu Met Met Ala Val Leu Gly Arg Leu Ala Asp Phe Ser Gly
965 970 975
Leu Trp Glu Arg Asp Leu Tyr Phe Ala Thr Leu Ala Leu Leu His Arg
980 985 990
Ala Gly Lys Thr Pro Arg Glu Val Phe Glu Asn Glu Gly Ile Asp Leu

995 1000 1005
Leu Arg Asn Gly Gln Ile Val Tyr Ala Leu Arg Lys Leu Asn Gly
1010 1015 1020
Ser Ser Asn Ala Ser Ala Leu Arg Ser Gly Leu Phe Pro His Phe
1025 1030 1035
Gly Ser Ala Phe Lys Arg Gly Asp Pro Ile Gly Gly Ile Arg Asn
1040 1045 1050
Ala Phe Ala His Phe Asn Met Leu Arg Ala Ala Gln Pro Pro Asn

1055 1060 1065
Leu Thr Glu Cys Ile Asn Arg Ala Arg Gln Leu Met Lys His Asp
1070 1075 1080
Arg Lys Leu Lys Asn Ala Val Ser Lys Ser Val Ile Asp Leu Leu
1085 1090 1095
Ala Arg Glu Gly Leu Asn Ile Ala Trp Ala Val His Thr Arg Ala
1100 1105 1110
Gly Ala His Asp Leu Ala Glu Ala Val Leu Ser Ser Arg Gln Ala

1115 1120 1125
Gln His Leu Gly Lys Leu Arg Leu Phe Pro Val Ser Gly Asp Gly
1130 1135 1140
Arg Asp Gly Lys Gly Phe Phe Ile Met Glu Asp Leu His Gly Ala
1145 1150 1155
Asp Phe Val Glu Met Ala Ala Glu Leu Phe Gly Gly Arg Val Ser
1160 1165 1170
Asp Arg Trp Arg Gly Lys Gly Cys Val Ser Glu Leu Arg Leu Asp

1175 1180 1185

Ser Ile Asp Trp Ser Arg Gln Arg Glu Gln Lys Lys His Gly Gly

1190 1195 1200

Gly Lys Lys Pro Thr Gly Arg Ala Arg Lys Ala Asn Arg Gly His

1205 1210 1215

Lys Asn Arg His Arg Arg Ala

1220 1225

<210> 51

<211> 1076

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12f sequence

<400> 51

Met Ser Ala Arg Asn Ile Lys Val Lys Ile Asp Thr Lys Gly Asn Pro

1 5 10 15

Glu Leu Arg Leu Gly Leu Trp Lys Thr His Gln Val Thr Asn Glu Gly

20 25 30

Val Lys Tyr Tyr Thr Glu Trp Leu Ile Lys Leu Arg Gln Gln Asp Ile

35 40 45

Tyr Arg Gln Ser Arg Glu Asp Ala Ser Pro Arg Val Ile Ile Ser Ala

50 55 60

Ser Asp Leu Lys Ala Asp Leu Leu Cys His Ala Arg Gln Leu Gln Lys

65 70 75 80

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

85 90 95

Leu Arg Gln Val Tyr Glu Leu Ile Val Pro Ser Ser Val Gly Lys Ser

100 105 110

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

115 120 125

Pro Gly Ser Ala Gly Gly Arg Asp Gln Ser Ala Ser Gly Arg Lys Pro

130 135 140

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

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

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

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

Val Ala His Pro Ile Trp Ser Arg Tyr Glu Gly Ala Asn Ala Ser Ser

385 390 395 400

Gly Asn Arg Tyr His Ile His Leu Pro Thr Lys Gly Gln Pro Gly Ser

405 410 415

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

420 425 430

Glu Arg Lys Arg Val Thr Val Phe Leu Arg Pro Ser His Gln Val Asp

435 440 445

Arg Ile His Glu Ala Pro Thr Asp Ser Val Val Asp Asn Phe Pro Leu

450 455 460

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

465 470 475 480

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

485 490 495

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

500 505 510

Thr Asn Lys Pro Ser Gly Leu Phe His Thr Gln Gln Asn Gly Arg Val

515 520 525

Trp Ile Arg Lys Asp Val Leu Met Gln Tyr Tyr Asn Glu Thr Pro Gly

530 535 540

Asp Asn Val Gln Phe Lys Pro Leu Tyr Val Met Ser Val Asp Leu Gly

545 550 555 560

Ile Arg Ser Ala Ala Ala Val Ser Ile Phe Ser Val Gln Leu Lys Ala

565 570 575

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

580 585 590

Leu Val Ala Val His Glu Arg Ser Val Leu Leu Thr Met Pro Gly Glu

595 600 605

Arg Arg Glu Gln Trp Asp Arg Arg Tyr Glu Gln Gln Arg Gln Gly Leu

610 615 620

Arg Glu Leu Arg Thr Asp Met Arg Gly Met Asn Asp Leu Leu Arg Gly

625 630 635 640

Ala Tyr Met Asp Gly Asp Arg Arg Glu Glu Phe Leu Ala Arg Leu Ser
645 650 655
Lys Leu Glu Glu Thr Ser Pro Glu Leu Trp Gly Pro Val Tyr Arg Ser
660 665 670
Leu Asn Asp Ser Lys Val Ala Ser Ala Thr Glu Trp Glu Arg Leu Val
675 680 685
Val Tyr Cys His Arg Gln Val Glu Gln Ser Leu Ser Ser Arg Ile Gln
690 695 700

Asn Leu Arg Ser Gly Arg Ser Ala Tyr Arg Met Ser Gly Gly Leu Ser
705 710 715 720
Leu Asp His Val Gln Asp Leu Glu Arg Ile Arg Gly Ile Ile Ala Ser
725 730 735
Trp Thr Asn His Pro Arg Ile Pro Gly Ser Val Val Arg Trp Gln Gln
740 745 750
Gly Arg Ser His Thr Val Ala Leu Gly Arg His Ile Leu Glu Leu Lys
755 760 765

Arg Asp Arg Val Lys Lys Val Ala Asn Tyr Leu Ile Met Thr Thr Leu
770 775 780
Gly Tyr Ala Tyr Asp Ser Lys Arg Ala Arg Gly Glu Lys Trp Val Arg
785 790 795 800
Arg Tyr Pro Ala Cys His Leu Met Val Phe Glu Asp Leu Thr Arg Tyr
805 810 815
Arg Phe Arg Thr Asp Arg Pro Arg Ser Glu Asn Arg Gln Leu Met Arg
820 825 830

Trp Thr His Gln Glu Leu Ile Ala Val Thr Gly Ile Gln Ala Glu Pro
835 840 845
His Gly Ile Ser Val Gly Thr Met Tyr Ala Gly Phe Ser Ser Arg Phe
850 855 860
Asp Ala Val Thr Lys Ala Pro Gly Val Arg Gly Ala Thr Val Arg Gln
865 870 875 880
Ile Leu Arg Thr Arg Gly Met Val Arg Leu Lys Glu Ile Ala Ala Asp

885 890 895

Val Gly Ile Asp Ile Asn Thr Leu Arg Pro His Asp Val Leu Pro Thr
900 905 910
Gly Asp Gly Glu Tyr Leu Leu Ser Val Val Arg His Gly Glu Ser Tyr
915 920 925
Arg Leu Lys Gln Val His Ala Asp Ile Asn Ala Ala His Asn Leu Gln
930 935 940
Arg Arg Leu Trp Thr Gln Asp Glu Val Phe Arg Val Ser Cys Arg Leu
945 950 955 960

Ala Leu Asn Ser Gly Arg Val Val Ala Met Pro Pro Pro Ser Tyr Asn
965 970 975
Lys Arg Tyr Gly Lys Gly Phe Phe Glu Lys Gly Asp Asn Gly Val Tyr
980 985 990
Ile Trp Lys Thr Gly Gly Lys Ile Lys Ile Ser Asp Thr Leu Glu Glu
995 1000 1005
Asp Met Asp Ile Pro Glu Asp Thr Ala Glu Leu Leu Arg Gly Asn
1010 1015 1020

Ser Val Thr Leu Phe Arg Asp Pro Ser Gly Thr Ile Ala Gly Gly
1025 1030 1035
Asn Trp Leu Glu Ala Lys Glu Phe Trp Gly Arg Val Asn Ser Leu
1040 1045 1050
Val Asn Lys Gly Val Arg Asp Lys Ile Leu Gly Gly Ile Pro Val
1055 1060 1065
Asp Asn Ser Ser Ala His Ala Glu
1070 1075

<210> 52
<211> 660
<212> PRT
<213> Unknown

<220><223> Description of Unknown:
cas12f sequence

<400> 52

Met Pro Met Ile Lys Ile Thr Glu Cys Val Thr Trp Gly Thr Thr Cys
1 5 10 15
Asp Gly Leu Trp Asp Ala Arg Pro His Leu Glu Val Arg Arg Ser Trp
20 25 30
Ser Pro Pro Val Gln Gly Gly Arg Thr Asn Arg Leu Asp Ala Pro Pro
35 40 45
Ala Ser Val Thr Leu Asn Ile His Gly Arg Val Glu His Pro Arg Asp

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

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

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

Ile Gln Lys Thr Asp Pro Asp Tyr Tyr Ala Glu Gln Arg Lys Lys Glu

245 250 255

Arg Glu Ala Ile Thr Pro Asn Val Val Ala Met Lys Arg Asp Leu Met

260 265 270

Ala Lys Gly Ala Tyr Phe Pro Ser Glu Tyr Asp Leu Gln Tyr Ile Trp

275 280 285

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

290 295 300

Pro Glu Cys Pro Thr Ile Leu Phe Tyr Asp Gly Ile Asn Arg Ala Arg

305 310 315 320

Thr Ala Trp Lys Asn Trp Met Asp Ser Ala Ser Gly Ala Arg Lys Gly

325 330 335

Pro Pro Val Gly Met Pro Arg Phe Lys Ser Lys Tyr Lys Ala Lys Asp

340 345 350

Thr Phe Thr Ile Thr Asn Pro Asn Arg Ser Val Ile Lys Phe Glu Thr

355 360 365

Tyr Arg Arg Ile Ala Ile Thr Gly Ile Gly Ser Met Arg Leu His Arg

370 375 380

Gly Ala Lys Leu Leu Ala Arg Arg Ile Ala Ala Gly Gln Ala Glu Ile

385 390 395 400

Thr Ser Ala Thr Ile Ser Arg Ser Gly Thr Ala Trp Tyr Val Ser Val

405 410 415

Leu Cys Thr Val His Thr Thr Ala Arg Thr Ala Pro Ser Lys Ala Gln

420 425 430

Arg Ser Arg Gly Ala Val Gly Val Asp Trp Gly Val Arg Ala Leu Ala

435 440 445

Thr Thr Ser Lys Pro Ile Ala Leu Thr Pro Gly Lys Pro Ala Ser Arg

450 455 460

Thr Val Pro Ala Glu Lys Tyr Gly Ala Ala Met Ser Gln Lys Ile Ala

465 470 475 480

Arg Ala Gln Arg Gln Leu Ala Arg Met Pro Lys Gly Ser Ser Arg Arg

485 490 495

Arg Lys Ala Ala Arg His Val Ala Asp Leu Gln His Leu Val Ala Gln

500 505 510

Arg Arg Ala Ser Ser Val His Gln Leu Ser Lys Ala Leu Ala Gln Ser

515 520 525

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

530 535 540

Ser Ala Lys Gly Thr Val Glu Asn Pro Gly Lys Asn Ile Arg Gln Lys

545 550 555 560

Ala Gly Leu Asn Arg Ala Ile Leu Asp Ala Thr Pro Gly Glu Leu Lys

565 570 575

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

580 585 590

Leu Asp Thr Trp Tyr Pro Ser Ser Lys Thr Cys Ser Arg Cys Gly Trp

595 600 605

Val His Pro Lys Leu Lys Leu Ser Met Arg Thr Phe Arg Cys Gln Gln

610 615 620

Cys Gly Leu Val Glu Asp Arg Asp Phe Asn Ala Ala Val Asn Ile Glu

625 630 635 640

Arg Gln Gly Ile Thr His Ile Val Lys Glu Asn Glu Gly Thr Asp Asp

645 650 655

Arg Glu Glu Gly

660

<210> 53

<211> 696

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12f sequence

<400> 53

Met Ser Thr Pro Met Gly Trp Thr Ala Val Asn Gly Gly Asp Ala Thr

1 5 10 15

Ser Pro Thr Thr Arg Val Ser Ser Pro Pro Gly Glu Pro Arg Thr Gly

20 25 30

Ala Cys Pro Arg Ala Ala Ala Ala Asp Ala Thr Arg Ala Glu Ser Ser

35 40 45

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

50 55 60

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

65 70 75 80

Pro Ser Ala Glu Gly Asp Arg His Gly Gln Ser Ser Leu Asp Cys Gly

85 90 95

Pro Cys Pro Val Arg Arg Ser Gly Ala Leu His Gln Ser Ser Gln Ala

100 105 110

Ala His Arg Arg Ser Met Thr Gly Ala Lys Gln Lys Thr Pro Ile Arg

115 120 125

Val Val Arg Phe Ser Ile Asp His Ser Ala Leu Thr Pro Ala Gln Val

130 135 140

Val Ala Phe Ala Arg His Ala Gly Ala Ala Arg Gln Thr Trp Asn Trp

145 150 155 160

Ala Leu Gly Arg Trp Met Asp Trp Arg Asn Asn Thr Lys Phe Tyr Val

165 170 175

Asp Tyr Lys Val Phe Lys Ala Ala Gly Met Gly Pro Gly Leu Ser Thr

180 185 190

Asp Asp Leu Ile Gln Val Ile Glu Arg Ala Val Ser Ile Arg Gln Asp

195 200 205

Asp Lys Trp Met Asp Ala Ala Trp Asp Glu Ala Arg Gln Ile His Gly

210 215 220

Glu Trp Asp Gln Phe Gln Lys Ala Ser Thr Leu Gln Ser Leu Tyr Leu

225 230 235 240

Ala Gly Ala Gln Glu Pro Phe Asp Pro Ser Arg Asp Asp Gly Ile Asn

245 250 255

Pro Tyr His Trp Trp Val Thr Glu Gly Asp Lys Ser Gly Leu Pro Lys

260 265 270

Ala Glu Arg His Asn Val Asn Ser Gly Ala Thr Tyr Thr Ala Pro Leu

275 280 285

Arg Ala Phe Glu Glu Ala Val Gly Arg Phe Tyr Lys Leu Pro Gly Lys

290 295 300

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

305 310 315 320

Cys Ile Gln Arg Leu Thr Glu Thr Gly Leu Ser Pro Trp Arg Ala Ile

325 330 335

Glu Gly Gly His Arg Ile Lys Val Pro Ser Ile Gly Ser Ile Arg Val

340 345 350

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

355 360 365

Thr Thr Ser Ala Arg Phe Thr Arg Arg Gly Gly Lys Trp Phe Val Ser

370 375 380

Val Ser Val Ala Phe Asp Leu Ser Ala Pro Arg Val Gln Arg Pro Ala

385 390 395 400

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

405 410 415

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

420 425 430

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

435 440 445

Lys Phe Asp Arg Gln His Arg Ala Gly Ser Pro Glu Cys Phe Asn Glu

450 455 460

Asp Gly Thr His Lys Lys Arg Cys Arg Trp Gly Arg Glu Asp Gly Pro

465 470 475 480

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

485 490 495

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

500 505 510

Lys Asp Leu Ala Thr Arg Phe Glu Leu Ile Gly Val Glu Asp Leu Asn
515 520 525
Val Ala Gly Met Thr Ala Lys Ser Lys Pro Lys Pro Asp Pro Asp Arg

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

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

660 665 670
Ser Leu Ala Pro Cys Glu Ser Thr Arg Pro Val Arg Asp Leu Ser Pro
675 680 685
Pro Ala Thr Gln Glu Glu Thr Ala
690 695
<210> 54
<211> 606
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
cas12f sequence
<400> 54
Met Ala Gln Ala Glu Ala Pro Arg Arg Leu Arg Ala Tyr Lys Phe Ala

1 5 10 15

Leu Asp Pro Thr Glu Ala Gln Leu Arg Glu Phe Glu Gln His Ala Gly
20 25 30
Ser Ala Arg Trp Ala Tyr Asn His Ala Asn Ala Ile Leu Ser Arg Tyr
35 40 45
Ser Asp Thr Leu Arg Asn Arg Trp Asn Ala Trp Ile Ala Gln His His
50 55 60
Gly Leu Ser Arg Glu Gln Leu Tyr Ala Leu Pro Asp Arg Glu Arg Thr
65 70 75 80

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

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

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

Arg Ser Phe Thr Leu Tyr Gly Ser Val Lys Leu Val Thr Tyr Arg Arg
260 265 270

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

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

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

Ala Lys Ala Gly Leu Asn Arg Ser Ile Leu Asp Thr Ser Pro Ala Glu
465 470 475 480
Phe Arg Arg Gln Leu Gln Tyr Lys Ala Ser Trp Tyr Gly Ala Thr Val
485 490 495
Ala Val Ile Asp Arg Trp Ala Pro Thr Ser Arg Thr Cys Ser Ser Cys

500 505 510

Gly Ala Val Lys Ala Lys Leu Ser Leu Ala Glu Arg Thr Phe Phe Cys
515 520 525

Glu His Cys Gly Met Glu Leu Asp Arg Asp Ile Asn Ala Ala Arg Asn
530 535 540

Ile Leu Ala Phe Ala Gln Ser Ala Tyr Pro Gly Glu Gly Lys Ala Leu
545 550 555 560

Asn Ala Cys Gly Gly Ser Val Ser Pro Gly Ser Gln Ser Val Val Gln
565 570 575

Ala Gly Ala Asp Glu Ala Gly Arg Pro Ala Arg Lys Pro Arg Arg Ser
580 585 590

Ser Arg Gly Ser Asp Pro Pro Ala Thr Pro Thr Thr Arg Ala
595 600 605

<210> 55

<211> 1421

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12a sequence

<400> 55

Met Thr Ser Ser Ser Pro Thr Gln Arg Ala Tyr Thr Leu Arg Leu Lys
1 5 10 15

Ser Ala Ala Gln Gly Asp Lys Ser Trp Ala Glu Lys Leu Trp Asp Thr
20 25 30

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

35 40 45

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

Glu Thr Gly Glu Glu Gly Lys Lys Arg Arg Arg Ile Leu Leu Ala Leu
65 70 75 80

Ser Trp Leu Ser Val Glu Ser Lys Asp Phe Ala Pro Glu Lys Tyr Ile
85 90 95

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

100 105 110

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

115 120 125

Val Asn Asp Cys Lys Asp Ser Leu Thr Ser Ser Ile Arg Asp Asp Ala

130 135 140

Val Trp Val Asn Arg Ser Arg Ala Phe Asp Asp Ala Val Arg Lys Ile

145 150 155 160

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

165 170 175

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

180 185 190

Asn Gly Lys Thr Lys Lys Glu Glu Pro Lys Asp Leu Ala Arg Lys Ala

195 200 205

Gly Gly Trp Leu Ser Lys Arg Phe Gly Lys Gly Lys Gly Thr Asp Phe

210 215 220

Ser Lys Leu Ser Lys Val Tyr Ser Glu Ile Val Lys Trp Ala Glu Glu

225 230 235 240

Pro Arg Lys Ser Glu Pro Arg Thr Leu Ala Asn Leu Ala Ser Ala Leu

245 250 255

Lys Glu Asp Ser Leu Gln Gly Ile Leu Asn Leu Ile Lys Asn Ser Gly

260 265 270

Ser Lys Ser Gly Thr Arg Asn Phe Leu Glu Glu Ile Gly Glu Gly Glu

275 280 285

Val Ser Lys Glu Asn Leu Ala Ile Leu Lys Ala Lys Ala Glu Gly Asn

290 295 300

Arg Asn Tyr Cys Lys Lys Glu Ile Gly Gly Lys Gly Arg Arg Glu Trp

305 310 315 320

Ser Asp Arg Ile Leu Lys Ser Ile Glu Glu Thr Leu Asp Gly Lys Phe

325 330 335

Thr Tyr Leu Gln Glu Lys Gly Pro Ala Arg His Trp Glu Phe Ala Val

340 345 350

Met Leu Asp His Ala Ala Arg Arg Ile Ser Ala Gly His Thr Trp Ile

355 360 365

Lys Leu Ala Glu Ala Arg Arg Arg Asn Phe Glu Glu Asp Ser Gln Lys

370 375 380

Ile Asn Glu Val Pro Glu Asn Ala Arg Gln Trp Leu Glu Thr Tyr Arg

385 390 395 400

Glu Asp Arg Ser Lys Ser Ser Gly Ala Ile Glu Gly Tyr Leu Ile Ser

405 410 415

Lys Arg Ala Val Thr Glu Trp Glu Thr Val Val Lys Ala Trp Lys Asn

420 425 430

Cys Lys Thr Glu Glu Asp Arg Ile Ala Ala Ala Gly Ala Leu Gln Asp

435 440 445

Asn Leu Gly Ile Asp Gln Phe Gly Asp Ile Asn Leu Phe Arg Ala Leu

450 455 460

Ala Ser Glu Asp Val Arg Cys Val Trp Gln Val Asp Gly Lys Pro Asp

465 470 475 480

Ala Asn Ile Leu Leu Asn Tyr Val Ala Ala Thr Lys Ala Glu Phe Asp

485 490 495

Lys Arg Arg Phe Lys Val Pro Ala Tyr Arg His Pro Asp Pro Leu Leu

500 505 510

His Pro Val Phe Cys Asp Tyr Gly Asn Ser Arg Trp Glu Ile Arg Phe

515 520 525

Asp Val His Glu Val Asn Arg Thr Gly Lys Lys Ala Lys Gln Asn Lys

530 535 540

Lys Thr Ile Glu Thr Ala Asp Val His Gly Leu Lys Met Asp Leu Trp

545 550 555 560

Thr Gly Ser Lys Ile Glu Asn Val Ser Leu Arg Trp Gln Ser Lys Leu

565 570 575

Leu Glu Lys Asp Leu Ala Val Lys Gln Leu Asp Gly Lys Glu Asp Gly

580 585 590

Lys Lys Glu Val Ser Arg Ala Ser Arg Leu Gly Arg Ala Ala Val Gly
595 600 605
Ala Gly Trp Glu Thr Pro Val Ser Ala Ser Ser Val Phe Ala Gln Lys

610 615 620
His Trp Asn Gly Arg Leu Gln Ala Ser Arg Lys Glu Leu Ser Arg Ile
625 630 635 640
Ala Arg Arg Val Lys Thr Arg Gly Trp Asp Glu Lys Ala Asn Ser Met
645 650 655
Lys Lys Asn Leu Lys Trp Phe Ile Thr Phe Ser Pro Lys Leu Lys Leu
660 665 670
Gln Gly Pro Trp Ile Ser Tyr Val Asp Asn Ser Glu Asp Lys Arg Pro

675 680 685
Phe Thr Phe Thr Ser Lys Gly Glu Pro Ile Leu Asp Glu Val Phe Ser
690 695 700
Ile Glu Asn Lys Asn Arg Lys Gly Arg Ala Arg Leu Ile Leu Ser Arg
705 710 715 720
Leu Pro Gly Leu Arg Val Leu Ser Met Asp Leu Gly His Arg His Ala
725 730 735
Ala Ala Cys Ala Val Trp Glu Thr Leu Ser Ser Arg Gln Leu Glu Asp

740 745 750
Ala Cys Ala Glu Gly Gly Tyr Asp Lys Pro Ala Pro Asp Ala Met Tyr
755 760 765
His His Ile Lys Ser Asn Arg Gly Lys Arg Val Ile Tyr Arg Arg Ile
770 775 780
Gly Ala Asp Glu Leu Ser Asp Asp Ser Ile His Pro Thr Pro Trp Ala
785 790 795 800
Arg Leu Glu Arg Gln Phe Leu Ile Lys Leu Gln Gly Glu Glu Arg Lys

805 810 815
Ala Arg Met Ala Thr Ala Asp Glu Ile Trp Glu Val His Glu Leu Glu
820 825 830
Arg Ala Leu Gly Arg Lys Thr Pro Leu Val Asp Arg Leu Thr Lys Ser

835 840 845

Gly Trp Gly Ser Asp Ser Gly Thr Pro Arg Gln Arg Gln Leu Leu Gly

850 855 860

Glu Leu Asn Gln Trp Gly Trp Glu Pro Asp Glu Ala Gln Glu Asn Ser

865 870 875 880

Glu Asp Asp Glu Ile Thr Ser Arg Glu Ser Leu Leu Val Asp Lys Leu

885 890 895

Met Ser Arg Thr Val Asp Thr Val Arg Lys Gly Leu Arg Arg His Gly

900 905 910

Asn Arg Ala Arg Ile Ala Asn Phe Leu Val Ala Arg Glu Lys Thr Val

915 920 925

Pro Gly Gly Gln Met Asp Thr Leu Asn Asn Glu Gly Arg Lys Glu Ile

930 935 940

Ile Ala Asp Ala Leu Ala Phe Trp Tyr Glu Leu Ala Asn Gly Gly Glu

945 950 955 960

Trp Lys Asp Thr Glu Ala Leu Asp Trp Trp Lys Ile His Ile Glu Pro

965 970 975

Glu Leu Ser Val Glu Glu Leu Pro Asp Ile Ala Gly Thr Gly Ile Ala

980 985 990

Pro Lys Glu Arg Lys Arg Lys Lys Lys Glu Leu Lys Glu Lys Leu Lys

995 1000 1005

Pro Val Ala Glu Arg Leu Leu Thr Ser Gly Ala Lys Lys Leu Ser

1010 1015 1020

Asp Gln Trp Cys Glu Arg Trp Lys Gln Asp Asp Lys Glu Trp Gln

1025 1030 1035

Lys Thr Leu Arg Trp Leu Arg Asp Trp Ile Leu Pro Arg Gly Val

1040 1045 1050

Arg Gly Lys Ser Glu Leu Ile Arg Asn Val Gly Gly Leu Ser Leu

1055 1060 1065

Asp Arg Leu Thr Thr Ile Gln Ser Leu Tyr Gln Ala Gln Lys Ala

1070 1075 1080

Tyr Phe Thr Arg Ile Thr Pro Lys Gly Ile Gln Met Asp Lys Asp

1085 1090 1095

Lys Pro Leu Thr Ala Val Met Asn Phe Gly Gly His Ile Leu Asn

1100 1105 1110

Asp Leu Glu Asn Met Arg Glu Gln Arg Val Lys Gln Leu Ala Ser

1115 1120 1125

Arg Ile Val Glu Ala Ala Leu Gly Val Gly Arg Val Lys Ile Pro

1130 1135 1140

Lys Lys Ser Lys Asp Pro Lys Arg His Tyr Glu Arg Val Asp Ala

1145 1150 1155

Pro Cys His Ala Val Val Ile Glu Asn Leu Thr Asn Tyr Arg Pro

1160 1165 1170

Glu Glu Thr Arg Thr Arg Arg Glu Asn Arg Gln Leu Met Thr Trp

1175 1180 1185

Cys Ser Gly Lys Val Lys Lys Tyr Leu Ser Glu Ser Cys Ser Leu

1190 1195 1200

His Gly Leu Phe Leu Trp Glu Val Pro Pro Ser Tyr Thr Ser Arg

1205 1210 1215

Gln Asp Ser Arg Thr Gly Ser Pro Gly Ile Arg Cys Glu Glu Val

1220 1225 1230

Ser Val Glu Lys Phe Phe Lys Thr Pro Phe Arg Gln Arg Glu Val

1235 1240 1245

Ala Arg Ala Glu Glu Lys Asp Ser Lys Asn Lys Ala Ser Ala Tyr

1250 1255 1260

Glu Gln Tyr Leu Ile Asp Leu Lys Glu Arg Trp Lys Ser Arg Gly

1265 1270 1275

Glu Glu Thr Ala Leu Leu Arg Ile Pro Arg Lys Gly Gly Glu Ile

1280 1285 1290

Phe Val Ser Ala Asn Ser Asn Ser Pro Ala Ser Lys Gly Leu Gln

1295 1300 1305

Ala Asp Leu Asn Ala Ala Ala Asn Ile Gly Leu Lys Ala Ile Thr

1310 1315 1320

Asp Pro Asp Trp Ser Gly Ser Trp Trp Tyr Val Pro Cys Ser Ser

1325 1330 1335

Lys Asp Phe Val Pro Ile Lys Asp Lys Ile Gly Gly Ser Arg Ala

1340 1345 1350

Phe Glu Asn Ile Thr Thr Pro Met Pro Asn Pro Asp Asp Ala Lys

1355 1360 1365

Glu Ala Thr Gly Lys Lys Arg Ser Gly Lys Lys Glu Ile Ile Asn

1370 1375 1380

Leu Trp Arg Asn Pro Ala Cys Ser Pro Leu Glu Arg Asp Glu Trp

1385 1390 1395

Glu Arg Thr Ala Lys Tyr Trp Asn Met Val Glu Tyr His Val Ile

1400 1405 1410

Lys Arg Leu Lys Arg Gln Met Gly

1415 1420

<210> 56

<211> 1333

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12a sequence

<400> 56

Met Lys Asn Phe Gln Asp Phe Thr Asn Leu Tyr Glu Leu Ser Lys Thr

1 5 10 15

Leu Arg Phe Glu Leu Lys Pro Ile Trp Gly Thr Lys Lys Leu Ile Glu

20 25 30

Glu Lys Asn Ile Leu Lys Leu Asp Lys Lys Lys Arg Glu Asn Tyr Glu

35 40 45

Lys Val Lys Pro Tyr Phe Asn Lys Ile His Gln Glu Phe Ile Asn Phe

50 55 60

Ala Leu Arg Asn Pro Asn Phe Asp Phe Ser Gln Phe Glu Glu Lys Tyr

65 70 75 80

Leu Asn Trp Leu Lys Asp Lys Lys Asn Lys Asp Leu Leu Lys Glu Lys
85 90 95
Glu Ser Ile Asp Lys Ile Phe Leu Glu Lys Ile Trp Lys Leu Phe Glu
100 105 110

Asn Ser Val Lys Asp Phe Leu Lys Glu Asn Gly Phe Glu Ser Ile Val
115 120 125
Lys Ser Glu Asp Gln Asn Leu Lys Phe Phe Arg Arg Lys Glu Ile Phe
130 135 140
Glu Val Leu Gln Glu Lys Tyr Gly Ser Glu Leu Glu Thr Gln Met Val
145 150 155 160
Asn Lys Asp Trp Glu Ile Lys Ser Ile Phe Asn Gly Trp Glu Lys Trp
165 170 175

Leu Trp Tyr Phe Asp Lys Phe Phe Asn Thr Arg Asp Asn Phe Tyr Lys
180 185 190
Thr Asp Trp Thr Ser Thr Ala Ile Ala Thr Arg Ile Ile Lys Asp Asn
195 200 205
Leu Lys Ile Phe Leu Glu Asn Thr Ile Ile Phe Glu Lys Val Lys Asn
210 215 220
Lys Lys Ile Asp Phe Ser Glu Val Glu Lys Asn Phe Ser Val Ser Ile
225 230 235 240

Asp Thr Phe Phe Glu Ile Asn Asn Phe Asn Asn Cys Phe Leu Gln Asp
245 250 255
Trp Ile Asp Phe Tyr Asn Lys Val Ile Trp Gly Glu Thr Leu Glu Asn
260 265 270
Trp Glu Lys Leu Lys Trp Leu Asn Glu Ile Ile Asn Lys Tyr Arg Gln
275 280 285
Asp Thr Gly Glu Lys Ile Pro Tyr Phe Lys Lys Leu Gln Lys Gln Ile
290 295 300

Leu Ser Glu Lys Asp Trp Val Phe Ile Asp Lys Ile Glu Asp Asp Gly
305 310 315 320
Gly Phe Tyr Glu Val Leu Lys Asn Phe Tyr Lys Asn Ala Ala Glu Lys

325 330 335

Glu Trp Phe Leu Lys Asn Ile Phe Glu Asn Phe Tyr Thr Ile Ser Asp

340 345 350

Lys Asn Leu Glu Lys Ile Tyr Phe Asn Lys Ile Ala Phe Asn Thr Ile

355 360 365

Ser His Lys Phe Trp Ser Ala Leu Glu Phe Glu Arg Ile Leu Tyr Glu

370 375 380

Glu Met Lys Lys Glu Lys Ala Asp Trp Ile Lys Phe Glu Lys Lys Glu

385 390 395 400

Asn Lys Tyr Lys Phe Pro Asp Phe Ile Gln Ile Ile Phe Ile Lys Arg

405 410 415

Ser Leu Glu Asn Tyr Asp Ser Glu Asn Leu Phe Trp Lys Glu Arg Tyr

420 425 430

Tyr Lys Ser Glu Glu Asn Val Asp Trp Phe Leu Glu Lys Asn Asn Asn

435 440 445

Asn Ile Trp Glu Gln Phe Cys Lys Ile Leu Asn Phe Glu Phe Leu Asn

450 455 460

Ile Leu Lys Arg Arg Ile Ile Asp Glu Ala Trp Glu Glu Tyr Glu Val

465 470 475 480

Trp Phe Glu Ile Ser Lys Asn Ile Leu Trp Glu Lys Leu Glu Asn Phe

485 490 495

Glu Leu Asn Gln Glu Asn Lys Trp Ile Ile Lys Asp Phe Ala Asp Tyr

500 505 510

Ser Leu Ala Leu Tyr Ser Phe Trp Lys Tyr Phe Ala Val Glu Lys Trp

515 520 525

Arg Asn Trp Asp Leu Asn Ile Asp Ile Ser Asp Asp Phe Tyr Gly Trp

530 535 540

Glu Asp Trp Tyr Ile Glu Lys Phe Tyr Asn Thr Gly Tyr Asp Glu Ile

545 550 555 560

Val Lys Pro Tyr Asn Leu Met Arg Asn Tyr Ile Ser Lys Lys Pro Trp

565 570 575

Glu Asp Ser Lys Lys Trp Lys Ile Asn Phe Glu Thr Ser Ser Leu Leu
580 585 590
Ser Trp Trp Asp Lys Asn Leu Glu Ser Asn Trp Ser Tyr Ile Phe Gln
595 600 605
Lys Trp Asn Lys Tyr Tyr Ile Trp Ile Ile Asn Trp Ser Lys Pro Ala
610 615 620

Lys Glu Val Leu Glu Lys Leu Tyr Ser Trp Asn Gly Glu Lys Ile Lys
625 630 635 640
Arg Phe Ile Tyr Asp Phe Gln Lys Pro Asp Asn Lys Asn Thr Pro Arg
645 650 655
Met Phe Ile Arg Ser Lys Lys Asp Ser Phe Ser Pro Ala Val Gly Lys
660 665 670
Tyr Asn Leu Pro Val Glu Asp Ile Leu Glu Ile Tyr Asp Asn Trp Leu
675 680 685

Phe Lys Thr Glu Asn Lys Asp Asn Ser Asn Tyr Lys Glu Ser Leu Ser
690 695 700
Lys Leu Ile Asp Tyr Phe Lys Leu Gly Phe Ser Lys His Glu Ser Phe
705 710 715 720
Lys His Phe Asn Phe Val Trp Lys Asp Ser Lys Glu Tyr Glu Asn Ile
725 730 735
Ala Asp Phe Tyr Arg Asp Val Glu Lys Ser Cys Tyr Gln Ile Thr Ser
740 745 750

Glu Phe Leu Asp Phe Glu Glu Leu Lys Lys Leu Thr Phe Lys Lys His
755 760 765
Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Glu Leu Asp Glu Ser
770 775 780
Leu Gln Lys Asn Trp Tyr Asn Phe Arg Asp Glu Trp Gln Lys Asn Ile
785 790 795 800
His Thr Lys Tyr Phe Glu Ala Leu Phe Leu Glu Glu Asn Ile Leu Arg
805 810 815

Lys Ser Trp Ala Val Phe Lys Leu Ser Trp Gly Trp Glu Val Phe Phe

820 825 830

Arg Lys Glu Ser Ile Lys Ala Glu Lys Glu Lys Arg Lys Asn Ile Glu

835 840 845

Val Thr Lys Asn Arg Arg Tyr Thr Glu Glu Lys Tyr Phe Leu His Phe

850 855 860

Pro Ile Gln Val Asn Phe Lys Asn Glu Ile Ser Trp Asn Phe Asn Gln

865 870 875 880

Glu Ile Asn Lys Phe Leu Ala Asn Asn Pro Asp Ile Asn Val Ile Trp

885 890 895

Ile Asp Arg Trp Glu Lys His Leu Ala Tyr Phe Ser Val Ile Asn Gln

900 905 910

Lys Trp Glu Ile Leu Glu Ser Trp Ser Phe Asn Lys Ile Glu Asn Tyr

915 920 925

Asn Lys Asn Trp Glu Lys Leu Leu Phe Pro Glu Arg Glu Ile Lys Glu

930 935 940

Ile His Lys Asp Trp Ser Leu Ile Asp Leu Glu Leu Val Glu Thr Trp

945 950 955 960

Arg Lys Val Asp Tyr Val Asp Tyr Lys Leu Leu Leu Glu Tyr Lys Glu

965 970 975

Arg Lys Arg Leu Leu Gln Arg Gln Ser Trp Lys Glu Val Glu Gln Ile

980 985 990

Lys Asp Leu Lys Lys Trp Tyr Ile Ser Ala Leu Val Arg Lys Ile Ala

995 1000 1005

Asp Leu Ile Ile Lys His Asn Ala Ile Val Ile Phe Glu Asp Leu

1010 1015 1020

Asn Phe Arg Phe Lys Gln Ile Arg Gly Trp Ile Glu Lys Ser Ile

1025 1030 1035

Tyr Gln Gln Leu Glu Lys Ala Leu Ile Asp Lys Leu Asn Phe Leu

1040 1045 1050

Val Asn Lys Asn Glu Ile Asn Leu Glu Lys Ala Gly Ser Ile Leu

1055 1060 1065

Lys Ala Tyr Gln Leu Thr Val Pro Val Asp Ser Leu Lys Glu Ile
1070 1075 1080
Trp Lys Gln Thr Trp Val Ile Phe Tyr Thr Glu Ala Ala Tyr Thr
1085 1090 1095
Ser Lys Ile Asp Pro Ile Lys Trp Trp Arg Pro Asn Leu Tyr Leu
1100 1105 1110
Lys Lys Gln Asn Ala Glu Ile Asn Lys Glu Asn Ile Leu Lys Phe
1115 1120 1125

Asp Asn Ile Ile Phe Asn Ser Lys Glu Asn Arg Phe Glu Phe Thr
1130 1135 1140
Tyr Asp Leu Lys Lys Phe Phe Trp Lys Asp Ser Lys Phe Pro Ala
1145 1150 1155
Lys Thr Val Asn Thr Val Cys Ser Cys Val Glu Arg Phe Lys Trp
1160 1165 1170
Asn Arg Asn Leu Asn Asn Asn Lys Trp Gly Tyr Ile His Tyr Glu
1175 1180 1185

Asn Leu Thr Asp Trp Lys Leu Ala Asn Lys Glu Gln Lys Glu Asp
1190 1195 1200
Glu Phe Ser Asn Phe Lys Glu Leu Phe Glu Lys Tyr Phe Ile Asp
1205 1210 1215
Ile Asn Trp Asn Ile Leu Glu Gln Ile Lys Asn Leu Asp Thr Lys
1220 1225 1230
Asn Asn Glu Lys Phe Phe Ser Ser Phe Ile Asp Leu Phe Thr Leu
1235 1240 1245

Val Cys Gln Ile Arg Asn Thr Asn Gln Asn Ala Lys Trp Asp Glu
1250 1255 1260
Asn Asp Phe Ile Leu Ser Pro Val Glu Pro Phe Phe Asp Ser Arg
1265 1270 1275
Lys Ser Gln Asn Phe Trp Lys Ser Leu Pro Lys Asn Trp Asp Glu
1280 1285 1290
Asn Trp Ala Phe Asn Ile Ala Arg Lys Gly Leu Ile Ile Leu Asn

1295 1300 1305

Arg Ile Ser Glu Asn Pro Glu Lys Pro Asp Leu Leu Ile Phe Asn

1310 1315 1320

Ala Asp Trp Asp Asn Phe Ala Arg Asn Ile

1325 1330

<210> 57

<211> 1175

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<400> 57

Met Thr Glu Gln Asn Glu Lys Pro Tyr Asn Gly Thr Tyr Tyr Thr Leu

1 5 10 15

Glu Asp Lys His Phe Trp Ala Ala Phe Phe Asn Leu Ala Arg His Asn

20 25 30

Ala Tyr Ile Thr Leu Ala His Ile Asp Arg Gln Leu Ala Tyr Ser Lys

35 40 45

Ala Asp Ile Thr Asn Asp Glu Asp Ile Leu Phe Phe Lys Gly Gln Trp

50 55 60

Lys Asn Leu Asp Asn Asp Leu Glu Arg Lys Ala Arg Leu Arg Ser Leu

65 70 75 80

Ile Leu Lys His Phe Ser Phe Leu Glu Gly Ala Ala Tyr Gly Lys Lys

85 90 95

Leu Phe Glu Ser Gln Ser Ser Gly Asn Lys Ser Ser Lys Lys Lys Glu

100 105 110

Leu Thr Lys Lys Glu Lys Glu Glu Leu Gln Ala Asn Ala Leu Ser Leu

115 120 125

Asp Asn Leu Lys Ser Ile Leu Phe Asp Phe Leu Gln Lys Leu Lys Asp

130 135 140

Phe Arg Asn Tyr Tyr Ser His Tyr Arg His Pro Glu Ser Ser Glu Leu

145 150 155 160

Pro Leu Phe Asp Gly Asn Met Leu Gln Arg Leu Tyr Asn Val Phe Asp

165 170 175

Val Ser Val Gln Arg Val Lys Arg Asp His Glu His Asn Asp Lys Val

180 185 190

Asp Pro His Arg His Phe Asn His Leu Val Arg Lys Gly Lys Lys Asp

195 200 205

Lys Tyr Gly Asn Asn Asp Asn Pro Phe Phe Lys His His Phe Val Asp

210 215 220

Arg Glu Glu Lys Val Thr Glu Ala Gly Leu Leu Phe Phe Val Ser Leu

225 230 235 240

Phe Leu Glu Lys Arg Asp Ala Ile Trp Met Gln Lys Lys Ile Arg Gly

245 250 255

Phe Lys Gly Gly Thr Glu Ala Tyr Gln Gln Met Thr Asn Glu Val Phe

260 265 270

Cys Arg Ser Arg Ile Ser Leu Pro Lys Leu Lys Leu Glu Ser Leu Arg

275 280 285

Thr Asp Asp Trp Met Leu Leu Asp Met Leu Asn Glu Leu Val Arg Cys

290 295 300

Pro Lys Ser Leu Tyr Asp Arg Leu Arg Glu Glu Asp Arg Ala Arg Phe

305 310 315 320

Arg Val Pro Val Asp Ile Leu Ser Asp Glu Asp Asp Thr Asp Gly Thr

325 330 335

Glu Glu Asp Pro Phe Lys Asn Thr Leu Val Arg His Gln Asp Arg Phe

340 345 350

Pro Tyr Phe Ala Leu Arg Tyr Phe Asp Leu Lys Lys Val Phe Thr Ser

355 360 365

Leu Arg Phe His Ile Asp Leu Gly Thr Tyr His Phe Ala Ile Tyr Lys

370 375 380

Lys Asn Ile Gly Glu Gln Pro Glu Asp Arg His Leu Thr Arg Asn Leu

385 390 395 400

Tyr Gly Phe Gly Arg Ile Gln Asp Phe Ala Glu Glu His Arg Pro Glu

405 410 415

Glu Trp Lys Arg Leu Val Arg Asp Leu Asp Tyr Phe Glu Thr Gly Asp

420 425 430

Lys Pro Tyr Ile Thr Gln Thr Thr Pro His Tyr His Ile Glu Lys Gly

435 440 445

Lys Ile Gly Leu Arg Phe Val Pro Glu Gly Gln Leu Leu Trp Pro Ser

450 455 460

Pro Glu Val Gly Ala Thr Arg Thr Gly Arg Ser Lys Tyr Ala Gln Asp

465 470 475 480

Lys Arg Phe Thr Ala Glu Ala Phe Leu Ser Val His Glu Leu Met Pro

485 490 495

Met Met Phe Tyr Tyr Phe Leu Leu Arg Glu Lys Tyr Ser Glu Glu Ala

500 505 510

Ser Ala Glu Lys Val Gln Gly Arg Ile Lys Arg Val Ile Glu Asp Val

515 520 525

Tyr Ala Val Tyr Asp Ala Phe Ala Arg Asp Glu Ile Asn Thr Arg Asp

530 535 540

Glu Leu Asp Ala Cys Leu Ala Asp Lys Gly Ile Arg Arg Gly His Leu

545 550 555 560

Pro Arg Gln Met Ile Ala Ile Leu Ser Gln Glu His Lys Asp Met Glu

565 570 575

Glu Lys Val Arg Lys Lys Leu Gln Glu Met Ile Ala Asp Thr Asp His

580 585 590

Arg Leu Asp Met Leu Asp Arg Gln Thr Asp Arg Lys Ile Arg Ile Gly

595 600 605

Arg Lys Asn Ala Gly Leu Pro Lys Ser Gly Val Ile Ala Asp Trp Leu

610 615 620

Val Arg Asp Met Met Arg Phe Gln Pro Val Ala Lys Asp Thr Ser Gly

625 630 635 640

Lys Pro Leu Asn Asn Ser Lys Ala Asn Ser Thr Glu Tyr Arg Met Leu

645 650 655

Gln Arg Ala Leu Ala Leu Phe Gly Gly Glu Lys Glu Arg Leu Thr Pro

660 665 670

Tyr Phe Arg Gln Met Asn Leu Thr Gly Gly Asn Asn Pro His Pro Phe

675 680 685

Leu His Glu Thr Arg Trp Glu Ser His Thr Asn Ile Leu Ser Phe Tyr

690 695 700

Arg Ser Tyr Leu Lys Ala Arg Lys Ala Phe Leu Gln Ser Ile Gly Arg

705 710 715 720

Ser Asp Arg Glu Glu Asn His Arg Phe Leu Leu Leu Lys Glu Pro Lys

725 730 735

Thr Asp Arg Gln Thr Leu Val Ala Gly Trp Lys Ser Glu Phe His Leu

740 745 750

Pro Arg Gly Ile Phe Thr Glu Ala Val Arg Asp Cys Leu Ile Glu Met

755 760 765

Gly Tyr Asp Glu Val Gly Ser Tyr Lys Glu Val Gly Phe Met Ala Lys

770 775 780

Ala Val Pro Leu Tyr Phe Glu Arg Ala Cys Lys Asp Arg Val Gln Pro

785 790 795 800

Phe Tyr Asp Tyr Pro Phe Asn Val Gly Asn Ser Leu Lys Pro Lys Lys

805 810 815

Gly Arg Phe Leu Ser Lys Glu Lys Arg Ala Glu Glu Trp Glu Ser Gly

820 825 830

Lys Glu Arg Phe Arg Asp Leu Glu Ala Trp Ser His Ser Ala Ala Arg

835 840 845

Arg Ile Glu Asp Ala Phe Val Gly Ile Glu Tyr Ala Ser Trp Glu Asn

850 855 860

Lys Lys Lys Ile Glu Gln Leu Leu Gln Asp Leu Ser Leu Trp Glu Thr

865 870 875 880

Phe Glu Ser Lys Leu Lys Val Lys Ala Asp Lys Ile Asn Ile Ala Lys

885 890 895

Leu Lys Lys Glu Ile Leu Glu Ala Lys Glu His Pro Tyr His Asp Phe

900 905 910

Lys Ser Trp Gln Lys Phe Glu Arg Glu Leu Arg Leu Val Lys Asn Gln

915 920 925

Asp Ile Ile Thr Trp Met Met Cys Arg Asp Leu Met Glu Glu Asn Lys

930 935 940

Val Glu Gly Leu Asp Thr Gly Thr Leu Tyr Leu Lys Asp Ile Arg Thr

945 950 955 960

Asp Val Gln Glu Gln Gly Ser Leu Asn Val Leu Asn His Val Lys Pro

965 970 975

Met Arg Leu Pro Val Val Val Tyr Arg Ala Asp Ser Arg Gly His Val

980 985 990

His Lys Glu Glu Ala Pro Leu Ala Thr Val Tyr Ile Glu Glu Arg Asp

995 1000 1005

Thr Lys Leu Leu Lys Gln Gly Asn Phe Lys Ser Phe Val Lys Asp

1010 1015 1020

Arg Arg Leu Asn Gly Leu Phe Ser Phe Val Asp Thr Gly Ala Leu

1025 1030 1035

Ala Met Glu Gln Tyr Pro Ile Ser Lys Leu Arg Val Glu Tyr Glu

1040 1045 1050

Leu Ala Lys Tyr Gln Thr Ala Arg Val Cys Ala Phe Glu Gln Thr

1055 1060 1065

Leu Glu Leu Glu Glu Ser Leu Leu Thr Arg Tyr Pro His Leu Pro

1070 1075 1080

Asp Glu Ser Phe Arg Glu Met Leu Glu Ser Trp Ser Asp Pro Leu

1085 1090 1095

Leu Asp Lys Trp Pro Asp Leu Gln Arg Glu Val Arg Leu Leu Ile

1100 1105 1110

Ala Val Arg Asn Ala Phe Ser His Asn Gln Tyr Pro Met Tyr Asp

1115 1120 1125

Glu Thr Ile Phe Ser Ser Ile Arg Lys Tyr Asp Pro Ser Ser Leu

1130 1135 1140

Asp Ala Ile Glu Glu Arg Met Gly Leu Asn Ile Ala His Arg Leu

1145 1150 1155

Ser Glu Glu Val Lys Leu Ala Lys Glu Met Val Glu Arg Ile Ile

1160 1165 1170

Gln Ala

1175

<210> 58

<211> 1115

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<400> 58

Met Glu Ser Ile Lys Asn Ser Gln Lys Ser Thr Gly Lys Thr Leu Gln

1 5 10 15

Lys Asp Pro Pro Tyr Phe Gly Leu Tyr Leu Asn Met Ala Leu Leu Asn

20 25 30

Val Arg Lys Val Glu Asn His Ile Arg Lys Trp Leu Gly Asp Val Ala

35 40 45

Leu Leu Pro Glu Lys Ser Gly Phe His Ser Leu Leu Thr Thr Asp Asn

50 55 60

Leu Ser Ser Ala Lys Trp Thr Arg Phe Tyr Tyr Lys Ser Arg Lys Phe

65 70 75 80

Leu Pro Phe Leu Glu Met Phe Asp Ser Asp Lys Lys Ser Tyr Glu Asn

85 90 95

Arg Arg Glu Thr Thr Glu Cys Leu Asp Thr Ile Asp Arg Gln Lys Ile

100 105 110

Ser Ser Leu Leu Lys Glu Val Tyr Gly Lys Leu Gln Asp Ile Arg Asn

115 120 125

Ala Phe Ser His Tyr His Ile Asp Asp Gln Ser Val Lys His Thr Ala

130 135 140

Leu Ile Ile Ser Ser Glu Met His Arg Phe Ile Glu Asn Ala Tyr Ser
145 150 155 160
Phe Ala Leu Gln Lys Thr Arg Ala Arg Phe Thr Gly Val Phe Val Glu

165 170 175
Thr Asp Phe Leu Gln Ala Glu Glu Lys Gly Asp Asn Lys Lys Phe Phe
180 185 190
Ala Ile Gly Gly Asn Glu Gly Ile Lys Leu Lys Asp Asn Ala Leu Ile
195 200 205
Phe Leu Ile Cys Leu Phe Leu Asp Arg Glu Glu Ala Phe Lys Phe Leu
210 215 220
Ser Arg Ala Thr Gly Phe Lys Ser Thr Lys Glu Lys Gly Phe Leu Ala

225 230 235 240
Val Arg Glu Thr Phe Cys Ala Leu Cys Cys Arg Gln Pro His Glu Arg
245 250 255
Leu Leu Ser Val Asn Pro Arg Glu Ala Leu Leu Met Asp Met Leu Asn
260 265 270
Glu Leu Asn Arg Cys Pro Asp Ile Leu Phe Glu Met Leu Asp Glu Lys
275 280 285
Asp Gln Lys Ser Phe Leu Pro Leu Leu Gly Glu Glu Glu Gln Ala His

290 295 300
Ile Leu Glu Asn Ser Leu Asn Asp Glu Leu Cys Glu Ala Ile Asp Asp
305 310 315 320
Pro Phe Glu Met Ile Ala Ser Leu Ser Lys Arg Val Arg Tyr Lys Asn
325 330 335
Arg Phe Pro Tyr Leu Met Leu Arg Tyr Ile Glu Glu Lys Asn Leu Leu
340 345 350
Pro Phe Ile Arg Phe Arg Ile Asp Leu Gly Cys Leu Glu Leu Ala Ser

355 360 365
Tyr Pro Lys Lys Met Gly Glu Glu Asn Asn Tyr Glu Arg Ser Val Thr
370 375 380
Asp His Ala Met Ala Phe Gly Arg Leu Thr Asp Phe His Asn Glu Asp

385 390 395 400

Ala Val Leu Gln Gln Ile Thr Lys Gly Ile Thr Asp Glu Val Arg Phe

405 410 415

Ser Leu Tyr Ala Pro Arg Tyr Ala Ile Tyr Asn Asn Lys Ile Gly Phe

420 425 430

Val Arg Thr Gly Gly Ser Asp Lys Ile Ser Phe Pro Thr Leu Lys Lys

435 440 445

Lys Gly Gly Glu Gly His Cys Val Ala Tyr Thr Leu Gln Asn Thr Lys

450 455 460

Ser Phe Gly Phe Ile Ser Ile Tyr Asp Leu Arg Lys Ile Leu Leu Leu

465 470 475 480

Ser Phe Leu Asp Lys Asp Lys Ala Lys Asn Ile Val Ser Gly Leu Leu

485 490 495

Glu Gln Cys Glu Lys His Trp Lys Asp Leu Ser Glu Asn Leu Phe Asp

500 505 510

Ala Ile Arg Thr Glu Leu Gln Lys Glu Phe Pro Val Pro Leu Ile Arg

515 520 525

Tyr Thr Leu Pro Arg Ser Lys Gly Gly Lys Leu Val Ser Ser Lys Leu

530 535 540

Ala Asp Lys Gln Glu Lys Tyr Glu Ser Glu Phe Glu Arg Arg Lys Glu

545 550 555 560

Lys Leu Thr Glu Ile Leu Ser Glu Lys Asp Phe Asp Leu Ser Gln Ile

565 570 575

Pro Arg Arg Met Ile Asp Glu Trp Leu Asn Val Leu Pro Thr Ser Arg

580 585 590

Glu Lys Lys Leu Lys Gly Tyr Val Glu Thr Leu Lys Leu Asp Cys Arg

595 600 605

Glu Arg Leu Arg Val Phe Glu Lys Arg Glu Lys Gly Glu His Pro Val

610 615 620

Pro Pro Arg Ile Gly Glu Met Ala Thr Asp Leu Ala Lys Asp Ile Ile

625 630 635 640

Arg Met Val Ile Asp Gln Gly Val Lys Gln Arg Ile Thr Ser Ala Tyr
645 650 655
Tyr Ser Glu Ile Gln Arg Cys Leu Ala Gln Tyr Ala Gly Asp Asp Asn
660 665 670
Arg Arg His Leu Asp Ser Ile Ile Arg Glu Leu Arg Leu Lys Asp Thr

675 680 685
Lys Asn Gly His Pro Phe Leu Gly Lys Val Leu Arg Pro Gly Leu Gly
690 695 700
His Thr Glu Lys Leu Tyr Gln Arg Tyr Phe Glu Glu Lys Lys Glu Trp
705 710 715 720
Leu Glu Ala Thr Phe Tyr Pro Ala Ala Ser Pro Lys Arg Val Pro Arg
725 730 735
Phe Val Asn Pro Pro Thr Gly Lys Gln Lys Glu Leu Pro Leu Ile Ile

740 745 750
Arg Asn Leu Met Lys Glu Arg Pro Glu Trp Arg Asp Trp Lys Gln Arg
755 760 765
Lys Asn Ser His Pro Ile Asp Leu Pro Ser Gln Leu Phe Glu Asn Glu
770 775 780
Ile Cys Arg Leu Leu Lys Asp Lys Ile Gly Lys Glu Pro Ser Gly Lys
785 790 795 800
Leu Lys Trp Asn Glu Met Phe Lys Leu Tyr Trp Asp Lys Glu Phe Pro

805 810 815
Asn Gly Met Gln Arg Phe Tyr Arg Cys Lys Arg Arg Val Glu Val Phe
820 825 830
Asp Lys Val Val Glu Tyr Glu Tyr Ser Glu Glu Gly Gly Asn Tyr Lys
835 840 845
Lys Tyr Tyr Glu Ala Leu Ile Asp Glu Val Val Arg Gln Lys Ile Ser
850 855 860
Ser Ser Lys Glu Lys Ser Lys Leu Gln Val Glu Asp Leu Thr Leu Ser

865 870 875 880
Val Arg Arg Val Phe Lys Arg Ala Ile Asn Glu Lys Glu Tyr Gln Leu

885 890 895

Arg Leu Leu Cys Glu Asp Asp Arg Leu Leu Phe Met Ala Val Arg Asp

900 905 910

Leu Tyr Asp Trp Lys Glu Ala Gln Leu Asp Leu Asp Lys Ile Asp Asn

915 920 925

Met Leu Gly Glu Pro Val Ser Val Ser Gln Val Ile Gln Leu Glu Gly

930 935 940

Gly Gln Pro Asp Ala Val Ile Lys Ala Glu Cys Lys Leu Lys Asp Val

945 950 955 960

Ser Lys Leu Met Arg Tyr Cys Tyr Asp Gly Arg Val Lys Gly Leu Met

965 970 975

Pro Tyr Phe Ala Asn His Glu Ala Thr Gln Glu Gln Val Glu Met Glu

980 985 990

Leu Arg His Tyr Glu Asp His Arg Arg Arg Val Phe Asn Trp Val Phe

995 1000 1005

Ala Leu Glu Lys Ser Val Leu Lys Asn Glu Lys Leu Arg Arg Phe

1010 1015 1020

Tyr Glu Glu Ser Gln Gly Gly Cys Glu His Arg Arg Cys Ile Asp

1025 1030 1035

Ala Leu Arg Lys Ala Ser Leu Val Ser Glu Glu Glu Tyr Glu Phe

1040 1045 1050

Leu Val His Ile Arg Asn Lys Ser Ala His Asn Gln Phe Pro Asp

1055 1060 1065

Leu Glu Ile Gly Lys Leu Pro Pro Asn Val Thr Ser Gly Phe Cys

1070 1075 1080

Glu Cys Ile Trp Ser Lys Tyr Lys Ala Ile Ile Cys Arg Ile Ile

1085 1090 1095

Pro Phe Ile Asp Pro Glu Arg Arg Phe Phe Gly Lys Leu Leu Glu

1100 1105 1110

Gln Lys

1115

<210> 59

<211> 1115

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<400> 59

Met Glu Ser Ile Lys Asn Ser Gln Lys Ser Thr Gly Lys Thr Leu Gln
1 5 10 15

Lys Asp Pro Pro Tyr Phe Gly Leu Tyr Leu Asn Met Ala Leu Leu Asn
20 25 30

Val Arg Lys Val Glu Asn His Ile Arg Lys Trp Leu Gly Asp Val Ala
35 40 45

Leu Leu Pro Glu Lys Ser Gly Phe His Ser Leu Leu Thr Thr Asp Asn
50 55 60

Leu Ser Ser Ala Lys Trp Thr Arg Phe Tyr Tyr Lys Ser Arg Lys Phe
65 70 75 80

Leu Pro Phe Leu Glu Met Phe Asp Ser Asp Lys Lys Ser Tyr Glu Asn
85 90 95

Arg Arg Glu Thr Ala Glu Cys Leu Asp Thr Ile Asp Arg Gln Lys Ile
100 105 110

Ser Ser Leu Leu Lys Glu Val Tyr Gly Lys Leu Gln Asp Ile Arg Asn
115 120 125

Ala Phe Ser His Tyr His Ile Asp Asp Gln Ser Val Lys His Thr Ala
130 135 140

Leu Ile Ile Ser Ser Glu Met His Arg Phe Ile Glu Asn Ala Tyr Ser
145 150 155 160

Phe Ala Leu Gln Lys Thr Arg Ala Arg Phe Thr Gly Val Phe Val Glu
165 170 175

Thr Asp Phe Leu Gln Ala Glu Glu Lys Gly Asp Asn Lys Lys Phe Phe
180 185 190

Ala Ile Gly Gly Asn Glu Gly Ile Lys Leu Lys Asp Asn Ala Leu Ile

195 200 205

Phe Leu Ile Cys Leu Phe Leu Asp Arg Glu Glu Ala Phe Lys Phe Leu

210 215 220

Ser Arg Ala Thr Gly Phe Lys Ser Thr Lys Glu Lys Gly Phe Leu Ala

225 230 235 240

Val Arg Glu Thr Phe Cys Ala Leu Cys Cys Arg Gln Pro His Glu Arg

245 250 255

Leu Leu Ser Val Asn Pro Arg Glu Ala Leu Leu Met Asp Met Leu Asn

260 265 270

Glu Leu Asn Arg Cys Pro Asp Ile Leu Phe Glu Met Leu Asp Glu Lys

275 280 285

Asp Gln Lys Ser Phe Leu Pro Leu Leu Gly Glu Glu Glu Gln Ala His

290 295 300

Ile Leu Glu Asn Ser Leu Asn Asp Glu Leu Cys Glu Ala Ile Asp Asp

305 310 315 320

Pro Phe Glu Met Ile Ala Ser Leu Ser Lys Arg Val Arg Tyr Lys Asn

325 330 335

Arg Phe Pro Tyr Leu Met Leu Arg Tyr Ile Glu Glu Lys Asn Leu Leu

340 345 350

Pro Phe Ile Arg Phe Arg Ile Asp Leu Gly Cys Leu Glu Leu Ala Ser

355 360 365

Tyr Pro Lys Lys Met Gly Glu Glu Asn Asn Tyr Glu Arg Ser Val Thr

370 375 380

Asp His Ala Met Ala Phe Gly Arg Leu Thr Asp Phe His Asn Glu Asp

385 390 395 400

Ala Val Leu Gln Gln Ile Thr Lys Gly Ile Thr Asp Glu Val Arg Phe

405 410 415

Ser Leu Tyr Ala Pro Arg Tyr Ala Ile Tyr Asn Asn Lys Ile Gly Phe

420 425 430

Val Arg Thr Ser Gly Ser Asp Lys Ile Ser Phe Pro Thr Leu Lys Lys

435 440 445

Lys Gly Gly Glu Gly His Cys Val Ala Tyr Thr Leu Gln Asn Thr Lys
450 455 460
Ser Phe Gly Phe Ile Ser Ile Tyr Asp Leu Arg Lys Ile Leu Leu Leu
465 470 475 480
Ser Phe Leu Asp Lys Asp Lys Ala Lys Asn Ile Val Ser Gly Leu Leu
485 490 495
Glu Gln Cys Glu Lys His Trp Lys Asp Leu Ser Glu Asn Leu Phe Asp

500 505 510
Ala Ile Arg Thr Glu Leu Gln Lys Glu Phe Pro Val Pro Leu Ile Arg
515 520 525
Tyr Thr Leu Pro Arg Ser Lys Gly Gly Lys Leu Val Ser Ser Lys Leu
530 535 540
Ala Asp Lys Gln Glu Lys Tyr Glu Ser Glu Phe Glu Arg Arg Lys Glu
545 550 555 560
Lys Leu Thr Glu Ile Leu Ser Glu Lys Asp Phe Asp Leu Ser Gln Ile

565 570 575
Pro Arg Arg Met Ile Asp Glu Trp Leu Asn Val Leu Pro Thr Ser Arg
580 585 590
Glu Lys Lys Leu Lys Gly Tyr Val Glu Thr Leu Lys Leu Asp Cys Arg
595 600 605
Glu Arg Leu Arg Val Phe Glu Lys Arg Glu Lys Gly Glu His Pro Leu
610 615 620
Pro Pro Arg Ile Gly Glu Met Ala Thr Asp Leu Ala Lys Asp Ile Ile

625 630 635 640
Arg Met Val Ile Asp Gln Gly Val Lys Gln Arg Ile Thr Ser Ala Tyr
645 650 655
Tyr Ser Glu Ile Gln Arg Cys Leu Ala Gln Tyr Ala Gly Asp Asp Asn
660 665 670
Arg Arg His Leu Asp Ser Ile Ile Arg Glu Leu Arg Leu Lys Asp Thr
675 680 685
Lys Asn Gly His Pro Phe Leu Gly Lys Val Leu Arg Pro Gly Leu Gly

690 695 700

His Thr Glu Lys Leu Tyr Gln Arg Tyr Phe Glu Glu Lys Lys Glu Trp

705 710 715 720

Leu Glu Ala Thr Phe Tyr Pro Ala Ala Ser Pro Lys Arg Val Pro Arg

725 730 735

Phe Val Asn Pro Pro Thr Gly Lys Gln Lys Glu Leu Pro Leu Ile Ile

740 745 750

Arg Asn Leu Met Lys Glu Arg Pro Glu Trp Arg Asp Trp Lys Gln Arg

755 760 765

Lys Asn Ser His Pro Ile Asp Leu Pro Ser Gln Leu Phe Glu Asn Glu

770 775 780

Ile Cys Arg Leu Leu Lys Asp Lys Ile Gly Lys Glu Pro Ser Gly Lys

785 790 795 800

Leu Lys Trp Asn Glu Met Phe Lys Leu Tyr Trp Asp Lys Glu Phe Pro

805 810 815

Asn Gly Met Gln Arg Phe Tyr Arg Cys Lys Arg Arg Val Glu Val Phe

820 825 830

Asp Lys Val Val Glu Tyr Glu Tyr Ser Glu Glu Gly Gly Asn Tyr Lys

835 840 845

Lys Tyr Tyr Glu Ala Leu Ile Asp Glu Val Val Arg Gln Lys Ile Ser

850 855 860

Ser Ser Lys Glu Lys Ser Lys Leu Gln Val Glu Asp Leu Thr Leu Ser

865 870 875 880

Val Arg Arg Val Phe Lys Arg Ala Ile Asn Glu Lys Glu Tyr Gln Leu

885 890 895

Arg Leu Leu Cys Glu Asp Asp Arg Leu Leu Phe Met Ala Val Arg Asp

900 905 910

Leu Tyr Asp Trp Lys Glu Ala Gln Leu Asp Leu Asp Lys Ile Asp Asn

915 920 925

Met Leu Gly Glu Pro Val Ser Val Ser Gln Val Ile Gln Leu Glu Gly

930 935 940

Gly Gln Pro Asp Ala Val Ile Lys Ala Glu Cys Lys Leu Lys Asp Val

945 950 955 960

Ser Lys Leu Met Arg Tyr Cys Tyr Asp Gly Arg Val Lys Gly Leu Met

965 970 975

Pro Tyr Phe Ala Asn His Glu Ala Thr Gln Glu Gln Val Glu Met Glu

980 985 990

Leu Arg His Tyr Glu Asp His Arg Arg Arg Val Phe Asn Trp Val Phe

995 1000 1005

Ala Leu Glu Lys Ser Val Leu Lys Asn Glu Lys Leu Arg Arg Phe

1010 1015 1020

Tyr Glu Glu Ser Gln Gly Gly Cys Glu His Arg Arg Cys Ile Asp

1025 1030 1035

Ala Leu Arg Lys Ala Ser Leu Val Ser Glu Glu Glu Tyr Glu Phe

1040 1045 1050

Leu Val His Ile Arg Asn Lys Ser Ala His Asn Gln Phe Pro Asp

1055 1060 1065

Leu Glu Ile Gly Lys Leu Pro Pro Asn Val Thr Ser Gly Phe Cys

1070 1075 1080

Glu Cys Ile Trp Ser Lys Tyr Lys Ala Ile Ile Cys Arg Ile Ile

1085 1090 1095

Pro Phe Ile Asp Pro Glu Arg Arg Phe Phe Gly Lys Leu Leu Glu

1100 1105 1110

Gln Lys

1115

<210> 60

<211> 1008

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<400> 60

Met Asp Thr Pro Asn Phe Ser Glu Arg Ile Pro Val Ser Leu Gln Ser

1 5 10 15

His Pro Tyr Tyr Phe Ala His Tyr Leu Asn Met Ala Arg His Asn Ala

20 25 30

Tyr Val Ile Leu Glu Tyr Val Asn Arg Glu Leu Ile Lys Pro Gly Lys

35 40 45

Asn Leu Asp Glu Asp Asn Leu Ile Gln Ser Thr Val Leu Lys Asp Gly

50 55 60

Tyr Phe Asp Arg Lys Pro Asp Glu Leu Ser His Arg Asn Arg Leu Leu

65 70 75 80

Val Gln His Phe Pro Phe Leu Arg Glu Ala Glu Asn Glu Gly Ala Arg

85 90 95

Thr Cys Asn Pro Val Ser Tyr Lys Leu Lys Thr Ala Leu Ala Ala Leu

100 105 110

Asn Gln Trp Arg Asn Asn Ala Ser His Tyr Pro Leu Asn Gln Asn His

115 120 125

Glu Lys Asp Phe Asp Leu Gln Pro Phe Phe Ser Phe Ala Ile Glu Ala

130 135 140

Cys Lys Lys Arg Met Arg Glu Val Phe Gln Pro Asp Asp Phe Tyr Leu

145 150 155 160

Leu Glu Thr Asn Glu Lys Gln Phe Tyr Thr Leu His Asn Glu Asn Gly

165 170 175

Phe Thr Glu Lys Gly Leu Tyr Cys Phe Ile Cys Phe Phe Leu Glu Lys

180 185 190

Lys Tyr Ala Phe Gln Phe Leu Ala Gly Ile Lys Gly Phe Lys Asn Thr

195 200 205

Thr Asp Asn Lys Phe Arg Ala Thr Leu Glu Thr Phe Thr Glu His Cys

210 215 220

Cys Arg Leu Pro Lys Pro Lys Leu Asp Ser Ser Asp Ile Lys Leu Asp

225 230 235 240

Met Leu Gly Glu Leu Ser Arg Cys Pro Ala Pro Leu Phe Asp Leu Leu

245 250 255

Asp Ile Glu Glu Arg Lys Lys Phe Ile Arg Glu Pro Glu Glu Val Lys

260 265 270

Pro Asp Glu Ser Gly Asp Arg Glu Glu Val Gln Gln Val Leu Met Lys

275 280 285

Arg Tyr Asp Asp Arg Phe Pro Tyr Phe Ala Leu Arg Tyr Phe Glu Glu

290 295 300

Lys Asn Leu Leu Lys Gly Ile Ser Phe His Ile His Ile Gly Arg Trp

305 310 315 320

Ile Lys Ser Glu His Thr Lys Lys Ile Met Gly Ala Glu Arg Asp Arg

325 330 335

Arg Leu Leu Lys Asp Ile Arg Thr Phe Gly Glu Leu Lys Glu Phe Ser

340 345 350

Pro Glu His Ala Pro Asp Tyr Trp Leu Arg Asp Gly Ile Thr Pro Asp

355 360 365

Asp Val Asp Gln Phe Ser Pro Gln Tyr Arg Ile Val Gly Asn Arg Ile

370 375 380

Gly Ile Lys Leu Asn Tyr Asn Gly His Asn Arg Trp Ser Val Pro Asp

385 390 395 400

Lys Glu Ile Asn Val Lys Pro Asp Ala Ile Ile Ser Thr Tyr Glu Phe

405 410 415

Leu Asn Leu Phe Leu Tyr Glu His Leu Tyr Gln Lys Lys Leu Thr Gly

420 425 430

Leu Ser Pro Ala Glu Phe Ile Gln Asp Tyr Leu Asp Arg Phe Asn Asn

435 440 445

Phe Leu Ser Glu Phe Lys Ala Gly His Ile Arg Pro Val Gly Asp Phe

450 455 460

Ser Leu Glu Lys Arg Arg Gly Gln Gly Asp Glu Pro Asp Leu Thr Ala

465 470 475 480

Arg Arg Lys Ser Leu Gln Lys Glu Leu Asp Arg Phe Val Leu Lys Gly

485 490 495

Lys Asp Leu Pro Asp Lys Ile Arg Glu Tyr Leu Leu Gly Tyr Lys Gln
500 505 510
Lys Ser Glu Lys Lys Gln Ala Lys Trp Ile Leu Gly Gly Met Ile Lys

515 520 525
Glu Thr Val Tyr Trp Arg Asn Lys Ala Glu Gln Ser Pro Glu Lys Met
530 535 540
Arg Ser Gly Asp Met Ala Gln Gln Leu Ala Arg Asp Ile Ile Phe Leu
545 550 555 560
Thr Pro Pro His Thr Val Lys Glu His Lys Gln Lys Leu Asn Ser Leu
565 570 575
Glu Tyr Asp Val Leu Gln Tyr Ala Leu Ala Tyr Phe Ser Ser Asn Arg

580 585 590
Glu Lys Leu Tyr Ser Phe Phe Lys Glu His Gln Leu Thr Val Lys Gly
595 600 605
Asp Arg Ala His Pro Phe Leu Tyr Lys Ile Arg Leu Asp Glu Cys Gln
610 615 620
Gly Ile Leu Asp Phe Phe Ile Val Tyr Met Gln Gln Lys Glu Lys Trp
625 630 635 640
Leu Gly Trp Leu Asp Arg Asn Leu Lys Ser Pro Arg Leu Asn Glu Glu

645 650 655
Glu Phe Phe Asn Thr Tyr Ser Tyr Phe Ile Lys Thr Asp Thr Lys Arg
660 665 670
Ala Ile Glu Met Asp Tyr Glu Ser Cys Pro Asn Tyr Leu Pro Arg Gly
675 680 685
Ile Phe Asn Glu Pro Ile Ala Lys Ala Leu Gln Lys Ala Gly Val Lys
690 695 700
Ile Lys Asp Glu Asp Asn Ala Ser Tyr Ala Leu Ser Val Tyr Ser Asn

705 710 715 720
Gly Lys Thr Gln Pro Phe Tyr Asn Lys Glu Arg Tyr Tyr Asn Lys Gly
725 730 735
Ile Phe Arg Met Glu Glu Leu Pro Glu Lys Leu Gln Pro Lys Glu Leu

740 745 750

Leu Gly Lys Ile Gln Trp Thr Ile Lys Ser Ser Gly Lys Asp Thr Glu

755 760 765

Glu Phe Arg Ser Leu Gln Asn Leu Lys Asn Arg Ile Leu Asn Thr Glu

770 775 780

Lys Glu Ile Arg Tyr Val Gln Ser Thr Asp Arg Ala Leu Trp Ile Met

785 790 795 800

Val Ala Asp Leu Phe Pro Glu Thr Phe Glu Leu Arg Pro Asp Asp Leu

805 810 815

Glu Cys Ile Gly His Asp Leu Ser Asp Asp Leu Leu Ser Arg Pro Tyr

820 825 830

Gln Met Lys Glu Lys Val Tyr Asn Tyr Thr Ile Thr Asp Tyr Leu Pro

835 840 845

Ile Lys Arg Tyr Gly Glu Phe Arg Arg Phe Leu Lys Asp Arg Arg Leu

850 855 860

Glu Asn Leu Leu Thr Tyr Phe Glu Glu Gly Val Pro Leu His Arg Glu

865 870 875 880

Ala Leu Val Ala Glu Leu Glu Ala Tyr Asp Leu Gln Arg Lys Asn Leu

885 890 895

Leu Glu Ile Ile Tyr Arg Phe Glu Lys Leu Val Phe Asp Arg His Arg

900 905 910

His Glu Leu Thr Phe Ser Gly Glu Gly Glu Asn Gln Tyr Val Asn His

915 920 925

Trp Asp Tyr Leu Asp Phe Val Ala Arg Lys Tyr Gly Leu Ser Ala Glu

930 935 940

Val Lys Glu Leu Asn Ser Glu Arg Phe Thr Glu Leu Arg Asn Lys Met

945 950 955 960

Leu His Asn Gln Ile Pro Tyr Gln Leu Trp Ile Lys Glu Ala Ile Ala

965 970 975

Ala Arg Glu Glu Asn Thr Val Cys Gly Arg Ile Met Gly Met Ile Gly

980 985 990

Glu Ile Tyr Glu Arg Met Thr Thr Glu Ile Glu Lys Gln Met Gln Val

995 1000 1005

<210> 61

<211> 1063

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<400> 61

Met Phe Asp Asn Glu Gln Lys Asn Leu Glu Lys Glu Pro Tyr Trp Gly

1 5 10 15

Val Phe Leu Asn Gln Ala Arg Leu Asn Ala Tyr Ile Ala Leu Arg Asp

20 25 30

Ile Ser Glu Arg Leu Glu Glu Asn Ala Ala Asp Glu Asp Ser Leu Ser

35 40 45

Glu Trp Pro Val Leu Lys Tyr Leu Asp Asn Asp Thr Asp Ala Val Lys

50 55 60

Ser Arg Arg Ile Phe Asp Leu Val Glu Lys His Phe Ser Met Leu Lys

65 70 75 80

Ile Ile Tyr Gly Gly Glu Lys Glu Gly Asp Leu Val Lys Arg Ser Lys

85 90 95

Glu Tyr Lys Ile Ile Leu Lys Cys Leu Phe Arg Ala Leu Asn Phe Tyr

100 105 110

Arg Asn Lys Phe Cys His Met Tyr Ser Gly Asn Arg Ala Arg Lys Tyr

115 120 125

Asn Glu Lys Glu Leu Ile Lys Tyr Leu Glu Asp Cys Phe Asp Ala Ser

130 135 140

Val Arg Lys Ile Lys Glu Leu Arg Arg Leu Asp Glu Lys Asp Val Leu

145 150 155 160

His Leu Arg Arg Lys Ile Ala Glu Gly Lys Asp Ala Asn Lys Arg Val

165 170 175

Ile Asp Asn Pro Gln Phe Arg Tyr Pro Phe Lys Asn Glu Lys Gly Glu

180 185 190

Leu Asn Glu Lys Gly Leu Tyr Phe Leu Ala Ser Ile Phe Leu Asp Lys

195 200 205

Lys Glu Ala His Glu Phe Leu Lys Lys Gln Glu Tyr Phe Lys Asn Asp

210 215 220

Ser Glu Pro Lys Tyr Arg Ala Thr Leu Glu Ser Phe Tyr His Tyr Arg

225 230 235 240

Ile Lys Leu Pro Arg Pro Val Ile Glu Ser Asp Val Asp Lys Asn Gly

245 250 255

Leu Ala Leu Asp Met Leu Asn Glu Leu Lys Lys Cys Pro Lys Glu Leu

260 265 270

Phe Asp Leu Leu Ser Lys Glu Gln Gln Glu Lys Phe Arg Val Val Asp

275 280 285

Ser Glu Asp Ala Asp Glu Glu Gly Asn Glu Ile Leu Met Arg Arg Tyr

290 295 300

Ser Asp Arg Phe Pro Tyr Leu Ala Leu Arg Tyr Cys Asp Glu Asn Gln

305 310 315 320

Val Phe Glu Arg Ile Arg Phe Gln Ile Asp Leu Gly Arg Tyr Tyr Phe

325 330 335

Lys Phe Tyr Pro Lys Glu Thr Ile Asp Gly Lys Thr Gln Gln Arg Ser

340 345 350

Leu Asp Lys Arg Leu Lys Ile Phe Gly Arg Ile Lys Asp Val Lys Ser

355 360 365

Lys Val Glu Gln Glu Trp Ser Gly Ile Ile Lys Ser Pro Asp Thr Ile

370 375 380

Glu Glu Asn Pro Asn Glu Pro Tyr Lys Leu Lys Thr Thr Pro Arg Tyr

385 390 395 400

Asn Ile Val Asp Asn Gln Ile Gly Phe Val Ile Thr Gly Asp Lys Asn

405 410 415

Leu Pro Asp Val Lys Arg Pro Asp Gly Arg Ile Glu Leu Glu Lys Pro

420 425 430

Asp Gly Trp Leu Ser Ile Tyr Glu Leu Pro Gly Met Leu Phe His Gly

435 440 445

Leu Lys Tyr Gly Phe Asp Lys Thr Glu Arg Met Ile Lys Ile Tyr Ile

450 455 460

Glu Lys Gln Arg Lys Ile Cys Lys Glu Ile Cys Glu Lys Gly Thr Ile

465 470 475 480

Thr Pro Asp Asp Gly Glu Ser Met Pro Glu Ala Leu Lys Gly Gly Ala

485 490 495

Lys Ala Ala Lys Arg Asn Tyr Ser Glu Lys Lys Leu Glu Arg Met Leu

500 505 510

Gln Asp Thr Glu Gln Arg Ile Arg Ala Ile Gln Thr Thr Gln Lys Arg

515 520 525

Met Asp Glu Pro Gly Asn Lys Pro Gly Lys Lys Lys Phe Phe Asp Ile

530 535 540

Arg Ala Gly Lys Leu Ala Asp Phe Leu Ala Arg Asp Ile Met Ala Leu

545 550 555 560

Gln Arg Phe Asp Pro Ala Lys His Gly Lys Asp Lys Leu Thr Ala Ile

565 570 575

Asn Phe Gln Val Leu Gln Ala Thr Leu Ala Phe Tyr Gly Ala Lys Lys

580 585 590

Asp Val Ile Glu Asp Met Phe Lys Gly Ile Gly Leu Leu Glu Gly Asp

595 600 605

Asn Pro His Pro Phe Leu Asn Gln Ile Asp Pro Ala Gln Tyr Asn Ser

610 615 620

Ile Ala Gly Phe Tyr Gln Ala Tyr Leu Gln Lys Lys Arg Ser Tyr Leu

625 630 635 640

Glu Asp Tyr Arg Lys Glu Glu Glu Tyr Asp Glu Gln Phe Leu Arg Pro

645 650 655

Lys Arg Gln Arg Tyr Ala Gln Glu Lys Arg Glu Ile Lys Thr Val Ala

660 665 670

Arg Gln Leu Leu Asp Asn Pro Val Asn Val Pro Lys Asn Phe Phe Lys

675 680 685

Lys Glu Ile Glu Glu Phe Val Phe Ser Gln Asp Pro Ser Leu Lys Lys

690 695 700

Ser Lys Met Asn Thr Ala Tyr Met Ile Gln Ala Leu Phe Glu Lys His

705 710 715 720

Tyr Gly Arg Gln Gln Pro Phe Tyr Ser Tyr Asn Arg Thr Tyr Pro Val

725 730 735

Val Ser Lys Ala Ile Glu Tyr Gly Lys Lys Gly Lys Asn Lys Lys Ile

740 745 750

Ala Lys Val Leu Met Ala Ile Glu Pro Lys Leu Asn Tyr Met Glu Ile

755 760 765

Lys Lys Ile Val Asn Glu Met Pro Asp Gly Gln Tyr Glu Pro Glu Asn

770 775 780

Leu Lys Arg Asn Leu Tyr Glu Gly Tyr Lys Asp Tyr Glu Lys Asp Glu

785 790 795 800

Arg Ile Ile Arg Arg Cys Lys Val Gln Asp Val Val Ser Phe Met Met

805 810 815

Val Glu Glu Thr Leu Lys Asp Gln Leu Asp Phe Asn Gly Asn Val Leu

820 825 830

Thr Leu Glu Lys Ile Thr Pro Trp Glu Ala Ser Pro Phe Lys Lys Pro

835 840 845

Val Leu Cys His Thr Ile Ile Ser Ile Pro Phe Asn Thr Lys Gly Gly

850 855 860

His Thr Asp Lys Asp Tyr Val Asp Phe Ile Lys Asn Asn Phe Glu Gly

865 870 875 880

Ser Tyr Asp Cys Glu Pro Asn Lys Ile Ile Leu Lys Tyr Lys Val Thr

885 890 895

Ser Lys Asp Thr Lys Leu Lys Asp Ile Gly Lys Tyr Arg Met Tyr Ser

900 905 910

His Asp Arg Arg Leu Pro Gly Leu Leu Ile Trp Lys Tyr Arg Pro Asn

915 920 925

Asp Gln Asn Gly Asn Glu Ile Lys Phe Thr Glu Ile Glu Gln Glu Ile

930 935 940

Lys Ala Phe Glu Arg Arg Arg Ile Glu Ile Ala Gln Cys Leu Tyr Thr

945 950 955 960

Leu Glu Lys Lys Val Ile Asp Ser Trp Phe Thr Gln Asp Glu Leu Gly

965 970 975

Glu Glu His Ile Pro Phe Asn Lys Val Ile Asp Val Ile Lys Ala Lys

980 985 990

Met Pro Asn Phe Glu Asp Lys Cys Asn Val Leu Leu Lys Ile Arg Asn

995 1000 1005

Ala Ile Asn His Asn Gln Phe Pro Val Tyr Glu Gln Ala Ile Gln

1010 1015 1020

Thr Ala Pro Gly Lys Glu Ile Ala Gly Lys Met Leu Arg Ile Thr

1025 1030 1035

Glu Ser Tyr Ile Glu Gln Ile Met Ala Lys Ile Asp Pro Asp Phe

1040 1045 1050

Gly Arg Thr Glu Asp Ala Glu Ser Ser Arg

1055 1060

<210> 62

<211> 1009

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<220><221> MOD_RES

<222> (375)..(375)

<223> Any amino acid

<400> 62

Met Asp Thr Pro Asn Phe Ser Glu Arg Ile Pro Val Ser Leu Gln Ser

1 5 10 15

His Pro Tyr Tyr Phe Ala His Tyr Leu Asn Met Ala Arg His Asn Ala

20 25 30

Tyr Val Ile Leu Glu Tyr Val Asn Arg Glu Leu Ile Lys Pro Gly Lys
35 40 45
Asn Leu Asp Glu Asp Asn Leu Ile Gln Ser Thr Val Leu Lys Asp Gly
50 55 60
Tyr Phe Asp Arg Lys Pro Asp Glu Leu Ser His Arg Asn Arg Leu Leu

65 70 75 80
Val Gln His Phe Pro Phe Leu Arg Glu Ala Glu Asn Glu Gly Ala Arg
85 90 95
Thr Cys Asn Pro Val Ser Tyr Lys Leu Lys Thr Ala Leu Ala Ala Leu
100 105 110
Asn Gln Trp Arg Asn Asn Ala Ser His Tyr Pro Leu Asn Gln Asn His
115 120 125
Glu Lys Asp Phe Asp Leu Gln Pro Phe Phe Ser Phe Ala Ile Glu Ala

130 135 140
Cys Lys Lys Arg Met Arg Glu Val Phe Gln Pro Asp Asp Phe Tyr Leu
145 150 155 160
Leu Glu Thr Asn Glu Lys Gln Phe Tyr Thr Leu His Asn Glu Asn Gly
165 170 175
Phe Thr Glu Lys Gly Leu Tyr Cys Phe Ile Cys Phe Phe Leu Glu Lys
180 185 190
Lys Tyr Ala Phe Gln Phe Leu Ala Gly Ile Lys Gly Phe Lys Asn Thr

195 200 205
Thr Asp Asn Lys Phe Arg Ala Thr Leu Glu Thr Phe Thr Glu His Cys
210 215 220
Cys Arg Leu Pro Lys Pro Lys Leu Asp Ser Ser Asp Ile Lys Leu Asp
225 230 235 240
Met Leu Gly Glu Leu Ser Arg Cys Pro Ala Pro Leu Phe Asp Leu Leu
245 250 255
Asp Ile Glu Glu Arg Lys Lys Phe Ile Arg Glu Pro Glu Glu Val Lys

260 265 270
Pro Asp Glu Ser Gly Asp Arg Glu Glu Val Gln Gln Val Leu Met Lys

275 280 285

Arg Tyr Asp Asp Arg Phe Pro Tyr Phe Ala Leu Arg Tyr Phe Glu Glu

290 295 300

Lys Asn Leu Leu Lys Gly Ile Ser Phe His Ile His Ile Gly Arg Trp

305 310 315 320

Ile Lys Ser Glu His Thr Lys Lys Ile Met Gly Ala Glu Arg Asp Arg

325 330 335

Arg Leu Leu Lys Asp Ile Arg Thr Phe Gly Glu Leu Lys Glu Phe Ser

340 345 350

Pro Glu His Ala Pro Asp Tyr Trp Leu Arg Asp Gly Ile Thr Pro Asp

355 360 365

Asp Val Asp Gln Phe Ser Xaa Pro Gln Tyr Arg Ile Val Gly Asn Arg

370 375 380

Ile Gly Ile Lys Leu Asn Tyr Asn Gly His Asn Arg Trp Ser Val Pro

385 390 395 400

Asp Lys Glu Ile Asn Val Lys Pro Asp Ala Ile Ile Ser Thr Tyr Glu

405 410 415

Phe Leu Asn Leu Phe Leu Tyr Glu His Leu Tyr Gln Lys Lys Leu Thr

420 425 430

Gly Leu Ser Pro Ala Glu Phe Ile Gln Asp Tyr Leu Asp Arg Phe Asn

435 440 445

Asn Phe Leu Ser Glu Phe Lys Ala Gly His Ile Arg Pro Val Gly Asp

450 455 460

Phe Ser Leu Glu Lys Arg Arg Gly Gln Gly Asp Glu Pro Asp Leu Thr

465 470 475 480

Ala Arg Arg Lys Ser Leu Gln Lys Glu Leu Asp Arg Phe Val Leu Lys

485 490 495

Gly Lys Asp Leu Pro Asp Lys Ile Arg Glu Tyr Leu Leu Gly Tyr Lys

500 505 510

Gln Lys Ser Glu Lys Lys Gln Ala Lys Trp Ile Leu Gly Gly Met Ile

515 520 525

Lys Glu Thr Val Tyr Trp Arg Asn Lys Ala Glu Gln Ser Pro Glu Lys
530 535 540
Met Arg Ser Gly Asp Met Ala Gln Gln Leu Ala Arg Asp Ile Ile Phe
545 550 555 560
Leu Thr Pro Pro His Thr Val Lys Glu His Lys Gln Lys Leu Asn Ser
565 570 575
Leu Glu Tyr Asp Val Leu Gln Tyr Ala Leu Ala Tyr Phe Ser Ser Asn

580 585 590
Arg Glu Lys Leu Tyr Ser Phe Phe Lys Glu His Gln Leu Thr Val Lys
595 600 605
Gly Asp Arg Ala His Pro Phe Leu Tyr Lys Ile Arg Leu Asp Glu Cys
610 615 620
Gln Gly Ile Leu Asp Phe Phe Ile Val Tyr Met Gln Gln Lys Glu Lys
625 630 635 640
Trp Leu Gly Trp Leu Asp Arg Asn Leu Lys Ser Pro Arg Leu Asn Glu

645 650 655
Glu Glu Phe Phe Asn Thr Tyr Ser Tyr Phe Ile Lys Thr Asp Thr Lys
660 665 670
Arg Ala Ile Glu Met Asp Tyr Glu Ser Cys Pro Asn Tyr Leu Pro Arg
675 680 685
Gly Ile Phe Asn Glu Pro Ile Ala Lys Ala Val Gln Lys Ala Gly Val
690 695 700
Lys Ile Lys Asp Glu Asp Asn Ala Ser Tyr Ala Leu Ser Val Tyr Ser

705 710 715 720
Asn Gly Lys Thr Gln Pro Phe Tyr Asn Lys Glu Arg Tyr Tyr Asn Lys
725 730 735
Gly Ile Phe Arg Met Glu Glu Leu Pro Glu Lys Leu Gln Pro Lys Glu
740 745 750
Leu Leu Gly Lys Ile Gln Trp Thr Ile Lys Ser Ser Gly Lys Asp Thr
755 760 765
Glu Glu Phe Arg Ser Leu Gln Asn Leu Lys Asn Arg Ile Leu Asn Thr

770 775 780

Glu Lys Glu Ile Arg Tyr Val Gln Ser Thr Asp Arg Ala Leu Trp Ile

785 790 795 800

Met Val Ala Asp Leu Phe Pro Glu Thr Phe Glu Leu Arg Pro Asp Asp

805 810 815

Leu Glu Cys Ile Gly His Asp Leu Ser Asp Asp Leu Leu Ser Arg Pro

820 825 830

Tyr Gln Met Lys Glu Lys Val Tyr Asn Tyr Thr Ile Thr Asp Tyr Leu

835 840 845

Pro Ile Lys Arg Tyr Gly Glu Phe Arg Arg Phe Leu Lys Asp Arg Arg

850 855 860

Leu Glu Asn Leu Leu Thr Tyr Phe Glu Glu Gly Val Pro Leu His Arg

865 870 875 880

Glu Ala Leu Val Ala Glu Leu Glu Ala Tyr Asp Leu Gln Arg Lys Asn

885 890 895

Leu Leu Glu Ile Ile Tyr Arg Phe Glu Lys Leu Val Phe Asp Arg His

900 905 910

Arg His Glu Leu Thr Phe Ser Gly Glu Gly Glu Asn Gln Tyr Val Asn

915 920 925

His Trp Asp Tyr Leu Asp Phe Val Ala Arg Lys Tyr Gly Leu Ser Ala

930 935 940

Glu Val Lys Glu Leu Asn Ser Glu Arg Phe Thr Glu Leu Arg Asn Lys

945 950 955 960

Met Leu His Asn Gln Ile Pro Tyr Gln Leu Trp Ile Lys Glu Ala Ile

965 970 975

Ala Ala Arg Glu Glu Asn Thr Val Cys Gly Arg Ile Met Gly Met Ile

980 985 990

Gly Glu Ile Tyr Glu Arg Met Thr Thr Glu Ile Glu Lys Gln Met Gln

995 1000 1005

Val

<210> 63

<211> 1160

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<400> 63

Met Lys Thr Leu Gly Ala Leu Ser Ser His Asn Tyr Asn Asn Lys Lys

1 5 10 15

Tyr Tyr Phe Ser Gly Leu Leu Asn Thr Ala Gln Tyr Asn Phe Asn Leu

20 25 30

Ala Leu Gln Glu Val Asn Asp Arg Leu Gly Lys Lys Gly Lys Asn Pro

35 40 45

Gly Lys Thr Met Ile Lys Asn Ile Phe Asp Gln Lys Asp Ser Phe Ser

50 55 60

Thr Gln Glu Arg Ala Met Tyr Tyr Leu Glu Glu Phe Phe Pro Trp Ile

65 70 75 80

Phe Leu Val Met Lys Gln Ser Gly Ile Asn Ile Pro Thr Glu Glu Gln

85 90 95

Glu Thr Lys Leu His Lys Glu Glu Ile Gln Leu Ile Gln Glu His Leu

100 105 110

Ile Ser Leu Tyr Glu Leu Leu Asp Asp Leu Arg Asn Glu Gln Thr His

115 120 125

Tyr Met His Asp Pro Val Ile Ile Pro Glu Glu Val Ser Lys Met Leu

130 135 140

Asp Ala Leu Leu Leu Gln Ile Leu Lys Asn Thr Arg Lys Lys Cys Lys

145 150 155 160

Asp Asp Glu Tyr Arg Thr Phe Ile Val Lys Lys Tyr Gln Glu Glu Phe

165 170 175

Gln Lys Glu Ile Lys Val Gln Val Lys Asp Arg Phe Gly Lys Glu Lys

180 185 190

Glu Lys Ile Val Thr Gly Glu Val Lys Glu Asn Tyr Val Ile Asn Arg

195 200 205

Cys Phe Arg Lys Trp Ile Gln Lys Glu Gly Glu Glu Glu Thr Leu Arg

210 215 220

Tyr Ser Thr Val Gln Glu Glu Gln Gly Lys Tyr Val Trp Ser Ser Ser

225 230 235 240

Gly Phe Val Phe Phe Leu Ser Leu Phe Leu Arg Arg Lys Glu Leu Glu

245 250 255

Asp Val Met Asn His Val Pro Tyr Phe Lys Asp Ser Arg Lys Leu Leu

260 265 270

Phe Tyr Leu Thr Arg Lys Thr Phe Ser Ser Tyr Cys Phe Arg Asp Leu

275 280 285

Arg Lys Ser Leu Arg Ser Asp Tyr Ser Asn Asp Ser Leu Leu Met Gln

290 295 300

Met Ile Glu Glu Leu Tyr Lys Cys Pro Gly Glu Leu Tyr Glu Val Leu

305 310 315 320

Leu Lys Glu Gln Lys Gln Glu Phe Ile Glu Asp Ile Asn Glu Tyr Tyr

325 330 335

Lys Asp Asn Pro Glu Phe Glu Gly Ser Ala Asn Glu Ala Gln Val Ile

340 345 350

His Pro Val Ile Arg Lys Arg Tyr Gln Asp Lys Phe Pro Tyr Phe Ala

355 360 365

Leu Arg Phe Ile Asp Glu Tyr Phe Asn Phe Pro Thr Leu Arg Phe Gln

370 375 380

Leu Val Leu Gly Glu Tyr Val Thr Asp Arg Arg Thr Lys Glu Leu Gln

385 390 395 400

Gly Thr Ala Leu Phe Thr Asp Arg Val Ile Ser Gln Arg Ile Ser Tyr

405 410 415

Val Gly Lys Leu Ser Glu Ala Glu Met Asn Lys Lys Arg Glu Gly Tyr

420 425 430

Thr Glu Thr Gly Trp Lys Glu Tyr Pro Asn Pro Tyr Tyr Lys Ile Glu

435 440 445

Asn Asn Arg Ile Pro Leu Tyr Ile Glu Phe Ser Lys Asn Glu Glu Leu

450 455 460

Ile Phe Lys Glu Lys Lys Phe Lys Tyr Asn Thr Leu Ala Lys Trp Glu

465 470 475 480

Asn Arg Glu Ile Asp Lys Arg Thr Gly Glu Phe Asn Gln Val Asn Lys

485 490 495

Gln Arg Arg Ile Thr Gln Leu Glu Glu Phe Lys Ile Asp Asn Pro Lys

500 505 510

Lys Met Lys Thr Pro Asn Val Phe Leu Ser Ile Tyr Glu Leu Pro Ala

515 520 525

Leu Leu His Ala Leu Leu Ile Glu Lys Lys Thr Glu Ala Glu Ile Glu

530 535 540

Asp Ile Ile Lys Ala Lys Ile Lys Lys Gln Leu Thr Glu Ile Ala Glu

545 550 555 560

Gly Arg Arg Asn Leu Ser Gly Leu Pro Lys Gly Ile Lys Lys Met Arg

565 570 575

Asn Cys Asn Ser Asp Phe Glu Lys Lys Lys Leu Ile Ser Asp Ile Asp

580 585 590

Asn Glu Ile Lys Lys Gly Glu Lys Ile Leu Glu Glu Val Gln Gln Trp

595 600 605

Leu Asn Pro Val Ile Asn Lys Lys Gly Thr Gly Lys Gln Glu Asn Asn

610 615 620

Lys Pro Phe Phe Ser Asn Thr Tyr Arg Gly Lys Tyr Ala Thr Trp Leu

625 630 635 640

Ala Tyr Asp Ile Lys Arg Phe Thr Gly Lys Asp His Ile Gln Asn Trp

645 650 655

Lys Gly Tyr Gln Phe Ser Glu Leu Gln Thr Leu Leu Ser Leu Tyr Thr

660 665 670

Leu Arg Lys Glu Glu Leu Lys Asn Phe Leu Glu Lys Asp Leu Gln Leu

675 680 685

Thr Ser His Pro Phe Leu Lys Glu Ala Leu Lys Ala Val Asn Leu Glu

690 695 700

Asp Phe Met Gly Ala Tyr Leu Arg Gly Arg Gln Phe Phe Leu Glu Lys

705 710 715 720

Ala Lys Lys Gln Ile Gly Ile Lys Gly Val Lys Lys Ser Ile Phe Gln

725 730 735

Tyr Phe Glu Glu Arg Lys Tyr Lys Ile Tyr Ser Ser Asn Leu Asp Tyr

740 745 750

Trp Glu Glu Leu Trp Lys His Pro Val Asn Leu Asp Arg Gly Leu Phe

755 760 765

Asp Glu Arg Gly Thr Val Tyr Asn Lys Asn Lys Glu Leu Asn Asp Leu

770 775 780

Gln Asn Arg Ala Ala Trp Phe Ser Phe Ala Glu Thr Asn Pro Lys Gln

785 790 795 800

Gln Phe Tyr His Phe Pro Arg Ile Tyr Ser Asp Glu Asp Ile Thr Lys

805 810 815

Pro Val Thr Asp Arg Tyr Gly Lys Thr Lys Glu Lys Leu Ile Leu Phe

820 825 830

Lys Leu Ser Pro Gln Lys Gly Phe Met Glu Gln Ile Pro Ser Asp Leu

835 840 845

Lys Lys Lys Tyr Gln Glu Asp Lys Gly Lys Val Glu His Pro Glu Val

850 855 860

Gln Lys Glu Lys Lys Tyr Glu Glu Lys Lys His Pro Gly Ile Asn Ala

865 870 875 880

Phe Ile Lys Asn Ala Tyr Lys Asn Glu Gln Lys Ile Arg Arg Ile Ser

885 890 895

Arg Asn Asp Ile Phe Leu Tyr Glu Met Val Lys Tyr Met Leu Asn Lys

900 905 910

Ile Ser Pro Ala Thr Glu Phe Ser Ser Leu Asp Lys Val Trp Leu Thr

915 920 925

Arg Ile Glu Arg Glu Lys Gln Ala Thr Glu Ala Arg Glu Gln Ser Phe

930 935 940

Lys Glu Lys Gly Asp Thr Ser Glu Asn Lys Ile Arg Gln Asp Tyr Leu
945 950 955 960
Leu Ser Phe Pro Ile Thr Leu Thr Leu Phe Asn Asp Ile Ile Lys Glu

965 970 975
Lys Val Lys Ile Lys Asp Ile Gly Arg Phe Arg Lys Leu Glu Lys Asp
980 985 990
Glu Arg Val Gln Thr Met Ile Ser Tyr Tyr Thr Ser Gly Leu Trp Lys
995 1000 1005
Asn Asp Gln Pro Ser Leu Thr Ile Lys Glu Leu Glu Ala Glu Leu
1010 1015 1020
Glu Ser Tyr His Lys Ile Arg Leu Gln Glu Ile Phe Lys Glu Val

1025 1030 1035
His Lys Leu Glu Lys Glu Ile Tyr Glu Phe Thr Pro Glu Glu Asp
1040 1045 1050
Lys Ser Lys Leu Leu Ala Arg Glu Ser Phe Pro Lys Phe Lys Tyr
1055 1060 1065
Tyr Ile Ser Phe Tyr Phe Ile Pro Lys Glu Asp Gln Glu Val Phe
1070 1075 1080
Asn Glu Ile Gln Phe Asp Lys Tyr Lys Asn Leu Glu Gln Ile Pro

1085 1090 1095
Gly Arg Lys Pro Glu Tyr Asp Pro Tyr Tyr Leu Leu Ile Phe Ile
1100 1105 1110
Arg Asn Lys Phe Ala His Asn Gln Leu Pro Ala Glu Pro Ile Tyr
1115 1120 1125
Lys Thr Ala Leu Thr Phe Leu Pro Asn Asn Phe Asn Thr Leu Ala
1130 1135 1140
Glu Tyr Tyr His Lys Leu Phe Ile Leu Leu Asn Asn Lys Asn Tyr

1145 1150 1155
Asn Asn
1160
<210> 64

<211> 1160

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<400> 64

Met Asn Ile Leu Pro Ala Ala Pro Glu Lys Glu Lys Ile Ala Tyr Ser
1 5 10 15

Thr Ala Thr Ala Pro Trp Phe Phe Gly Ala Phe Leu Asn Gln Ala Arg
20 25 30

His Asn Leu Phe Leu Thr Val Asn Asp Leu Ala Ile Arg Leu Gly Glu
35 40 45

Lys Val Ile Asp Tyr Asp Asp Gln Leu Leu Asn Ser Asn Val Val Arg
50 55 60

Met Leu Val Asn Glu Lys Ala Ser Pro Leu Gln Leu Glu Ile Leu Met
65 70 75 80

Lys Tyr Leu Asp Arg His Leu Pro Phe Leu Ile Pro Met Gln Val Ala
85 90 95

Leu Lys Gly His Gln Gly Asp Ala Ser Asp Asn Pro Val Ile Gly Ser
100 105 110

Pro Ala Asp Tyr Gly Ala Ile Leu Ser Lys Leu Ile Val Cys Leu Asn
115 120 125

Ala Ala Arg Asn His Phe Ser His Tyr His Ser Thr Ser Gly Trp Ser
130 135 140

Gly Tyr Asn Glu Val Ile Glu Trp Met Glu His Val Phe Thr Arg Asn
145 150 155 160

Ile Glu Thr Val Val Lys Arg Phe Thr Leu Thr Glu Glu Glu Val Gln
165 170 175

His Leu Lys Lys Pro Val Asp Lys Ser Pro Lys Gly Thr Ile Pro Pro
180 185 190

Tyr Tyr Phe Ser Phe Cys Lys Gly Asp Ile Trp Thr Asp Thr Gly Leu
195 200 205

Ala Phe Phe Ile Cys Leu Phe Leu Thr Arg Glu Glu Ala Tyr Leu Phe
210 215 220
Leu Lys Lys Leu Arg Gly Phe Lys Arg Gly Glu Glu Arg Phe His Lys

225 230 235 240
Ala Thr Leu Glu Ala Phe Cys Val Gly Ser Leu Lys Val Pro Arg Glu
245 250 255
Arg Leu Glu Ser Asn Asn Ser Pro Gln Ser Ala Phe Leu Asp Met Cys
260 265 270
Asn Glu Leu Val Arg Cys Pro Lys Ser Leu Phe Asp Leu Leu Glu Pro
275 280 285
Glu Lys Gln Glu Leu Phe Arg Arg Asp Pro Glu Pro Glu Asp Ala Glu

290 295 300
Asp Asn Gly Ile Glu Glu Glu Glu Asp Gln Pro Gln Ala Leu Leu Val
305 310 315 320
Arg Lys Glu Asn Arg Phe Ser Tyr Phe Ala Leu Arg Tyr Leu Asp Ile
325 330 335
Ala Lys Ala Phe Pro Arg Leu Arg Phe Gly Val Asp Leu Gly Thr Tyr
340 345 350
Phe Phe Ser Val Tyr Pro Lys Thr Phe Ala Gly Ile Glu Glu Thr Arg

355 360 365
Gln Leu Ser Lys Arg Leu Ile Gly Tyr Gly Lys Leu Glu Glu Phe Ala
370 375 380
Arg Glu Lys Arg Pro Glu His Ile Ala Ala Leu Phe Arg Ser Lys Glu
385 390 395 400
Glu Ala Asn Ala Ala Pro Thr Glu Pro Phe Ile Arg Glu Thr Ala Pro
405 410 415
His Tyr His Leu Asp Gly Asn Asn Val Tyr Leu Tyr Met Ser Gly Asp

420 425 430
Gly Glu Ala Gln Trp Pro Ala Val Glu Leu Glu Glu Val Thr Gly Lys
435 440 445
Ser Tyr Pro Arg Lys Leu Val Lys Lys Ser Thr Leu Leu Pro Phe Ala

450 455 460

Val Leu Thr Val Asn Glu Leu Pro Ala Leu Leu Phe Tyr His Leu Leu

465 470 475 480

His Lys Glu Lys Gly Ala Gly Asp Ala Ala Glu Arg Val Ile Ile Asn

485 490 495

His Met Glu Arg Val Lys Arg Phe Phe Lys Ala Leu Gln Asp Asp Lys

500 505 510

Val Asp Gln Val Ala Gly Gln Pro Ile Arg Lys Pro Asp Val Asp Ala

515 520 525

Asp Glu Ser Leu His Met Glu Tyr Asp Arg Arg Trp Lys Leu Leu Lys

530 535 540

Lys Lys Leu Ser Glu Tyr Gln Leu Arg Ala Ser Tyr Ile Pro Glu Lys

545 550 555 560

Ile Ile Asn Tyr Leu Leu Asn Ile Glu Ala Val Asp Leu Gly Asp Lys

565 570 575

Ala Met Ala Gln Leu Lys Asn Leu Gln Arg Gln Ala Gln Asp Asp Ile

580 585 590

Ala Ala Ile Glu Arg Arg Met Glu His Leu Met Lys Lys Gly Ala Asp

595 600 605

Gly Arg Lys Thr Leu Lys Val Gly Asn Leu Ala Gln Gln Leu Ala Glu

610 615 620

Asp Met Leu Gln Met Gln Pro Val Gln Ile Gly Thr Asp Gly Glu Pro

625 630 635 640

Val Pro Ala Ser Lys Ala Asn Asn Leu Ala Phe Arg Leu Leu Gln Ser

645 650 655

His Leu Ala Tyr Phe Ala Glu Asn Arg His Asn Leu Pro Ala Val Phe

660 665 670

Glu Ala Cys Gly Leu Ile Gly Ala Ser Asn Lys His Pro Phe Leu Asp

675 680 685

Asn Ile Asn Ile Glu Ser Cys Lys Gly Val Val Asp Phe Phe Ile Leu

690 695 700

Asn Phe Arg Asn Lys Leu Asp Phe Leu Asp Arg Cys Leu Gln Glu Gly
705 710 715 720
Glu Trp His Arg Tyr His Phe Ile Ser Ala Ala Lys Leu Lys Ser Gly
725 730 735
Ala Lys Val Thr Ile Lys Lys Tyr Leu Asn Glu Ala Phe Glu Ser Lys

740 745 750
Gly Arg Asn His Ile Pro Phe Thr Leu Pro Pro Ser Leu Phe Leu Asp
755 760 765
Ala Ser Leu Asp Trp Leu Ala Lys Phe Gly Asp Gly Lys Ala Lys Lys
770 775 780
Val Leu Ala Glu Asn Glu Tyr Val Asn Ser Val Phe Leu Ile Arg Arg
785 790 795 800
Leu Phe Ala Asp Gly Gly Leu Gln Pro Phe Tyr Ala Trp Lys Arg Glu

805 810 815
Tyr Arg Leu Phe Glu Lys Lys Ala Gly Lys Ala Val Phe Leu Asp Glu
820 825 830
Ala Gly Arg Met Arg Lys Ala Asp Lys Ile Gly Ile Glu Val Glu Arg
835 840 845
His Arg Glu Phe Leu Ala Arg Pro Val Lys Lys Gly Lys Gln Tyr Asp
850 855 860
Ile Lys Lys Ala Ala Ala Glu Gln Phe Leu Arg Ser Tyr Arg Phe Tyr

865 870 875 880
Leu Gln Glu Glu Lys Tyr Ile Arg Leu Leu Ala Ala Gln Asp Met Leu
885 890 895
Leu Phe Arg Cys Ile Cys Asp Leu Leu Thr Tyr His Val Gly Asp Ile
900 905 910
Gly Leu Glu Glu Leu Ala Glu Ala Lys Ala Gly Thr Phe Ser Leu Ala
915 920 925
Asn Ile Thr Pro Glu Lys Thr Glu Thr Ala Lys Ser Leu Leu Asn Tyr

930 935 940
Arg Pro Ala Gly Gly Val Val Leu Asp Arg His Phe Tyr Ala Thr Asp

945 950 955 960

Glu Lys Gly Ala Phe Val Lys Gln Glu Gly Lys Leu Val Pro Gly Gly

965 970 975

Gln Val Arg Ile Phe Asp Asn Thr Leu Lys Ile Lys Asn Ala Gly Asn

980 985 990

Phe Arg Lys Leu Leu Lys Asp Arg Arg Met Asn Asn Leu Phe Phe Tyr

995 1000 1005

Phe Lys Gln His Ala Asp Glu Pro Val Val Leu His Arg Met Val

1010 1015 1020

Leu Glu Asn Glu Leu Arg Ala Tyr Asp Arg Met Arg Leu Lys Val

1025 1030 1035

Leu Pro Val Ile Ala Glu Phe Glu Lys Lys Leu Tyr Gln His Cys

1040 1045 1050

Thr Asp Val Glu Lys Glu Arg Leu Val Val Asn Gly Ser Met His

1055 1060 1065

His Arg Cys Tyr Leu Asp Val Tyr Arg Glu Lys Tyr Gln Pro Asp

1070 1075 1080

Trp Gly Trp Glu Ala Ala Gly Asn Leu Leu Arg Ile Arg Asn Ala

1085 1090 1095

Phe Val His Asn Gln Phe Pro Leu Met Glu Gly Asp Gly Phe Lys

1100 1105 1110

Leu Glu Val Ala His Trp Lys Lys Ile Asn Ala Asp Phe Val Pro

1115 1120 1125

Ser Glu Gln Gly Ser Ser Leu Gly Tyr Gly Ile Ile Asp Arg Leu

1130 1135 1140

Gly Gln Leu Ala Val Glu Gly Tyr Glu Gly Leu Ile Lys Asn Ile

1145 1150 1155

His Val

1160

<210> 65

<211> 817

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<400> 65

Met Gly Glu Glu Glu Gln Ala His Ile Leu Glu Asn Ser Leu Asn Asp

1 5 10 15

Glu Leu Cys Glu Ala Ile Asp Asp Pro Phe Glu Met Ile Ala Ser Leu

20 25 30

Ser Lys Arg Ala Arg Tyr Lys Asp Arg Phe Pro Tyr Leu Met Leu Arg

35 40 45

Tyr Ile Glu Glu Lys Asn Leu Leu Pro Phe Ile Arg Phe Arg Ile Asp

50 55 60

Leu Gly Cys Leu Glu Leu Ala Ser Tyr Pro Lys Lys Met Gly Glu Glu

65 70 75 80

Asn Asn Tyr Glu Arg Ser Val Thr Asp His Ala Met Ala Phe Gly Arg

85 90 95

Leu Thr Asp Phe His Asn Glu Asp Glu Val Leu Gln Gln Ile Thr Lys

100 105 110

Gly Ile Thr Asp Glu Val Arg Phe Ser Leu Tyr Ala Pro Arg Tyr Ala

115 120 125

Ile Tyr Asn Asn Lys Ile Gly Phe Val Trp Thr Ser Arg Ser Lys Lys

130 135 140

Lys Ser Phe Pro Thr Leu Lys Lys Lys Glu Gly Glu Gly His Arg Val

145 150 155 160

Ala Tyr Thr Leu Gln Asn Glu Glu Ser Phe Gly Phe Ile Ser Ile Tyr

165 170 175

Asp Leu Arg Lys Ile Leu Leu Leu Ser Phe Leu Asp Glu Gly Lys Asn

180 185 190

Ile Val Ser Gly Leu Phe Lys Gln Ser Lys Ala Asn Trp Glu Asn Leu

195 200 205

Ser Glu Asn Leu Phe Asp Ala Ile Arg Thr Glu Leu Gln Lys Glu Phe

210 215 220

Pro Val Pro Leu Ile Arg Tyr Thr Leu Pro Arg Ser Lys Gly Gly Lys

225 230 235 240

Phe Val Asp Pro Lys Leu Ala Asp Lys Gln Glu Lys Tyr Glu Ser Glu

245 250 255

Phe Glu Arg Arg Lys Glu Lys Leu Ser Glu Ile Leu Ser Glu Lys Gly

260 265 270

Phe Asp Leu Ser Gln Ile Pro Arg Arg Met Ile Asp Glu Trp Leu Asn

275 280 285

Val Leu Pro Thr Ser Lys Glu Lys Lys Leu Lys Gly Tyr Val Glu Thr

290 295 300

Leu Lys Leu Asp Cys Arg Glu Arg Leu Arg Val Phe Glu Lys Arg Glu

305 310 315 320

Lys Gly Glu His Pro Val Pro Pro Arg Ile Gly Glu Met Ala Thr Asp

325 330 335

Leu Ala Lys Asp Ile Ile Arg Met Val Ile Asp Gln Gly Met Lys Gln

340 345 350

Arg Ile Thr Ser Ala Tyr Tyr Ser Glu Ile Gln Arg Cys Leu Ala Gln

355 360 365

Tyr Ala Gly Asp Asp Asn Arg Arg His Leu Asp Ser Ile Ile Arg Glu

370 375 380

Leu Gly Leu Lys Asp Arg Lys Lys Gly His Pro Phe Leu Gly Lys Val

385 390 395 400

Leu Arg Pro Asp Leu Asp His Thr Glu Lys Leu Tyr Gln Arg Tyr Phe

405 410 415

Lys Glu Lys Lys Glu Trp Leu Glu Ala Thr Phe Tyr Pro Ala Ala Asn

420 425 430

Pro Lys Arg Val Pro Arg Phe Val Asn Pro Pro Ala Glu Lys Gln Lys

435 440 445

Glu Leu Pro Leu Ile Ile His Asn Leu Met Lys Glu Arg Pro Glu Trp

450 455 460

Arg Asp Trp Lys Gln Arg Lys Asn Ser His Pro Ile Asp Leu Pro Ser
465 470 475 480
Gln Leu Phe Glu Asn Glu Ile Cys Arg Leu Leu Lys Asp Lys Ile Gly
485 490 495
Lys Glu Ser Ser Gly Lys Leu Lys Trp Asn Glu Met Phe Lys Leu Tyr
500 505 510
Trp Asp Lys Glu Phe Pro Asn Gly Met Gln Arg Phe Tyr Arg Cys Lys

515 520 525
Arg Arg Val Glu Val Phe Asp Lys Val Val Glu Tyr Glu Tyr Ser Glu
530 535 540
Glu Gly Gly Asn Tyr Lys Lys Tyr Tyr Glu Ala Leu Ile Asn Glu Val
545 550 555 560
Val Arg Gln Lys Ile Ser Ser Ser Lys Glu Asn Ser Lys Leu Gln Val
565 570 575
Glu Asp Leu Thr Leu Ser Val Arg Arg Ala Phe Lys Arg Ala Ile Asn

580 585 590
Glu Lys Glu Tyr Gln Leu Arg Leu Val Cys Glu Asp Asp Arg Leu Leu
595 600 605
Phe Met Ala Val Arg Asp Leu Tyr Asp Trp Lys Glu Val Gln Leu Asp
610 615 620
Leu Asn Lys Ile Asp Asn Met Leu Gly Glu Pro Val Ser Val Ser Gln
625 630 635 640
Val Ile Gln Leu Glu Asn Gly Gln Pro Asp Ala Val Ile Lys Ala Glu

645 650 655
Cys Lys Leu Lys Asp Val Ser Lys Leu Met Arg Tyr Cys Tyr Asp Gly
660 665 670
Arg Val Lys Gly Leu Met Pro Tyr Phe Ala Asn His Glu Ala Thr Gln
675 680 685
Glu Gln Val Glu Val Glu Leu Arg His Tyr Glu Asp His Arg Arg Arg
690 695 700
Val Phe Asp Trp Val Phe Ala Leu Glu Lys Ser Val Leu Lys Asn Glu

705 710 715 720

Lys Leu Arg Arg Leu Tyr Glu Lys Ser Gln Glu Gly Cys Glu His Arg

725 730 735

Arg Cys Ile Asp Ala Leu Arg Lys Ala Thr Leu Val Ser Glu Glu Glu

740 745 750

Tyr Lys Phe Leu Val His Ile Arg Asn Lys Ser Ala His Asn Gln Phe

755 760 765

Pro Asp Leu Glu Phe Gly Lys Leu Thr Pro Asn Val Thr Ser Gly Phe

770 775 780

Cys Glu Cys Ile Trp Ser Lys Tyr Lys Ala Ile Ile Cys Arg Ile Ile

785 790 795 800

Pro Phe Ile Asp Pro Glu Arg Arg Phe Phe Gly Lys Leu Leu Glu Gln

805 810 815

Lys

<210> 66

<211> 1114

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<400> 66

Met Arg Ile Pro Lys Leu Ile Glu Glu His Lys Ser Val Phe Gly Ala

1 5 10 15

Tyr Ser Thr Met Ala Leu Ser Asn Val Glu Thr Val Leu Asn His Ile

20 25 30

Ala Glu Arg Ala Gly Leu Asp Gly Tyr Glu Arg Asp Arg Gly Pro Gly

35 40 45

Val Glu Asp Tyr Trp Glu His Pro Val Met Gln Cys Leu Cys Arg Lys

50 55 60

Asp Lys Pro Arg Ser Ile Pro Ser Asp Val Leu Leu Asp Val Arg Asn

65 70 75 80

Arg Leu Phe Arg Ser Phe Pro Phe Leu Lys Ile Met Ala Glu Asn Gln
85 90 95
Arg Asp Tyr Arg Asn Ala Lys Gly Lys Val Glu Cys Val Glu Ile Asn
100 105 110
Glu Ser Asp Ile Phe Val Val Leu Asn Asn Ser Phe Arg Val Leu Lys
115 120 125
Ala Tyr Arg Asp Thr Cys Thr His Tyr Leu Ile Glu Asn Arg Ile Trp

130 135 140
Glu Asp Asn Ser Pro Met Leu Met Tyr Asn Glu Cys Pro Leu Ala Ala
145 150 155 160
Met Val Asn Gln Tyr Tyr Thr Ala Ala Leu Arg Val Thr Lys Glu Arg
165 170 175
Tyr Gly Tyr Glu Thr Arg Asp Leu Thr Phe Ile Gln Lys Arg Arg Phe
180 185 190
Lys Gln Glu Pro Glu Lys Glu Ala Ser Gly Asn Val Lys Lys Lys Ala

195 200 205
Val Pro Asp Leu Ala Phe Phe Leu Ser Leu Val Ala Leu Asn Gly Asp
210 215 220
Gly Arg Lys Trp Leu His Leu Ser Gly Trp Gly Val Val Leu Leu Ile
225 230 235 240
Cys Leu Phe Leu Glu Lys Lys Tyr Val Asn Val Phe Leu Ser Lys Leu
245 250 255
Pro Asn Pro Gly Asn Tyr Pro Pro Ser Ser Lys Glu Arg Arg Ile Ile

260 265 270
Arg Arg Ser Met Gly Val Cys Ser Val Val Leu Pro Lys Glu Arg Ile
275 280 285
His Ser Glu Thr Gly Asp Leu Ser Val Ala Leu Asp Met Leu Asn Glu
290 295 300
Leu Lys Arg Cys Pro Arg Glu Leu Phe Asp Thr Leu Ser Pro Gly Asp
305 310 315 320
Gln Glu Arg Phe Arg Thr Ile Ser Ser Asp His Asn Glu Val Leu Gln

325 330 335

Met Arg Ser Lys Asp Arg Phe Ala Gln Leu Val Leu Gln Tyr Ile Asp

340 345 350

His Asn Arg Leu Phe Glu Asn Leu Arg Phe His Val Asn Met Gly Lys

355 360 365

Leu Arg Tyr Leu Phe Asn Pro Lys Lys Tyr Cys Ile Asp Gly Gln Thr

370 375 380

Arg Val Arg Val Leu Glu His Pro Leu Asn Gly Phe Gly Arg Leu Gln

385 390 395 400

Glu Met Glu Glu Lys Arg Leu Gln Glu Asn Gly Pro Phe Ala Arg Ser

405 410 415

Gly Ile Lys Val Arg Cys Phe Asp Glu Val Arg Arg Asp Asp Ala Asn

420 425 430

Glu Ser Asn Tyr Pro Tyr Ile Val Asp Thr Tyr Thr His Tyr Val Leu

435 440 445

Glu Asn Asp Met Val Glu Met Phe Phe Cys Pro Glu Gly Ser Gly Met

450 455 460

Lys Met Pro Glu Val Thr Ser Arg Glu Gly Lys Trp Tyr Val Asp Lys

465 470 475 480

Lys Val Pro His Cys Arg Met Arg Met Ser Val Leu Glu Leu Pro Ala

485 490 495

Met Leu Phe His Leu Leu Leu Cys Gly Ala Lys Asn Thr Glu Val His

500 505 510

Ile Gly Lys Val Cys Asp Asn Tyr Cys His Leu Phe Ser Asp Met Ala

515 520 525

Gln Gly Asn Leu Thr Glu Glu Asn Ile Leu Ser Tyr Gly Ile Lys Lys

530 535 540

Glu Asp Ile Pro Gln Lys Val Trp Asp Cys Val Arg Gly Val His Met

545 550 555 560

Gly Lys Asp Ser Arg Ala Tyr Arg Glu Lys Glu Ile Arg Glu Arg Tyr

565 570 575

Glu Asp Val Thr Arg Arg Leu Glu Arg Leu Glu Ala Asp Arg Lys Ala

580 585 590

Val Leu Gly Gly Glu Asn Lys Ile Gly Lys Arg Gly Phe Val Gln Ile

595 600 605

Val Pro Gly Arg Leu Ala Ala Tyr Leu Ala Thr Asp Ile Cys Arg Leu

610 615 620

Gln Pro Ser Leu Arg Lys Gly Asp Gly Tyr Gly Thr Asp Arg Leu Thr

625 630 635 640

Gly Leu Asn Phe Arg Leu Leu Gln Ser Ser Ile Ala Thr Tyr Asn Cys

645 650 655

Gly Glu Ser Asp Ile Leu Tyr Gly Arg Phe Arg Asp Val Phe Cys Ser

660 665 670

Ala Gly Leu Ile Gly Gly Asp Asn Pro His Pro Phe Leu Asp Lys Val

675 680 685

Leu Pro Glu Ala Tyr Ser Val Cys Cys Pro Arg Asn Thr Ile Glu Phe

690 695 700

Tyr Glu Arg Tyr Leu Glu Glu Tyr Gln Arg Tyr Leu Lys Pro Leu Val

705 710 715 720

Ile Lys Leu Glu Lys Gly Lys Val Pro Ser Leu Ser Phe Val Asn Glu

725 730 735

Gly Gln Arg Arg Trp Ala Arg Arg Asp Asp Ala Tyr Tyr His Glu Leu

740 745 750

Gly Asn Leu Tyr Leu Ser Gln Ala Ile Glu Leu Pro Arg Gln Met Phe

755 760 765

Asp Asp Glu Ile Lys Asp Lys Leu Arg Glu Met Pro Glu Met Arg Asp

770 775 780

Val Asp Phe Asp His Ala Asn Val Thr Phe Leu Ile Gly Glu Tyr Leu

785 790 795 800

Lys Arg Val Arg His Asp Glu Ser Gln Glu Phe Tyr Ser Trp Pro Arg

805 810 815

His Tyr Lys Tyr Val Asp Met Leu Lys Cys Ile Leu Asn Pro Lys Asn

820 825 830

Gly Ser Leu Gln Ala Val Tyr Ile Gln Met Gly Glu Arg Glu Gly Leu

835 840 845

Trp Gln Glu Arg Ser Glu Leu Glu Glu Lys Tyr Ala Lys Ile Arg Leu

850 855 860

Arg Asp Leu Gly Arg Lys Gly Leu Asp Lys Asp Glu Ala Asn Glu Arg

865 870 875 880

Ile Lys Thr Gly Leu Gly Asn Arg Lys Lys Glu Tyr Gln Lys Ala Glu

885 890 895

Lys Val Ile Arg Arg Tyr Lys Val Gln Asp Ala Leu Leu Phe Met Leu

900 905 910

Ala Lys Asn Thr Leu Phe Asn Ser Val Glu Val Asp Asp Glu Arg Phe

915 920 925

Lys Leu Lys Asp Ile Met Pro Asp Gly Glu Lys Gly Ile Leu Ser Glu

930 935 940

Val Val Pro Met Asp Phe Cys Phe Arg Ser Gly Asn Ser Ala Thr Arg

945 950 955 960

Lys Leu Met Gly Thr Ile His Ser Asp Asn Thr Lys Ile Lys Asn Tyr

965 970 975

Gly Asp Phe Phe Ala Leu Ala Asn Asp Lys Arg Met Val Thr Leu Leu

980 985 990

Pro Leu Val Gly Glu Gln Cys Leu Val Lys Glu Glu Val Lys Glu Glu

995 1000 1005

Phe Asp Lys Tyr Asp Asp Cys Arg Pro Glu Met Ile Ser Met Val

1010 1015 1020

Phe Asp Phe Glu Gln Trp Ala Tyr Ser Ala Tyr Pro Glu Leu Lys

1025 1030 1035

Glu Leu Val Ser Asn Glu Ala Ile Lys Gly Arg Leu Phe Ser Asn

1040 1045 1050

Leu Leu Gln Glu Leu Leu Gly Arg Gly Glu Leu Thr Tyr Glu Glu

1055 1060 1065

Lys Tyr Ala Leu Val Gly Ile Arg Asn Ala Phe Leu His Asn Ser

1070 1075 1080

Tyr Pro Lys Asp Gly Gly Val Val Lys Val Arg Thr Leu Pro Asp

1085 1090 1095

Ile Ala Lys Ser Leu Lys Asp Val Phe Lys Glu Tyr Ile Arg Leu

1100 1105 1110

Glu

<210> 67

<211> 909

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas13b sequence

<400> 67

Met Lys Met Phe Tyr Lys Ser Val Leu Thr Ala Phe Phe Thr Ala Val

1 5 10 15

Asp Ser Leu Arg Asn Lys Tyr Thr His Tyr Ser His Lys Asp Leu Asn

20 25 30

Ile Arg Glu Ile Lys Ile Glu Cys Thr Leu Gly Gly Lys Asp Tyr Cys

35 40 45

Ile Gly Leu Leu Asn Ala Leu Asp Cys Ile Tyr Asp Ser Ala Val Asn

50 55 60

Leu Leu Lys Leu Arg Phe Met Ala Gly Glu Asp Glu Val Ala His Leu

65 70 75 80

Arg Arg Cys Lys Ala Val Asn Lys Lys Val Val Val Arg Thr Glu Lys

85 90 95

Asp Gly Phe Tyr Tyr Arg Leu Ser Asp Asn Gly Gly Val Thr Glu Lys

100 105 110

Gly Val Ile Phe Ile Ala Ser Met Phe Leu Asn Arg Lys Tyr Gly Phe

115 120 125

Leu Phe Leu Lys Gln Leu Glu Gly Phe Lys Arg Ser Asp Glu Lys Arg

130 135 140

Tyr Arg Leu Thr Leu Glu Ala Phe Leu Ala Phe Ser Asn Ile Lys Pro

145 150 155 160

Val Asp Arg Leu Lys Ser Asp Lys Leu Asp Arg Ala Ser Leu Gly Leu

165 170 175

Asp Met Leu Asn Glu Leu Thr Lys Ile Pro Lys Glu Leu Ser Glu Thr

180 185 190

Leu Ser Val Asp Cys Leu Tyr Lys Tyr Leu Ala Ser Asp Gly Glu Asp

195 200 205

Asp Leu Arg Ser Arg Ile Arg Tyr Gln Asp Arg Phe Val Pro Leu Ala

210 215 220

Leu Glu Phe Ile Ser Gln Ser Asp Glu Phe Lys Asp Phe Arg Phe Tyr

225 230 235 240

Thr Tyr Val Gly Asn Tyr Val Tyr Lys Gly Tyr Ile Lys Arg Leu Ile

245 250 255

Asp Gly Thr Asp Lys Glu Arg Tyr Leu Ser Asp Arg Leu Cys Gly Phe

260 265 270

Tyr Lys Ser Val Asn Asp Ala Ser Ser Asp Ala Ile Ala Gln Lys Tyr

275 280 285

Gly Val Glu Ile Lys Asp Ser Asn Glu Pro Asp Tyr Met Leu Pro Asp

290 295 300

Ser Phe Arg Pro His Val Leu Arg Ala Thr Pro His Phe Val Ile Asn

305 310 315 320

Thr Asn Asn Ile Gly Ile Lys Ile Cys Gly Asn Asp Cys Leu Pro Ile

325 330 335

Val Asn Gly Lys Gly Val Glu Ser Pro Glu Pro Asp Tyr Trp Leu Ser

340 345 350

Ile Tyr Glu Leu Pro Ala Met Leu Phe Tyr Ala Tyr Leu Arg Glu Lys

355 360 365

Asn Gly Lys Arg Phe Lys Asp Tyr Lys Ser Ile Arg Glu Leu Ile Glu

370 375 380

Gly Val Glu Lys Lys Ala Asp Glu Lys Asn Asp Arg Asp Lys Gly Ala
385 390 395 400
Leu Met Ala Arg His Ile Asp Lys Glu Ile Ile Trp Thr Gln Thr Lys

405 410 415
Leu Asp Glu Val Lys Arg Leu Glu Glu Lys Lys Val Ala Ala Tyr Gly
420 425 430
Lys Lys Gly Arg Val Val Leu Lys Ala Gly Arg Met Ala Asp Leu Leu
435 440 445
Ala His Asp Met Val Arg Leu Gln Pro Ala Thr Lys Gly Ser Asp Lys
450 455 460
Ile Thr Gly Ala Asn Phe Gln Ala Leu Gln Val Ser Leu Ala Tyr Phe

465 470 475 480
Lys Arg Asp Ile Leu Ala Asp Val Phe Ser Arg Ala Met Leu Thr Thr
485 490 495
Gly Asn His Arg His Pro Phe Leu Tyr Arg Ile Asp Val Ser His Cys
500 505 510
Ser Ser Leu Arg Asp Phe Tyr Val Ala Tyr Leu Gly Glu Arg Arg Lys
515 520 525
Tyr Phe Glu Asp Val Ala Lys Lys Ile Ala Lys Asn Lys Leu Asn Thr

530 535 540
Pro Cys His Ile Leu Arg Arg Leu Gln Arg Glu Gly Ser Gly Glu Glu
545 550 555 560
Ala Gly Lys Asp Val Lys Pro Lys Phe Leu Pro Arg Gly Ile Phe Thr
565 570 575
Asp Ser Ile Lys Asn Cys Leu Glu Gln Ser Lys Leu Asn Ile Tyr Ile
580 585 590
Arg Asn Ala Arg Asn Asp Val Lys Pro Ala Ile Asn Ala Ala Tyr Leu

595 600 605
Ile Leu Met Tyr Tyr Lys Glu Ile Glu Lys Gly Glu Phe Gln Gly Phe
610 615 620
Tyr Gly Glu Lys Arg Arg Tyr Asp Ile Leu Glu Glu Gly Lys Pro Leu

625 630 635 640

Asp Leu Ala Glu Arg Lys Lys Ala Leu Ala Ser Ile Lys Pro Ala Lys

645 650 655

Ile Asp Val Ser Glu Ala Asn Met Pro Met Ser Lys Glu Glu His Leu

660 665 670

Met Arg Lys Arg Tyr His Ala Val Cys Asn Asn Glu Ser Ala Ile Arg

675 680 685

Met Tyr Gln Val Gln Asp Ile Leu Leu Leu Leu Met Ala Lys Asp Ile

690 695 700

Phe Lys Lys Ala Leu Ser Glu Gly Val Met Ser Lys Lys Ile Gly Leu

705 710 715 720

Glu Asn Leu Asn Gly Ile Phe Asp Ala Pro Val Asn Phe Val Lys Asn

725 730 735

Phe Asp Asn Ile Lys Leu Thr Ala Thr Gly Ile Lys Ile Lys Asp Tyr

740 745 750

Gly Lys Val Cys Arg Leu Gly Thr Asp Phe Lys Phe Asn Ser Leu Ile

755 760 765

Lys Ala Phe His Lys Val Tyr Ser Lys Ser Val Glu Met Asp Tyr Ser

770 775 780

Asp Tyr Leu Lys Glu Glu Glu Glu Phe Glu Lys Tyr Arg Leu Asn Met

785 790 795 800

Val Lys Leu Cys Arg Glu Val Glu Arg Gly Ile Thr Glu Asp Leu His

805 810 815

Leu Ser Leu Asp Gly Lys Ser His Leu Ser Phe Asn Asp Asp Val Ile

820 825 830

Lys Pro Tyr Asn Asp Lys Tyr Asn Val Phe Asn Gly Gly Asp Leu Thr

835 840 845

Phe Phe Ile Asn Ala Arg Asn Met Phe Met His Gly Asp Tyr Lys Tyr

850 855 860

Glu Cys Val Lys Tyr Val Val Ser Glu His Phe Lys Gly Ser Leu Asn

865 870 875 880

Asp Val Ser Phe Ala Lys Glu Thr Tyr Gly His Phe Cys Asn Leu Leu
885 890 895

Glu Ser Met Arg Lys Lys Thr Gly Leu Arg Ile Asp Ile
900 905

<210> 68

<211> 821

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12g sequence

<400> 68

Met Leu Pro Thr Arg Tyr Lys Pro Ala Arg Thr Leu Val Arg Pro Leu
1 5 10 15

Gly Arg Leu Pro His Glu Pro Arg Lys Glu Phe Val Glu Lys Cys Arg
20 25 30

Arg Val Arg Met His Phe Glu Gln Phe Asn Ile Asp Val Ala Asp Leu
35 40 45

Cys Gln Trp Leu Met Ser Leu Arg Pro Asn Thr Arg Ile Gly Asp Ala
50 55 60

Gln Ser Thr Val Phe Trp Asp Phe Phe Leu Asn Pro Ser Ile Leu Thr
65 70 75 80

Val Glu Ala Asp Glu Lys Glu Arg Asp Arg Trp Arg Leu Ala Ala Phe
85 90 95

Asp Glu Leu Leu Gln Ile Arg Phe Gly His Asp Pro Asn Ala Pro Pro
100 105 110

Trp Ser Glu Glu Phe Arg Ser Ala Ile Arg His Val Ala Gln Arg Pro
115 120 125

Lys Ser Ala Thr Ala Gln Arg Leu Phe Asp Arg Leu Arg Ser Leu Thr
130 135 140

Ala Pro His Arg Leu Val Leu Leu Lys Ser Ala Ala Glu Trp Ile Ile
145 150 155 160

Ala Arg Tyr Gln Arg Gly Met Glu Asn Trp Gln Arg Gln Phe Ala Glu

165 170 175

Trp Gln Arg Glu Lys Glu Glu Trp Glu Ala Ala His Pro Asn Leu Thr

180 185 190

Pro Glu Val Arg Asp Ala Phe Thr Arg Val Phe Lys Asn Leu Phe Glu

195 200 205

Asn Pro Asp Gly Asp Gly Lys Ile Gly Val Arg Arg Lys Asn Pro Arg

210 215 220

Ile Cys Ser Trp Glu Arg Leu Lys Leu Asn Lys Asp Asn Cys Val Tyr

225 230 235 240

Ala Gly Gln Lys Gly His Gly Pro Leu Cys Trp Glu Phe Ser Lys Phe

245 250 255

Val Lys Ala Gln Lys Asn Ala Gly Thr Ile Lys Thr Phe Phe Val Asp

260 265 270

Val Ala Asn Lys Tyr Leu His Val Arg Arg Asn Leu Ser Lys Pro Gly

275 280 285

Val Lys Leu Lys Lys Ser Pro Arg Gln Glu Ala Phe Lys Arg Leu Tyr

290 295 300

Asn Gln Lys Gly Met Glu Lys Ala Arg Asn Trp Phe Thr Asp Ala Trp

305 310 315 320

Ser Gly Tyr Leu Thr Ala Leu Asn Leu Asn Glu Lys Thr Ile Leu Asp

325 330 335

His Gly Cys Leu Lys His Cys Gly Ala Ile Gly Ala Glu Phe Glu Lys

340 345 350

Ser Leu Cys Gln Phe Asn Pro His Thr His Leu Cys Val Gln Tyr Arg

355 360 365

Asn Ala Leu Glu Ser Leu Glu Pro Ala Ile Arg Glu Leu Glu Gly Asp

370 375 380

Tyr Arg Glu Trp Arg Arg Leu Phe Leu Ala Pro Pro Arg Lys Pro Ser

385 390 395 400

Phe Arg Tyr Pro Ser Ser Arg Arg Leu Pro Met Pro Lys Ile Phe Gly

405 410 415

Glu His Phe His Gln Ile Asp Phe Asp Gln Ser Ile Leu Arg Leu Arg
420 425 430
Leu Glu Asp Met Ala Glu Gly Glu Trp Ile Glu Phe Gly Phe Lys Pro
435 440 445

Trp Pro Lys Asp Tyr Arg Pro Gly Lys Asp Glu Val Arg Val Thr Ser
450 455 460
Val His Val Asn Phe His Gly Asn Arg Met Arg Ala Gly Phe His Phe
465 470 475 480
Glu Ala Pro Ala Lys Pro Ser Arg Phe Ala Cys Thr Gln Asp Glu Leu
485 490 495
Asp Asp Leu Arg Ser Lys Gln Phe Pro Arg Gln Ser Gln Asp Arg Gln
500 505 510

Leu Leu Glu Val Ala Arg Arg Arg Leu Leu Glu Ser Phe Asp Gly Met
515 520 525
Leu Glu Ser Asp Leu Arg Ile Leu Ala Val Asp Leu Gly Glu Lys Gly
530 535 540
Ala Ala Ala Ala Val Tyr Gln Gly His Gly His Glu Ala Asp Val Ala
545 550 555 560
Ile Pro Ile Val Lys Ile Asp Arg Leu Tyr Asp His Val Pro Asp Val
565 570 575

Leu Asp Val Glu Ser Ala Arg Val Pro Pro Pro Lys Phe Asp Asp Ser
580 585 590
Arg Asp Pro Arg Gly Val Arg Lys Glu His Val Gly Arg His Leu Gly
595 600 605
Gln Leu Gln Arg Gly Ala Gln Thr Leu Ala Gln His Arg Gln Gln Asp
610 615 620
Glu Ser Ala Pro Ala Ala Leu Arg Arg His Asp Phe Arg Ser Leu Thr
625 630 635 640

Arg His Ile Arg Trp Met Ile Arg Asp Trp Thr Arg His Asn Ala Ala
645 650 655
Gln Ile Thr Ala Ala Ala Glu Thr His Arg Cys His Leu Ile Val Phe

660 665 670

Glu Ser Leu Arg Gly Phe Lys Pro Arg Gly Tyr Asp Gln Met Asp Phe

675 680 685

Ala Gln Lys Ala Arg Leu Ala Phe Phe Ala Tyr Gly Arg Val Arg Arg

690 695 700

Lys Val Val Glu Lys Ala Val Glu Arg Gly Leu Arg Val Val Thr Val

705 710 715 720

Pro Tyr Gly Phe Thr Ser Gln Ile Cys Ser Glu Cys Gly His Arg Gln

725 730 735

Arg Asn Lys Gly Arg Leu Arg Lys Asn Lys Tyr Gln Arg Arg Phe Val

740 745 750

Cys Glu Cys Gly Glu Pro Lys Lys Ser Ala Asn Lys Thr Ala Ala Pro

755 760 765

Asp Arg Ser Ala Thr Val Ser Pro Cys Thr Cys Arg Leu Gln Leu Gly

770 775 780

Ser Asp Val Asn Ala Ala Arg Val Leu Ala Arg Val Phe Trp Asp Glu

785 790 795 800

Ile Val Leu Pro Thr Arg Glu Glu Met Arg Glu Pro Ala Val Asp Ser

805 810 815

Ala Pro Pro Ser Lys

820

<210> 69

<211> 797

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12g sequence

<400> 69

Met Cys Leu Cys Thr Leu Ser Gly Arg Thr Arg Gln Glu Glu Glu Ile

1 5 10 15

Ile Gly Ser Thr Gln Tyr Thr Glu Ala Arg Ser Leu Val Arg Arg Ile

20 25 30

Arg Arg Pro Arg Gly Glu Ser Arg Arg Gln Phe Lys Ser Asn Val Leu
35 40 45
Leu Leu Arg Arg His Phe Glu Gln Phe Asn Val Asp Ala Ser Glu Ile
50 55 60

Cys Gln Trp Leu Met Gly Ile Arg Pro Gly Gly Arg His Ala Asp Glu
65 70 75 80
Ser Thr Gly Pro Phe Trp Glu Phe Phe Leu Asp Pro Gly Arg Phe Leu
85 90 95
Arg Glu Thr Gly Arg Gly Pro Glu Asp Ala Asp Glu Arg Ile Asp Ala
100 105 110
Tyr Arg Arg Ile Ala Phe Asp Val Val Ala Gly Ile Glu Asp Glu Ser
115 120 125

Arg Met Ser Asp Pro Ser Ile Pro Arg Gln Ile Val Glu Ser Leu His
130 135 140
Ala Val Ser Met Ala Thr Arg Thr Glu Ser Ala Arg Arg Leu Phe Glu
145 150 155 160
Arg Leu Ala Gly Leu Glu Pro Ser His Arg Gln Ile Leu Leu Lys Ala
165 170 175
Ala Ala Glu Trp Ile Val Ser Arg Tyr Trp Arg Ser Val Gln Gly Trp
180 185 190

Pro Asp Arg Tyr Lys His Trp Ser Asp Glu Lys Glu Glu Trp Glu Lys
195 200 205
Ala His Pro Arg Leu Thr Glu Ser Leu Arg Glu Glu Phe Thr Gly Ile
210 215 220
Phe Arg Asp Leu Gly Ile Arg Arg Lys Lys Pro Arg Val Cys Pro Trp
225 230 235 240
Glu Arg Leu Glu Lys Gly Met Asp Asn Cys Met Tyr Ala Gly Glu Arg
245 250 255

Ile Lys Val Gly Tyr Ser Arg Gln Ser His Ser Gln Leu Cys Ala Lys
260 265 270
Tyr Glu Arg Phe Ser Tyr Lys Gln Arg Gln Arg Thr Lys Ser Gly Lys

275 280 285

Asn Phe Lys Ser Tyr Phe Val Lys Asn Ala Glu Leu Tyr Leu Lys Leu

290 295 300

Arg Arg Lys Asn Arg Ser Leu Ile Lys Lys Asp Val Met Lys Leu Phe

305 310 315 320

Arg Lys Lys Val Pro Gln Ala Leu Trp Phe Glu Lys Ala Trp Asp Glu

325 330 335

Tyr Leu Lys Ala Leu Gly Val Asp Glu Ala Thr Leu Thr Lys Asp Gly

340 345 350

Lys Leu Pro His Cys Thr Gln Phe Ala Asp Asp Lys Glu Cys Leu Phe

355 360 365

Asn Arg His Thr Glu Leu Cys Leu Gln Tyr Arg Glu Arg Leu Leu Arg

370 375 380

Leu Pro His Leu Gln Glu Leu Glu Gln Leu Tyr Arg Glu Trp Arg Asp

385 390 395 400

Lys Tyr Leu Ser Gly Pro Arg Arg Pro Ser Leu Arg Tyr Pro Ser Lys

405 410 415

Arg Thr Leu Pro Met Pro Lys Val Phe Gly Arg Gly Tyr Phe Cys Ala

420 425 430

Asp Phe Thr Asn Ser Leu Leu Asp Leu Arg Leu Glu Gly Met Gly Glu

435 440 445

Gly Asp Phe Val Arg Phe Gly Phe Ala Pro Trp Pro Ala Asp Tyr Asp

450 455 460

Ala Gln Pro Ser Asp Ala Thr Val Thr Ser Val His Ile His Phe Val

465 470 475 480

Gly Thr Arg Ala Arg Ala Gly Phe Arg Phe Gln Ala Pro His Lys Thr

485 490 495

Ser Arg Phe Ala Ser Ser Gln Asp Glu Ile Asp Asp Leu Arg Ser Arg

500 505 510

Lys Phe Pro Arg Ala Ala Gln Asp Gly Glu Phe Leu Asp Ala Ala Arg

515 520 525

Lys Leu Leu Leu Glu Ser Phe Thr Gly Asp Ala Glu Arg Glu Met Lys
530 535 540
Leu Leu Ala Val Asp Leu Gly Asp Arg Gly Ala Gly Ala Ala Val Phe
545 550 555 560
Glu Gly Arg Cys Phe Lys Glu Ala Met Pro Leu Lys Ile Ile Lys Thr
565 570 575

Asp Thr Leu Ile Asp Lys Pro Pro Pro Val Thr Lys Thr Pro Arg Lys
580 585 590
Gly Lys Pro Gly Lys Arg Glu Ser Lys Arg Ala Arg Gly Leu Asp Lys
595 600 605
Tyr His Val Ala Arg His Leu Asp Thr Trp Arg Lys Gly Ala Arg Lys
610 615 620
Ile Ala Glu Arg Arg Ala Lys Gly Glu Ala Asp Pro Val Lys Leu Gly
625 630 635 640

Ala His Asp Met Arg Ser Leu Ser Leu His Val Arg Trp Met Ile Arg
645 650 655
Asp Trp Val Arg Leu Asn Ala Ser Gln Ile Ile Lys Thr Ala Glu Ser
660 665 670
His Lys Thr Asp Leu Ile Val Leu Glu Ser Leu Arg Gly Phe Ser Ala
675 680 685
Pro Gly Tyr His Lys Leu Asp Asp Glu Lys Lys Arg Thr Leu Ala Phe
690 695 700

Phe Ala Tyr Gly Arg Ile Arg Arg Lys Leu Thr Glu Lys Ala Val Glu
705 710 715 720
Arg Gly Met Arg Val Val Val Ala Pro Tyr Leu Arg Ser Ser Gln Val
725 730 735
Cys Ala Glu Cys Gly Arg Glu Gln Ile Asp Arg Asn Lys Leu Met Lys
740 745 750
Asp Lys Arg Lys Arg Arg Phe Ile Cys Glu Tyr Ser Asp Cys Thr Trp
755 760 765

Gln Cys Asp Ser Asp Gln Asn Ala Ala Cys Val Leu Gly Arg Val Phe

770 775 780

Trp Gly Glu Ile Glu Leu Pro Ser Glu Arg Lys Lys Asp

785 790 795

<210> 70

<211> 830

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

cas12g sequence

<400> 70

Met His Pro Ser Arg Tyr Lys Thr Ala Arg Thr Leu Val Arg Arg Leu

1 5 10 15

Cys Arg Leu Pro Gly Glu Asp Arg Ser Ala Phe Arg Ser Lys Val Gly

20 25 30

Leu Leu Arg Gly His Phe Glu Gln Phe Asn Val Asp Val Ser Glu Leu

35 40 45

Cys Gln Trp Leu Met Ser Leu Arg Lys Arg Asn Lys Val Pro Glu Asn

50 55 60

Pro Ala Thr Phe Gly Ala Leu Gly Asp Phe Leu Leu Gln Pro Gly Leu

65 70 75 80

Pro Gly Glu Glu Thr Asp Glu Lys Glu Ala Asp Arg Leu Arg Leu Ala

85 90 95

Val Phe Asp Ala Val Ala Gly Phe Arg Met Leu Glu Asp Arg Leu Ala

100 105 110

Ala Ser Ile Pro Ala Ser Leu Ser Asp Ala Ile Arg Asp Glu Ala Val

115 120 125

Phe Leu Ala Gly Val Arg Ala Ala Gly Lys Pro Ser Gly Leu Ala Arg

130 135 140

Val Leu Ala Arg Leu Glu Ala Cys Ala Pro Ala Gln Arg Leu Val Leu

145 150 155 160

Leu Lys Ser Ala Ala Glu Trp Ile Val Ala Arg Phe Leu Arg Gly Thr

165 170 175

Glu Asn Trp Met Arg Gln Arg Ala Glu Trp Glu Lys Glu Lys Ala Ala
180 185 190
Trp Glu Ala Ala His Pro His Leu Thr Pro Glu Val Arg Ala Gln Phe
195 200 205
Asn Lys Ile Phe Glu Ser Leu His Asp Pro Glu Asn Ser Gly Lys Pro

210 215 220
Gly Val Ser Arg Lys Asn Pro Arg Ile Cys Pro Trp Asp Arg Leu Lys
225 230 235 240
Gln Asn Leu Asp Asn Cys Cys Tyr Gly Glu Lys Gly His Ser Ala Leu
245 250 255
Cys Trp Arg Tyr Gln Asp Phe Leu Lys Gln Arg Met Gly Glu Asn Arg
260 265 270
Arg Asp Lys Lys Asn Phe Ser Ala Thr Ala Met Asp Leu Ala Gln Ile

275 280 285
Cys Arg Glu Trp Lys Ile Gln His Ser Arg Asn Ala Leu Asn Asn Pro
290 295 300
Arg Val Leu Asp Arg Leu Phe Ala Glu His Glu Arg Arg Lys Gln Asp
305 310 315 320
Lys Thr Lys Lys Glu Ser Arg Ser Pro Lys Pro Arg Gln Gly Gly Tyr
325 330 335
Lys Ala Asn Pro Lys Ala Asp Tyr Leu Arg Ser Phe Lys Ala His Trp

340 345 350
Lys Ala Tyr Leu Glu His Met Lys Leu Asn Asp Thr Thr Val Leu Glu
355 360 365
Arg Gly Cys Leu Pro His Cys Leu Ser Ile Lys Lys Asn Gly Lys Glu
370 375 380
Ser Thr Cys Lys Trp Asn Lys His Thr Glu Leu Cys Leu Glu Tyr Lys
385 390 395 400
Arg Ser Leu Ala Pro Leu Pro Asp Ser Val Leu Glu Leu Glu Pro Glu

405 410 415
Tyr Arg Glu Trp Arg Arg Leu Tyr Leu His Gly Pro Gly Arg Pro His

420 425 430

Phe Arg Tyr Pro Ser Ala Gly Glu Leu Pro Leu Pro Lys Val Phe Gly

435 440 445

Glu Gly Phe His Gln Val Asp Leu Asp Arg Ser Ile Val Arg Leu Arg

450 455 460

Leu Glu Gly Ala Ala Glu Gly Glu Trp Leu Glu Phe Gly Phe Ile Pro

465 470 475 480

Trp Pro Arg Gly Tyr Gln Pro Ser Arg Arg Glu Val Leu Ile Thr Ser

485 490 495

Val Gln Val His Phe Val Gly Thr Arg Pro Arg Ala Gly Phe Arg Phe

500 505 510

Asp Val Ser His Arg Thr Ser Arg Phe Gly Cys Ser Gln Asp Glu Leu

515 520 525

Asp Glu Leu Arg Ser Arg Arg Tyr Pro Arg Gln Ala Gln Asp Lys Glu

530 535 540

Phe Leu Ala Ala Ala Arg Ala Gln Leu Ile Gln Thr Phe Glu Gly Gly

545 550 555 560

Glu Gly Ala Ala Arg Gln Gln Met Arg Val Met Ser Val Asp Leu Gly

565 570 575

Glu Gly Gly Ala Cys Ala Ser Ile Tyr Glu Gly Arg Thr His Gln Lys

580 585 590

Asp Glu Ser Leu Lys Val Ile Lys Ile Asp Arg Arg Tyr Asp Gln His

595 600 605

Pro Glu Val Leu Glu Lys Asp Val Gly Ala Ala Lys Pro Gln Lys Phe

610 615 620

Glu Lys Ser Asp Pro Arg Gly Val Arg Lys Glu His Val Ala Arg His

625 630 635 640

Leu Asn Arg Ile Ala Ala Gly Ala Ser Ala Ile Ala Glu His Arg Arg

645 650 655

Lys Glu Arg Ser Asp Ala Glu Cys Ser Val Gly Glu Leu Gln Glu His

660 665 670

Asp Phe Arg Ser Leu Lys Arg His Ile Ala Trp Met Ile Arg Asp Trp
675 680 685
Val Arg Leu Asn Ala Ala Gln Ile Ile Asp Val Ala Lys Gln His Cys
690 695 700
Cys Asp Leu Ile Val Phe Glu Ser Gln Arg Gly Phe Arg Leu Pro Gly
705 710 715 720
Tyr Asp Glu Leu Asp Arg Gly Lys Lys Gln Arg Phe Ala Ile Leu Ala

725 730 735
Phe Gly Arg Ile Arg Arg Lys Val Val Glu Lys Ala Val Glu His Gly
740 745 750
Met Arg Val Val Thr Val Pro Tyr Phe Ala Ser Ser Gln Val Cys Ser
755 760 765
Ala Cys Lys Arg Val Gln Glu Asn Arg Gly Ser Trp Arg Glu Asn Lys
770 775 780
Lys Lys Arg Val Phe Ala Cys Glu Phe Cys Lys Leu Lys Leu Asn Ser

785 790 795 800
Asp Ala Asn Ala Ser Arg Val Leu Ala Arg Val Phe Trp Gly Glu Ile
805 810 815
Glu Leu Pro Glu Pro Thr Arg Ala His Leu Pro Ser Lys Ala
820 825 830

<210> 71
<211> 864
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
cas12g sequence
<400> 71
Met Pro Val Ser Arg Tyr Ser Glu Ser Arg Thr Leu Val Arg Pro Leu
1 5 10 15

Ala Arg Leu Pro His Glu Glu Arg Gln Asp Val Thr Pro Lys Val Ala
20 25 30
Arg Leu Arg Arg His Phe Glu Arg Phe Asn Val Asp Val Ala Glu Leu

35 40 45

Cys Gln Trp Leu Met Gly Leu Arg Asn Gln Phe Gly Pro Lys Glu Ser

50 55 60

Pro Ala Ser Phe Gly Pro Leu Gly Asp Phe Leu Ile Glu Pro Ala Leu

65 70 75 80

Asp Asn Ile Asp Ala Asp Glu Thr Glu Arg Asp Arg Trp Arg Leu Ala

85 90 95

Val Phe Asp Ala Val Ala Gly Phe Arg Pro Ile Arg Gly Leu Gly Asp

100 105 110

His Pro Val Pro Asp Thr Leu Arg Leu Ala Met Gln Gln Ala Ala Ser

115 120 125

Leu Ser Pro Thr Pro Thr Thr Ala Arg Leu Leu Glu Arg Leu Arg Pro

130 135 140

Leu Ser Pro Ala His Arg Leu Val Leu Leu Lys Ser Ala Ala Glu Trp

145 150 155 160

Ile Val Ala Arg Tyr Gln Arg Gly Met Glu Asn Trp Val Ile Gln His

165 170 175

Ala Ala Trp His Lys Glu Lys Glu Ala Trp Glu Arg Glu His Pro Ala

180 185 190

Leu Thr Pro Ala Val Arg Glu Arg Phe Thr Ala Leu Tyr Lys Gln Leu

195 200 205

Ser Asp Ser Lys Pro Thr Asp Arg Pro Val Ser Arg Arg Lys Asn Pro

210 215 220

Arg Ile Cys Glu Trp Glu Arg Leu Arg Gln Asn Ile Asp Asn Cys Cys

225 230 235 240

Tyr Ala Gly Glu Lys Gly His Gly Pro Leu Cys Arg Lys Tyr Ala Asn

245 250 255

Phe Val Lys Ala Arg Lys Ala Val Asp Gly Lys Phe Asn Asp Leu Leu

260 265 270

Phe Trp Asp Thr Ala Thr Ser Phe Ile Ala Leu Cys Arg Lys Phe Asn

275 280 285

Val Thr Arg Ala Arg Asn Ala Leu Gln Ser Gln Leu Asp Ala Leu Phe
290 295 300
Ala Glu Asp Gln Arg Arg Lys Ala Glu Arg Asp Gln Ala Lys Gly Arg
305 310 315 320
Gln Pro Arg Pro Leu His Pro Gln Ala Ala Ala Arg Ala Lys Ser Asp
325 330 335

Phe Leu Arg Ile Phe Lys Asp Gly Trp Asn Ala Tyr Leu Ser Ala Met
340 345 350
Gly Leu Asn Asp Ser Thr Ala Ile Glu Lys Gly Arg Leu Pro His Cys
355 360 365
Gln Lys Ile Gly Gly Thr Phe Glu Asn Ser Lys Cys Glu Trp Asn Pro
370 375 380
His Thr Asp Leu Cys His Gln Tyr Arg Arg Leu Ala Gly Gln Leu Asp
385 390 395 400

Asp Ala Thr Leu Ala Leu Glu Lys Asp Tyr Arg Glu Trp Arg Arg Leu
405 410 415
Tyr Leu Ala Gly Pro Arg Lys Pro Ser Phe Gln Tyr Pro Ser Ser Arg
420 425 430
Asp Leu Pro Met Pro Lys Ile Phe Gly Ala Gly Phe Phe Glu Leu Asp
435 440 445
Met Asp Arg Ser Ile Leu Arg Leu Arg Leu Asp Asp Met Val Glu Gly
450 455 460

Glu Trp Leu Glu Phe Gly Phe Lys Pro Trp Pro Arg Glu Tyr Thr Pro
465 470 475 480
Ser Arg Ala Gln Val Ala Arg Pro Gly Arg Ile Thr Ser Val His Val
485 490 495
Asn Phe Ile Gly Ser Arg Cys Arg Val Gly Phe Arg Phe Glu Ala Pro
500 505 510
His Ala Gly Ser Arg Phe Gly Cys Ser Gln Asp Glu Ile Asp Gln Leu
515 520 525

Arg Arg Asp His Pro Arg Glu Arg Asp Asp Gln Pro Phe Leu Glu Ala

530 535 540

Ala Arg Lys Arg Leu Val Glu Thr Phe Ala Gly Asp Ala Arg Arg Asp

545 550 555 560

Leu Arg Leu Leu Ala Val Asp Val Gly Glu Lys Gly Cys Cys Ala Ala

565 570 575

Val Tyr Gln Gly Thr Arg Tyr Val Ala Asp Ala Leu Leu Pro Ile Ile

580 585 590

Lys Ile Asn Gln Leu Tyr Thr Glu Pro Pro Thr Glu Leu Lys Pro Asp

595 600 605

Ser His Asn Arg Pro Ala Pro Asp Arg Arg Pro Phe Asn Asp Glu Lys

610 615 620

Asp Pro Arg Asp Pro Arg Gly Val Arg Lys Glu His Val Ala Arg His

625 630 635 640

Leu Lys Arg Met Ala Asp Lys Ala Pro Glu Val Ala Ala Tyr Arg Leu

645 650 655

Ala Gln Arg Glu Lys Ala Ala Pro Ser Pro Ser Ala Ser Pro Pro Pro

660 665 670

Val Thr Leu Gly Val His Asp Phe Arg Arg Leu Lys Arg His Val Thr

675 680 685

Trp Met Ile Arg Asp Trp Ala Arg His Asn Ala Ala Arg Ile Val Ala

690 695 700

Glu Ala Gln Arg His Gly Cys Asp Leu Ile Val Phe Glu Ser His Arg

705 710 715 720

Gly Arg Arg Pro Pro Gly Tyr His Glu Val Gly Asp Asp Ala Glu Arg

725 730 735

Arg Lys Leu Asp Asn Ala Thr Phe Ala Phe Gly Arg Ile Arg Arg Lys

740 745 750

Val Thr Glu Lys Ala Val Glu Arg Gly Leu Arg Val Val Thr Val Pro

755 760 765

Tyr His Cys Ser Ser Lys Val Cys Ser Arg Cys Gly Arg Leu Gln Glu

770 775 780

Asn Asp Gly Leu Leu Arg Arg Asn Lys Lys Glu Arg Lys Phe Ile Cys
785 790 795 800
Glu Gln Cys Lys Phe Glu Thr Asn Ser Asp Gly Asn Ala Ala Arg Val
805 810 815
Leu Ala Arg Val Phe Trp Gly Glu Ile Met Leu Pro Ser Pro Glu Glu
820 825 830
Arg Arg Lys Lys Arg Glu Gly Ser Gly Gly Arg Ser Pro Thr Pro Ala
835 840 845

Asn Pro Gly Gly Leu Val Asp Ala Pro Pro Ser Arg Arg Asn Leu Arg
850 855 860

<210> 72
<211> 1263
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 72

Met Glu Asp Tyr Ser Gly Phe Val Asn Ile Tyr Ser Ile Gln Lys Thr
1 5 10 15
Leu Arg Phe Glu Leu Lys Pro Val Gly Lys Thr Leu Glu His Ile Glu
20 25 30

Lys Lys Gly Phe Leu Lys Lys Asp Lys Ile Arg Ala Glu Asp Tyr Lys
35 40 45
Ala Val Lys Lys Ile Ile Asp Lys Tyr His Arg Ala Tyr Ile Glu Glu
50 55 60
Val Phe Asp Ser Val Leu His Gln Lys Lys Lys Lys Asp Lys Thr Arg
65 70 75 80
Phe Ser Thr Gln Phe Ile Lys Glu Ile Lys Glu Phe Ser Glu Leu Tyr
85 90 95

Tyr Lys Thr Glu Lys Asn Ile Pro Asp Lys Glu Arg Leu Glu Ala Leu
100 105 110
Ser Glu Lys Leu Arg Lys Met Leu Val Gly Ala Phe Lys Gly Glu Phe

115 120 125

Ser Glu Glu Val Ala Glu Lys Tyr Lys Asn Leu Phe Ser Lys Glu Leu

130 135 140

Ile Arg Asn Glu Ile Glu Lys Phe Cys Glu Thr Asp Glu Glu Arg Lys

145 150 155 160

Gln Val Ser Asn Phe Lys Ser Phe Thr Thr Tyr Phe Thr Gly Phe His

165 170 175

Ser Asn Arg Gln Asn Ile Tyr Ser Asp Glu Lys Lys Ser Thr Ala Ile

180 185 190

Gly Tyr Arg Ile Ile His Gln Asn Leu Pro Lys Phe Leu Asp Asn Leu

195 200 205

Lys Ile Ile Glu Ser Ile Gln Arg Arg Phe Lys Asp Phe Pro Trp Ser

210 215 220

Asp Leu Lys Lys Asn Leu Lys Lys Ile Asp Lys Asn Ile Lys Leu Thr

225 230 235 240

Glu Tyr Phe Ser Ile Asp Gly Phe Val Asn Val Leu Asn Gln Lys Gly

245 250 255

Ile Asp Ala Tyr Asn Thr Ile Leu Gly Gly Lys Ser Glu Glu Ser Gly

260 265 270

Glu Lys Ile Gln Gly Leu Asn Glu Tyr Ile Asn Leu Tyr Arg Gln Lys

275 280 285

Asn Asn Ile Asp Arg Lys Asn Leu Pro Asn Val Lys Ile Leu Phe Lys

290 295 300

Gln Ile Leu Gly Asp Arg Glu Thr Lys Ser Phe Ile Pro Glu Ala Phe

305 310 315 320

Pro Asp Asp Gln Ser Val Leu Asn Ser Ile Thr Glu Phe Ala Lys Tyr

325 330 335

Leu Lys Leu Asp Lys Lys Lys Lys Ser Ile Ile Ala Glu Leu Lys Lys

340 345 350

Phe Leu Ser Ser Phe Asn Arg Tyr Glu Leu Asp Gly Ile Tyr Leu Ala

355 360 365

Asn Asp Asn Ser Leu Ala Ser Ile Ser Thr Phe Leu Phe Asp Asp Trp
370 375 380
Ser Phe Ile Lys Lys Ser Val Ser Phe Lys Tyr Asp Glu Ser Val Gly
385 390 395 400
Asp Pro Lys Lys Lys Ile Lys Ser Pro Leu Lys Tyr Glu Lys Glu Lys
405 410 415

Glu Lys Trp Leu Lys Gln Lys Tyr Tyr Thr Ile Ser Phe Leu Asn Asp
420 425 430
Ala Ile Glu Ser Tyr Ser Lys Ser Gln Asp Glu Lys Arg Val Lys Ile
435 440 445
Arg Leu Glu Ala Tyr Phe Ala Glu Phe Lys Ser Lys Asp Asp Ala Lys
450 455 460
Lys Gln Phe Asp Leu Leu Glu Arg Ile Glu Glu Ala Tyr Ala Ile Val
465 470 475 480

Glu Pro Leu Leu Gly Ala Glu Tyr Pro Arg Asp Arg Asn Leu Lys Ala
485 490 495
Asp Lys Lys Glu Val Gly Lys Ile Lys Asp Phe Leu Asp Ser Ile Lys
500 505 510
Ser Leu Gln Phe Phe Leu Lys Pro Leu Leu Ser Ala Glu Ile Phe Asp
515 520 525
Glu Lys Asp Leu Gly Phe Tyr Asn Gln Leu Glu Gly Tyr Tyr Glu Glu
530 535 540

Ile Asp Ser Ile Gly His Leu Tyr Asn Lys Val Arg Asn Tyr Leu Thr
545 550 555 560
Gly Lys Ile Tyr Ser Lys Glu Lys Phe Lys Leu Asn Phe Glu Asn Ser
565 570 575
Thr Leu Leu Lys Gly Trp Asp Glu Asn Arg Glu Val Ala Asn Leu Cys
580 585 590
Val Ile Phe Arg Glu Asp Gln Lys Tyr Tyr Leu Gly Val Met Asp Lys
595 600 605

Glu Asn Asn Thr Ile Leu Ser Asp Ile Pro Lys Val Lys Pro Asn Glu

610 615 620

Leu Phe Tyr Glu Lys Met Val Tyr Lys Leu Ile Pro Thr Pro His Met
625 630 635 640

Gln Leu Pro Arg Ile Ile Phe Ser Ser Asp Asn Leu Ser Ile Tyr Asn
645 650 655

Pro Ser Lys Ser Ile Leu Lys Ile Arg Glu Ala Lys Ser Phe Lys Glu
660 665 670

Gly Lys Asn Phe Lys Leu Lys Asp Cys His Lys Phe Ile Asp Phe Tyr
675 680 685

Lys Glu Ser Ile Ser Lys Asn Glu Asp Trp Ser Arg Phe Asp Phe Lys
690 695 700

Phe Ser Lys Thr Ser Ser Tyr Glu Asn Ile Ser Glu Phe Tyr Arg Glu
705 710 715 720

Val Glu Arg Gln Gly Tyr Asn Leu Asp Phe Lys Lys Val Ser Lys Phe
725 730 735

Tyr Ile Asp Ser Leu Val Glu Asp Gly Lys Leu Tyr Leu Phe Gln Ile
740 745 750

Tyr Asn Lys Asp Phe Ser Ile Phe Ser Lys Gly Lys Pro Asn Leu His
755 760 765

Thr Ile Tyr Phe Arg Ser Leu Phe Ser Lys Glu Asn Leu Lys Asp Val
770 775 780

Cys Leu Lys Leu Asn Gly Glu Ala Glu Met Phe Phe Arg Lys Lys Ser
785 790 795 800

Ile Asn Tyr Asp Glu Lys Lys Lys Arg Glu Gly His His Pro Glu Leu
805 810 815

Phe Glu Lys Leu Lys Tyr Pro Ile Leu Lys Asp Lys Arg Tyr Ser Glu
820 825 830

Asp Lys Phe Gln Phe His Leu Pro Ile Ser Leu Asn Phe Lys Ser Lys
835 840 845

Glu Arg Leu Asn Phe Asn Leu Lys Val Asn Glu Phe Leu Lys Arg Asn
850 855 860

Lys Asp Ile Asn Ile Ile Gly Ile Asp Arg Gly Glu Arg Asn Leu Leu
865 870 875 880
Tyr Leu Val Met Ile Asn Gln Lys Gly Glu Ile Leu Lys Gln Thr Leu
885 890 895
Leu Asp Ser Met Gln Ser Gly Lys Gly Arg Pro Glu Ile Asn Tyr Lys
900 905 910
Glu Lys Leu Gln Glu Lys Glu Ile Glu Arg Asp Lys Ala Arg Lys Ser
915 920 925

Trp Gly Thr Val Glu Asn Ile Lys Glu Leu Lys Glu Gly Tyr Leu Ser
930 935 940
Ile Val Ile His Gln Ile Ser Lys Leu Met Val Glu Asn Asn Ala Ile
945 950 955 960
Val Val Leu Glu Asp Leu Asn Ile Gly Phe Lys Arg Gly Arg Gln Lys
965 970 975
Val Glu Arg Gln Val Tyr Gln Lys Phe Glu Lys Met Leu Ile Asp Lys
980 985 990

Leu Asn Phe Leu Val Phe Lys Glu Asn Lys Pro Thr Glu Pro Gly Gly
995 1000 1005
Val Leu Lys Ala Tyr Gln Leu Thr Asp Glu Phe Gln Ser Phe Glu
1010 1015 1020
Lys Leu Ser Lys Gln Thr Gly Phe Leu Phe Tyr Val Pro Ser Trp
1025 1030 1035
Asn Thr Ser Lys Ile Asp Pro Arg Thr Gly Phe Ile Asp Phe Leu
1040 1045 1050

His Pro Ala Tyr Glu Asn Ile Glu Lys Ala Lys Gln Trp Ile Asn
1055 1060 1065
Lys Phe Asp Ser Ile Arg Phe Asn Ser Lys Met Asp Trp Phe Glu
1070 1075 1080
Phe Thr Ala Asp Thr Arg Lys Phe Ser Glu Asn Leu Met Leu Gly
1085 1090 1095
Lys Asn Arg Val Trp Val Ile Cys Thr Thr Asn Val Glu Arg Tyr

1100 1105 1110

Phe Thr Ser Lys Thr Ala Asn Ser Ser Ile Gln Tyr Asn Ser Ile
1115 1120 1125
Gln Ile Thr Glu Lys Leu Lys Glu Leu Phe Val Asp Ile Pro Phe
1130 1135 1140
Ser Asn Gly Gln Asp Leu Lys Pro Glu Ile Leu Arg Lys Asn Asp
1145 1150 1155
Ala Val Phe Phe Lys Ser Leu Leu Phe Tyr Ile Lys Thr Thr Leu
1160 1165 1170

Ser Leu Arg Gln Asn Asn Gly Lys Lys Gly Glu Glu Glu Lys Asp
1175 1180 1185
Phe Ile Leu Ser Pro Val Val Asp Ser Lys Gly Arg Phe Phe Asn
1190 1195 1200
Ser Leu Glu Ala Ser Asp Asp Glu Pro Lys Asp Ala Asp Ala Asn
1205 1210 1215
Gly Ala Tyr His Ile Ala Leu Lys Gly Leu Met Asn Leu Leu Val
1220 1225 1230

Leu Asn Glu Thr Lys Glu Glu Asn Leu Ser Arg Pro Lys Trp Lys
1235 1240 1245
Ile Lys Asn Lys Asp Trp Leu Glu Phe Val Trp Glu Arg Asn Arg
1250 1255 1260

<210> 73
<211> 1222
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 73

Met Lys Lys Phe Thr Asn Leu Tyr Ser Leu Ser Lys Thr Leu Arg Phe
1 5 10 15

Glu Leu Ile Pro Gln Gly Lys Thr Leu Glu Asn Ile Gln Lys Ser Gly

20 25 30

Ile Leu Glu Gln Asp Asn Ser Arg Ala Glu Lys Tyr Glu Lys Ile Lys

35 40 45

Lys Ile Ile Asp Asp Tyr His Lys Phe Phe Ile Glu Lys Ser Phe Thr

50 55 60

Gly Lys Lys Ile Asp Asp Tyr Phe Leu Asn Gln Tyr Phe Glu Leu Phe

65 70 75 80

Lys Ile Lys Asp Lys Asp Glu Glu Gln Lys Lys Asp Phe Lys Ser Ile

85 90 95

Gln Glu Asn Leu Arg Lys Asn Ile Ile Ser Phe Phe Asp Lys Asn Lys

100 105 110

Leu Lys Arg Leu Phe Glu Lys Glu Ile Ile Lys Glu Asp Leu Pro Asn

115 120 125

Phe Val Lys Glu Glu Glu Asp Lys Lys Leu Ile Ser Glu Phe Asp Lys

130 135 140

Phe Thr Thr Tyr Phe Val Gly Phe His Glu Asn Arg Lys Ser Met Tyr

145 150 155 160

Ser Glu Glu Glu Lys Ser Thr Ser Ile Ala Tyr Arg Thr Ile Asn Glu

165 170 175

Asn Leu Pro Lys Phe Ile Asn Asn Ile Phe Val Phe Glu Lys Ile Ser

180 185 190

Lys Thr Pro Ile Ser Glu Asn Phe Arg Glu Leu Tyr Lys Asp Leu Glu

195 200 205

Glu Tyr Leu Asn Val Asn Asp Ile Gln Asp Ile Phe Lys Leu Asn Tyr

210 215 220

Phe Ser Asn Val Ile Thr Gln Lys Gln Ile Asp Val Tyr Asn Leu Val

225 230 235 240

Ile Gly Gly Lys Thr Leu Glu Asn Gly Thr Lys Ile Lys Gly Leu Asn

245 250 255

Glu Tyr Ile Asn Leu Tyr Asn Gln Asn Gln Thr Asp Lys Lys Asn Lys

260 265 270

Leu Pro Leu Leu Thr Val Leu Phe Lys Gln Ile Leu Cys Asp Arg Asp
275 280 285

Thr Ile Ser Phe Leu Pro Glu Gln Phe Glu Asn Asp Ile Asp Val Leu
290 295 300

Asp Asn Ile Lys Asn Thr Tyr Ser Asn Met Glu Lys Ser Ile Lys Asp
305 310 315 320

Ile Lys Asp Leu Leu Ser Asn Leu Lys Asp Phe Asp Leu Ser Lys Ile
325 330 335

Tyr Ile Thr Asn Asp Ile Ala Leu Thr Asp Ile Ser Gln Gln Val Phe
340 345 350

Asn Asn Tyr Ser Ile Ile Ile Asn Ala Ile Lys Glu Asn Ile Lys Lys
355 360 365

Glu Asn Pro Lys Lys Lys Thr Glu Asn Glu Glu Lys Tyr Gly Glu Arg
370 375 380

Ile Asp Lys Ile Phe Lys Ser Asn Asn Ser Phe Ser Ile Lys Tyr Ile
385 390 395 400

Asn Asp Cys Ile Lys Glu Lys Asn Ile Glu Ile Tyr Phe Met Asp Phe
405 410 415

Gly Lys Lys Glu Asn Asn Lys Lys Val Lys Asn Leu Phe Asp Glu Leu
420 425 430

Gln Asn Asn Tyr Ser Met Val Lys Asp Leu Leu Glu Tyr Lys Lys Ile
435 440 445

Gln Ser Leu Ile Gln Asp Glu Lys Ser Ile Glu Leu Ile Lys Asn Phe
450 455 460

Leu Asp Ser Ile Lys Asn Ile Gln His Phe Leu Lys Pro Leu Tyr Val
465 470 475 480

Lys Asp Asn Asp Ile Val Lys Asp Ile Ser Phe Tyr Arg Asp Phe Glu
485 490 495

Glu Leu Tyr Leu Asn Ile Asp Lys Ile Thr Pro Leu Tyr Asn Lys Val
500 505 510

Arg Asn Tyr Val Thr Gln Lys Pro Tyr Ser Val Lys Lys Ile Lys Leu

515 520 525

Asn Phe Glu Asn Ser Thr Leu Leu Ala Gly Trp Asp Leu Asn Lys Glu
530 535 540
Arg Asp Asn Thr Cys Ala Ile Leu Arg Lys Asp Asp Leu Tyr Tyr Leu
545 550 555 560
Ala Ile Met Asp Val Asn Asn Arg Asn Val Phe Asn Glu Lys Gly Ile
565 570 575
Asp Gly Ile Gly Tyr Glu Lys Met Glu Tyr Lys Leu Leu Pro Gly Ala
580 585 590

Asn Lys Met Leu Pro Lys Val Phe Phe Ser Lys Ser Arg Ile Lys Asp
595 600 605
Phe Asn Pro Ser Glu Gln Ile Ile Arg Asn Tyr Glu Lys Glu Thr His
610 615 620
Lys Lys Gly Ser Asn Phe Ser Leu Lys Asp Cys His Lys Leu Ile Asp
625 630 635 640
Phe Phe Lys Ser Ser Ile Asn Lys His Glu Asp Trp Lys Asn Phe Asn
645 650 655

Phe Lys Phe Ser Asn Thr Asp Lys Tyr Glu Asp Leu Ser Gly Phe Tyr
660 665 670
Arg Glu Val Glu Gln Gln Gly Tyr Lys Ile Thr Phe Arg Asn Ile Ser
675 680 685
Lys Glu Tyr Val Asp Lys Leu Val Glu Glu Gly Lys Ile Tyr Leu Phe
690 695 700
Gln Ile Tyr Asn Lys Asp Phe Ser Lys Tyr Ser Lys Gly Thr Pro Asn
705 710 715 720

Met His Thr Leu Tyr Trp Lys Ala Leu Phe Asp Glu Asp Asn Leu Lys
725 730 735
Asn Val Val Tyr Lys Leu Asn Gly Gln Ala Glu Ile Phe Tyr Arg Lys
740 745 750
Gly Ser Ile Glu Lys Glu Asn Ile Val Ile His Lys Ala Asn Asn Ala
755 760 765

Ile Glu Asn Lys Asn Met Asp Asn Lys Lys Lys Gln Ser Lys Phe Glu
770 775 780

Tyr Asp Ile Ile Lys Asp Arg Arg Tyr Thr Val Asp Lys Phe Gln Phe
785 790 795 800
His Val Pro Ile Thr Leu Asn Phe Lys Ala Ile Gly Asn Glu Arg Ile
805 810 815
Asn Glu Gln Val Asn Gln Tyr Ile Lys Asp Asn Asn Ile Lys His Ile
820 825 830
Ile Gly Ile Asp Arg Gly Glu Arg His Leu Leu Phe Leu Ser Leu Ile
835 840 845

Asp Leu Lys Gly Asn Ile Ile Lys Gln Phe Ser Leu Asn Glu Ile Val
850 855 860
Asn Glu Tyr Asn Gly Asn Ser Tyr Lys Thr Asn Tyr His Met Leu Leu
865 870 875 880
Glu Lys Arg Glu Glu Glu Arg Asp Lys Ala Arg Lys Ser Trp Lys Thr
885 890 895
Ile Glu Asn Ile Lys Glu Leu Lys Glu Gly Tyr Ile Ser Gln Val Ile
900 905 910

His Lys Ile Thr Gln Leu Met Ile Glu Tyr Asn Ala Ile Val Val Leu
915 920 925
Glu Asp Leu Asn Phe Gly Phe Met Arg Gly Arg Gln Lys Val Glu Lys
930 935 940
Gln Val Tyr Gln Lys Phe Glu Lys Met Leu Ile Asp Lys Leu Asn Tyr
945 950 955 960
Leu Val Asp Lys Lys Lys Asp Lys Asn Glu Ala Gly Gly Leu Leu Lys
965 970 975

Ala His Gln Leu Thr Asn Lys Phe Glu Ser Phe Gln Lys Met Gly Lys
980 985 990
Gln Asn Gly Phe Leu Phe Tyr Ile Pro Ala Trp Asn Thr Ser Lys Leu
995 1000 1005
Asp Pro Ile Thr Gly Phe Val Asn Leu Phe Asp Thr His Tyr Thr

1010 1015 1020

Asn Val Asp Asn Ala Lys Lys Phe Phe Glu Asn Phe Glu Asp Ile

1025 1030 1035

Arg Phe Asn Glu Lys Lys Asn Tyr Phe Glu Phe Ile Val Asn Asp

1040 1045 1050

Tyr Thr Lys Phe Asn Thr Lys Ala Glu Gly Thr Lys Leu Asn Trp

1055 1060 1065

Thr Ile Cys Ser Asn Glu Asp Arg Ile Lys Thr Phe Arg Ser Ser

1070 1075 1080

Ser Lys Asn Asn Gln Trp Val Ser Glu Thr Val Asn Leu Thr Asp

1085 1090 1095

Ser Leu Ile Glu Leu Phe Lys Lys Tyr Asp Ile Asp Tyr Lys Leu

1100 1105 1110

Glu Leu Lys Glu Gln Ile Ile Ser Lys Ser Glu Lys Asn Phe Phe

1115 1120 1125

Glu Thr Leu Leu Tyr Leu Phe Lys Leu Thr Leu Gln Met Arg Asn

1130 1135 1140

Ser Ile Thr Gly Thr Glu Thr Asp Tyr Leu Ile Ser Pro Val Ala

1145 1150 1155

Asp Lys Thr Gly Asn Phe Phe Asp Ser Arg Lys Gly Ile Glu Asn

1160 1165 1170

Leu Pro Asn Asn Ala Asp Ala Asn Gly Ala Tyr Asn Ile Ala Arg

1175 1180 1185

Lys Gly Leu Trp Val Ile Glu Gln Ile Lys Lys Ala Lys Asp Leu

1190 1195 1200

Lys Lys Val Lys Leu Ala Ile Ser Asn Lys Glu Trp Leu Gln Phe

1205 1210 1215

Val Gln Gly Lys

1220

<210> 74

<211> 1262

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 74

Met Ala Lys Asn Thr Ile Phe Ser Gln Phe Thr Gly Leu Tyr Pro Val
1 5 10 15

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Met Gly Lys Thr Leu Glu
20 25 30

Lys Ile Lys Glu Thr Gly Val Ile Glu Asn Asp Lys Lys Arg His Asn
35 40 45

Asp Tyr Phe Asp Ala Lys Lys Ile Ile Asp Lys Tyr His Lys Tyr Phe
50 55 60

Ile Asp Ala Ala Leu Ser Lys Phe Pro Arg Ile Asp Trp Ser Pro Leu
65 70 75 80

Lys Glu Ala Ile Glu Arg Ser Leu Asp Arg Ser Asp Ala Ser Lys Lys
85 90 95

Lys Leu Glu Lys Thr Gln Thr Glu Phe Arg Lys Lys Ile Ala Lys Ala
100 105 110

Leu Thr Thr His Asp His Tyr Lys Glu Leu Thr Ala Ser Thr Pro Lys
115 120 125

Asp Leu Phe Leu Lys Val Phe Pro Asp His Phe Gly Lys Gln Pro Ala
130 135 140

Ile Asp Thr Phe Asp Gly Phe Ser Ser Tyr Phe Thr Gly Phe Gln Glu
145 150 155 160

Asn Arg Gln Asn Ile Tyr Ser Asp Glu Ala Ile Ser Thr Ala Ile Pro
165 170 175

Tyr Arg Leu Val His Asp Asn Phe Pro Lys Phe Leu Ser Asn Ile Glu
180 185 190

Val Tyr Lys Thr Leu Lys Asp Asn Ala Pro Ser Val Leu Ser Asp Ala
195 200 205

Glu Asn Glu Leu Arg Asp Phe Leu Asn Gly Lys Ser Leu Ala Asn Ile

210 215 220

Phe Glu Leu Asn Ala Tyr Asn Glu Val Leu Thr Gln Ser Gly Ile Asp

225 230 235 240

Phe Phe Asn Gln Val Ile Gly Gly Ile Ser Asp Glu Gly Gly Glu Lys

245 250 255

Lys Thr Arg Gly Ile Asn Glu Phe Ser Asn Leu Tyr Arg Gln Gln His

260 265 270

Pro Glu Phe Ala Gln Lys Arg Leu Ala Thr Lys Met Ile Pro Leu Tyr

275 280 285

Lys Gln Ile Leu Ser Asp Arg Glu Thr Lys Ser Phe Ile Leu Glu Ser

290 295 300

Tyr Ser Asn Asp Ser Gln Val Gln Asn Ser Val Lys Glu Phe Phe Glu

305 310 315 320

Ser Gln Ile Leu Asn Trp Asp Ile Ala Gly Arg Arg Val Asn Val Leu

325 330 335

Asn Glu Leu Thr Ser Leu Val Lys Arg Ile Ser Glu Phe Asp Leu Gly

340 345 350

Asn Ile Tyr Val Asn Gln Glu Glu Leu Ser Asn Ile Ser Leu Lys Leu

355 360 365

Phe Asp Asn Trp Asn Ser Ile Asn Gly Leu Leu Phe Lys His Ala Glu

370 375 380

Asn Arg Ile Gly Ser Ala Glu Lys Ser Ala Asn Lys Lys Lys Ile Asp

385 390 395 400

Ala Trp Met Lys Asn Lys Glu Phe Ser Ile Ala Thr Leu Asn Leu Ala

405 410 415

Ile Ala Glu Ser Asn Ser Glu Glu Ile Ser Arg Val Lys Ile Glu Ser

420 425 430

Tyr Trp Asn Asn Phe Glu Ala Lys Val Gln Ser Ile Leu Cys Gly Asp

435 440 445

Asn Arg Arg Asn Leu Asp Glu Phe Ile Ser Ala Thr Phe Asn Glu Asn

450 455 460

Asn Ala Leu Arg Glu Asp Ser Lys Ile Ile Glu Lys Leu Lys Ala Phe
465 470 475 480
Leu Asp Ala Leu Ile Glu Ile Met His Ser Ile Lys Pro Leu Ile Ser
485 490 495

Asp Ala Glu Asn Arg Asp Leu Ser Phe Tyr Asn Glu Leu Ile Pro Leu
500 505 510
Tyr Asp Gln Leu Ser Leu Val Val Pro Leu Tyr Asn Lys Ile Arg Asn
515 520 525
Tyr Ala Thr Gln Lys Leu Thr Glu Ser Glu Lys Phe Lys Leu Asn Phe
530 535 540
Asp Asn Pro Thr Leu Ala Asp Gly Trp Asp Gln Asn Lys Glu Glu Ala
545 550 555 560

Asn Thr Ala Ile Leu Leu Leu Lys Asn Gly Leu Tyr Tyr Leu Gly Ile
565 570 575
Met Asn Ala Lys Asn Lys Pro Lys Ile Lys Asp Phe Lys Thr Ser Glu
580 585 590
Ser Glu Asp Cys Tyr Asp Lys Met Val Tyr Lys Leu Leu Pro Gly Pro
595 600 605
Asn Lys Met Leu Pro Lys Val Phe Phe Ser Glu Lys Gly Leu Ala Thr
610 615 620

Phe Lys Pro Pro Lys Asp Ile Leu Asp Gly Tyr Asn Ala Gly Lys His
625 630 635 640
Lys Lys Gly Asp Leu Phe Asp Ile Gly Phe Cys His Gln Leu Ile Asp
645 650 655
Phe Phe Lys Glu Ser Ile Ala Lys His Pro Asp Trp Lys Lys Phe Asp
660 665 670
Phe Asn Phe Ser Asp Thr Ser Ser Tyr Glu Asp Ile Ser Gly Phe Tyr
675 680 685

Lys Glu Val Thr Asp Gln Gly Tyr Lys Ile Thr Phe Ser Lys Ile Pro
690 695 700
Thr Ser Gln Ile Asp Glu Trp Val Lys Glu Gly Lys Leu Phe Leu Phe

705 710 715 720

Gln Ile Tyr Asn Lys Asp Phe Ala Pro Gly Ala Lys Gly Ser Pro Asn

725 730 735

Leu His Thr Leu Tyr Trp Lys Ser Val Phe Ser Pro Glu Asn Leu Lys

740 745 750

Asp Val Val Val Lys Leu Asn Gly Glu Ala Glu Leu Phe Tyr Arg Pro

755 760 765

Ser Ser Val Lys Lys Pro Tyr Ser His Lys Val Gly Glu Lys Leu Val

770 775 780

Asn Arg Ile Gly Lys Asp Gly Leu Pro Leu Pro Glu Ser Val Phe Gly

785 790 795 800

Glu Leu Phe Arg Tyr Phe Asn Gly Lys Leu Glu Gly Glu Leu Ser Asp

805 810 815

Glu Ala Lys Arg Tyr Leu Asp Val Ala Val Val Lys Asp Val Lys His

820 825 830

Glu Ile Val Lys Asp Arg Arg Tyr Thr Gln Asp Lys Phe Glu Phe His

835 840 845

Val Pro Leu Thr Leu Asn Phe Lys Ala Asp Ser Lys Asn Glu Tyr Met

850 855 860

Asn Glu Arg Val Arg His Phe Leu Lys Asp Asn Pro Asp Val Asn Ile

865 870 875 880

Ile Gly Ile Asp Arg Gly Glu Arg His Leu Leu Tyr Met Thr Leu Ile

885 890 895

Asn Gln Lys Gly Glu Ile Leu Lys Gln Lys Ser Phe Asn Val Val Glu

900 905 910

Ser Val Asn Tyr Gln Ala Lys Leu Val Gln Arg Glu Lys Glu Arg Asp

915 920 925

Ala Ala Arg Arg Ser Trp Ser Ser Val Gly Lys Ile Lys Asp Leu Lys

930 935 940

Glu Gly Phe Leu Ser Gln Val Ile His Glu Ile Thr Thr Thr Met Ile

945 950 955 960

Glu Asn Asn Ala Ile Val Val Leu Glu Asp Leu Asn Phe Gly Phe Lys
965 970 975
Arg Gly Arg Phe Cys Val Glu Arg Gln Val Tyr Gln Lys Phe Glu Lys
980 985 990
Met Leu Ile Asp Lys Leu Asn Tyr Leu Val Phe Lys Asn Lys Pro Glu
995 1000 1005

Gly Asp Val Gly Gly Val Leu Lys Gly Tyr Gln Leu Ala Glu Lys
1010 1015 1020
Phe Asp Ser Phe Gln Lys Leu Gly Lys Gln Ser Gly Phe Leu Phe
1025 1030 1035
Tyr Ile Pro Ala Ala Tyr Thr Ser Lys Ile Asp Pro Thr Thr Gly
1040 1045 1050
Phe Ala Asn Leu Phe Asn Met Thr Glu Leu Thr Ser Ala Glu Lys
1055 1060 1065

Lys Lys Glu Phe Leu Ser His Phe Glu Asp Ile Thr Tyr Asp Gly
1070 1075 1080
Lys Asn Asp Arg Phe Leu Phe Ser Phe Asp Tyr Lys Asn Phe Lys
1085 1090 1095
Cys Phe Gln Thr Asp Tyr Ile Lys Lys Trp Thr Val Tyr Ser Gln
1100 1105 1110
Gly Lys Arg Ile Val Tyr Asp Lys Glu Ser Lys Ser Ala Lys Glu
1115 1120 1125

Ile Ser Pro Val Glu Ile Ile Lys Ala Ala Leu Ala Lys Gln Asn
1130 1135 1140
Ile Ala Leu Thr Asp Gln Leu Asp Val Leu Ser Ala Ile Asn Ser
1145 1150 1155
Val Glu Ala Ser Pro Lys Ser Ala Ser Phe Phe Gly Asp Ile Cys
1160 1165 1170
Tyr Ala Phe Glu Lys Thr Leu Gln Met Arg Asn Ser Ile Pro Asn
1175 1180 1185

Thr Asp Glu Asp Tyr Leu Ala Ser Pro Val Met Asn Lys Arg Gly

1190 1195 1200

Glu Phe Tyr Asp Ser Arg Ser Cys Asp Asp Ala Leu Pro Gln Asn

1205 1210 1215

Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu Lys Gly Leu Tyr

1220 1225 1230

Leu Ile Lys Asn Val Phe Asp Ala Gly Gly Lys Glu Leu Lys Ile

1235 1240 1245

Ser His Glu Asp Trp Phe Lys Phe Ala Gln Ser Arg Asn Cys

1250 1255 1260

<210> 75

<211> 1253

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 75

Met Ser Lys Gly Lys Ile Trp Glu Asn Phe Ile Asn Gln Tyr Ser Val

1 5 10 15

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Val Gly Lys Thr Leu Glu

20 25 30

Asn Ile Asn Ala Lys Gly Leu Ile Glu Glu Asp Glu Gln Arg Ala Glu

35 40 45

Asp Tyr Lys Lys Ala Lys Lys Ile Ile Asp Glu Tyr His Lys Tyr Phe

50 55 60

Ile Glu Gly Ala Leu Gly Ser Cys Ser Leu Asp Leu Asn Ile Leu Asn

65 70 75 80

Glu Phe Leu Gln Leu Tyr Asn Lys Ala Gln Lys Thr Asp Ala Asp Lys

85 90 95

Lys Glu Tyr Glu Lys Ile Gln Thr Thr Leu Arg Lys Asn Ile Ala Glu

100 105 110

Ser Phe Gly Lys Asn Ala Asp Lys Lys Thr Lys Glu Gln Tyr Glu Asn

115 120 125

Leu Phe Lys Lys Glu Leu Leu Arg Asn Asp Leu Pro Asp Trp Val Glu
130 135 140
Asp Glu Glu Asp Ala Lys Ile Ile Glu Arg Phe Lys Thr Phe Thr Thr
145 150 155 160
Tyr Phe Thr Gly Phe His Glu Asn Arg Lys Asn Ile Tyr Asp Asn Glu

165 170 175
Glu Lys Ser Thr Ala Ile Gly Tyr Arg Ile Val His Glu Asn Leu Pro
180 185 190
Lys Phe Ile Asp Asn Met Asn Ala Phe Glu Lys Ile Ser Lys Ala Leu
195 200 205
Asp Leu Ser Glu Ile Asp Arg Asp Phe Gln Ser Glu Leu Gly Glu Ile
210 215 220
Lys Ala Glu Glu Phe Phe Thr Ile Glu Phe Phe Asn Gln Cys Leu Asn

225 230 235 240
Gln Phe Gly Ile Asp Arg Tyr Asn Thr Leu Leu Gly Gly Ile Ser Glu
245 250 255
Gly Glu Asn Ile Lys Lys Lys Gln Gly Leu Asn Glu Arg Ile Asn Leu
260 265 270
Tyr Asn Gln Gln Leu Lys Gly Glu Arg Lys Lys Glu Arg Leu Pro Lys
275 280 285
Leu Lys Val Leu Tyr Lys Gln Ile Leu Ser Asp Ser Ser Ser His Ser

290 295 300
Phe Ser Ile Asp Glu Phe Glu Asn Asp Asn Glu Leu Leu Glu Ser Leu
305 310 315 320
Glu Ile Phe Tyr Lys Asn Glu Leu Ile Gly Phe Asn His Ser Gly Val
325 330 335
Asp Ser Asn Ile Phe Asp Leu Val Lys Asp Leu Leu Leu Lys Ile Asp
340 345 350
Glu Ser Glu Gln Ser Ser Ile Tyr Leu Lys Asn Asp Lys Gly Leu Thr

355 360 365
Glu Ile Ser Gln Arg Ile Phe Gly Asp Trp Asn Ile Ile Lys Ser Ala

370 375 380

Leu Glu Glu Tyr Tyr Asp Glu His Tyr Pro Pro Lys Lys Asp Thr Phe

385 390 395 400

Asn Lys Lys Glu Leu Asp Glu Arg Ser Arg Trp Leu Lys Glu Asn His

405 410 415

Ser Ile Gly Val Ile Glu Lys Ala Leu Ala Asn Tyr Glu Asn Glu Ile

420 425 430

Val Arg Glu His Leu Lys Gln Asn Ser Ala Pro Ile Val Ser Tyr Phe

435 440 445

Lys Ser Leu Glu Val Asp Gly Glu Asn Leu Ile Asp Lys Ile Tyr Ser

450 455 460

Ala Tyr Gly Asn Ile Ser Asp Leu Leu Asn Ser Ser Tyr Pro Asp Glu

465 470 475 480

Lys Lys Leu Val Ser Asp Arg Thr Ser Lys Asp Lys Ile Lys Val Phe

485 490 495

Leu Asp Ser Leu Met Ser Leu Leu His Phe Leu Lys Pro Leu Asp Val

500 505 510

Lys Asp Leu Gly Asn Lys Asp Ser Ala Phe Tyr Gly Asp Tyr Asp Phe

515 520 525

Ile Val Glu Gln Leu Ser Lys Leu Val Arg Leu Tyr Asn Lys Thr Arg

530 535 540

Asn Tyr Leu Thr Arg Lys Pro Tyr Ser Ile Glu Lys Ile Lys Leu Asn

545 550 555 560

Phe Glu Asn Ser Thr Leu Leu Ala Gly Trp Asp Val Asn Lys Glu Arg

565 570 575

Asp Asn Asn Cys Val Ile Phe Lys Arg Gln Asp Gly Asp Arg Glu Leu

580 585 590

Phe Tyr Leu Gly Ile Met Asp Lys Ser His Asn Lys Ile Phe Thr Lys

595 600 605

Ile Glu Glu Ala Lys Ser Asp Asp Val Tyr Gln Lys Met Asn Tyr Lys

610 615 620

Leu Leu Pro Gly Pro Asn Lys Met Leu Pro Lys Val Phe Phe Ser Lys
625 630 635 640
Lys Ser Ile Asp Phe Tyr Ala Pro Gly Glu Glu Leu Leu Lys Asn Tyr
645 650 655
Lys Asn Gly Thr His Lys Lys Gly Glu Asn Phe Asn Leu Gln His Cys
660 665 670
His Glu Leu Ile Asp Phe Phe Lys Arg Ser Ile Asn Lys His Glu Asp

675 680 685
Trp Ser Gln Phe Asn Phe Lys Phe Ser Asp Thr Ser Glu Tyr Glu Asp
690 695 700
Thr Ser Phe Phe Phe Lys Glu Val Ser Gln Gln Gly Tyr Ser Ile Thr
705 710 715 720
Phe Lys Asn Ile Asp Arg Glu Thr Ile Glu Lys Phe Val Asp Glu Gly
725 730 735
Lys Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Pro Lys Ser

740 745 750
Lys Gly Arg Pro Asn Leu His Thr Leu Tyr Trp Lys Met Leu Phe Asp
755 760 765
Glu Arg Asn Leu Ala Asn Thr Val Tyr Gln Leu Asn Gly Glu Ala Glu
770 775 780
Val Phe Tyr Arg Lys Lys Ser Ile Ser Glu Lys Asp Arg Val Val His
785 790 795 800
Arg Ala Asp Glu Pro Ile Gly Leu Lys Asn Ser Glu Asn Ser Ala Gln

805 810 815
Lys Ser Leu Phe Pro Tyr Asp Ile Val Lys Asp Arg Arg Phe Thr Val
820 825 830
Asp Lys Phe Gln Phe His Val Pro Ile Thr Leu Asn Phe Lys Ser Glu
835 840 845
Gly Asn Glu Arg Leu Asn Ile Ser Val Asn Lys Phe Leu Lys Asp Asn
850 855 860
Pro Asp Val Asn Ile Ile Gly Leu Asp Arg Gly Glu Arg His Leu Ile

865 870 875 880

Tyr Leu Thr Leu Ile Asn Gln Lys Gly Glu Ile Leu His Gln Glu Ser

885 890 895

Leu Asn Glu Val Met Gly Val Asn Tyr Gln Gln Lys Leu His Arg Val

900 905 910

Glu Lys Asp Arg Thr Glu Glu Arg Arg Asn Trp Asp Arg Ile Glu Asn

915 920 925

Ile Lys Glu Leu Lys Ser Gly Tyr Leu Ser Gln Val Val His Lys Ile

930 935 940

Ser Gln Leu Met Val Glu Tyr Asn Ala Ile Val Val Met Glu Asp Leu

945 950 955 960

Asn Phe Gly Phe Lys Arg Gly Arg Ile Lys Val Glu Lys Gln Val Tyr

965 970 975

Gln Lys Phe Glu Lys Thr Leu Ile Asp Lys Leu Asn Tyr Leu Val Phe

980 985 990

Lys Asp Arg Glu Pro Glu Glu Pro Ala Gly Val Leu Asn Ala Leu Gln

995 1000 1005

Leu Thr Asn Lys Phe Glu Ser Phe Lys Lys Leu Gly Lys Gln Cys

1010 1015 1020

Gly Phe Leu Phe Tyr Val Thr Ser Asp Tyr Thr Ser Lys Ile Asp

1025 1030 1035

Pro Ala Thr Gly Phe Val Asn Leu Leu Tyr Pro Lys Tyr Glu Ser

1040 1045 1050

Val Glu Lys Ser Gln Asn Phe Phe Arg Lys Phe Asp Asn Ile Cys

1055 1060 1065

Phe Asn Ser Gly Ala Gly Tyr Phe Glu Phe Asp Phe Asp Tyr Ser

1070 1075 1080

Asn Phe Thr Asp Arg Ala Asp Gly Thr Arg Thr Arg Trp Lys Val

1085 1090 1095

Cys Thr Val Gly Asn Glu Arg Phe Gly Tyr Asn Pro Lys Thr Lys

1100 1105 1110

Ala Ser Glu Thr Val Asn Val Thr Glu Ser Leu Lys Glu Leu Leu

1115 1120 1125

Leu Gln His Glu Ile Ala Phe Glu Asn Gly Glu Ser Leu Val Glu

1130 1135 1140

Ser Ile Ser Lys Asn Thr Thr Lys Tyr Phe His Lys Ser Leu Leu

1145 1150 1155

Asn Phe Leu Arg Leu Thr Leu Thr Leu Arg His Ser Lys Thr Gly

1160 1165 1170

Thr Asp Ile Asp Tyr Ile Leu Ser Pro Val Ala Asn Glu Glu Gly

1175 1180 1185

Val Phe Phe Asp Ser Arg Asn Ala Ser Asp Lys Met Pro Lys Asp

1190 1195 1200

Ala Asp Ala Asn Gly Ala Tyr Asn Val Ala Leu Lys Gly Leu Met

1205 1210 1215

Val Leu Glu Arg Ile Asn Ala Ala Glu Asp Leu Ser Gln Phe Lys

1220 1225 1230

Phe Lys Asp Met Ser Ile Lys Asn Lys Asp Trp Leu Lys Phe Val

1235 1240 1245

Gln Asp Arg Gln Gly

1250

<210> 76

<211> 1271

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 76

Met Lys Asn Leu Ala Asn Phe Thr Asn Leu Tyr Ser Leu Gln Lys Thr

1 5 10 15

Leu Arg Phe Glu Leu Lys Pro Ile Gly Lys Thr Leu Asp Trp Ile Ile

20 25 30

Lys Lys Asp Leu Leu Lys Gln Asp Glu Ile Leu Ala Glu Asp Tyr Lys

35 40 45

Ile Val Lys Lys Ile Ile Asp Arg Tyr His Lys Asp Phe Ile Asp Leu

50 55 60

Ala Phe Glu Ser Ala Tyr Leu Gln Lys Lys Ser Ser Asp Ser Phe Thr

65 70 75 80

Ala Ile Met Glu Ala Ser Ile Gln Ser Tyr Ser Glu Leu Tyr Phe Ile

85 90 95

Lys Glu Lys Ser Asp Arg Asp Lys Lys Ala Met Glu Glu Ile Ser Gly

100 105 110

Ile Met Arg Lys Glu Ile Val Glu Cys Phe Thr Gly Lys Tyr Ser Glu

115 120 125

Val Val Lys Lys Lys Phe Gly Asn Leu Phe Lys Lys Glu Leu Ile Lys

130 135 140

Glu Asp Leu Leu Asn Phe Cys Glu Pro Asp Glu Leu Pro Ile Ile Gln

145 150 155 160

Lys Phe Ala Asp Phe Thr Thr Tyr Phe Thr Gly Phe His Glu Asn Arg

165 170 175

Glu Asn Met Tyr Ser Asn Glu Glu Lys Ala Thr Ala Ile Ala Asn Arg

180 185 190

Leu Ile Arg Glu Asn Leu Pro Arg Tyr Leu Asp Asn Leu Arg Ile Ile

195 200 205

Arg Ser Ile Gln Gly Arg Tyr Lys Asp Phe Gly Trp Lys Asp Leu Glu

210 215 220

Ser Asn Leu Lys Arg Ile Asp Lys Asn Leu Gln Tyr Ser Asp Phe Leu

225 230 235 240

Thr Glu Asn Gly Phe Val Tyr Thr Phe Ser Gln Lys Gly Ile Asp Arg

245 250 255

Tyr Asn Leu Ile Leu Gly Gly Gln Ser Val Glu Ser Gly Glu Lys Ile

260 265 270

Gln Gly Leu Asn Glu Leu Ile Asn Leu Tyr Arg Gln Lys Asn Gln Leu

275 280 285

Asp Arg Arg Gln Leu Pro Asn Leu Lys Glu Leu Tyr Lys Gln Ile Leu

290 295 300

Ser Asp Arg Thr Arg His Ser Phe Val Pro Glu Lys Phe Ser Ser Asp

305 310 315 320

Lys Ala Leu Leu Arg Ser Leu Leu Asp Phe His Lys Glu Val Ile Gln

325 330 335

Asn Lys Asn Leu Phe Glu Glu Lys Gln Val Ser Leu Leu Gln Ala Ile

340 345 350

Arg Glu Thr Leu Thr Asp Leu Lys Ser Phe Asp Leu Asp Arg Ile Tyr

355 360 365

Leu Thr Asn Asp Thr Ser Leu Thr Gln Ile Ser Asn Phe Val Phe Gly

370 375 380

Asp Trp Ser Lys Val Lys Thr Ile Leu Ala Ile Tyr Phe Asp Glu Asn

385 390 395 400

Ile Ala Asn Pro Lys Asp Arg Gln Arg Gln Ser Asn Ser Tyr Leu Lys

405 410 415

Ala Lys Glu Asn Trp Leu Lys Lys Asn Tyr Tyr Ser Ile His Glu Leu

420 425 430

Asn Glu Ala Ile Ser Val Tyr Gly Lys His Ser Asp Glu Glu Leu Pro

435 440 445

Asn Thr Lys Ile Glu Asp Tyr Phe Ser Gly Leu Gln Thr Lys Asp Glu

450 455 460

Thr Lys Lys Pro Ile Asp Val Leu Asp Ala Ile Val Ser Lys Tyr Ala

465 470 475 480

Asp Leu Glu Ser Leu Leu Thr Lys Glu Tyr Pro Glu Asp Lys Asn Leu

485 490 495

Lys Ser Asp Lys Gly Ser Ile Glu Lys Ile Lys Asn Tyr Leu Asp Ser

500 505 510

Ile Lys Leu Leu Gln Asn Phe Leu Lys Pro Leu Lys Pro Lys Lys Val

515 520 525

Gln Asp Glu Lys Asp Leu Gly Phe Tyr Asn Asp Leu Glu Leu Tyr Leu

530 535 540

Glu Ser Leu Glu Ser Ala Asn Ser Leu Tyr Asn Lys Val Arg Asn Tyr

545 550 555 560

Leu Thr Gly Lys Glu Tyr Ser Asp Glu Lys Ile Lys Leu Asn Phe Lys

565 570 575

Asn Ser Thr Leu Leu Asp Gly Trp Asp Glu Asn Lys Glu Thr Ser Asn

580 585 590

Leu Ser Val Ile Phe Arg Asp Thr Asn Asn Tyr Tyr Leu Gly Ile Leu

595 600 605

Asp Lys Gln Asn Asn Arg Ile Phe Glu Ser Ile Pro Glu Ile Gln Ser

610 615 620

Gly Glu Glu Thr Ile Gln Lys Met Val Tyr Lys Leu Leu Pro Gly Ala

625 630 635 640

Asn Asn Met Leu Pro Lys Val Phe Phe Ser Glu Lys Gly Leu Leu Lys

645 650 655

Phe Asn Pro Ser Asp Glu Ile Thr Ser Leu Tyr Ser Glu Gly Arg Phe

660 665 670

Lys Lys Gly Asp Lys Phe Ser Ile Asn Ser Leu His Thr Leu Ile Asp

675 680 685

Phe Tyr Lys Lys Ser Leu Ala Val His Glu Asp Trp Ser Val Phe Asn

690 695 700

Phe Lys Phe Asp Glu Thr Ser His Tyr Glu Asp Ile Ser Gln Phe Tyr

705 710 715 720

Arg Gln Val Glu Ser Gln Gly Tyr Lys Ile Thr Phe Lys Pro Ile Ser

725 730 735

Lys Lys Tyr Ile Asp Thr Leu Val Glu Asp Gly Lys Leu Tyr Leu Phe

740 745 750

Gln Ile Tyr Asn Lys Asp Phe Ser Gln Asn Lys Lys Gly Gly Gly Lys

755 760 765

Pro Asn Leu His Thr Ile Tyr Phe Lys Ser Leu Phe Glu Lys Glu Asn

770 775 780

Leu Lys Asp Val Ile Val Lys Leu Asn Gly Gln Ala Glu Val Phe Phe

785 790 795 800

Arg Lys Lys Ser Ile His Tyr Asp Glu Asn Ile Thr Arg Tyr Gly His

805 810 815

His Ser Glu Leu Leu Lys Gly Arg Phe Ser Tyr Pro Ile Leu Lys Asp

820 825 830

Lys Arg Phe Thr Glu Asp Lys Phe Gln Phe His Phe Pro Ile Thr Leu

835 840 845

Asn Phe Lys Ser Gly Glu Ile Lys Gln Phe Asn Ala Arg Val Asn Ser

850 855 860

Tyr Leu Lys His Asn Lys Asp Val Lys Ile Ile Gly Ile Asp Arg Gly

865 870 875 880

Glu Arg His Leu Leu Tyr Leu Ser Leu Ile Asp Gln Asp Gly Lys Ile

885 890 895

Leu Arg Gln Glu Ser Leu Asn Leu Ile Lys Asn Asp Gln Asn Phe Lys

900 905 910

Ala Ile Asn Tyr Gln Glu Lys Leu His Lys Lys Glu Ile Glu Arg Asp

915 920 925

Gln Ala Arg Lys Ser Trp Gly Ser Ile Glu Asn Ile Lys Glu Leu Lys

930 935 940

Glu Gly Tyr Leu Ser Gln Val Val His Thr Ile Ser Lys Leu Met Val

945 950 955 960

Glu His Asn Ala Ile Val Val Leu Glu Asp Leu Asn Phe Gly Phe Lys

965 970 975

Arg Gly Arg Gln Lys Val Glu Arg Gln Val Tyr Gln Lys Phe Glu Lys

980 985 990

Met Leu Ile Glu Lys Leu Asn Phe Leu Val Phe Lys Asp Lys Glu Met

995 1000 1005

Asp Glu Pro Gly Gly Ile Leu Lys Ala Tyr Gln Leu Thr Asp Asn

1010 1015 1020

Phe Val Ser Phe Glu Lys Met Gly Lys Gln Thr Gly Phe Val Phe
1025 1030 1035
Tyr Val Pro Ala Trp Asn Thr Ser Lys Ile Asp Pro Lys Thr Gly
1040 1045 1050
Phe Val Asn Phe Leu His Leu Asn Tyr Glu Asn Val Asn Gln Ala

1055 1060 1065
Lys Glu Leu Ile Gly Lys Phe Asp Gln Ile Arg Tyr Asn Gln Asp
1070 1075 1080
Arg Asp Trp Phe Glu Phe Gln Val Thr Thr Asp Gln Phe Phe Thr
1085 1090 1095
Lys Glu Asn Ala Pro Asp Thr Arg Thr Trp Ile Ile Cys Ser Thr
1100 1105 1110
Pro Thr Lys Arg Phe Tyr Ser Lys Arg Thr Val Asn Gly Ser Val

1115 1120 1125
Ser Thr Ile Glu Ile Asp Val Asn Gln Lys Leu Lys Glu Leu Phe
1130 1135 1140
Asn Asp Cys Asn Tyr Gln Asp Gly Glu Asp Leu Val Asp Arg Ile
1145 1150 1155
Leu Glu Lys Asp Ser Lys Asp Phe Phe Ser Lys Leu Ile Ala Tyr
1160 1165 1170
Leu Arg Ile Leu Thr Ser Leu Arg Gln Asn Asn Gly Glu Gln Gly

1175 1180 1185
Phe Glu Glu Arg Asp Phe Ile Leu Ser Pro Val Val Gly Ser Asp
1190 1195 1200
Gly Lys Phe Phe Asn Ser Leu Asp Ala Ser Ser Gln Glu Pro Lys
1205 1210 1215
Asp Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu Lys Gly Leu
1220 1225 1230
Met Asn Leu His Val Ile Asn Glu Thr Asp Asp Glu Ser Leu Gly

1235 1240 1245
Lys Pro Ser Trp Lys Ile Ser Asn Lys Asp Trp Leu Asn Phe Val

1250 1255 1260

Trp Gln Arg Pro Ser Leu Lys Ala

1265 1270

<210> 77

<211> 816

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 77

Met Asn Leu Ile Glu Asn Glu Thr Lys Ser Glu Glu Ile Lys Ser Lys

1 5 10 15

Leu Asp Ser Ile Met Glu Ile Met His Trp Thr Lys Met Phe Ile Ile

20 25 30

Glu Glu Glu Ile Glu Lys Asp Val Asn Phe Tyr Asn Glu Ile Glu Glu

35 40 45

Ile Tyr Asp Glu Leu Gln Pro Leu Val Thr Ile Tyr Asn Arg Ile Arg

50 55 60

Asn Tyr Val Thr Gln Lys Pro Tyr Ser Glu Glu Lys Ile Lys Leu Asn

65 70 75 80

Phe Gly Ile Pro Thr Leu Ala Asn Gly Trp Ser Lys Thr Lys Glu Tyr

85 90 95

Asp Asn Asn Ala Ile Ile Met Ile Arg Asp Gly Lys Tyr Tyr Leu Gly

100 105 110

Ile Phe Asn Ala Lys Asn Lys Pro Asp Lys Lys Ile Met Glu Gly His

115 120 125

Gln Ser Glu Glu Asn Gly Asp Tyr Lys Lys Met Ile Tyr Arg Leu Leu

130 135 140

Pro Gly Pro Asn Lys Met Leu Pro Lys Val Phe Met Ser Lys Thr Gly

145 150 155 160

Ile Ala Glu Tyr Lys Pro Ser Gln Tyr Ile Leu Glu Cys Tyr Glu Gln

165 170 175

Asn Lys His Ile Lys Ser Asp Lys Asn Phe Asp Ile Lys Phe Cys Arg
180 185 190
Asp Leu Ile Asp Phe Phe Lys Thr Ser Ile Asn Arg His Pro Glu Trp
195 200 205

Ser Lys Phe Asn Phe Lys Phe Ser Glu Thr Ser Glu Tyr Glu Asp Ile
210 215 220
Ser Thr Phe Tyr Arg Glu Val Glu Lys Gln Gly Tyr Lys Ile Glu Trp
225 230 235 240
Thr Tyr Ile Ser Glu Lys Glu Ile Lys Glu Leu Asp Glu Asn Gly Gln
245 250 255
Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Glu Lys Ser Lys
260 265 270

Gly Lys Glu Asn Leu His Thr Met Tyr Leu Lys Asn Leu Phe Ser Glu
275 280 285
Glu Asn Leu Lys Asn Ile Val Leu Lys Leu Asn Gly Glu Ala Glu Val
290 295 300
Phe Phe Arg Lys Ser Ser Ile Lys Lys Pro Ile Ile His Lys Lys Gly
305 310 315 320
Ser Val Leu Val Asn Lys Thr Tyr Asn Glu Asn Gly Glu Arg Lys Ser
325 330 335

Ile Pro Glu Glu Gln Tyr Thr Glu Ile Tyr Lys Tyr Leu Asn Ser Ile
340 345 350
Gly Thr Asn Glu Leu Ser Glu Lys Ser Lys Lys Leu Met Glu Glu Gly
355 360 365
Lys Val Glu Tyr Tyr Lys Ala Asn Tyr Asp Ile Val Lys Asp Tyr Arg
370 375 380
Tyr Ser Val Asp Lys Phe Phe Ile His Leu Pro Met Thr Ile Asn Phe
385 390 395 400

Lys Ala Ala Gly Phe Ser Pro Ile Asn Asn Ile Ala Leu Lys Ser Ile
405 410 415
Ala Leu Lys Glu Asp Met His Ile Ile Gly Ile Asp Arg Gly Glu Arg

420 425 430

Asn Leu Ile Tyr Val Ser Val Ile Asp Thr Lys Gly Asn Ile Val Glu

435 440 445

Gln Arg Asn Phe Asn Ile Val Asn Gly Ile Asp Tyr Lys Glu Lys Leu

450 455 460

Lys Gln Lys Glu Leu Asp Arg Asp Asn Ala Arg Lys Asn Trp Lys Glu

465 470 475 480

Ile Gly Lys Ile Lys Asp Leu Lys Glu Gly Tyr Leu Ser Leu Val Val

485 490 495

His Glu Ile Ala Lys Leu Val Val Lys Tyr Asn Ala Ile Ile Thr Met

500 505 510

Glu Asp Leu Asn Gln Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Arg

515 520 525

Gln Val Tyr Gln Lys Phe Glu Thr Met Leu Ile Asn Lys Leu Asn Tyr

530 535 540

Leu Val Asp Lys Asp Leu Ala Val Asp Gln Glu Gly Gly Leu Leu Arg

545 550 555 560

Gly Tyr Gln Leu Thr Tyr Ile Pro Glu Ser Leu Lys Val Leu Gly Arg

565 570 575

Gln Cys Gly Tyr Ile Phe Tyr Val Pro Val Ala Tyr Thr Ser Lys Ile

580 585 590

Asp Pro Thr Thr Gly Phe Val Ala Ile Phe Asn Tyr Lys Gly Met Thr

595 600 605

Asp Lys Asp Phe Val Thr Ser Phe Asp Ser Ile Lys Tyr Asp Asp Glu

610 615 620

Arg Gly Leu Phe Ala Phe Glu Phe Asp Tyr Glu Asn Phe Val Thr His

625 630 635 640

Lys Val Glu Met Ala Arg Asn Lys Trp Thr Val Tyr Thr Tyr Gly Glu

645 650 655

Arg Ile Lys Arg Lys Phe Lys Asn Gly Leu Trp Asp Thr Ala Glu Lys

660 665 670

Val Asp Leu Thr Tyr Gln Met Arg Ser Ile Leu Glu Lys Tyr Glu Ile
675 680 685

Glu Tyr Asn Lys Gly Gln Asp Ile Leu Glu Gln Ile Glu Glu Leu Asp
690 695 700

Glu Lys Ala Gln Asn Gly Ile Cys Lys Glu Ile Lys Tyr Leu Val Lys
705 710 715 720

Asp Ile Val Gln Met Arg Asn Ser Leu Pro Asp Asn Ala Val Glu Asp
725 730 735

Tyr Asp Ala Ile Ile Ser Pro Val Ile Asn Asn Asn Gly Glu Phe Phe
740 745 750

Asp Ser Thr Arg Gly Asp Glu Asp Lys Pro Leu Asp Ala Asp Ala Asn
755 760 765

Gly Ala Tyr Cys Ile Ala Leu Lys Gly Leu Tyr Glu Val Met Gln Ile
770 775 780

Lys Lys Asn Trp Asn Glu Glu Thr Glu Phe Pro Arg Lys Glu Leu Lys
785 790 795 800

Ile Arg His Gln Asp Trp Phe Asp Phe Ile Gln Asn Lys Arg Tyr Leu
805 810 815

<210> 78

<211> 869

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas12 sequence

<400> 78

Met Glu Asn Arg Tyr Gln Val Leu Gln Gly Leu Thr Ala Ala Gln Lys
1 5 10 15

Lys Ala Ala Ala Ala Ala Lys Lys Arg Ser Ser Phe Ser Ile Val Glu
20 25 30

Leu Asn Ala Ala Thr Arg Ser Arg Val Pro Asp Glu Lys Tyr Val Pro
35 40 45

Val Gln Asn Tyr Phe Ser Ala Met Gly Lys Val Cys Ser Gln Gly Glu

50 55 60

Pro Lys Arg Glu Asn Phe Val Thr Arg Ile Cys Ala Ala Tyr Gln Glu
65 70 75 80

Leu Glu Glu Tyr Ile Pro Ser Ile Arg Lys Ser Leu Leu Gln Glu Lys
85 90 95

Arg Ala Thr Glu Leu Ile Lys Asn Tyr Leu Asp Ala Val Asn Asp Leu
100 105 110

Leu Arg Phe Ile Lys Pro Leu Leu Gly Arg Gly Asn Glu Thr Asp Lys
115 120 125

Asp Ala Asn Phe Tyr Gly Glu Phe Ser Phe Leu Thr Asp Cys Leu Phe
130 135 140

Ala Ile Val Pro Leu Tyr Asn Glu Val Arg Asn Tyr Leu Thr Gln Lys
145 150 155 160

Pro Tyr Ser Thr Glu Lys Phe Lys Leu Asn Phe Arg Gly Ser Thr Leu
165 170 175

Leu Asn Gly Trp Asp Lys Asn Lys Glu Arg Asp Asn Leu Gly Val Ile
180 185 190

Leu Arg Lys Glu Gly Lys Tyr Phe Leu Ala Ile Met Asn Lys Lys His
195 200 205

Asn Thr Leu Phe Thr Glu Gly Lys Leu Gln Gln His Thr Gly Gly Glu
210 215 220

Cys Tyr Gln Lys Met Glu Tyr Lys Leu Ile Pro Gly Ser Lys Met Leu
225 230 235 240

Pro Lys Val Phe Phe Ser Lys Lys Gly Ile Ser Thr Phe Gln Pro Ser
245 250 255

Glu Glu Leu Leu Leu Asn Tyr Arg Ile Gly Thr Tyr Lys Lys Gly Glu
260 265 270

Lys Phe Asn Leu Glu His Leu His Lys Leu Ile Asp Phe Tyr Lys His
275 280 285

Ser Ile Ala Val His Glu Asp Trp Ser Lys Phe Asp Phe His Phe Ser
290 295 300

Asp Thr Ser Ser Tyr Arg Asp Ile Ser Gly Phe Tyr Lys Glu Val Glu
305 310 315 320
Gln Gln Gly Tyr Lys Leu Thr Phe Arg Asn Val Ser Val Ser Tyr Ile
325 330 335

Asn Arg Leu Val Glu Glu Gly Lys Leu Tyr Leu Phe Gln Ile Tyr Asn
340 345 350
Lys Asp Phe Ser Glu Tyr Ser Lys Gly Thr Pro Asn Leu His Thr Leu
355 360 365
Tyr Trp Lys Met Leu Phe Asp Pro Glu Asn Leu Lys Asp Val Val Tyr
370 375 380
Lys Leu Ser Gly Glu Ala Glu Val Phe Phe Arg Lys Lys Ser Leu Asp
385 390 395 400

Val Ser His Pro Thr His Pro Lys Asn Glu Pro Ile Glu Lys Lys Asn
405 410 415
Ile Asn Asn Lys Gly Glu Lys Ser Leu Phe Ser Tyr Asp Leu Ile Lys
420 425 430
Asp Arg Arg Phe Thr Val Asp Lys Phe Gln Phe His Val Pro Ile Thr
435 440 445
Met Asn Phe Lys Gly Glu Gln Gly Asp Arg Val Asn Gln Met Val Gln
450 455 460

Ser Tyr Val Arg Asn Asn Lys Gly Leu Asn Val Ile Gly Ile Asp Arg
465 470 475 480
Gly Glu Arg Asn Leu Leu Tyr Leu Val Val Ile Asn Glu His Gly Glu
485 490 495
Ile Leu Glu Gln Phe Ser Leu Asn Glu Ile Arg Asn Ala Tyr Asn Gly
500 505 510
Lys Glu His Lys Ile Asp Tyr His Thr Leu Leu Glu Glu Arg Ser Lys
515 520 525

Lys Arg Gln Asp Ala Arg Gln Ser Trp Gln Thr Ile Glu Gly Ile Lys
530 535 540
Asp Leu Lys Thr Gly Tyr Leu Ser Gln Val Ile His Val Ile Thr Gln

545 550 555 560

Leu Met Val Lys Tyr Asn Ala Ile Val Val Leu Glu Asp Leu Asn Phe

565 570 575

Gly Phe Lys Ser Ser Arg Gln Lys Phe Glu Gln Ser Val Tyr Gln Gln

580 585 590

Phe Glu Arg Lys Leu Ile Asp Lys Leu Asn Phe Leu Val Asn Lys Lys

595 600 605

Ala Ala Pro Asn Glu Val Gly Gly Leu Leu Asn Ala Tyr Gln Leu Thr

610 615 620

Ala Pro Leu Gly Asn Ser Arg Lys Met Gly Lys Gln Asn Gly Phe Leu

625 630 635 640

Phe Tyr Val Pro Ala Trp His Thr Ser Lys Ile Asp Pro Arg Thr Gly

645 650 655

Phe Val Asn Leu Leu Asp Thr Arg Tyr Glu Asn Val Ala Lys Ala Lys

660 665 670

Glu Phe Phe Ala Lys Phe Ala Ser Ile Thr Tyr Asn Pro Glu Lys Lys

675 680 685

Trp Phe Glu Phe Ala Phe Asp Tyr Lys Ala Phe Gly Asn Arg Ala Asp

690 695 700

Gly Ser Arg Thr Lys Trp Thr Ile Cys Ser Tyr Gly Glu Arg Ile Glu

705 710 715 720

Thr Phe Arg Asn Pro Glu Asn Asn Asn Gln Trp Asp Thr Lys Ser Val

725 730 735

Pro Leu Thr Glu Arg Leu Thr Glu Leu Phe Ser Lys Tyr Gly Ile Asp

740 745 750

Tyr Thr Thr Asn Leu Lys Glu Gln Ile Leu Asn Gln Thr Asp Lys Ala

755 760 765

Phe Phe Val Glu Leu Leu Gly Ala Leu Arg Leu Thr Leu Gln Leu Arg

770 775 780

Asn Ser Arg Lys Ser Thr Gly Glu Asp Phe Leu Phe Ser Pro Val Ala

785 790 795 800

Asp Glu Asn Gly Cys Phe Phe Asp Ser Arg Glu Ala Asn Asp Asn Glu
805 810 815

Pro Lys Asp Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu Lys Gly
820 825 830

Leu Trp Val Leu Asp Thr Ile Arg Asn Thr Glu Glu Gly Lys Asn Pro
835 840 845

Lys Leu Ala Ile Thr Asn Lys Glu Trp Leu Ser Phe Ala Gln Ala Lys
850 855 860

Pro Phe Ala His Glu
865

<210> 79

<211> 884

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas12 sequence

<400> 79

Met Ser Asp Ser Tyr Asp Glu Leu Thr Lys Ala Gln Lys Glu Lys Gln
1 5 10 15

Glu Lys Arg Lys His Val Ala Leu Thr Glu Val Val Ala Ala Leu Glu
20 25 30

Lys Tyr Thr Ile Ala Leu Asp Asn Gly His Glu His Lys Asn Ala Val
35 40 45

Asn Thr Phe Lys Asn Tyr Phe Gln Asn Tyr Phe Phe His Phe Asp Thr
50 55 60

Asp Lys Lys Lys Thr Ala Lys Thr Leu Asp Cys Gln Ile Lys Asp Glu
65 70 75 80

Tyr Asn Gly Leu Lys Gly Ile Leu Asn Thr Pro Trp Asp Lys Asn Lys
85 90 95

Lys Leu Gln Gln Asp Lys Lys Leu Val Gln Gln Ile Lys Ser Phe Leu
100 105 110

Asp Ser Ile Gln Glu Leu Leu Trp Phe Ile Lys Pro Leu Val Leu Thr

115 120 125

Asp Asn Thr Leu Glu Lys Asp Glu Arg Phe Tyr Gly Glu Phe Met Pro

130 135 140

Leu Tyr Asp Glu Ile Ser Asn Ile Ile Lys Leu Tyr Asn Lys Ile Arg

145 150 155 160

Asn Tyr Leu Thr Lys Lys Pro Tyr Ser Ile Glu Lys Tyr Lys Leu Asn

165 170 175

Phe Glu Asn Gly Ser Leu Leu Ser Gly Trp Asp Val Asn Lys Glu Lys

180 185 190

Asp Asn Thr Ser Val Leu Leu Cys Lys Asp Asn Gln Tyr Tyr Leu Ala

195 200 205

Ile Met His Ile Asp His Asn Lys Val Phe Glu Leu Asp Glu Leu Ile

210 215 220

Lys His Ala Gly Lys Gly Tyr Gln Lys Ile Asn Tyr Lys Leu Leu Pro

225 230 235 240

Gly Ala Asn Lys Met Leu Pro Lys Val Phe Phe Ser Gly Lys Asn Ile

245 250 255

Ser Tyr Tyr Asp Pro Ser Lys Glu Ile Leu Lys Ile Arg Asn Tyr Gly

260 265 270

Thr His Thr Lys Asn Gly Asp Pro Gln Pro Gly Phe Ser Lys Arg Asp

275 280 285

Phe Ser Val Asp Asp Cys Arg Lys Met Ile Asp Phe Phe Lys Asn Ser

290 295 300

Ile Ala Lys His Glu Asp Trp Lys Asn Phe Asp Phe Lys Phe Gln Pro

305 310 315 320

Thr Lys Asn Tyr Asn Ser Ile Asp Glu Phe Tyr Arg Glu Val Glu Glu

325 330 335

Gln Gly Tyr Lys Ile Thr Tyr Ser Asn Val Ser Glu Asp Tyr Ile Asp

340 345 350

Ser Leu Val Glu Tyr Gly Lys Ile Tyr Leu Phe His Ile Tyr Asn Lys

355 360 365

Asp Phe Ser Asp Lys Arg Asp Glu Ser Lys Lys His Thr Asp Asn Met
370 375 380
His Thr Leu Tyr Trp Lys Ala Leu Phe Asp Ala Lys Asn Leu Lys Asp
385 390 395 400
Val Val Tyr Lys Leu Asn Gly Glu Ala Glu Ile Phe Tyr Arg Lys Lys
405 410 415

Ser Ile Asp Ile Lys Lys Pro Thr His Glu Lys Gly Lys Pro Ile Asp
420 425 430
Asn Lys Asn Pro Asn Ala Arg Lys Lys Thr Ser Val Phe Lys Tyr Asp
435 440 445
Leu Ile Lys Asp Lys Arg Phe Thr Val Asp Lys Phe Phe Phe His Val
450 455 460
Pro Ile Thr Leu Asn Phe Lys Ser Lys Ser Gly Tyr Leu Ser Asn Asp
465 470 475 480

Asp Val Asn Ala Ala Ile Lys Lys Asn Asn Asp Ile Lys Ile Ile Gly
485 490 495
Leu Asp Arg Gly Glu Arg Asn Leu Ile Tyr Leu Ser Leu Ile Asn Ser
500 505 510
Lys Gly Glu Ile Ala Tyr Gln Glu Ser Leu Asn Val Val Ser Thr Asp
515 520 525
Lys Gly Phe Asp Val Asn Tyr His Lys Leu Leu Asp Asp Lys Glu Gly
530 535 540

Asn Arg Asp Glu Ala Arg Lys Asn Trp Asp Lys Ile Glu Asn Ile Lys
545 550 555 560
Glu Leu Lys Ala Gly Tyr Leu Ser Gln Val Ile His Lys Ile Ala Lys
565 570 575
Leu Met Ile Asp Asn Asn Ala Ile Val Val Met Glu Asp Leu Asn Phe
580 585 590
Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Lys Gln Ile Tyr Gln Lys
595 600 605

Phe Glu Lys Met Leu Ile Asp Lys Leu Asn Tyr Leu Val Phe Lys Asn

610 615 620

Val His Pro Glu Gln Ala Gly Gly Leu Tyr Lys Ala Tyr Gln Leu Thr
625 630 635 640

Ala Gln Phe Glu Ser Phe Lys Lys Leu Gly Lys Gln Ser Gly Phe Leu
645 650 655

Phe Tyr Ile Pro Ala Trp Asn Thr Ser Lys Ile Asp Pro Thr Ala Gly
660 665 670

Phe Val Asp Phe Leu Lys Pro Arg Tyr Glu Ser Val Thr Gln Ala Lys
675 680 685

Ser Phe Leu Gln Arg Phe Asp Lys Ile Asn Tyr Asn Lys Thr Lys Asp
690 695 700

Tyr Phe Glu Phe Ala Phe Asp Tyr Lys Asn Phe Thr Asp Lys Ala Asn
705 710 715 720

Asp Thr Lys Thr Asp Trp Val Val Cys Thr Tyr Gly Thr Glu Arg Tyr
725 730 735

Tyr Tyr Asp Val Arg Thr Lys Thr Thr Gln Lys Ile Asp Ile Thr Ala
740 745 750

Glu Leu Lys Lys Leu Leu Glu Lys Ser Glu Ile Asn Tyr Leu Asn Gly
755 760 765

Lys Asp Ile Lys Glu Leu Ile Ile Ala Val Asp Ser Lys Glu Phe His
770 775 780

Ser Ala Leu Leu Lys Tyr Leu Ala Ile Val Leu Ala Leu Arg Tyr Ser
785 790 795 800

Asp Ser Gln Ser Gly Arg Asp Phe Ile Leu Ser Pro Val Ala Asn Glu
805 810 815

Gln Gly His Phe Phe Asn Ser Asp Lys Thr Asp Asp Thr Leu Pro Lys
820 825 830

Asp Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu Lys Gly Leu Trp
835 840 845

Ala Ile Asn Gln Ile Arg Lys Thr Lys Asn Gly Asp Lys Leu Lys Leu
850 855 860

Thr Ile Ser Asn Lys Asp Trp Leu Asn Phe Val Gln Lys Lys Glu Tyr
865 870 875 880
Arg Lys Gly Val

<210> 80
<211> 1250
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 80
Met Gln Thr Leu Phe Glu Asn Phe Thr Asn Gln Tyr Pro Val Ser Lys
1 5 10 15
Thr Leu Arg Phe Glu Leu Ile Pro Gln Gly Lys Thr Lys Asp Phe Ile
20 25 30

Glu Gln Lys Gly Leu Leu Lys Lys Asp Glu Asp Arg Ala Glu Lys Tyr
35 40 45
Lys Lys Val Lys Asn Ile Ile Asp Glu Tyr His Lys Asp Phe Ile Glu
50 55 60
Lys Ser Leu Asn Gly Leu Lys Leu Asp Gly Leu Glu Lys Tyr Lys Thr
65 70 75 80
Leu Tyr Leu Lys Gln Glu Lys Asp Asp Lys Asp Lys Lys Ala Phe Asp
85 90 95

Lys Glu Lys Glu Asn Leu Arg Lys Gln Ile Ala Asn Ala Phe Arg Asn
100 105 110
Asn Glu Lys Phe Lys Thr Leu Phe Ala Lys Glu Leu Ile Lys Asn Asp
115 120 125
Leu Met Ser Phe Ala Cys Glu Glu Asp Lys Lys Asn Val Lys Glu Phe
130 135 140
Glu Ala Phe Thr Thr Tyr Phe Thr Gly Phe His Gln Asn Arg Ala Asn
145 150 155 160

Met Tyr Val Ala Asp Glu Lys Arg Thr Ala Ile Ala Ser Arg Leu Ile

165 170 175

His Glu Asn Leu Pro Lys Phe Ile Asp Asn Ile Lys Ile Phe Glu Lys

180 185 190

Met Lys Lys Glu Ala Pro Glu Leu Leu Ser Pro Phe Asn Gln Thr Leu

195 200 205

Lys Asp Met Lys Asp Val Ile Lys Gly Thr Thr Leu Glu Glu Ile Phe

210 215 220

Ser Leu Asp Tyr Phe Asn Lys Thr Leu Thr Gln Ser Gly Ile Asp Ile

225 230 235 240

Tyr Asn Ser Val Ile Gly Gly Arg Thr Pro Glu Glu Gly Lys Thr Lys

245 250 255

Ile Lys Gly Leu Asn Glu Tyr Ile Asn Thr Asp Phe Asn Gln Lys Gln

260 265 270

Thr Asp Lys Lys Lys Arg Gln Pro Lys Phe Lys Gln Leu Tyr Lys Gln

275 280 285

Ile Leu Ser Asp Arg Gln Ser Leu Ser Phe Ile Ala Glu Ala Phe Lys

290 295 300

Asn Asp Ala Glu Ile Leu Glu Ala Ile Glu Lys Phe Tyr Val Asn Glu

305 310 315 320

Leu Leu His Phe Ser Asn Glu Gly Lys Ser Thr Asn Val Leu Asp Ala

325 330 335

Ile Lys Asn Ala Val Ser Asn Leu Glu Ser Phe Asn Leu Thr Lys Met

340 345 350

Tyr Phe Arg Ser Gly Thr Ser Leu Thr Asp Val Ser Arg Lys Val Phe

355 360 365

Gly Glu Trp Ser Ile Ile Asn Arg Ala Leu Asp Asn Tyr Tyr Ala Thr

370 375 380

Thr Tyr Pro Ile Lys Pro Arg Glu Lys Ser Glu Lys Tyr Glu Glu Arg

385 390 395 400

Lys Glu Lys Trp Leu Lys Gln Asp Phe Asn Val Arg Leu Ile Gln Thr

405 410 415

Ala Ile Asp Glu Tyr Asp Asn Glu Thr Val Lys Gly Lys Asn Ser Gly
420 425 430

Lys Val Ile Ala Asp Tyr Phe Ala Lys Phe Cys Asp Asp Lys Glu Thr
435 440 445

Asp Leu Ile Gln Lys Val Asn Glu Gly Tyr Ile Ala Val Lys Asp Leu
450 455 460

Leu Asn Thr Pro Tyr Pro Glu Asn Glu Lys Ile Gly Ser Asn Lys Asp
465 470 475 480

Gln Val Lys Gln Ile Lys Ala Phe Met Asp Ser Ile Met Asp Ile Met
485 490 495

His Phe Val Arg Pro Leu Ser Leu Lys Asp Thr Asp Lys Glu Lys Asp
500 505 510

Glu Thr Phe Tyr Ser Leu Phe Thr Pro Leu Tyr Asp His Leu Thr Gln
515 520 525

Thr Ile Ala Leu Tyr Asn Lys Val Arg Asn Tyr Leu Thr Gln Lys Pro
530 535 540

Tyr Ser Thr Glu Lys Ile Lys Leu Asn Phe Glu Asn Ser Thr Leu Leu
545 550 555 560

Gly Gly Trp Asp Leu Asn Lys Glu Thr Asp Asn Thr Ala Ile Ile Leu
565 570 575

Arg Lys Asp Asn Leu Tyr Tyr Leu Gly Ile Met Asp Lys Arg His Asn
580 585 590

Arg Ile Phe Arg Asn Val Pro Lys Ala Asp Lys Lys Asp Phe Cys Tyr
595 600 605

Glu Lys Met Val Tyr Lys Leu Leu Pro Gly Ala Asn Lys Met Leu Pro
610 615 620

Lys Val Phe Phe Ser Gln Ser Arg Ile Gln Glu Phe Thr Pro Ser Ala
625 630 635 640

Lys Leu Leu Glu Asn Tyr Ala Asn Glu Thr His Lys Lys Gly Asp Asn
645 650 655

Phe Asn Leu Asn His Cys His Lys Leu Ile Asp Phe Phe Lys Asp Ser

660 665 670

Ile Asn Lys His Glu Asp Trp Lys Asn Phe Asp Phe Arg Phe Ser Ala
675 680 685
Thr Ser Thr Tyr Ala Asp Leu Ser Gly Phe Tyr His Glu Val Glu His
690 695 700
Gln Gly Tyr Lys Ile Ser Phe Gln Ser Ile Ala Asp Ser Phe Ile Asp
705 710 715 720
Asp Leu Val Asn Glu Gly Lys Leu Tyr Leu Phe Gln Ile Tyr Asn Lys
725 730 735

Asp Phe Ser Pro Phe Ser Lys Gly Lys Pro Asn Leu His Thr Leu Tyr
740 745 750
Trp Lys Met Leu Phe Asp Glu Asn Asn Leu Lys Asp Val Val Tyr Lys
755 760 765
Leu Asn Gly Glu Ala Glu Val Phe Tyr Arg Lys Lys Ser Ile Ala Glu
770 775 780
Lys Asn Thr Thr Ile His Lys Ala Asn Glu Ser Ile Ile Asn Lys Asn
785 790 795 800

Pro Asp Asn Pro Lys Ala Thr Ser Thr Phe Asn Tyr Asp Ile Val Lys
805 810 815
Asp Lys Arg Tyr Thr Ile Asp Lys Phe Gln Phe His Ile Pro Ile Thr
820 825 830
Met Asn Phe Lys Ala Glu Gly Ile Phe Asn Met Asn Gln Arg Val Asn
835 840 845
Gln Phe Leu Lys Ala Asn Pro Asp Ile Asn Ile Ile Gly Ile Asp Arg
850 855 860

Gly Glu Arg His Leu Leu Tyr Tyr Ala Leu Ile Asn Gln Lys Gly Lys
865 870 875 880
Ile Leu Lys Gln Asp Thr Leu Asn Val Ile Ala Asn Glu Lys Gln Lys
885 890 895
Val Asp Tyr His Asn Leu Leu Asp Lys Lys Glu Gly Asp Arg Ala Thr
900 905 910

Ala Arg Gln Glu Trp Gly Val Ile Glu Thr Ile Lys Glu Leu Lys Glu
915 920 925

Gly Tyr Leu Ser Gln Val Ile His Lys Leu Thr Asp Leu Met Ile Glu
930 935 940
Asn Asn Ala Ile Ile Val Met Glu Asp Leu Asn Phe Gly Phe Lys Arg
945 950 955 960
Gly Arg Gln Lys Val Glu Lys Gln Val Tyr Gln Lys Phe Glu Lys Met
965 970 975
Leu Ile Asp Lys Leu Asn Tyr Leu Val Asp Lys Asn Lys Lys Ala Asn
980 985 990

Glu Leu Gly Gly Leu Leu Asn Ala Phe Gln Leu Ala Asn Lys Phe Glu
995 1000 1005
Ser Phe Gln Lys Met Gly Lys Gln Asn Gly Phe Ile Phe Tyr Val
1010 1015 1020
Pro Ala Trp Asn Thr Ser Lys Thr Asp Pro Ala Thr Gly Phe Ile
1025 1030 1035
Asp Phe Leu Lys Pro Arg Tyr Glu Asn Leu Asn Gln Ala Lys Asp
1040 1045 1050

Phe Phe Glu Lys Phe Asp Ser Ile Arg Leu Asn Ser Lys Ala Asp
1055 1060 1065
Tyr Phe Glu Phe Ala Phe Asn Phe Lys Asn Phe Thr Glu Lys Ala
1070 1075 1080
Asp Gly Gly Arg Thr Lys Trp Thr Val Cys Thr Thr Asn Glu Asp
1085 1090 1095
Arg Tyr Ala Trp Asn Arg Ala Leu Asn Asn Asn Arg Gly Ser Gln
1100 1105 1110

Glu Lys Tyr Asp Ile Thr Ala Glu Leu Lys Ser Leu Phe Asp Gly
1115 1120 1125
Lys Val Asp Tyr Lys Ser Gly Lys Asp Leu Lys Gln Gln Ile Ala
1130 1135 1140
Ser Gln Glu Ser Ala Asp Phe Phe Lys Ala Leu Met Lys Asn Leu

1145 1150 1155

Ser Ile Thr Leu Ser Leu Arg His Asn Asn Gly Glu Lys Gly Asp

1160 1165 1170

Asn Glu Gln Asp Tyr Ile Leu Ser Pro Val Ala Asp Ser Lys Gly

1175 1180 1185

Arg Phe Phe Asp Ser Arg Lys Ala Asp Asp Asp Met Pro Lys Asn

1190 1195 1200

Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu Lys Gly Leu Trp

1205 1210 1215

Cys Leu Glu Gln Ile Ser Lys Thr Asp Asp Leu Lys Lys Val Lys

1220 1225 1230

Leu Ala Ile Ser Asn Lys Glu Trp Leu Glu Phe Val Gln Thr Leu

1235 1240 1245

Lys Gly

1250

<210> 81

<211> 810

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 81

Met Gln Leu Thr Asp Asn Leu Ser Asp Lys Tyr Lys Glu Ala Ala Pro

1 5 10 15

Leu Leu Asn Glu Asn Tyr Ser Asn Glu Lys Gly Leu Lys Asn Asp Asp

20 25 30

Lys Ser Ile Ser Leu Ile Lys Asn Phe Leu Asp Ala Ile Lys Glu Ile

35 40 45

Glu Lys Phe Ile Lys Pro Leu Ser Glu Thr Asn Ile Thr Gly Glu Lys

50 55 60

Asn Asp Leu Phe Tyr Ser Gln Phe Thr Pro Leu Leu Asp Asn Ile Ser

65 70 75 80

Arg Ile Asp Ile Leu Tyr Asp Lys Val Arg Asn Tyr Val Thr Gln Lys
85 90 95

Pro Phe Ser Thr Asp Lys Ile Lys Leu Asn Phe Gly Asn Ser Gln Leu
100 105 110
Leu Asn Gly Trp Asp Arg Asn Lys Glu Lys Asp Cys Gly Ala Val Trp
115 120 125
Leu Cys Lys Asp Glu Lys Tyr Tyr Leu Ala Ile Ile Asp Lys Ser Asn
130 135 140
Asn Ser Ile Leu Glu Asn Ile Asp Phe Gln Asp Cys Asp Glu Ser Asp
145 150 155 160

Cys Tyr Glu Lys Ile Ile Tyr Lys Leu Leu Pro Gly Pro Asn Lys Met
165 170 175
Leu Pro Lys Val Phe Phe Ser Glu Lys Cys Lys Lys Leu Leu Ser Pro
180 185 190
Ser Asp Glu Ile Leu Lys Ile Arg Lys Asn Gly Thr Phe Lys Lys Gly
195 200 205
Asp Lys Phe Ser Leu Asp Asp Cys His Lys Leu Ile Asp Phe Tyr Lys
210 215 220

Glu Ser Phe Lys Lys Tyr Pro Asn Trp Leu Ile Tyr Asn Phe Lys Phe
225 230 235 240
Lys Lys Thr Asn Glu Tyr Asn Asp Ile Arg Glu Phe Tyr Asn Asp Val
245 250 255
Ala Ser Gln Gly Tyr Asn Ile Ser Lys Met Lys Ile Pro Thr Ser Phe
260 265 270
Ile Asp Lys Leu Val Asp Glu Gly Lys Ile Tyr Leu Phe Gln Leu Tyr
275 280 285

Asn Lys Asp Phe Ser Pro His Ser Lys Gly Thr Pro Asn Leu His Thr
290 295 300
Leu Tyr Phe Lys Met Leu Phe Asp Glu Arg Asn Leu Glu Asp Val Val
305 310 315 320
Tyr Lys Leu Asn Gly Glu Ala Glu Met Phe Tyr Arg Pro Ala Ser Ile

325 330 335

Lys Tyr Asp Lys Pro Thr His Pro Lys Asn Thr Pro Ile Lys Asn Lys

340 345 350

Asn Thr Leu Asn Asp Lys Lys Thr Ser Ala Phe Pro Tyr Asp Leu Ile

355 360 365

Lys Asp Lys Arg Tyr Thr Lys Trp Gln Phe Ser Leu His Phe Pro Ile

370 375 380

Thr Met Asn Phe Lys Ala Pro Asp Arg Ala Met Ile Asn Asp Asp Val

385 390 395 400

Arg Asn Leu Leu Lys Ser Cys Asn Asn Asn Phe Ile Ile Gly Ile Asp

405 410 415

Arg Gly Glu Arg Asn Leu Leu Tyr Val Ser Val Ile Asp Ser Asn Gly

420 425 430

Thr Ile Ile Tyr Gln His Ser Leu Asn Ile Ile Gly Asn Lys Phe Lys

435 440 445

Gly Lys Thr Tyr Lys Thr Asn Tyr Arg Glu Lys Leu Ala Thr Arg Glu

450 455 460

Lys Asp Arg Thr Glu Gln Arg Arg Asn Trp Lys Ala Ile Glu Ser Ile

465 470 475 480

Lys Glu Leu Lys Glu Gly Tyr Ile Ser Gln Ala Val His Val Ile Cys

485 490 495

Gln Leu Val Val Lys Tyr Asp Ala Ile Ile Val Met Glu Lys Leu Thr

500 505 510

Glu Gly Phe Lys Arg Gly Arg Thr Lys Phe Glu Lys Gln Val Tyr Gln

515 520 525

Lys Phe Glu Lys Met Leu Ile Asp Lys Leu Asn Tyr Tyr Val Asp Lys

530 535 540

Lys Leu Asp Pro Asp Glu Glu Gly Gly Leu Leu His Ala Tyr Gln Leu

545 550 555 560

Thr Asn Lys Leu Glu Ser Phe Asp Lys Leu Gly Thr Gln Ser Gly Phe

565 570 575

Ile Phe Tyr Val Arg Pro Asp Phe Thr Ser Lys Ile Asp Pro Val Thr
580 585 590
Gly Phe Val Asn Leu Leu Tyr Pro Arg Tyr Glu Asn Ile Asp Lys Ala
595 600 605

Lys Asp Met Ile Ser Arg Phe Asp Glu Ile Arg Tyr Asn Ala Gly Glu
610 615 620
Asp Phe Phe Glu Phe Asp Ile Asp Tyr Asp Lys Phe Pro Lys Thr Ala
625 630 635 640
Ser Asp Tyr Arg Lys Lys Trp Thr Ile Cys Thr Asn Gly Glu Arg Ile
645 650 655
Glu Ala Phe Arg Asn Pro Ala Asn Asn Asn Glu Trp Ser Tyr Arg Thr
660 665 670

Ile Ile Leu Ala Glu Lys Phe Lys Glu Leu Phe Asp Asn Asn Ser Ile
675 680 685
Asn Tyr Arg Asp Ser Asp Asp Leu Lys Ala Glu Ile Leu Ser Gln Thr
690 695 700
Lys Gly Lys Phe Phe Glu Asp Phe Phe Lys Leu Leu Arg Leu Thr Leu
705 710 715 720
Gln Met Arg Asn Ser Asn Pro Glu Thr Gly Glu Asp Arg Ile Leu Ser
725 730 735

Pro Val Lys Asp Lys Asn Gly Asn Phe Tyr Asp Ser Ser Lys Tyr Asp
740 745 750
Glu Lys Ser Lys Leu Pro Cys Asp Ala Asp Ala Asn Gly Ala Tyr Asn
755 760 765
Ile Ala Arg Lys Gly Leu Trp Ile Val Glu Gln Phe Lys Lys Ala Asp
770 775 780
Asn Val Ser Thr Val Glu Pro Val Ile His Asn Asp Lys Trp Leu Lys
785 790 795 800

Phe Val Gln Glu Asn Asp Met Thr Asn Asn
805 810

<210> 82

<211> 875

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 82

Met Leu Pro Asn Glu Lys Glu Arg Asn Glu Phe Lys Asn Ser Asn Ala
1 5 10 15

Lys Gln Tyr Ile Arg Glu Ile Ser Asn Ile Ile Thr Asp Thr Glu Thr
20 25 30

Ala His Leu Glu Tyr Asp Glu His Ile Ser Leu Ile Glu Ser Glu Glu
35 40 45

Lys Ala Asp Glu Met Lys Lys Arg Leu Asp Met Tyr Met Asn Met Tyr
50 55 60

His Trp Ala Lys Ala Phe Ile Val Asp Glu Val Leu Asp Arg Asp Glu
65 70 75 80

Met Phe Tyr Ser Asp Ile Asp Asp Ile Tyr Asn Ile Leu Glu Asn Ile
85 90 95

Val Pro Leu Tyr Asn Arg Val Arg Asn Tyr Val Thr Gln Lys Pro Tyr
100 105 110

Asn Ser Lys Lys Ile Lys Leu Asn Phe Gln Ser Pro Thr Leu Ala Asn
115 120 125

Gly Trp Ser Gln Ser Lys Glu Phe Asp Asn Asn Ala Ile Ile Leu Ile
130 135 140

Arg Asp Asn Lys Tyr Tyr Leu Ala Ile Phe Asn Ala Lys Asn Lys Pro
145 150 155 160

Asp Lys Lys Ile Ile Gln Gly Asn Ser Asp Lys Lys Asn Asp Asn Asp
165 170 175

Tyr Lys Lys Met Val Tyr Asn Leu Leu Pro Gly Ala Asn Lys Met Leu
180 185 190

Pro Lys Val Phe Leu Ser Lys Lys Gly Ile Glu Thr Phe Lys Pro Ser
195 200 205

Asp Tyr Ile Ile Ser Gly Tyr Asn Ala His Lys His Ile Lys Thr Ser

210 215 220

Glu Asn Phe Asp Ile Ser Phe Cys Arg Asp Leu Ile Asp Tyr Phe Lys

225 230 235 240

Asn Ser Ile Glu Lys His Ala Glu Trp Arg Lys Tyr Glu Phe Lys Phe

245 250 255

Ser Ala Thr Asp Ser Tyr Asn Asp Ile Ser Glu Phe Tyr Arg Glu Val

260 265 270

Glu Met Gln Gly Tyr Arg Ile Asp Trp Thr Tyr Ile Ser Glu Ala Asp

275 280 285

Ile Asn Lys Leu Asp Glu Glu Gly Lys Ile Tyr Leu Phe Gln Ile Tyr

290 295 300

Asn Lys Asp Phe Ala Glu Asn Ser Thr Gly Lys Glu Asn Leu His Thr

305 310 315 320

Met Tyr Phe Lys Asn Ile Phe Ser Glu Glu Asn Leu Lys Asp Ile Ile

325 330 335

Ile Lys Leu Asn Gly Gln Ala Glu Leu Phe Tyr Arg Arg Ala Ser Val

340 345 350

Lys Asn Pro Val Lys His Lys Lys Asp Ser Val Leu Val Asn Lys Thr

355 360 365

Tyr Lys Asn Gln Leu Asp Asn Gly Asp Val Val Arg Ile Pro Ile Pro

370 375 380

Asp Asp Ile Tyr Asn Glu Ile Tyr Lys Met Tyr Asn Gly Tyr Ile Lys

385 390 395 400

Glu Asn Asp Leu Ser Glu Ala Ala Lys Glu Tyr Leu Asp Lys Val Glu

405 410 415

Val Arg Thr Ala Gln Lys Asp Ile Val Lys Asp Tyr Arg Tyr Thr Val

420 425 430

Asp Lys Tyr Phe Ile His Thr Pro Ile Thr Ile Asn Tyr Lys Val Thr

435 440 445

Ala Arg Asn Asn Val Asn Asp Met Ala Val Lys Tyr Ile Ala Gln Asn

450 455 460

Asp Asp Ile His Val Ile Gly Ile Asp Arg Gly Glu Arg Asn Leu Ile

465 470 475 480

Tyr Ile Ser Val Ile Asp Ser His Gly Asn Ile Val Lys Gln Lys Ser

485 490 495

Tyr Asn Ile Leu Asn Asn Tyr Asp Tyr Lys Lys Lys Leu Val Glu Lys

500 505 510

Glu Lys Thr Arg Glu Tyr Ala Arg Lys Asn Trp Lys Ser Ile Gly Asn

515 520 525

Ile Lys Glu Leu Lys Glu Gly Tyr Ile Ser Gly Val Val His Glu Ile

530 535 540

Ala Met Leu Met Val Glu Tyr Asn Ala Ile Ile Ala Met Glu Asp Leu

545 550 555 560

Asn Tyr Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Arg Gln Val Tyr

565 570 575

Gln Lys Phe Glu Ser Met Leu Ile Asn Lys Leu Asn Tyr Phe Ala Ser

580 585 590

Lys Gly Lys Ser Val Asp Glu Pro Gly Gly Leu Leu Lys Gly Tyr Gln

595 600 605

Leu Thr Tyr Val Pro Asp Asn Ile Lys Asn Leu Gly Lys Gln Cys Gly

610 615 620

Val Ile Phe Tyr Val Pro Ala Ala Phe Thr Ser Lys Ile Asp Pro Ser

625 630 635 640

Thr Gly Phe Ile Ser Ala Phe Asn Phe Lys Ser Ile Ser Thr Asn Ala

645 650 655

Ser Arg Lys Gln Phe Phe Met Gln Phe Asp Glu Ile Arg Tyr Cys Ala

660 665 670

Glu Lys Asp Met Phe Ser Phe Gly Phe Asp Tyr Asn Asn Phe Asp Thr

675 680 685

Tyr Asn Ile Thr Met Ser Lys Thr Gln Trp Thr Val Tyr Thr Asn Gly

690 695 700

Glu Arg Leu Gln Ser Glu Phe Asn Asn Ala Arg Arg Thr Gly Lys Thr
705 710 715 720
Lys Ser Ile Asn Leu Thr Glu Thr Ile Lys Leu Leu Leu Glu Asp Asn
725 730 735
Glu Ile Asn Tyr Ala Asp Gly His Asp Val Arg Ile Asp Met Glu Lys

740 745 750
Met Asp Glu Asp Lys Asn Ser Glu Phe Phe Ala Gln Leu Leu Ser Leu
755 760 765
Tyr Lys Leu Thr Val Gln Met Arg Asn Ser Tyr Thr Glu Ala Glu Glu
770 775 780
Gln Glu Lys Gly Ile Ser Tyr Asp Lys Ile Ile Ser Pro Val Ile Asn
785 790 795 800
Asp Glu Gly Glu Phe Phe Asp Ser Asp Asn Tyr Lys Glu Ser Asp Asp

805 810 815
Lys Glu Cys Lys Met Pro Lys Asp Ala Asp Ala Asn Gly Ala Tyr Cys
820 825 830
Ile Ala Leu Lys Gly Leu Tyr Glu Val Leu Lys Ile Lys Ser Glu Trp
835 840 845
Thr Glu Asp Gly Phe Asp Arg Asn Cys Leu Lys Leu Pro His Ala Glu
850 855 860
Trp Leu Asp Phe Ile Gln Asn Lys Arg Tyr Glu
865 870 875

<210> 83
<211> 1238
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 83
Met Ser Asn Leu Tyr Ser Asn Leu His Asn Leu Tyr Pro Val Gln Lys
1 5 10 15
Thr Leu Arg Phe Glu Leu Lys Pro Gln Gly Lys Thr Lys Glu Asn Met

20 25 30

Glu Lys Ala Gly Ile Leu Lys Ala Asp Glu His Arg Ala Glu Val Tyr

35 40 45

Gly Lys Val Lys Lys Tyr Cys Asp Glu Tyr His Lys Thr Phe Ile Asp

50 55 60

Arg Cys Leu Ser Asn Ile Glu Leu Asn Glu Ile Asp Lys Tyr Tyr Glu

65 70 75 80

Leu Tyr Ser Ile Asn Asn Arg Asp Asp Lys Gln Lys Glu Glu Leu Asp

85 90 95

Gln Leu Glu Thr Gly Leu Arg Lys Gln Ile Ser Asp Ala Phe Lys Lys

100 105 110

Ser Ala Glu Tyr Lys Gly Leu Phe Gln Lys Asp Met Ile Thr Ser Tyr

115 120 125

Leu Val Thr Met Tyr Lys Glu Asn Gln Glu Lys Met Gln Asp Ile Gly

130 135 140

Glu Phe Asn Arg Phe Thr Thr Tyr Phe Thr Gly Tyr Asn Lys Asn Arg

145 150 155 160

Glu Asn Met Tyr Ser Glu Glu Asp Lys Ser Thr Ala Ile Ser Tyr Arg

165 170 175

Leu Ile Asn Glu Asn Leu Pro Thr Phe Ile Asp Asn Ile Lys Ile Tyr

180 185 190

Lys Lys Ile Val Ser Leu Met Pro Glu Asn Ile Glu Lys Ile Tyr Lys

195 200 205

Asp Leu Glu Glu Tyr Ile Gln Val Asn Ser Val Asp Glu Ile Phe Asn

210 215 220

Ile Ser Tyr Tyr Asn Asp Val Leu Thr Gln Arg Gly Ile Glu Cys Tyr

225 230 235 240

Asn Ile Leu Ile Ser Gly Arg Thr Lys Asn Asp Gly Asp Lys Ile Lys

245 250 255

Gly Leu Asn Glu Tyr Ile Asn Glu Phe Asn Gln Thr His Asn Glu Lys

260 265 270

Ile Pro Lys Leu Gln Glu Leu Tyr Lys Gln Ile Leu Ser Asp Ala Glu
275 280 285
Ser Ala Ser Phe Lys Val Asp Ile Ile Glu Asn Asp Lys Glu Leu Leu
290 295 300

Asn Leu Ile Glu Val Tyr Tyr Ala Asn Ile Leu Pro Thr Leu Asn Lys
305 310 315 320
Ile Glu Asp Leu Phe Thr Arg Ile Ser Asn Tyr Asn Leu Glu Leu Ile
325 330 335
Leu Val Asn Asn Asp Gly Ser Leu Ser Thr Leu Ser Asn Met Val Phe
340 345 350
Asn Glu Trp Ser Tyr Ile Lys Gly Ile Ile Ser Gln Lys Tyr Asp Ala
355 360 365

Glu Tyr Ser Gly Lys Glu Lys Tyr Gly Thr Glu Lys Tyr Ala Gln Lys
370 375 380
Lys Gln Glu Tyr Leu Lys Lys Gln Lys Ile Tyr Ser Leu Lys Phe Leu
385 390 395 400
Asn Asp Cys Ile Gly Asn Asn Ala Ile Cys Glu Tyr Leu Lys Asn Tyr
405 410 415
Ile Ile Gln Asn Lys Asn Ile Glu Thr Ile Lys Glu Asp Tyr Asn Glu
420 425 430

Val Gln Asn Ile Lys Ala Glu Asp Asp Thr Lys Glu Leu Ile Lys Asp
435 440 445
Glu Lys Ser Ile Glu Lys Ile Lys Lys Phe Leu Asp Asp Val Lys Ser
450 455 460
Leu Gln Glu Phe Val Lys Leu Val Ile Pro Lys Asp Arg Thr Val Glu
465 470 475 480
Lys Asp Ala Lys Phe Tyr Ser Glu Leu Thr Pro Tyr Tyr Glu Lys Ile
485 490 495

Lys Glu Ile Ile Pro Leu Tyr Asn Lys Val Arg Asn Tyr Val Thr Gln
500 505 510
Lys Pro Tyr Ser Thr Glu Lys Ile Lys Leu Asn Phe Glu Cys Pro Thr

515 520 525

Leu Leu Asn Gly Trp Asp Ala Asn Lys Glu Glu Ala Asn Leu Gly Val

530 535 540

Ile Leu Leu Lys Glu Gly Lys Tyr Tyr Leu Gly Ile Met Asn Pro Tyr

545 550 555 560

Cys Lys Lys Ile Phe Glu Val Tyr Glu Lys Asp Ser Asn Glu Gln Asn

565 570 575

Asn Tyr Lys Lys Met Glu Tyr Lys Leu Leu Pro Gly Pro Asn Lys Met

580 585 590

Leu Pro Lys Val Phe Phe Ser Asn Ser Arg Ile Glu Glu Phe Asn Pro

595 600 605

Ser Lys Glu Leu Gln Glu Lys Tyr Asn Lys Gly Tyr His Lys Lys Gly

610 615 620

Lys Asp Phe Asp Ile Asn Phe Cys His Glu Leu Ile Asp Phe Tyr Lys

625 630 635 640

Gln Ser Leu Asn Lys His Glu Asp Trp Lys Lys Phe Asn Phe Lys Phe

645 650 655

Lys Asp Thr Ser Glu Tyr Asn Asp Ile Ser Glu Phe Tyr Arg Glu Val

660 665 670

Glu Glu Gln Gly Tyr Lys Ile Glu Tyr Thr Glu Tyr Ser Glu Lys Tyr

675 680 685

Ile Asn Glu Leu Val Asp Arg Gly Glu Leu Tyr Leu Phe Gln Ile Tyr

690 695 700

Asn Lys Asp Phe Ser Glu Tyr Ser Lys Gly Lys Glu Asn Leu His Thr

705 710 715 720

Leu Tyr Trp Lys Ala Val Phe Asp Pro Asp Asn Ile Met Asn Pro Val

725 730 735

Tyr Lys Leu Asn Gly Asn Ala Glu Ile Phe Tyr Arg Lys Lys Ser Leu

740 745 750

Glu Met Lys Val Thr His Pro Ala Asn Gln Pro Ile Ala Asn Lys Asn

755 760 765

Ile Ser Thr Ile Glu Ala Gly Arg Ser Thr Ser Thr Phe Lys Tyr Asp
770 775 780
Leu Ile Lys Asp Lys Arg Tyr Thr Met Asp Lys Phe Gln Phe His Val
785 790 795 800
Pro Ile Thr Val Asn Phe Lys Ser Glu Arg Leu Phe Asn Ile Asn Gln
805 810 815

Ile Val Asn Lys Tyr Leu Lys Tyr Asn Asp Asp Ile His Val Ile Gly
820 825 830
Ile Asp Arg Gly Glu Arg Asn Leu Leu Tyr Val Cys Val Ile Asp Lys
835 840 845
Asn Glu Lys Ile Val Tyr Gln Lys Ser Leu Asn Glu Ile Val Ser Glu
850 855 860
Tyr Asn Asn Asn Arg Tyr Thr Thr Asp Tyr His Gly Leu Leu Asp Arg
865 870 875 880

Lys Glu Lys Glu Arg Glu Ile Ala Arg Glu Asp Trp Lys Asn Ile Glu
885 890 895
Asn Ile Lys Glu Leu Lys Glu Gly Tyr Met Ser Gln Ile Ile His Ile
900 905 910
Leu Val Glu Leu Met Lys Lys Tyr Asn Ala Ile Ile Val Ile Glu Asp
915 920 925
Leu Asn Lys Gly Phe Lys Asn Ser Arg Ile Lys Val Glu Lys Gln Val
930 935 940

Tyr Gln Lys Phe Glu Lys Met Phe Ile Asp Lys Leu Asn Tyr Leu Val
945 950 955 960
Phe Lys Asp Glu Asp Lys Met Asp Glu Gly Gly Val Leu Asn Ala Tyr
965 970 975
Gln Leu Thr Asn Lys Phe Glu Ser Phe Thr Lys Leu Gly Lys Gln Ser
980 985 990
Gly Ile Leu Tyr Tyr Ile Pro Ala Trp Cys Thr Ser Lys Ile Asp Pro
995 1000 1005

Thr Thr Gly Phe Ile Asn Arg Phe Tyr Leu Lys Tyr Glu Asn Phe

1010 1015 1020

Asp Lys Ser Lys Glu Phe Val Asn Arg Ile Asp Asp Ile Arg Tyr

1025 1030 1035

Asn Glu Lys Glu Asn Leu Phe Glu Phe Asp Ile Asp Tyr Ser Lys

1040 1045 1050

Phe Thr Asp Arg Leu Asn Asp Thr Lys Asn Lys Trp Thr Leu Cys

1055 1060 1065

Ser Tyr Gly Glu Arg Ile Leu Thr Gln Lys Asn Ala Asn Gly Glu

1070 1075 1080

Trp Phe Asp Arg Arg Ile Gln Leu Ser Ile Glu Phe Lys Asn Leu

1085 1090 1095

Phe Glu Lys Tyr Val Ile Asn Leu Asn Asn Ile Lys Asp Ser Ile

1100 1105 1110

Leu Lys Leu Asp Lys Asp Asn Ile Glu Phe Tyr Lys Gly Asn Gly

1115 1120 1125

Glu Asn Leu Gly Phe Ile Gln Leu Phe Lys Leu Met Val Gln Met

1130 1135 1140

Arg Asn Ser Leu Thr Gly Lys Glu Glu Asp Asn Leu Ile Ser Pro

1145 1150 1155

Val Lys Asn Gln His Gly Lys Phe Phe Asn Thr Ser Glu Arg Val

1160 1165 1170

Glu Gly Leu Pro Ile Asp Ala Asp Ala Asn Gly Ala Tyr Asn Ile

1175 1180 1185

Ala Arg Lys Gly Phe Met Leu Val Glu Gln Met Lys Asn Val Glu

1190 1195 1200

Asp Glu Lys Leu Asn Lys Ile Lys Tyr Asn Ile Thr Glu Lys Glu

1205 1210 1215

Trp Leu Asn Tyr Val Gln Asn Arg Gly Met Trp Trp Lys Arg Gln

1220 1225 1230

Tyr Leu Tyr His Ile

1235

<210> 84

<211> 1262

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 84

Met Ala Lys Asn Thr Ile Phe Ser Gln Phe Thr Gly Leu Tyr Pro Val
1 5 10 15

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Met Gly Lys Thr Leu Glu
20 25 30

Lys Ile Lys Glu Thr Gly Val Ile Glu Asn Asp Lys Lys Arg His Asn
35 40 45

Asp Tyr Phe Asp Ala Lys Lys Ile Ile Asp Lys Tyr His Lys Tyr Phe
50 55 60

Ile Asp Ala Ala Leu Ser Lys Phe Pro Arg Ile Asp Trp Ser Pro Leu
65 70 75 80

Lys Glu Ala Ile Glu Arg Ser Leu Asp Arg Ser Asp Ala Ser Lys Lys
85 90 95

Lys Leu Glu Lys Thr Gln Thr Glu Phe Arg Lys Lys Ile Ala Lys Ala
100 105 110

Leu Thr Thr His Asp His Tyr Lys Glu Leu Thr Ala Ser Thr Pro Lys
115 120 125

Asp Leu Phe Leu Lys Val Phe Pro Asp His Phe Gly Lys Gln Pro Ala
130 135 140

Ile Asp Thr Phe Asp Gly Phe Ser Ser Tyr Phe Thr Gly Phe Gln Glu
145 150 155 160

Asn Arg Gln Asn Ile Tyr Ser Asp Glu Ala Ile Ser Thr Ala Ile Pro
165 170 175

Tyr Arg Leu Val His Asp Asn Phe Pro Lys Phe Leu Ser Asn Ile Glu
180 185 190

Val Tyr Lys Thr Leu Lys Asp Asn Ala Pro Ser Val Leu Ser Asp Ala

195 200 205

Glu Asn Glu Leu Arg Asp Phe Leu Asn Gly Lys Ser Leu Ala Asn Ile

210 215 220

Phe Glu Leu Asn Ala Tyr Asn Glu Val Leu Thr Gln Ser Gly Ile Asp

225 230 235 240

Phe Phe Asn Gln Val Ile Gly Gly Ile Ser Asp Glu Gly Gly Glu Lys

245 250 255

Lys Thr Arg Gly Ile Asn Glu Phe Ser Asn Leu Tyr Arg Gln Gln His

260 265 270

Pro Glu Phe Ala Gln Lys Arg Leu Ala Thr Lys Met Ile Pro Leu Tyr

275 280 285

Lys Gln Ile Leu Ser Asp Arg Glu Thr Lys Ser Phe Ile Leu Glu Ser

290 295 300

Tyr Ser Asn Asp Ser Gln Val Gln Asn Ser Val Lys Glu Phe Phe Glu

305 310 315 320

Ser Gln Ile Leu Asn Trp Asp Ile Ala Gly Arg Arg Val Asn Val Leu

325 330 335

Asn Glu Leu Thr Ser Leu Val Lys Arg Ile Ser Glu Phe Asp Leu Gly

340 345 350

Asn Ile Tyr Val Asn Gln Glu Glu Leu Ser Asn Ile Ser Leu Lys Leu

355 360 365

Phe Asp Asn Trp Asn Ser Ile Asn Gly Leu Leu Phe Lys His Ala Glu

370 375 380

Asn Arg Ile Gly Ser Ala Glu Lys Ser Ala Asn Lys Lys Lys Ile Asp

385 390 395 400

Ala Trp Met Lys Asn Lys Glu Phe Ser Ile Ala Thr Leu Asn Leu Ala

405 410 415

Ile Ala Glu Ser Asn Ser Glu Glu Ile Ser Arg Val Lys Ile Glu Ser

420 425 430

Tyr Trp Asn Asn Phe Glu Ala Lys Val Gln Ser Ile Leu Cys Gly Asp

435 440 445

Asn Arg Arg Asn Leu Asp Glu Phe Ile Ser Ala Thr Phe Asn Glu Asn
450 455 460
Asn Ala Leu Arg Glu Asp Ser Lys Ile Ile Glu Lys Leu Lys Ala Phe
465 470 475 480
Leu Asp Ala Leu Ile Glu Ile Met His Ser Ile Lys Pro Leu Ile Ser
485 490 495
Asp Ala Glu Asn Arg Asp Leu Ser Phe Tyr Asn Glu Leu Ile Pro Leu
500 505 510

Tyr Asp Gln Leu Ser Leu Val Val Pro Leu Tyr Asn Lys Ile Arg Asn
515 520 525
Tyr Ala Thr Gln Lys Leu Thr Glu Ser Glu Lys Phe Lys Leu Asn Phe
530 535 540
Asp Asn Pro Thr Leu Ala Asp Gly Trp Asp Gln Asn Lys Glu Glu Ala
545 550 555 560
Asn Thr Ala Ile Leu Leu Leu Lys Asn Gly Leu Tyr Tyr Leu Gly Ile
565 570 575

Met Asn Ala Lys Asn Lys Pro Lys Ile Lys Asp Phe Lys Thr Ser Glu
580 585 590
Ser Glu Asp Cys Tyr Asp Lys Met Val Tyr Lys Leu Leu Pro Gly Pro
595 600 605
Asn Lys Met Leu Pro Lys Val Phe Phe Ser Glu Lys Gly Leu Ala Thr
610 615 620
Phe Lys Pro Pro Lys Asp Ile Leu Asp Gly Tyr Asn Ala Gly Lys His
625 630 635 640

Lys Lys Gly Asp Leu Phe Asp Ile Gly Phe Cys His Gln Leu Ile Asp
645 650 655
Phe Phe Lys Glu Ser Ile Ala Lys His Pro Asp Trp Lys Lys Phe Asp
660 665 670
Phe Asn Phe Ser Asp Thr Ser Ser Tyr Glu Asp Ile Ser Gly Phe Tyr
675 680 685
Lys Glu Val Thr Asp Gln Gly Tyr Lys Ile Thr Phe Ser Lys Ile Pro

690 695 700

Thr Ser Gln Ile Asp Glu Trp Val Lys Glu Gly Lys Leu Phe Leu Phe
705 710 715 720
Gln Ile Tyr Asn Lys Asp Phe Ala Pro Gly Ala Lys Gly Ser Pro Asn
725 730 735
Leu His Thr Leu Tyr Trp Lys Ser Val Phe Ser Pro Glu Asn Leu Lys
740 745 750
Asp Val Val Val Lys Leu Asn Gly Glu Ala Glu Leu Phe Tyr Arg Pro
755 760 765

Ser Ser Val Lys Lys Pro Tyr Ser His Lys Val Gly Glu Lys Leu Val
770 775 780
Asn Arg Ile Gly Lys Asp Gly Leu Pro Leu Pro Glu Ser Val Phe Gly
785 790 795 800
Glu Leu Phe Arg Tyr Phe Asn Gly Lys Leu Glu Gly Glu Leu Ser Asp
805 810 815
Glu Ala Lys Arg Tyr Leu Asp Val Ala Val Val Lys Asp Val Lys His
820 825 830

Glu Ile Val Lys Asp Arg Arg Tyr Thr Gln Asp Lys Phe Glu Phe His
835 840 845
Val Pro Leu Thr Leu Asn Phe Lys Ala Asp Ser Lys Asn Glu Tyr Met
850 855 860
Asn Glu Arg Val Arg His Phe Leu Lys Asp Asn Pro Asp Val Asn Ile
865 870 875 880
Ile Gly Ile Asp Arg Gly Glu Arg His Leu Leu Tyr Met Thr Leu Ile
885 890 895

Asn Gln Lys Gly Glu Ile Leu Lys Gln Lys Ser Phe Asn Val Val Glu
900 905 910
Ser Val Asn Tyr Gln Ala Lys Leu Val Gln Arg Glu Lys Glu Arg Asp
915 920 925
Ala Ala Arg Arg Ser Trp Ser Ser Val Gly Lys Ile Lys Asp Leu Lys
930 935 940

Glu Gly Phe Leu Ser Gln Val Ile His Glu Ile Thr Thr Thr Met Ile
945 950 955 960

Glu Asn Asn Ala Ile Val Val Leu Glu Asp Leu Asn Phe Gly Phe Lys
965 970 975
Arg Gly Arg Phe Cys Val Glu Arg Gln Val Tyr Gln Lys Phe Glu Lys
980 985 990
Met Leu Ile Asp Lys Leu Asn Tyr Leu Val Phe Lys Asn Lys Pro Glu
995 1000 1005
Gly Asp Val Gly Gly Val Leu Lys Gly Tyr Gln Leu Ala Glu Lys
1010 1015 1020

Phe Asp Ser Phe Gln Lys Leu Gly Lys Gln Ser Gly Phe Leu Phe
1025 1030 1035
Tyr Ile Pro Ala Ala Tyr Thr Ser Lys Ile Asp Pro Thr Thr Gly
1040 1045 1050
Phe Ala Asn Leu Phe Asn Met Thr Glu Leu Thr Ser Ala Glu Lys
1055 1060 1065
Lys Lys Glu Phe Leu Ser His Phe Glu Asp Ile Thr Tyr Asp Gly
1070 1075 1080

Lys Asn Asp Arg Phe Leu Phe Ser Phe Asp Tyr Lys Asn Phe Lys
1085 1090 1095
Cys Phe Gln Thr Asp Tyr Ile Lys Lys Trp Thr Val Tyr Ser Gln
1100 1105 1110
Gly Lys Arg Ile Val Tyr Asp Lys Glu Ser Lys Ser Ala Lys Glu
1115 1120 1125
Ile Ser Pro Val Glu Ile Ile Lys Ala Ala Leu Ala Lys Gln Asn
1130 1135 1140

Ile Ala Leu Thr Asp Gln Leu Asp Val Leu Ser Ala Ile Asn Ser
1145 1150 1155
Val Glu Ala Ser Pro Lys Ser Ala Ser Phe Phe Gly Asp Ile Cys
1160 1165 1170
Tyr Ala Phe Glu Lys Thr Leu Gln Met Arg Asn Ser Ile Pro Asn

1175 1180 1185

Thr Asp Glu Asp Tyr Leu Ala Ser Pro Val Met Asn Lys Arg Gly

1190 1195 1200

Glu Phe Tyr Asp Ser Arg Ser Cys Asp Asp Ala Leu Pro Gln Asn

1205 1210 1215

Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu Lys Gly Leu Tyr

1220 1225 1230

Leu Ile Lys Asn Val Phe Asp Ala Gly Gly Lys Glu Leu Lys Ile

1235 1240 1245

Ser His Glu Asp Trp Phe Lys Phe Ala Gln Ser Arg Asn Cys

1250 1255 1260

<210> 85

<211> 1140

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 85

Met Tyr Lys Asp Lys Thr Asp Lys Thr Lys Ile Ile Asp Ser Asp Leu

1 5 10 15

Ile Lys Phe Ile Asn Ile Ala Glu Ser Thr Gln Leu Asp Ser Met Ser

20 25 30

Gln Asp Glu Ala Lys Glu Leu Val Lys Glu Phe Trp Gly Phe Thr Thr

35 40 45

Tyr Phe Val Gly Phe Tyr Asp Asn Arg Lys Asn Met Tyr Thr Ala Glu

50 55 60

Glu Lys Ser Thr Gly Ile Ala Tyr Arg Leu Val Asn Glu Asn Leu Pro

65 70 75 80

Lys Phe Ile Asp Asn Met Glu Ala Phe Lys Lys Ala Ile Ala Arg Pro

85 90 95

Glu Ile Gln Ala Asn Met Glu Glu Leu Tyr Ser Asp Phe Ser Glu Tyr

100 105 110

Leu Asn Val Glu Ser Val Gln Glu Met Phe Gln Leu Asp Tyr Tyr Asn
115 120 125
Met Leu Leu Thr Gln Lys Gln Ile Asp Val Tyr Asn Ala Ile Ile Gly
130 135 140
Gly Lys Thr Asp Asp Glu His Asp Val Lys Ile Lys Gly Ile Asn Glu
145 150 155 160
Tyr Ile Asn Leu Tyr Asn Gln Gln His Lys Asp Asp Lys Leu Pro Lys
165 170 175

Leu Lys Ala Leu Phe Lys Gln Ile Leu Ser Asp Arg Asn Ala Ile Ser
180 185 190
Trp Leu Pro Glu Glu Phe Asn Gly Asp Gln Glu Val Leu Asn Ala Ile
195 200 205
Lys Asp Cys Tyr Glu Arg Leu Ser Glu Asn Val Leu Gly Asp Lys Val
210 215 220
Leu Lys Ser Leu Leu Gly Ser Leu Ser Asp Tyr Ser Leu Asp Gly Ile
225 230 235 240

Phe Ile Arg Asn Asp Leu Gln Leu Thr Asp Ile Ser Gln Lys Met Phe
245 250 255
Gly Asn Trp Cys Val Ile Gln Asn Ala Ile Met Gln Asn Ile Lys His
260 265 270
Val Ala Pro Ala Arg Lys His Lys Glu Ser Glu Glu Asp Tyr Glu Lys
275 280 285
Arg Ile Ala Gly Ile Phe Lys Lys Val Asp Ser Phe Ser Ile Ser Phe
290 295 300

Ile Asn Asp Cys Leu Asn Glu Ala Asp Pro Asn Asn Ala Tyr Phe Val
305 310 315 320
Glu Asn Tyr Phe Ala Thr Phe Gly Ala Val Asn Thr Pro Thr Met Gln
325 330 335
Arg Glu Asn Leu Phe Ala Leu Val Gln Asn Ala Tyr Thr Glu Val Ala
340 345 350

Ala Leu Leu His Ser Asp Tyr Pro Thr Ala Lys His Leu Ala Gln Asp
355 360 365

Lys Val Asn Val Ala Lys Ile Lys Ala Leu Leu Asp Ala Ile Lys Ser
370 375 380
Leu Gln His Phe Val Lys Pro Leu Leu Gly Lys Gly Asp Glu Ser Asp
385 390 395 400
Lys Asp Glu Arg Phe Tyr Gly Glu Leu Ala Ser Leu Trp Ala Glu Leu
405 410 415
Asp Thr Val Thr Pro Leu Tyr Asn Met Ile Arg Asn Tyr Met Thr Arg
420 425 430

Lys Pro Tyr Ser Gln Lys Lys Ile Lys Leu Asn Phe Glu Asn Pro Gln
435 440 445
Leu Leu Gly Gly Trp Asp Ala Asn Lys Glu Lys Asp Tyr Ala Thr Ile
450 455 460
Ile Leu Arg Arg Asp Gly Leu Tyr Tyr Leu Ala Ile Met Asn Lys Glu
465 470 475 480
Ser Lys Lys Leu Leu Gly Lys Ala Met Pro Ser Asp Gly Glu Cys Tyr
485 490 495

Glu Lys Met Val Tyr Lys Leu Leu Pro Gly Ala Asn Lys Met Leu Pro
500 505 510
Lys Val Phe Phe Ala Lys Ser Arg Met Glu Asp Phe Lys Pro Ser Lys
515 520 525
Glu Leu Val Glu Lys Tyr Asn Asn Gly Thr His Lys Lys Gly Lys Asn
530 535 540
Phe Asn Ile Gln Asp Cys His Asn Leu Ile Asp Tyr Phe Lys Gln Ser
545 550 555 560

Ile Ser Lys His Glu Asp Trp Gly Lys Phe Gly Phe Asn Phe Ser Asp
565 570 575
Thr Ser Thr Tyr Glu Asp Leu Ser Gly Phe Tyr Arg Glu Val Glu Gln
580 585 590
Gln Gly Tyr Lys Leu Ser Phe Ala Arg Val Ser Val Ser Tyr Ile Ser

595 600 605

Gln Leu Val Glu Glu Gly Lys Met Tyr Leu Phe Gln Ile Tyr Asn Lys

610 615 620

Asp Phe Ser Glu Tyr Ser Lys Gly Thr Pro Asn Met His Thr Leu Tyr

625 630 635 640

Trp Lys Ala Leu Phe Asp Glu Arg Asn Leu Ala Asp Val Val Tyr Lys

645 650 655

Leu Asn Gly Gln Ala Glu Met Phe Tyr Arg Lys Lys Ser Ile Glu Asn

660 665 670

Thr His Pro Thr His Pro Ala Asn His Pro Ile Leu Asn Lys Asn Lys

675 680 685

Asp Asn Lys Lys Lys Glu Ser Leu Phe Asp Tyr Asp Leu Ile Lys Asp

690 695 700

Arg Arg Tyr Thr Val Asp Lys Phe Met Phe His Val Pro Ile Thr Met

705 710 715 720

Asn Phe Lys Ser Ser Gly Ser Glu Asn Ile Asn Gln Asp Val Lys Ala

725 730 735

Tyr Leu Arg His Ala Asp Asp Met His Ile Ile Gly Ile Asp Arg Gly

740 745 750

Glu Arg His Leu Leu Tyr Leu Val Val Ile Asp Leu Gln Gly Asn Ile

755 760 765

Lys Glu Gln Tyr Ser Leu Asn Glu Ile Val Asn Glu Tyr Asn Gly Asn

770 775 780

Thr Tyr His Thr Asn Tyr His Asp Leu Leu Asp Val Cys Glu Glu Glu

785 790 795 800

Arg Leu Lys Ala Arg Gln Ser Trp Gln Thr Ile Glu Asn Ile Lys Glu

805 810 815

Leu Lys Glu Gly Tyr Leu Ser Gln Val Ile His Lys Ile Thr Gln Leu

820 825 830

Met Val Lys Tyr His Ala Ile Val Val Leu Glu Asp Leu Asn Met Gly

835 840 845

Phe Met Arg Gly Arg Gln Lys Val Glu Lys Gln Val Tyr Gln Lys Phe
850 855 860
Glu Lys Met Leu Ile Asp Lys Leu Asn Tyr Leu Val Asp Lys Lys Ala
865 870 875 880

Asp Ala Ser Val Ser Gly Gly Leu Leu Asn Ala Tyr Gln Leu Thr Ser
885 890 895
Lys Phe Asp Ser Phe Gln Lys Leu Gly Lys Gln Ser Gly Phe Leu Phe
900 905 910
Tyr Ile Pro Ala Trp Asn Thr Ser Lys Ile Asp Pro Val Thr Gly Phe
915 920 925
Val Asn Leu Leu Asp Thr Arg Tyr Gln Asn Val Glu Lys Ala Lys Val
930 935 940

Phe Phe Ser Lys Phe Asp Ala Ile Arg Tyr Asn Lys Asp Lys Asp Trp
945 950 955 960
Phe Glu Phe Asn Leu Asp Tyr Asp Lys Phe Gly Lys Lys Ala Glu Gly
965 970 975
Thr Arg Thr Lys Trp Ala Leu Cys Thr Arg Gly Met Arg Ile Asp Thr
980 985 990
Phe Arg Asn Lys Glu Lys Asn Ser Gln Trp Asp Asn Gln Glu Val Asp
995 1000 1005

Leu Thr Ala Glu Met Lys Ser Leu Leu Glu His Tyr Tyr Ile Asp
1010 1015 1020
Ile His Gly Asn Leu Lys Asp Ala Ile Ser Ala Gln Thr Asp Lys
1025 1030 1035
Ala Phe Phe Thr Gly Leu Leu His Ile Leu Lys Leu Thr Leu Gln
1040 1045 1050
Met Arg Asn Ser Ile Thr Gly Thr Glu Thr Asp Tyr Leu Val Ser
1055 1060 1065

Pro Val Ala Asp Glu Asn Gly Ile Phe Tyr Asp Ser Arg Ser Cys
1070 1075 1080
Gly Asp Glu Leu Pro Glu Asn Ala Asp Ala Asn Gly Ala Tyr Asn

1085 1090 1095

Ile Ala Arg Lys Gly Leu Met Met Ile Glu Gln Ile Lys Asp Ala

1100 1105 1110

Lys Asp Leu Asp Asn Leu Lys Phe Asp Ile Ser Asn Lys Ser Trp

1115 1120 1125

Leu Asn Phe Ala Gln Gln Lys Pro Tyr Lys Asn Glu

1130 1135 1140

<210> 86

<211> 832

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 86

Met Asn Glu Ala Asp Pro Asn Asn Ala Tyr Phe Val Glu Asn Tyr Phe

1 5 10 15

Ala Thr Phe Gly Ala Val Asn Thr Pro Thr Met Gln Arg Glu Asn Leu

20 25 30

Phe Ala Leu Val Leu Asn Ala Tyr Thr Glu Val Ala Ser Leu Leu His

35 40 45

Ser Tyr Tyr Pro Ala Glu Lys Asn Leu Ala Gln Asp Lys Ala Asn Val

50 55 60

Ala Lys Ile Lys Ala Leu Leu Asp Ala Ile Lys Ser Leu Gln His Phe

65 70 75 80

Val Lys Pro Leu Leu Gly Lys Gly Asp Glu Ser Asp Lys Asp Glu Arg

85 90 95

Phe Tyr Gly Glu Leu Ala Ser Leu Trp Ala Glu Leu Glu Thr Val Thr

100 105 110

Pro Leu Tyr Asn Met Ile Arg Asn Tyr Met Thr Arg Lys Pro Tyr Ser

115 120 125

Gln Lys Lys Ile Lys Leu Asn Phe Glu Asn Pro Gln Leu Leu Gly Gly

130 135 140

Trp Asp Ala Asn Lys Glu Lys Asp Tyr Ala Thr Ile Ile Leu Arg Arg
145 150 155 160
Asn Gly Leu Tyr Tyr Leu Ala Ile Met Asp Lys Asp Ser Arg Lys Leu

165 170 175
Leu Gly Lys Ala Met Pro Ser Asp Gly Glu Cys Tyr Glu Lys Met Val
180 185 190
Tyr Lys Leu Leu Pro Gly Ala Asn Lys Met Leu Pro Lys Val Phe Phe
195 200 205
Ala Lys Ser Arg Met Glu Asp Phe Lys Pro Ser Lys Glu Leu Val Glu
210 215 220
Lys Tyr Asn Asn Gly Thr His Lys Lys Gly Lys Asn Phe Asn Ile Gln

225 230 235 240
Asp Cys His Asn Leu Ile Asp Tyr Phe Lys Gln Ser Ile Ser Lys His
245 250 255
Glu Asp Trp Gly Lys Phe Gly Phe Asn Phe Ser Asp Thr Ser Thr Tyr
260 265 270
Glu Asp Leu Ser Gly Phe Tyr Arg Glu Val Glu Gln Gln Gly Tyr Lys
275 280 285
Leu Ser Phe Ala Arg Val Ser Val Ser Tyr Ile Ser Gln Leu Val Glu

290 295 300
Glu Gly Lys Met Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Glu
305 310 315 320
Tyr Ser Lys Gly Thr Pro Asn Met His Thr Leu Tyr Trp Lys Ala Leu
325 330 335
Phe Asp Glu Arg Asn Leu Ala Asp Val Val Tyr Lys Leu Asn Gly Gln
340 345 350
Ala Glu Met Phe Tyr Arg Lys Lys Ser Ile Glu Asn Thr His Pro Thr

355 360 365
His Pro Ala Thr His Pro Ile Leu Asn Lys Asn Lys Asp Asn Lys Lys
370 375 380
Lys Glu Ser Leu Phe Glu Tyr Asp Leu Ile Lys Asp Arg Arg Tyr Thr

385 390 395 400

Val Asp Lys Phe Met Phe His Val Pro Ile Thr Met Asn Phe Lys Ser

405 410 415

Val Gly Ser Glu Asn Ile Asn Gln Gly Val Lys Glu Tyr Leu His His

420 425 430

Ala Asp Asp Met His Ile Ile Gly Ile Asp Arg Gly Glu Arg His Leu

435 440 445

Leu Tyr Leu Val Val Ile Asp Leu Gln Gly Asn Ile Lys Glu Gln Tyr

450 455 460

Ser Leu Asn Glu Ile Val Asn Glu Tyr Asn Gly Asn Thr Tyr His Thr

465 470 475 480

Asn Tyr His Asp Leu Leu Asp Ala Arg Glu Asp Glu Arg Leu Lys Ala

485 490 495

Arg Gln Ser Trp Gln Thr Ile Glu Asn Ile Lys Glu Leu Lys Glu Gly

500 505 510

Tyr Leu Ser Gln Val Ile His Lys Ile Thr Gln Leu Met Val Lys Tyr

515 520 525

His Ala Ile Val Val Leu Glu Asp Leu Asn Met Gly Phe Met Arg Gly

530 535 540

Arg Gln Lys Val Glu Lys Gln Val Tyr Gln Lys Phe Glu Lys Met Leu

545 550 555 560

Ile Asp Lys Leu Asn Tyr Leu Val Asp Lys Lys Ala Asp Ala Ser Val

565 570 575

Ser Gly Gly Leu Leu Asn Ala Tyr Gln Leu Thr Ser Lys Phe Asp Ser

580 585 590

Phe Gln Lys Leu Gly Lys Gln Ser Gly Phe Leu Phe Tyr Ile Pro Ala

595 600 605

Trp Asn Thr Ser Lys Ile Asp Pro Val Thr Gly Phe Val Asn Leu Leu

610 615 620

Asp Ala Arg Tyr Gln Asn Val Glu Lys Ala Lys Ala Phe Phe Ser Lys

625 630 635 640

Phe Asp Ala Ile Arg Tyr Asn Lys Asp Lys Asp Trp Phe Glu Phe Asn
645 650 655
Leu Asp Tyr Asp Lys Phe Gly Lys Lys Ala Glu Gly Thr Arg Thr Lys
660 665 670
Trp Thr Leu Cys Thr Arg Gly Met Arg Ile Asp Thr Phe Arg Asn Lys

675 680 685
Glu Lys Asn Ser Gln Trp Asp Asn Gln Glu Val Asp Leu Thr Ala Glu
690 695 700
Leu Lys Ser Leu Leu Glu His Tyr Tyr Ile Asp Ile His Gly Asn Leu
705 710 715 720
Lys Glu Ala Ile Ser Thr Gln Thr Asp Lys Ala Phe Phe Thr Gly Leu
725 730 735
Leu His Ile Leu Lys Leu Thr Leu Gln Met Arg Asn Ser Ile Thr Gly

740 745 750
Thr Glu Thr Asp Tyr Leu Val Ser Pro Val Ala Asp Glu Asn Gly Ile
755 760 765
Phe Tyr Asp Ser Arg Thr Cys Gly Asp Glu Leu Pro Glu Asn Ala Asp
770 775 780
Ala Asn Gly Ala Tyr Asn Ile Ala Arg Lys Gly Leu Met Met Ile Glu
785 790 795 800
Gln Ile Lys Asn Ala Glu Asp Leu Gly Asn Leu Lys Phe Asp Ile Ser

805 810 815
Asn Lys Ala Trp Leu Asn Phe Ala Gln Gln Lys Pro Tyr Lys Asn Gly
820 825 830

<210> 87
<211> 831
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 87
Met Asp Asn Asn Asn Leu His Ala Val Asp Gly Tyr Phe Ala Thr Leu

1 5 10 15

Gly Ala Val Asn Thr Pro Thr Met Gln Arg Glu Asn Leu Phe Ala Leu

20 25 30

Ile Gln Asn Ala Tyr Thr Asp Ile Ser Asp Leu Leu Asp Thr Pro Tyr

35 40 45

Pro Glu Asn Lys Asn Leu Ala Gln Asp Lys Thr Asn Val Ala Lys Val

50 55 60

Lys Ala Leu Leu Asp Ala Ile Lys Ser Leu Gln His Phe Val Lys Pro

65 70 75 80

Leu Leu Gly Met Gly Asp Glu Ser Asp Lys Asp Glu Arg Phe Tyr Gly

85 90 95

Glu Leu Ala Ser Leu Trp Thr Glu Leu Asp Thr Val Thr Pro Leu Tyr

100 105 110

Asn Met Ile Arg Asn Tyr Met Thr Arg Lys Pro Tyr Ser Glu Lys Lys

115 120 125

Ile Lys Leu Asn Phe Glu Asn Pro Gln Leu Leu Gly Gly Trp Asp Ala

130 135 140

Asn Lys Glu Lys Asp Tyr Ala Thr Ile Ile Leu Arg Arg Asn Gly Met

145 150 155 160

Tyr Tyr Leu Ala Ile Met Asp Lys Asp Ser Lys Lys Leu Leu Gly Lys

165 170 175

Thr Met Pro Ser Asp Gly Glu Cys Tyr Glu Lys Met Val Tyr Lys Leu

180 185 190

Leu Pro Gly Ala Asn Lys Met Leu Pro Lys Val Phe Phe Ala Lys Ser

195 200 205

Arg Ile Asn Asp Phe Lys Pro Ser Lys Lys Ile Val Glu Asn Tyr Asn

210 215 220

Asn Gly Thr His Lys Lys Gly Lys Asn Phe Asn Ile Asn Asp Cys His

225 230 235 240

Asp Leu Ile Asp Tyr Phe Lys Gln Ser Ile Asp Lys His Glu Asp Trp

245 250 255

Ser Lys Phe Gly Phe Asn Phe Ser Asp Thr Ser Thr Tyr Glu Asp Leu
260 265 270
Ser Gly Phe Tyr Arg Glu Val Glu Gln Gln Gly Tyr Lys Leu Ser Phe

275 280 285
Thr Asn Ile Ser Val Ser Phe Ile Asp Lys Leu Val Asp Glu Gly Lys
290 295 300
Met Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Asp Tyr Ser Lys
305 310 315 320
Gly Thr Pro Asn Met His Thr Leu Tyr Trp Lys Ala Leu Phe Asp Glu
325 330 335
Arg Asn Leu Ala Asp Val Val Tyr Lys Leu Asn Gly Glu Ala Glu Met

340 345 350
Phe Tyr Arg Lys Lys Ser Ile Asn Asn Thr His Pro Thr His His Ala
355 360 365
Asn His Pro Ile Gln Asn Lys Asn Lys Asp Asn Lys Lys Lys Glu Ser
370 375 380
Val Phe Glu Tyr Asp Leu Val Lys Asp Arg Arg Tyr Thr Glu Asp Lys
385 390 395 400
Phe Leu Phe His Val Pro Ile Thr Met Asn Phe Asn Ser Val Gly Ala

405 410 415
Glu Asn Ile Asn Gln Gln Val Arg Lys Tyr Leu Gln Gln Ala Asp Asp
420 425 430
Thr His Ile Ile Gly Ile Asp Arg Gly Glu Arg His Leu Leu Tyr Leu
435 440 445
Val Val Ile Asp Met Gln Gly Asn Ile Lys Glu Gln Phe Ser Leu Asn
450 455 460
Glu Ile Val Asn Glu Tyr Asn Gly Asn Thr Tyr Arg Thr Asn Tyr His

465 470 475 480
Asp Leu Leu Asp Val Arg Ala Asp Lys Arg Leu Lys Ala Ser Gln Ser
485 490 495
Trp Gln Thr Ile Glu Asn Ile Lys Glu Leu Lys Glu Gly Tyr Leu Ser

500 505 510

Gln Ala Ile His Lys Ile Thr Gln Leu Met Val Lys Tyr His Ala Val

515 520 525

Val Val Leu Glu Asp Leu Asn Lys Gly Phe Met Arg Gly Arg Gln Lys

530 535 540

Val Glu Lys Gln Val Tyr Gln Lys Phe Glu Lys Met Leu Ile Asp Lys

545 550 555 560

Leu Asn Tyr Leu Val Asp Lys His Lys Asp Ala Asn Glu Thr Gly Gly

565 570 575

Leu Leu His Ala Leu Gln Leu Thr Ser Glu Phe Lys Asn Phe Lys Lys

580 585 590

Ser Glu Tyr Gln Asn Gly Phe Leu Phe Tyr Ile Pro Ala Trp Asn Thr

595 600 605

Ser Lys Ile Asp Pro Val Thr Gly Phe Val Asn Arg Phe Asp Thr Arg

610 615 620

Tyr Thr Asn Ala Val Glu Ala Gln Lys Phe Phe Arg Lys Phe Asp Glu

625 630 635 640

Ile Arg Tyr Asn Glu Glu Lys Asp Trp Phe Glu Phe Glu Phe Asp Tyr

645 650 655

Asp Lys Phe Thr Gln Lys Ala His Gly Thr Arg Thr Arg Trp Thr Leu

660 665 670

Cys Thr His Gly Lys Arg Leu Arg Ser Phe Arg Asn Pro Ala Lys Gln

675 680 685

Tyr Asn Trp Asp Ser Glu Val Val Ala Leu Thr Asp Glu Phe Lys Arg

690 695 700

Ile Leu Gly Glu Ala Gly Ile Asp Ile His Glu Asn Leu Lys Asp Ala

705 710 715 720

Ile Ser Asn Leu Glu Gly Lys Arg Arg Lys Tyr Leu Glu Pro Leu Met

725 730 735

Gln Phe Met Lys Leu Leu Leu Gln Leu Arg Asn Ser Arg Lys Asn Pro

740 745 750

Glu Glu Asp Tyr Ile Leu Ser Pro Val Ala Asp Glu Asn Gly Val Phe

755 760 765

Tyr Asp Ser Arg Ser Cys Gly Asp Lys Leu Pro Glu Asn Ala Asp Ala

770 775 780

Asn Gly Ala Tyr Asn Ile Ala Arg Lys Gly Leu Met Leu Ile Arg Gln

785 790 795 800

Ile Lys Glu Ala Lys Glu Leu Gly Lys Val Lys Tyr Asp Ile Ser Asn

805 810 815

Lys Ala Trp Leu Asn Phe Ala Gln Gln Lys Pro Tyr Lys Asn Glu

820 825 830

<210> 88

<211> 1177

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 88

Met Gln Lys Lys Ala Phe Glu Glu Asn Gln Gln Asn Leu Arg Ser Ile

1 5 10 15

Ile Ala Lys Lys Leu Thr Glu Asp Lys Ala Tyr Ala Asn Leu Phe Gly

20 25 30

Lys Asn Leu Leu Glu Ser Tyr Lys Asp Lys Thr Asp Lys Thr Lys Ile

35 40 45

Ile Asp Ser Asp Leu Ile Lys Phe Ile Asn Thr Ala Glu Ser Thr Gln

50 55 60

Leu Asp Ser Met Ser Gln Asp Glu Ala Lys Glu Ile Val Lys Glu Phe

65 70 75 80

Trp Gly Phe Thr Thr Tyr Phe Val Gly Phe Phe Asp Asn Arg Lys Asn

85 90 95

Met Tyr Thr Ala Glu Glu Lys Ser Thr Gly Ile Ala Tyr Arg Leu Ile

100 105 110

Asn Glu Asn Leu Pro Lys Phe Ile Asp Asn Met Glu Ala Phe Lys Lys

115 120 125

Ala Ile Ala Arg Pro Glu Ile Gln Ala Asp Met Glu Glu Leu Tyr Ser

130 135 140

Asn Phe Ser Glu Tyr Leu Asn Val Glu Ser Ile Gln Glu Met Phe Leu

145 150 155 160

Leu Asp Tyr Tyr Asn Met Leu Leu Thr Gln Lys Gln Ile Asp Val Tyr

165 170 175

Asn Ala Ile Ile Gly Gly Lys Thr Asp Asp Glu His Asp Val Lys Ile

180 185 190

Lys Gly Ile Asn Glu Tyr Ile Asn Leu Tyr Asn Gln Gln His Lys Asp

195 200 205

Asp Lys Leu Pro Lys Leu Lys Ala Leu Phe Lys Gln Ile Leu Ser Asp

210 215 220

Arg Asn Ala Ile Ser Trp Leu Pro Glu Glu Phe Asn Ser Asp Gln Glu

225 230 235 240

Val Leu Asn Ala Ile Lys Asp Cys Tyr Glu Arg Leu Ser Glu Asn Val

245 250 255

Leu Gly Asp Lys Val Leu Lys Ser Met Leu Gly Ser Leu Ala Asp Tyr

260 265 270

Ser Leu Asp Gly Ile Phe Ile Arg Asn Asp Leu Gln Leu Thr Asp Ile

275 280 285

Ser Gln Lys Met Phe Gly Asn Trp Ser Val Ile Gln Asn Ala Ile Met

290 295 300

Gln Asn Ile Lys His Val Ala Pro Ala Arg Lys His Lys Glu Ser Glu

305 310 315 320

Glu Glu Tyr Glu Asn Arg Ile Ala Gly Ile Phe Lys Lys Ala Asp Ser

325 330 335

Phe Ser Ile Ser Tyr Ile Asp Ala Cys Leu Asn Glu Thr Asp Pro Asn

340 345 350

Asn Ala Tyr Phe Val Glu Asn Tyr Phe Ala Thr Leu Gly Ala Val Asp

355 360 365

Thr Pro Thr Met Gln Arg Glu Asn Leu Phe Ala Leu Val Gln Asn Ala

370 375 380

Tyr Thr Glu Ile Thr Ala Leu Leu His Ser Asp Tyr Pro Thr Glu Lys

385 390 395 400

Asn Leu Ala Gln Asp Lys Ala Asn Val Ala Lys Ile Lys Ala Leu Leu

405 410 415

Asp Ala Ile Lys Ser Leu Gln His Phe Val Lys Pro Leu Leu Gly Lys

420 425 430

Gly Asp Glu Ser Asp Lys Asp Glu Arg Phe Tyr Gly Glu Leu Ala Ser

435 440 445

Leu Trp Ala Glu Leu Asp Thr Met Thr Pro Leu Tyr Asn Met Ile Arg

450 455 460

Asn Tyr Met Thr Arg Lys Pro Tyr Ser Gln Lys Lys Ile Lys Leu Asn

465 470 475 480

Phe Glu Asn Pro Gln Leu Leu Gly Gly Trp Asp Ala Asn Lys Glu Lys

485 490 495

Asp Tyr Ala Thr Ile Ile Leu Arg Arg Asn Gly Leu Tyr Tyr Leu Ala

500 505 510

Ile Met Asn Lys Asp Ser Lys Lys Leu Leu Gly Lys Ala Met Pro Ser

515 520 525

Asp Gly Glu Cys Tyr Glu Lys Met Val Tyr Lys Leu Leu Pro Gly Ala

530 535 540

Asn Lys Met Leu Pro Lys Val Phe Phe Ala Lys Ser Arg Met Glu Asp

545 550 555 560

Phe Lys Pro Ser Lys Glu Leu Val Glu Lys Tyr Asn Asn Gly Thr His

565 570 575

Lys Lys Gly Lys Asn Phe Asn Ile Gln Asp Cys His Asn Leu Ile Asp

580 585 590

Tyr Phe Lys Gln Ser Ile Asp Lys His Glu Asp Trp Ser Lys Phe Gly

595 600 605

Phe Lys Phe Ser Asp Thr Ser Thr Tyr Glu Asp Leu Ser Gly Phe Tyr

610 615 620

Arg Glu Val Glu Gln Gln Gly Tyr Lys Leu Ser Phe Ala Arg Val Ser

625 630 635 640

Val Ser Tyr Ile Asn Gln Leu Val Glu Glu Gly Lys Met Tyr Leu Phe

645 650 655

Gln Ile Tyr Asn Lys Asp Phe Ser Glu Tyr Ser Lys Gly Thr Pro Asn

660 665 670

Met His Thr Leu Tyr Trp Lys Ala Leu Phe Asp Glu Arg Asn Leu Ala

675 680 685

Asp Val Val Tyr Lys Leu Asn Gly Gln Ala Glu Met Phe Tyr Arg Lys

690 695 700

Lys Ser Ile Glu Asn Thr His Pro Thr His Pro Ala Asn His Pro Ile

705 710 715 720

Leu Asn Lys Asn Lys Asp Asn Lys Lys Lys Glu Ser Leu Phe Glu Tyr

725 730 735

Asp Leu Ile Lys Asp Arg Arg Tyr Thr Val Asp Lys Phe Met Phe His

740 745 750

Val Pro Ile Thr Met Asn Phe Lys Ser Val Gly Ser Glu Asn Ile Asn

755 760 765

Gln Asp Val Lys Ala Tyr Leu Arg His Ala Asp Asp Met His Ile Ile

770 775 780

Gly Ile Asp Arg Gly Glu Arg His Leu Leu Tyr Leu Val Val Ile Asp

785 790 795 800

Leu Gln Gly Asn Ile Lys Glu Gln Phe Ser Leu Asn Glu Ile Val Asn

805 810 815

Asp Tyr Asn Gly Asn Thr Tyr His Thr Asn Tyr His Asp Leu Leu Asp

820 825 830

Val Arg Glu Asp Glu Arg Leu Lys Ala Arg Gln Ser Trp Gln Thr Ile

835 840 845

Glu Asn Ile Lys Glu Leu Lys Glu Gly Tyr Leu Ser Gln Val Ile His

850 855 860

Lys Ile Thr Gln Leu Met Val Lys Tyr His Ala Ile Val Val Leu Glu
865 870 875 880
Asp Leu Asn Met Gly Phe Met Arg Gly Arg Gln Lys Val Glu Lys Gln
885 890 895
Val Tyr Gln Lys Phe Glu Lys Met Leu Ile Glu Lys Leu Asn Tyr Leu

900 905 910
Val Asp Lys Lys Ala Asp Ala Ser Val Ser Gly Gly Leu Leu Asn Ala
915 920 925
Tyr Gln Leu Thr Ser Lys Phe Asp Ser Phe Gln Lys Leu Arg Lys Gln
930 935 940
Ser Gly Phe Leu Phe Tyr Ile Pro Ala Trp Asn Thr Ser Lys Ile Asp
945 950 955 960
Pro Ile Thr Gly Phe Val Asn Leu Leu Asp Thr Arg Tyr Gln Asn Val

965 970 975
Glu Lys Ala Lys Ala Phe Phe Ser Lys Phe Asp Ala Ile Arg Tyr Asn
980 985 990
Lys Asp Lys Glu Trp Phe Glu Phe Asp Leu Asp Tyr Asp Lys Phe Gly
995 1000 1005
Arg Lys Ala Glu Gly Thr Arg Thr Lys Trp Thr Leu Cys Thr Arg
1010 1015 1020
Gly Met Arg Ile Asp Thr Phe Arg Asn Lys Glu Lys Asn Ser Gln

1025 1030 1035
Trp Asp Asn Gln Glu Ile Asp Leu Thr Ala Glu Met Lys Ser Leu
1040 1045 1050
Leu Glu His Tyr Tyr Ile Asp Ile Gln Gly Asn Leu Lys Glu Ala
1055 1060 1065
Ile Cys Thr Gln Thr Asp Lys Ala Phe Phe Thr Gly Leu Leu His
1070 1075 1080
Ile Leu Lys Leu Thr Leu Gln Met Arg Asn Ser Ile Thr Gly Thr

1085 1090 1095
Gln Thr Asp Tyr Leu Val Ser Pro Val Ala Asp Glu Asn Gly Ile

1100 1105 1110

Phe Tyr Asp Ser Arg Ser Cys Gly Asp Ser Leu Pro Glu Asn Ala

1115 1120 1125

Asp Ala Asn Gly Ala Tyr Asn Ile Ala Arg Lys Gly Leu Met Leu

1130 1135 1140

Ile Glu Lys Ile Lys Asn Ala Glu Asp Leu Asp Thr Ile Lys Phe

1145 1150 1155

Asp Ile Ser Asn Lys Ala Trp Leu Asn Phe Ala Gln Gln Lys Pro

1160 1165 1170

Tyr Lys Asn Gly

1175

<210> 89

<211> 814

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 89

Met Leu Glu Asn Glu Gln Glu Ala Glu Lys Ile Lys Asn Lys Leu Asp

1 5 10 15

Asp Ile Met Asn Ile Tyr His Trp Ile Lys Ile Phe Leu Val Asp Glu

20 25 30

Glu Ile Glu Lys Asp Met Asp Phe Tyr Ser Glu Ile Glu Asp Ile Tyr

35 40 45

Glu Glu Leu Ser Pro Leu Val Ser Leu Tyr Asn Arg Val Arg Asn Tyr

50 55 60

Val Thr Gln Lys Pro Tyr Ser Gln Glu Lys Met Lys Leu Asn Phe Gly

65 70 75 80

Ser Pro Thr Leu Ala Asp Gly Trp Ser Lys Ser Lys Glu Phe Ser Asn

85 90 95

Asn Ala Ile Ile Met Leu Lys Asp Gly Lys Tyr Tyr Ile Gly Ile Phe

100 105 110

Asn Ile Arg Asn Lys Pro Asn Lys Glu Val Ile Glu Gly Arg Asn Asn
115 120 125
Arg Ile Asn Asp Ser Asp Tyr Lys Lys Met Val Tyr Arg Leu Leu Pro
130 135 140
Gly Ala Asn Lys Met Leu Pro Lys Val Met Phe Ser Lys Lys Gly Ile

145 150 155 160
Glu Tyr Tyr Asn Pro Ser Gln Tyr Ile Leu Ser Gly Tyr Asn Ser Lys
165 170 175
Lys His Ile Lys Ser Asn Glu Asn Phe Asp Ile Asn Phe Cys His Asp
180 185 190
Leu Ile Asp Phe Phe Lys Glu Ser Ile Asn Lys Asn Glu Glu Trp Lys
195 200 205
Asn Phe Asp Phe Lys Phe Ser Asp Thr Glu Ser Tyr Asn Asp Ile Ser

210 215 220
Glu Phe Tyr Arg Glu Val Glu Gln Gln Gly Tyr Lys Ile Glu Trp Val
225 230 235 240
Tyr Ile Ser Glu Gln Asp Ile Glu Gln Leu Glu Lys Asn Gly Gln Leu
245 250 255
Tyr Ile Phe Gln Ile Tyr Asn Lys Asp Phe Ala Lys Lys Ser Ile Gly
260 265 270
Asn Lys Asn Leu His Thr Met Tyr Leu Glu Asn Leu Phe Ser Glu Glu

275 280 285
Asn Leu Lys Asp Val Val Leu Lys Leu Asn Gly Glu Ala Glu Ile Phe
290 295 300
Phe Arg Lys Ser Ser Ile Lys Lys Pro Ile Val His Lys Ala Gly Ser
305 310 315 320
Ile Leu Val Asn Lys Cys Ile Glu Asp Glu Thr Gly Asn Lys Val Ser
325 330 335
Phe Pro Asp Asp Ile Tyr Asn Glu Ile Tyr Gln Tyr Met Asn Gly Met

340 345 350
Thr Asp Val Leu Ser Glu Arg Ala Gln Asn Tyr Tyr Glu Lys Val Lys

355 360 365

His Ser Val Ser Lys Gln Asp Ile Val Lys Asp Tyr Arg Tyr Thr Val

370 375 380

Asp Lys Tyr Phe Ile His Leu Pro Ile Thr Ile Asn Phe Lys Ala Ser

385 390 395 400

Ser Phe Met Pro Ile Asn Asp Ile Ala Leu Lys Tyr Ile Ala Lys Arg

405 410 415

Asp Asp Ile His Ile Ile Gly Ile Asp Arg Gly Glu Arg Asn Leu Ile

420 425 430

Tyr Val Ser Val Ile Asp Leu Gln Gly Asn Ile Val Tyr Gln Lys Asn

435 440 445

Tyr Asn Val Val Asn Gly Tyr Asp Tyr Lys Ala Lys Leu Arg Glu Thr

450 455 460

Glu Ile Gln Arg Asp Asn Ala Arg Lys Asn Trp Lys Glu Ile Gly Lys

465 470 475 480

Ile Lys Gln Leu Lys Glu Gly Tyr Leu Ser Leu Val Val His Glu Ile

485 490 495

Ala Gln Leu Ile Val Lys Tyr Asn Ala Ile Val Val Met Glu Asp Leu

500 505 510

Asn Met Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Arg Gln Val Tyr

515 520 525

Gln Lys Phe Glu Asn Met Leu Ile Asn Lys Leu Asn Tyr Leu Val Asp

530 535 540

Lys Asn Lys Lys Val Asp Glu Asp Gly Gly Leu Leu Arg Gly Tyr Gln

545 550 555 560

Leu Thr Tyr Val Pro Gly Gln Lys Glu His Val Gly Lys Gln Cys Gly

565 570 575

Phe Ile Phe Tyr Val Pro Ala Ala Tyr Thr Ser Lys Ile Asp Pro Thr

580 585 590

Thr Gly Phe Val Ser Ile Phe Asn Asn Lys Val Asn Ala Lys Glu Phe

595 600 605

Val Thr Lys Phe Asp Ser Ile Lys Tyr Asn Lys Asn Met Lys Met Phe
610 615 620
Glu Leu Lys Phe Asp Tyr Asn Asn Phe Glu Thr Tyr Asn Ile Thr Leu
625 630 635 640
Ala Lys Ser Lys Trp Thr Ile Tyr Thr Asn Gly Ile Arg Leu Lys Arg
645 650 655
Glu Tyr Asn Asn Gly Arg Trp Asn Lys Ile Thr Glu Val Asp Leu Thr

660 665 670
Lys Glu Met Ala Asn Thr Leu Lys Lys Tyr Asp Ile Glu Phe Glu Asn
675 680 685
Asn Glu Glu Ile Leu Lys Ser Ile Ser Gln Leu Asp Glu Lys Asn Gln
690 695 700
Arg Asn Ile Cys Asn Glu Ile Lys Glu Ile Ile Lys Leu Ile Val Gln
705 710 715 720
Leu Arg Asn Ser Met Pro Asp Asn Gly Ser Lys Asp Asn Glu Tyr Asp

725 730 735
Lys Ile Ile Ser Pro Val Leu Asn Glu Asn Asn Tyr Phe Tyr Asp Ser
740 745 750
Ser Glu Val Cys Asp Asn Ser Ala Pro Glu Asn Ala Asp Ala Asn Gly
755 760 765
Ala Tyr Cys Ile Ala Met Lys Gly Leu Tyr Gln Val Ile Gln Ile Lys
770 775 780
Glu Asn Trp Ser Gln Asp Ser Asn Pro Lys Asn Ile Leu Gly Ile Lys

785 790 795 800
His Tyr Glu Trp Phe Asp Phe Met Gln Asn Lys Arg Tyr Leu
805 810

<210> 90
<211> 1262
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence

<400> 90

Met Ala Lys Asn Thr Ile Phe Thr Gln Phe Thr Gly Leu Tyr Pro Val
1 5 10 15

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Met Gly Lys Thr Leu Glu
20 25 30

Lys Ile Lys Glu Thr Gly Val Ile Glu Asn Asp Lys Lys Arg His Asn
35 40 45

Asp Tyr Phe Asp Ala Lys Lys Ile Ile Asp Lys Tyr His Lys Tyr Phe
50 55 60

Ile Asp Ala Ala Leu Ser Lys Phe Ser Arg Ile Asp Trp Asn Pro Leu
65 70 75 80

Lys Glu Ala Ile Glu Gly Ser Leu Asp Arg Ser Asp Ala Ser Lys Lys
85 90 95

Lys Leu Glu Lys Thr Gln Thr Glu Phe Arg Lys Lys Ile Ala Lys Ala
100 105 110

Leu Thr Thr His Asp His Tyr Lys Glu Leu Thr Ala Ser Thr Pro Lys
115 120 125

Asp Leu Phe Leu Lys Val Phe Pro Asp His Phe Gly Lys Gln Pro Ala
130 135 140

Ile Asp Thr Phe Asp Gly Phe Ser Ser Tyr Phe Thr Gly Phe Gln Glu
145 150 155 160

Asn Arg Gln Asn Ile Tyr Ser Asp Glu Ala Ile Ser Thr Ala Ile Pro
165 170 175

Tyr Arg Leu Val His Asp Asn Phe Pro Lys Phe Leu Ser Asn Ile Glu
180 185 190

Val Tyr Lys Thr Leu Lys Asp Asn Ala Pro Ser Val Leu Ser Asp Ala
195 200 205

Glu Asn Glu Leu Lys Asp Phe Leu Asn Gly Lys Pro Leu Ala Asn Ile
210 215 220

Phe Glu Leu Asn Ala Tyr Asn Asp Val Leu Thr Gln Ser Gly Ile Asp
225 230 235 240

Phe Phe Asn Gln Val Ile Gly Gly Ile Ser Gly Glu Gly Gly Glu Lys
245 250 255
Lys Thr Arg Gly Ile Asn Glu Phe Ser Asn Leu Tyr Arg Gln Gln His
260 265 270
Pro Glu Phe Ala Gln Lys Arg Leu Ala Thr Lys Met Ile Pro Leu Tyr
275 280 285

Lys Gln Ile Leu Ser Asp Arg Glu Thr Lys Ser Phe Ile Leu Glu Ser
290 295 300
Tyr Ser Thr Asp Ser Gln Val Gln Glu Ser Val Lys Glu Phe Phe Glu
305 310 315 320
Ser Gln Ile Leu Asn Cys Asp Ile Ala Gly Arg Lys Val Asn Val Leu
325 330 335
Asn Glu Leu Thr Ser Leu Ile Lys Arg Ile Ala Glu Phe Asp Leu Gly
340 345 350

Ser Ile Tyr Ile Asn Gln Glu Glu Leu Ser Asn Ile Ser Leu Glu Leu
355 360 365
Phe Lys Ser Trp Asn Thr Ile Asn Ala Val Leu Phe Lys Asn Ala Glu
370 375 380
Asn Arg Ile Gly Ser Ala Glu Lys Ala Ala Asn Lys Lys Lys Ile Asp
385 390 395 400
Ala Trp Met Lys Ser Asn Glu Phe Ser Ile Ala Thr Leu Asn Leu Ala
405 410 415

Ile Ala Glu Ser Asp Ser Glu Glu Ile Ser Arg Val Lys Ile Glu Ser
420 425 430
Tyr Trp Asn Asp Phe Glu Ala Lys Val Gln Ser Ile Leu Cys Gly Asp
435 440 445
Asn Arg Arg Asn Leu Asp Glu Phe Leu Ser Ala Thr Phe Asn Glu Asn
450 455 460
Asn Ala Leu Arg Glu Asp Ser Glu Ile Ile Gly Lys Leu Lys Ala Phe
465 470 475 480

Leu Asp Ala Leu Ile Glu Ile Met His Ser Ile Lys Pro Leu Ile Ser

485 490 495

Asp Ala Glu Asn Arg Asp Leu Ser Phe Tyr Asn Glu Leu Met Pro Leu

500 505 510

Tyr Asp Gln Leu Ser Leu Val Val Pro Leu Tyr Asn Lys Ile Arg Asn

515 520 525

Tyr Ala Thr Gln Lys Leu Thr Glu Ser Glu Lys Phe Lys Leu Asn Phe

530 535 540

Asp Asn Pro Thr Leu Ala Asp Gly Trp Asp Gln Asn Lys Glu Asp Ala

545 550 555 560

Asn Thr Ala Ile Leu Leu Leu Lys Asn Gly Leu Tyr Tyr Leu Gly Ile

565 570 575

Met Asn Ala Lys Asn Lys Pro Lys Ile Lys Asp Phe Lys Thr Ser Glu

580 585 590

Ser Glu Asp Cys Tyr Asp Lys Met Val Tyr Lys Leu Leu Pro Gly Pro

595 600 605

Asn Lys Met Leu Pro Lys Val Phe Phe Ser Glu Lys Gly Leu Ala Thr

610 615 620

Phe Lys Pro Pro Lys Asp Ile Leu Asp Gly Tyr Asn Ala Gly Lys His

625 630 635 640

Lys Lys Gly Asp Leu Phe Asp Ile Gly Phe Cys His Gln Leu Ile Asp

645 650 655

Phe Phe Lys Glu Ser Ile Ala Lys His Pro Asp Trp Lys Lys Phe Asp

660 665 670

Phe Lys Phe Ser Asp Thr Ser Ser Tyr Glu Asp Ile Ser Gly Phe Tyr

675 680 685

Lys Glu Val Thr Asp Gln Gly Tyr Lys Ile Thr Phe Ser Lys Ile Pro

690 695 700

Thr Ser Gln Ile Asp Glu Trp Val Asn Glu Gly Lys Leu Phe Leu Phe

705 710 715 720

Gln Ile Tyr Asn Lys Asp Phe Ala Pro Gly Ala Lys Gly Ser Pro Asn

725 730 735

Leu His Thr Leu Tyr Trp Lys Ser Val Phe Ser Pro Glu Asn Leu Lys
740 745 750

Asp Val Val Val Lys Leu Asn Gly Glu Ala Glu Leu Phe Tyr Arg Pro
755 760 765

Ser Ser Val Lys Lys Pro Tyr Ser His Lys Val Gly Glu Lys Leu Val
770 775 780

Asn Arg Ile Gly Lys Asp Gly Leu Pro Leu Pro Glu Ser Val Phe Gly
785 790 795 800

Glu Leu Phe Arg Tyr Phe Asn Gly Lys Leu Asp Gly Glu Leu Ser Asp
805 810 815

Glu Ala Lys Arg Tyr Leu Asp Val Ala Val Val Lys Asp Val Lys His
820 825 830

Glu Ile Val Lys Asp Arg Arg Tyr Thr Gln Asp Lys Phe Glu Phe His
835 840 845

Val Pro Leu Thr Leu Asn Phe Lys Ala Asp Ser Lys Asn Glu Tyr Met
850 855 860

Asn Glu Arg Val Arg His Phe Leu Lys Asp Asn Pro Asp Val Asn Ile
865 870 875 880

Ile Gly Ile Asp Arg Gly Glu Arg His Leu Leu Tyr Met Thr Leu Ile
885 890 895

Asn Gln Lys Gly Glu Ile Leu Lys Gln Lys Ser Phe Asn Ile Val Glu
900 905 910

Ser Val Asn Tyr Gln Ala Lys Leu Val Gln Arg Glu Lys Glu Arg Asp
915 920 925

Ala Ala Arg Lys Ser Trp Ser Ser Val Gly Lys Ile Lys Asp Leu Lys
930 935 940

Glu Gly Phe Leu Ser Gln Val Ile His Glu Ile Thr Thr Thr Met Ile
945 950 955 960

Glu Asn Asn Ala Ile Val Val Leu Glu Asp Leu Asn Phe Gly Phe Lys
965 970 975

Arg Gly Arg Phe Cys Val Glu Arg Gln Val Tyr Gln Lys Phe Glu Lys

980 985 990

Met Leu Ile Asp Lys Leu Asn Tyr Leu Val Phe Lys Asn Lys Pro Glu

995 1000 1005

Gly Asp Val Gly Gly Val Leu Lys Gly Tyr Gln Leu Ala Glu Lys

1010 1015 1020

Phe Asp Ser Phe Gln Lys Leu Gly Lys Gln Ser Gly Phe Leu Phe

1025 1030 1035

Tyr Ile Pro Ala Ala Tyr Thr Ser Lys Ile Asp Pro Thr Thr Gly

1040 1045 1050

Phe Ala Asn Leu Phe Asn Met Thr Glu Leu Thr Ser Ala Glu Lys

1055 1060 1065

Lys Lys Asp Phe Leu Ser His Phe Asp Asp Ile Thr Tyr Asp Gly

1070 1075 1080

Lys Asn Asp Arg Phe Leu Phe Gly Phe Asp Tyr Lys Asn Phe Lys

1085 1090 1095

Cys Phe Gln Thr Asp Phe Ile Lys Lys Trp Thr Val Tyr Thr Gln

1100 1105 1110

Gly Lys Arg Ile Val Tyr Asp Lys Glu Ser Lys Ser Ala Lys Glu

1115 1120 1125

Ile Phe Pro Val Glu Ile Ile Lys Ala Ala Leu Ala Lys Gln Asn

1130 1135 1140

Ile Ala Leu Thr Asp Gln Leu Asp Val Leu Ser Ala Ile Asn Ser

1145 1150 1155

Val Glu Ala Ser Pro Lys Ser Ala Ser Phe Phe Gly Asn Ile Cys

1160 1165 1170

Tyr Ala Phe Glu Lys Thr Leu Gln Met Arg Asn Ser Ile Pro Asn

1175 1180 1185

Thr Asp Glu Asp Tyr Leu Val Ser Pro Val Met Asn Lys Arg Gly

1190 1195 1200

Glu Phe Tyr Asp Ser Arg Ser Cys Asp Asp Ala Leu Pro Gln Asn

1205 1210 1215

Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu Lys Gly Leu Tyr
1220 1225 1230

Leu Ile Lys Asn Val Phe Asp Ala Gly Gly Lys Asp Leu Lys Ile
1235 1240 1245
Ser His Glu Asp Trp Phe Lys Phe Ala Gln Ser Arg Asn Cys
1250 1255 1260

<210> 91

<211> 791

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas12 sequence

<400> 91

Met Arg Pro Val Leu Gln Leu Thr Asp Thr Glu Asp Lys Leu Ser Gln
1 5 10 15
Asn Lys Pro Ala Val Gly Lys Ile Lys Ala Leu Leu Asp Ala Phe Lys

20 25 30
Asp Leu Gln His Phe Ile Lys Pro Leu Leu Gly Ser Gly Glu Glu Asn
35 40 45
Glu Lys Asp Glu Leu Phe Tyr Gly Ala Phe Gln Leu Ile Trp Asp Glu
50 55 60
Leu Asp Thr Val Thr Pro Leu Tyr Asn Lys Val Arg Asn Trp Leu Thr
65 70 75 80
Arg Lys Pro Tyr Ser Thr Glu Lys Ile Lys Leu Asn Phe Asp Asn Ala

85 90 95
Gln Leu Leu Gly Gly Trp Asp Val Asn Lys Glu Pro Asp Cys Thr Gly
100 105 110
Val Leu Leu Arg Lys Asp Gly Phe Tyr Tyr Leu Gly Ile Met Asn Lys
115 120 125
Lys Ser Asn Arg Ile Phe Asp Ala Asp Val Thr Pro Ala Asp Gly Ile
130 135 140

Cys Tyr Glu Lys Ile Asp Tyr Lys Leu Leu Pro Gly Ala Asn Lys Met

145 150 155 160

Leu Pro Lys Val Phe Phe Ser Lys Ser Arg Ile Asp Glu Phe Ala Pro

165 170 175

Ser Glu Ala Ile Leu Ser Ser Tyr Lys Arg Gly Thr His Lys Lys Gly

180 185 190

Ala Asp Phe Ser Leu Ser Asp Cys His Arg Leu Ile Asp Phe Phe Lys

195 200 205

Ala Ser Ile Asn Lys His Glu Asp Trp Ser Lys Phe Gly Phe Gln Phe

210 215 220

Ser Asp Thr Lys Thr Tyr Glu Asp Ile Ser Gly Phe Tyr Arg Glu Val

225 230 235 240

Glu Gln Gln Gly Tyr Met Leu Ser Ser His Gln Val Ser Glu Ala Tyr

245 250 255

Ile Asn Gln Met Val Glu Glu Gly Lys Leu Phe Leu Phe Arg Ile Trp

260 265 270

Asn Lys Asp Phe Ser Glu Tyr Ser Lys Gly Thr Pro Asn Met His Thr

275 280 285

Leu Tyr Trp Arg Met Leu Phe Asp Glu Arg Asn Leu Ala Asp Val Val

290 295 300

Tyr Lys Leu Asn Gly Gln Ala Glu Val Phe Tyr Arg Lys Ala Ser Ile

305 310 315 320

Lys Ala Glu Asn Gln Ile Met His Pro Ala His His Pro Ile Glu Asn

325 330 335

Lys Asn Thr Leu Asn Glu Lys Arg Ser Ser Thr Phe Asp Tyr Asp Leu

340 345 350

Val Lys Asp Arg Arg Tyr Thr Val Asp Lys Phe Gln Phe His Val Pro

355 360 365

Ile Thr Ile Asn Phe Lys Ala Ile Gly Gln Thr Asn Val Asn Pro Ile

370 375 380

Val His Glu Thr Ile Arg Arg Gly Gly Phe Thr His Val Ile Gly Ile

385 390 395 400

Asp Arg Gly Glu Arg His Leu Leu Tyr Leu Ser Leu Ile Asp Leu Lys

405 410 415

Gly His Ile Val Lys Gln Met Thr Leu Asn Glu Ile Ile Asn Glu Tyr

420 425 430

Asn Gly Leu Ala His Lys Thr Asn Tyr Tyr Asp Leu Leu Val Lys Arg

435 440 445

Glu Gly Glu Arg Thr Thr Ala Arg Arg Ser Trp Asp Thr Ile Glu Asn

450 455 460

Ile Lys Glu Leu Lys Glu Gly Tyr Leu Ser Gln Val Ile His Ile Ile

465 470 475 480

Ser Lys Met Met Val Glu Tyr Asn Ala Ile Val Val Leu Glu Asp Leu

485 490 495

Asn Met Gly Phe Met Arg Gly Arg Gln Lys Ile Glu Arg Gln Val Tyr

500 505 510

Glu Lys Phe Glu Lys Met Leu Ile Asp Lys Leu Asn Cys Tyr Ile Asp

515 520 525

Lys Gln Ala Asp Ser Gln Ser Glu Gly Gly Leu Leu His Pro Ile Gln

530 535 540

Leu Ala Asn Lys Phe Glu Ser Phe Arg Lys Leu Gly Lys Gln Ser Gly

545 550 555 560

Cys Leu Phe Tyr Ile Pro Ala Trp Asn Thr Ser Lys Ile Asp Pro Val

565 570 575

Thr Gly Phe Val Asn Leu Phe Asp Thr Arg Tyr Glu Thr Arg Glu Lys

580 585 590

Ala Lys Leu Phe Phe Ser His Phe Gln Arg Ile Cys Phe Asn Ala Glu

595 600 605

Lys Asp Trp Phe Glu Phe Ser Phe Asp Tyr Asn Asp Phe Thr Thr Lys

610 615 620

Ala Glu Gly Thr Arg Thr Gln Trp Thr Leu Cys Ser Tyr Gly Thr Arg

625 630 635 640

Ile Arg Asn Phe Arg Asn Pro Leu Gln Asn His Gln Trp Asp Asp Glu
645 650 655
Glu Ile Val Leu Thr Glu Ala Phe Lys Ala Leu Phe Asp Lys Tyr Asp

660 665 670
Ile Asp Ile His Ala Asn Leu Lys Glu Ala Ile Asn Ala Gln Thr Asp
675 680 685
Ala Gln Phe Phe Lys Asp Leu Met Gly Leu Met Lys Leu Leu Leu Gln
690 695 700
Met Arg Asn Ser Lys Thr Asn Ser Glu Val Asp Tyr Leu Leu Ser Pro
705 710 715 720
Val Ala Asp Glu His Gly Arg Phe Phe Asp Ser Arg Ala Gly Ala Gly

725 730 735
Ser Leu Pro Asp Asn Ala Asp Ala Asn Gly Ala Tyr Asn Ile Ala Arg
740 745 750
Lys Gly Leu Trp Val Ile Arg Lys Ile Gln Glu Thr Pro Glu Gly Glu
755 760 765
Lys Leu Ser Leu Ala Ile Thr Asn Lys Glu Trp Leu Glu Phe Ala Gln
770 775 780
Thr Lys Pro Tyr Leu Asn Asp
785 790

<210> 92
<211> 1262
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 92
Met Asn Leu Asn Thr Tyr Phe Ser Gln Phe Thr Gly Leu Tyr Pro Val
1 5 10 15
Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Met Gly Lys Thr Leu Glu
20 25 30
Lys Ile Lys Glu Thr Gly Ile Ile Glu Asn Asp Lys Lys Arg His Asn

35 40 45

Asp Tyr Phe Asp Ala Lys Lys Ile Ile Asp Lys Tyr His Lys Tyr Phe
50 55 60
Ile Asp Ala Ala Leu Ser Lys Phe Pro Cys Ile Asp Trp Asn Pro Leu
65 70 75 80
Lys Glu Ala Ile Glu Arg Ser Leu Asp Arg Ser Asp Ala Ser Lys Lys
85 90 95
Lys Leu Glu Lys Thr Gln Thr Glu Phe Arg Lys Lys Ile Ala Lys Ala
100 105 110

Leu Thr Thr His Gly His Tyr Lys Glu Leu Thr Ala Ser Thr Pro Lys
115 120 125
Asp Leu Phe Leu Lys Val Phe Pro Asp His Phe Gly Lys Gln Pro Ala
130 135 140
Ile Asp Thr Phe Asp Gly Phe Ser Ser Tyr Phe Thr Gly Phe Gln Glu
145 150 155 160
Asn Arg Gln Asn Ile Tyr Ser Asp Glu Ala Ile Ser Thr Ala Ile Pro
165 170 175

Tyr Arg Leu Val His Asp Asn Phe Pro Lys Phe Leu Ser Asn Ile Glu
180 185 190
Val Tyr Asn Ile Leu Lys Asp Asn Ala Pro Ser Val Leu Ser Asp Ala
195 200 205
Glu Asn Glu Leu Lys Asp Phe Leu Asn Gly Lys Pro Leu Ala Asn Ile
210 215 220
Phe Glu Leu Asn Ala Tyr Asn Asp Val Leu Thr Gln Ser Gly Ile Asp
225 230 235 240

Phe Phe Asn Gln Val Ile Gly Gly Phe Ser Gly Glu Gly Gly Glu Lys
245 250 255
Lys Thr Arg Gly Ile Asn Glu Phe Ser Asn Leu Tyr Arg Gln Gln His
260 265 270
Pro Glu Phe Ala Gln Lys Arg Leu Ala Thr Lys Met Ile Pro Leu Tyr
275 280 285

Lys Gln Ile Leu Ser Asp Arg Glu Thr Lys Ser Phe Ile Leu Glu Ser
290 295 300

Tyr Ser Thr Asp Ser Gln Val Gln Glu Ser Val Lys Glu Phe Phe Glu
305 310 315 320
Ser Gln Ile Leu Asn Cys Asp Ile Ala Gly Arg Lys Val Asn Val Leu
325 330 335
Lys Glu Leu Ser Ser Leu Ile Lys Arg Ile Thr Glu Phe Asp Leu Gly
340 345 350
Ser Ile Tyr Val Asn Gln Glu Glu Leu Ser Ser Ile Ser Leu Glu Leu
355 360 365

Phe Lys Ser Trp Asn Thr Ile Asn Ala Ile Leu Phe Lys Asn Ala Glu
370 375 380
Asn Arg Ile Gly Ser Ala Glu Lys Ala Ala Asn Lys Lys Lys Ile Asp
385 390 395 400
Ala Trp Met Lys Ser Asn Glu Phe Ser Ile Ala Thr Leu Asn Leu Ala
405 410 415
Ile Ala Glu Ser Asp Ser Glu Glu Ile Ser Arg Val Lys Ile Glu Ser
420 425 430

Tyr Trp Asn Asn Phe Glu Ala Lys Val Gln Ser Ile Leu Cys Gly Asp
435 440 445
Asn Arg Arg Asn Leu Asp Glu Phe Ile Ser Ala Thr Phe Asn Glu Asn
450 455 460
Asn Ala Leu Arg Glu Asp Ser Lys Val Ile Glu Lys Leu Lys Ala Phe
465 470 475 480
Leu Asp Ala Leu Ile Glu Ile Met His Ser Ile Lys Pro Leu Ile Ser
485 490 495

Asp Ala Glu Asn Arg Asp Leu Ser Phe Tyr Asn Glu Leu Met Pro Leu
500 505 510
Tyr Asp Gln Leu Ser Leu Val Val Pro Leu Tyr Asn Lys Ile Arg Asn
515 520 525
Tyr Ala Thr Gln Lys Leu Thr Glu Ser Glu Lys Phe Lys Leu Asn Phe

530 535 540

Asp Asn Pro Thr Leu Ala Asp Gly Trp Asp Gln Asn Lys Glu Glu Ala

545 550 555 560

Asn Thr Ala Ile Leu Leu Leu Lys Asn Gly Leu Tyr Tyr Leu Gly Ile

565 570 575

Met Asn Ala Lys Asn Lys Pro Lys Ile Lys Asp Phe Lys Thr Ser Glu

580 585 590

Ser Glu Asp Cys Tyr Asp Lys Met Val Tyr Lys Leu Leu Pro Gly Pro

595 600 605

Asn Lys Met Leu Pro Lys Val Phe Phe Ser Glu Lys Gly Leu Ala Thr

610 615 620

Phe Lys Pro Pro Lys Asp Ile Leu Asp Gly Tyr Asn Ala Gly Lys His

625 630 635 640

Lys Lys Gly Asp Leu Phe Asp Ile Gly Phe Cys His Gln Leu Ile Asp

645 650 655

Phe Phe Lys Glu Ser Ile Ala Lys His Pro Asp Trp Lys Lys Phe Asp

660 665 670

Phe Lys Phe Ser Asp Thr Ser Ser Tyr Glu Asp Ile Ser Gly Phe Tyr

675 680 685

Lys Glu Val Thr Asp Gln Gly Tyr Lys Ile Thr Phe Ser Lys Ile Pro

690 695 700

Thr Pro Gln Ile Asp Glu Trp Val Asn Glu Gly Lys Leu Phe Leu Phe

705 710 715 720

Gln Ile Tyr Asn Lys Asp Phe Ala Pro Gly Ala Lys Gly Ser Pro Asn

725 730 735

Leu His Thr Leu Tyr Trp Lys Ser Val Phe Ser Pro Glu Asn Leu Lys

740 745 750

Asp Val Val Val Lys Leu Asn Gly Glu Ala Glu Leu Phe Tyr Arg Pro

755 760 765

Ser Ser Val Lys Lys Pro Tyr Ser His Lys Val Gly Glu Lys Leu Val

770 775 780

Asn Arg Ile Gly Lys Asp Gly Leu Pro Leu Pro Glu Ser Val Phe Gly
785 790 795 800
Glu Leu Phe Arg Tyr Phe Asn Gly Lys Leu Asp Gly Glu Leu Ser Asp
805 810 815

Glu Ala Lys Arg Tyr Leu Asp Val Ala Val Val Lys Asp Val Lys His
820 825 830
Glu Ile Val Lys Asp Arg Arg Tyr Thr Gln Asp Lys Phe Glu Phe His
835 840 845
Val Pro Leu Thr Leu Asn Phe Lys Ala Asp Ser Lys Asn Glu Tyr Met
850 855 860
Asn Glu Arg Val Arg His Phe Leu Lys Asp Asn Pro Asp Val Asn Ile
865 870 875 880

Ile Gly Ile Asp Arg Gly Glu Arg His Leu Leu Tyr Met Thr Leu Ile
885 890 895
Asn Gln Lys Gly Glu Ile Leu Lys Gln Lys Ser Phe Asn Ile Val Glu
900 905 910
Ser Val Asn Tyr Gln Ala Lys Leu Val Gln Arg Glu Lys Glu Arg Asp
915 920 925
Thr Ala Arg Arg Ser Trp Ser Ser Val Gly Lys Ile Lys Asp Leu Lys
930 935 940

Glu Gly Phe Leu Ser Gln Val Ile His Glu Ile Thr Thr Thr Met Ile
945 950 955 960
Glu Asn Asn Ala Ile Val Val Leu Glu Asp Leu Asn Phe Gly Phe Lys
965 970 975
Arg Gly Arg Phe Cys Val Glu Arg Gln Val Tyr Gln Lys Phe Glu Lys
980 985 990
Met Leu Ile Asp Lys Leu Asn Tyr Leu Val Phe Lys Asn Lys Pro Glu
995 1000 1005

Gly Asp Val Gly Gly Val Leu Lys Gly Tyr Gln Leu Ala Glu Lys
1010 1015 1020
Phe Asp Ser Phe Gln Lys Leu Gly Lys Gln Ser Gly Phe Leu Phe

1025 1030 1035

Tyr Ile Pro Ala Ala Tyr Thr Ser Lys Ile Asp Pro Thr Thr Gly

1040 1045 1050

Phe Ala Asn Leu Phe Asn Met Thr Glu Leu Thr Ser Ala Glu Lys

1055 1060 1065

Lys Lys Glu Phe Leu Ser His Phe Glu Asp Ile Thr Tyr Asp Gly

1070 1075 1080

Lys Asn Asp Arg Phe Leu Phe Ser Phe Asp Tyr Lys Lys Phe Lys

1085 1090 1095

Cys Phe Gln Thr Asp Tyr Ile Lys Lys Trp Thr Val Tyr Ser Gln

1100 1105 1110

Gly Lys Arg Ile Val Tyr Asp Lys Glu Ser Lys Ser Ala Lys Ala

1115 1120 1125

Ile Ser Pro Val Glu Ile Ile Lys Ala Ala Leu Ala Lys Gln Asn

1130 1135 1140

Ile Ala Leu Thr Asp Gln Leu Asp Val Leu Ser Ala Ile Asn Ser

1145 1150 1155

Val Glu Ala Ser Arg Glu Thr Ala Ser Phe Phe Gly Asp Ile Cys

1160 1165 1170

Tyr Ala Phe Glu Lys Thr Leu Gln Met Arg Asn Ser Ile Pro Asn

1175 1180 1185

Thr Asp Glu Asp Tyr Leu Val Ser Pro Val Met Asn Lys Lys Gly

1190 1195 1200

Glu Phe Tyr Asp Ser Arg Ser Cys Gly Asp Ser Leu Pro Lys Asn

1205 1210 1215

Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu Lys Gly Leu Tyr

1220 1225 1230

Leu Ile Lys Asn Val Phe Asp Ala Gly Gly Lys Asp Leu Lys Ile

1235 1240 1245

Ser His Glu Asp Trp Phe Lys Phe Ala Gln Ser Arg Asn Arg

1250 1255 1260

<210> 93

<211> 1250

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 93

Met Gln Thr Leu Phe Glu Asn Phe Thr Asn Gln Tyr Pro Val Ser Lys
1 5 10 15

Thr Leu Arg Phe Glu Leu Ile Pro Gln Gly Lys Thr Lys Asp Phe Ile
20 25 30

Glu Gln Lys Gly Leu Leu Lys Lys Asp Glu Asp Arg Ala Glu Lys Tyr
35 40 45

Lys Lys Val Lys Asn Ile Ile Asp Glu Tyr His Lys Asp Phe Ile Glu
50 55 60

Lys Ser Leu Asn Gly Leu Lys Leu Asp Gly Leu Glu Glu Tyr Lys Thr
65 70 75 80

Leu Tyr Leu Lys Gln Glu Lys Asp Asp Lys Asp Lys Lys Ala Phe Asp
85 90 95

Lys Glu Lys Glu Asn Leu Arg Lys Gln Ile Ala Asn Ala Phe Arg Asn
100 105 110

Asn Glu Lys Phe Lys Thr Leu Phe Ala Lys Glu Leu Ile Lys Asn Asp
115 120 125

Leu Met Ser Phe Ala Cys Glu Glu Asp Lys Lys Asn Val Lys Glu Phe
130 135 140

Glu Ala Phe Thr Thr Tyr Phe Thr Gly Phe His Gln Asn Arg Ala Asn
145 150 155 160

Met Tyr Val Ala Asp Glu Lys Arg Thr Ala Ile Ala Ser Arg Leu Ile
165 170 175

His Glu Asn Leu Pro Lys Phe Ile Asp Asn Ile Lys Ile Phe Glu Lys
180 185 190

Met Lys Lys Glu Ala Pro Glu Leu Leu Ser Pro Phe Asn Gln Thr Leu

195 200 205

Lys Asp Met Lys Asp Val Ile Lys Gly Thr Thr Leu Glu Glu Ile Phe

210 215 220

Ser Leu Asp Tyr Phe Asn Lys Thr Leu Thr Gln Ser Gly Ile Asp Ile

225 230 235 240

Tyr Asn Ser Val Ile Gly Gly Arg Thr Pro Glu Glu Gly Lys Thr Lys

245 250 255

Ile Lys Gly Leu Asn Glu Tyr Ile Asn Thr Asp Phe Asn Gln Lys Gln

260 265 270

Thr Asp Lys Lys Lys Arg Gln Pro Lys Phe Lys Gln Leu Tyr Lys Gln

275 280 285

Ile Leu Ser Asp Arg Gln Ser Leu Ser Phe Ile Ala Glu Ala Phe Lys

290 295 300

Asn Asp Thr Glu Ile Leu Glu Ala Ile Glu Lys Phe Tyr Val Asn Glu

305 310 315 320

Leu Leu His Phe Ser Asn Glu Gly Lys Ser Thr Asn Val Leu Asp Ala

325 330 335

Ile Lys Asn Ala Val Ser Asn Leu Glu Ser Phe Asn Leu Thr Lys Ile

340 345 350

Tyr Phe Arg Ser Gly Thr Ser Leu Thr Asp Val Ser Arg Lys Val Phe

355 360 365

Gly Glu Trp Ser Ile Ile Asn Arg Ala Leu Asp Asn Tyr Tyr Ala Thr

370 375 380

Thr Tyr Pro Ile Lys Pro Arg Glu Lys Ser Glu Lys Tyr Glu Glu Arg

385 390 395 400

Lys Glu Lys Trp Leu Lys Gln Asp Phe Asn Val Ser Leu Ile Gln Thr

405 410 415

Ala Ile Asp Glu Tyr Asp Asn Glu Thr Val Lys Gly Lys Asn Ser Gly

420 425 430

Lys Val Ile Val Asp Tyr Phe Ala Lys Phe Cys Asp Asp Lys Glu Thr

435 440 445

Asp Leu Ile Gln Lys Val Asn Glu Gly Tyr Ile Ala Val Lys Asp Leu
450 455 460
Leu Asn Thr Pro Tyr Pro Glu Asn Glu Lys Leu Gly Ser Asn Lys Asp
465 470 475 480
Gln Val Lys Gln Ile Lys Ala Phe Met Asp Ser Ile Met Asp Ile Met

485 490 495
His Phe Val Arg Pro Leu Ser Leu Lys Asp Thr Asp Lys Glu Lys Asp
500 505 510
Glu Thr Phe Tyr Ser Leu Phe Thr Pro Leu Tyr Asp His Leu Thr Gln
515 520 525
Thr Ile Ala Leu Tyr Asn Lys Val Arg Asn Tyr Leu Thr Gln Lys Pro
530 535 540
Tyr Ser Thr Glu Lys Ile Lys Leu Asn Phe Glu Asn Ser Thr Leu Leu

545 550 555 560
Gly Gly Trp Asp Leu Asn Lys Glu Thr Asp Asn Thr Ala Ile Ile Leu
565 570 575
Arg Lys Glu Asn Leu Tyr Tyr Leu Gly Ile Met Asp Lys Arg His Asn
580 585 590
Arg Ile Phe Arg Asn Val Pro Lys Ala Asp Lys Lys Asp Ser Cys Tyr
595 600 605
Glu Lys Met Val Tyr Lys Leu Leu Pro Gly Ala Asn Lys Met Leu Pro

610 615 620
Lys Val Phe Phe Ser Gln Ser Arg Ile Gln Glu Phe Thr Pro Ser Ala
625 630 635 640
Lys Leu Leu Glu Asn Tyr Glu Asn Glu Thr His Lys Lys Gly Asp Asn
645 650 655
Phe Asn Leu Asn His Cys His Gln Leu Ile Asp Phe Phe Lys Asp Ser
660 665 670
Ile Asn Lys His Glu Asp Trp Lys Asn Phe Asp Phe Arg Phe Ser Ala

675 680 685
Thr Ser Thr Tyr Ala Asp Leu Ser Gly Phe Tyr His Glu Val Glu His

690 695 700

Gln Gly Tyr Lys Ile Ser Phe Gln Ser Ile Ala Asp Ser Phe Ile Asp

705 710 715 720

Asp Leu Val Asn Glu Gly Lys Leu Tyr Leu Phe Gln Ile Tyr Asn Lys

725 730 735

Asp Phe Ser Pro Phe Ser Lys Gly Lys Pro Asn Leu His Thr Leu Tyr

740 745 750

Trp Lys Met Leu Phe Asp Glu Asn Asn Leu Lys Asp Val Val Tyr Lys

755 760 765

Leu Asn Gly Glu Ala Glu Val Phe Tyr Arg Lys Lys Ser Ile Ala Glu

770 775 780

Lys Asn Thr Thr Ile His Lys Ala Asn Glu Ser Ile Ile Asn Lys Asn

785 790 795 800

Pro Asp Asn Pro Lys Ala Thr Ser Thr Phe Asn Tyr Asp Ile Val Lys

805 810 815

Asp Lys Arg Tyr Thr Ile Asp Lys Phe Gln Phe His Val Pro Ile Thr

820 825 830

Met Asn Phe Lys Ala Glu Gly Ile Phe Asn Met Asn Gln Arg Val Asn

835 840 845

Gln Phe Leu Lys Ala Asn Pro Asp Ile Asn Ile Ile Gly Ile Asp Arg

850 855 860

Gly Glu Arg His Leu Leu Tyr Tyr Thr Leu Ile Asn Gln Lys Gly Lys

865 870 875 880

Ile Leu Lys Gln Asp Thr Leu Asn Val Ile Ala Asn Glu Lys Gln Lys

885 890 895

Val Asp Tyr His Asn Leu Leu Asp Lys Lys Glu Gly Asp Arg Ala Thr

900 905 910

Ala Arg Gln Glu Trp Gly Val Ile Glu Thr Ile Lys Glu Leu Lys Glu

915 920 925

Gly Tyr Leu Ser Gln Val Ile His Lys Leu Thr Asp Leu Met Ile Glu

930 935 940

Asn Asn Ala Ile Ile Val Met Glu Asp Leu Asn Phe Gly Phe Lys Arg
945 950 955 960
Gly Arg Gln Lys Val Glu Lys Gln Val Tyr Gln Lys Phe Glu Lys Met
965 970 975
Leu Ile Asp Lys Leu Asn Tyr Leu Val Asp Lys Asn Lys Lys Ala Asn
980 985 990
Glu Leu Gly Gly Leu Leu Asn Ala Phe Gln Leu Ala Asn Lys Phe Glu

995 1000 1005
Ser Phe Gln Lys Met Gly Lys Gln Asn Gly Phe Ile Phe Tyr Val
1010 1015 1020
Pro Ala Trp Asn Thr Ser Lys Thr Asp Pro Ala Thr Gly Phe Ile
1025 1030 1035
Asp Phe Leu Lys Pro Arg Tyr Glu Asn Leu Lys Gln Ala Lys Asp
1040 1045 1050
Phe Phe Glu Lys Phe Asp Ser Ile Arg Leu Asn Ser Lys Ala Asp

1055 1060 1065
Tyr Phe Glu Phe Ala Phe Asp Phe Lys Asn Phe Thr Gly Lys Ala
1070 1075 1080
Asp Gly Gly Arg Thr Lys Trp Thr Val Cys Thr Thr Asn Glu Asp
1085 1090 1095
Arg Tyr Ala Trp Asn Arg Ala Leu Asn Asn Asn Arg Gly Ser Gln
1100 1105 1110
Glu Lys Tyr Asp Ile Thr Ala Glu Leu Lys Ser Leu Phe Asp Gly

1115 1120 1125
Lys Val Asp Tyr Lys Ser Gly Lys Asp Leu Lys Gln Gln Ile Ala
1130 1135 1140
Ser Gln Glu Leu Ala Asp Phe Phe Arg Thr Leu Met Lys Tyr Leu
1145 1150 1155
Ser Val Thr Leu Ser Leu Arg His Asn Asn Gly Glu Lys Gly Glu
1160 1165 1170
Thr Glu Gln Asp Tyr Ile Leu Ser Pro Val Ala Asp Ser Met Gly

1175 1180 1185

Lys Phe Phe Asp Ser Arg Lys Ala Gly Asp Asp Met Pro Lys Asn

1190 1195 1200

Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu Lys Gly Leu Trp

1205 1210 1215

Cys Leu Glu Gln Ile Ser Lys Thr Asp Asp Leu Lys Lys Val Lys

1220 1225 1230

Leu Ala Ile Ser Asn Lys Glu Trp Leu Glu Phe Met Gln Thr Leu

1235 1240 1245

Lys Gly

1250

<210> 94

<211> 1390

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 94

Met Ile Asp Asn Thr Lys Glu Lys Lys Glu Gly Ser Val Phe Asp Gly

1 5 10 15

Phe Thr Arg Lys Tyr Gln Leu Ser Lys Thr Leu Arg Phe Glu Leu Arg

20 25 30

Pro Ile Leu Asn Thr Pro Lys Met Leu Asp Asp Glu Gln Val Ile Lys

35 40 45

Asn Asp Glu Thr Arg Arg Lys Lys Tyr Glu Ala Val Lys Pro Trp Phe

50 55 60

Asp Gln Leu His Arg Glu Phe Ile Glu Asp Ala Leu Lys Ser Phe Lys

65 70 75 80

Phe Lys Asn Leu Ala Ile Tyr Gln Asp Thr Phe Gln Thr Trp Gln Lys

85 90 95

Asp Arg Lys Ser Lys Gln Lys Lys Asp Thr Leu Val Lys Ile Glu Val

100 105 110

Gly Leu Arg Glu Glu Ile Val Arg Arg Phe Glu Glu Val Ala Asn Ile
115 120 125
Trp Val Arg Ser Glu Gln Tyr Lys Leu Leu Gly Ile Lys Lys Glu Gly
130 135 140
Leu Gly Met Leu Phe Glu Ala Gly Val Phe Arg Leu Leu Lys Glu Arg
145 150 155 160
Phe Lys Asn Glu Lys Asp Thr Thr Val Asp Gly Asn Asn Ile Phe Asp

165 170 175
Glu Trp Thr Arg Trp Thr Gly Tyr Phe Lys Lys Phe Phe Glu Thr Arg
180 185 190
Lys Asn Phe Tyr Lys Ser Asp Asp Thr Ser Thr Ala Ile Ala Tyr Arg
195 200 205
Val Ile Asn Gln Asn Leu Arg Arg Phe Cys Glu Asn Ile Gln Ile Phe
210 215 220
Glu Lys Ile Ser Glu Lys Ile Glu Phe Ser Glu Val Glu Lys Ser Phe

225 230 235 240
Asp Ile Ser Cys Ala Gly Ile Phe Ser Leu Ala Tyr Tyr Asn Ala Cys
245 250 255
Leu Leu Gln Gly Gly Ile Asp Thr Tyr Asn Lys Ile Ile Gly Gly Glu
260 265 270
Val Asp Glu Lys Asp Lys Lys Ile Pro Gly Ile Asn Glu Leu Ile Asn
275 280 285
Lys Tyr Arg Gln Asp Asn Ser Gly Glu Lys Ile Pro Phe Leu Lys Gln

290 295 300
Leu Asp Lys Gln Ile His Ser Ala Lys Glu Ala Phe Ile Glu Ser Ile
305 310 315 320
Glu Thr Asn Lys Glu Leu Val Gly Lys Leu Lys Thr Phe Tyr Glu Asn
325 330 335
Ala Glu Val Lys Ile Gln Ser Phe Arg Asn Leu Ile Ala Asp Ile Val
340 345 350
Thr Asp Tyr Ser Gly Tyr Asp Ile Asp Lys Ile Tyr Leu Thr Lys Glu

355 360 365

Ala Val Ser His Asn Ala Ser Arg Trp Phe Ala Ser Phe Glu Ser Phe

370 375 380

Glu Arg Asp Leu Phe Ala Val Val Ala Glu Lys Gln Asn Lys Leu Val

385 390 395 400

Tyr Glu Leu Leu Arg Thr His Lys Asn Asp Ser Lys Ile Ser Asp Lys

405 410 415

Asp Gly Lys Phe Ser Phe Pro Asp Phe Ile Lys Cys Ser His Ile Lys

420 425 430

Arg Ala Leu Glu Lys Gln Glu Gly Arg Ile Trp Lys Gly Glu Tyr Tyr

435 440 445

Glu Asp Ile Val Asp Phe Glu Lys Ile Lys Asp Val Phe Thr Gln Phe

450 455 460

Leu Cys Val Phe Lys Phe Glu Leu Glu Gln Gln Phe Phe Arg Lys Thr

465 470 475 480

Thr Ser Ala Gln Thr Gly Glu Gln Thr Lys Ile Gly Tyr Glu Ile Phe

485 490 495

Val Thr Lys Ile Asn Glu Leu Ile Thr Arg Glu Asn Pro Val Ile Asp

500 505 510

Leu Glu Glu Lys Ile Ala Ile Lys Asn Phe Ala Asp Ala Thr Leu Leu

515 520 525

Ile Tyr Gln Ile Ala Lys Tyr Phe Ala Val Glu Lys Arg Arg Gly Trp

530 535 540

Leu Asp Asn Tyr Asp Leu Asp Asp Arg Phe Tyr Lys Ser Ser Asp Ile

545 550 555 560

Gly Tyr Leu Asn Phe Tyr Arg Asp Ala Phe Glu Gln Ile Val Arg Pro

565 570 575

Tyr Asn Leu Phe Arg Asn Tyr Leu Thr Lys Lys Pro Tyr Asn Thr Asn

580 585 590

Lys Trp Val Leu Ser Phe Glu Asn Pro Thr Leu Ala Asp Gly Trp Asp

595 600 605

Lys Asn Lys Glu Lys Thr Asn Ala Ala Val Ile Leu Arg Lys Asp Gly

610 615 620

Arg Tyr Tyr Leu Gly Ile Ile Lys Glu Asp Cys Lys Ser Leu Phe Ala

625 630 635 640

Asp Arg Tyr Ser Lys Glu Met Ser Glu Gly Ile Glu Ser Gly Ser Phe

645 650 655

Gln Lys Met Ala Tyr Lys Phe Phe Pro Glu Ala Ser Lys Met Ile Pro

660 665 670

Lys Cys Ser Thr Gln Thr Lys Asn Val Lys Glu His Phe Arg Lys Ser

675 680 685

Ser Ser Asp Tyr Asn Leu Phe His Glu Lys Asp Tyr Lys Ile Ser Val

690 695 700

Ala Ile Thr Lys Asn Ile Tyr Glu Leu Asn Asn Val Phe Tyr Arg Lys

705 710 715 720

Asp Asn Ile Glu Glu Ser Phe Val Pro Lys Asn Asp Phe Glu Lys Lys

725 730 735

Leu Gly Val Lys Lys Phe Gln Arg Gln Tyr Leu Glu Ile Ser Arg Asp

740 745 750

Asn Asn Gly Tyr Lys Gln Ala Leu Ala Gln Trp Ile Glu Phe Cys Ile

755 760 765

Arg Phe Leu Lys Ala Tyr Lys Ser Thr Thr Ile Phe Asp Tyr Ser Arg

770 775 780

Leu Arg Glu Ala Lys Glu Tyr Glu Ser Leu Asp Ala Phe Tyr Gln Asp

785 790 795 800

Ile Asn Ala Leu Thr Tyr Asn Ile Ser Phe Val Pro Ile Ser Glu Gln

805 810 815

Tyr Ile Lys Glu Lys Asn Asp Asn Gly Glu Leu Phe Leu Phe Glu Ile

820 825 830

Tyr Asn Lys Asp Trp Ser Leu Gly Pro Met Asp Lys Asn Arg Lys Arg

835 840 845

Thr Lys Asn Leu His Thr Leu Tyr Phe Glu Gln Leu Phe Ser Lys Glu

850 855 860

Asn Glu Gln Glu Asn Phe Leu Phe Gln Leu Asn Gly Glu Ala Glu Leu

865 870 875 880

Phe Phe Arg Pro Lys Thr Glu Glu Lys Arg Leu Gly Tyr Lys Val Trp

885 890 895

Asp Ala Gly Glu Lys Lys Trp Val Lys Ala Lys Glu Lys Glu Asp Gly

900 905 910

Ala Val Ile Asp Arg Lys Arg Tyr Ala Lys Asp Ile Ile Leu Phe His

915 920 925

Cys Pro Ile Thr Leu Asn Arg Val Ser Glu Ser Lys Thr Lys Arg Glu

930 935 940

Met Asp Val Glu Ile Arg Glu Val Leu Ser Ser Thr Pro Gly Val His

945 950 955 960

Ile Ile Gly Val Asp Arg Gly Glu Lys His Leu Ala Tyr Tyr Ser Val

965 970 975

Ile Asp Gln Asn Gly Lys Ile Ile Glu Thr Asp Thr Leu Asn Ser Ile

980 985 990

Gly Lys Asp Gly Arg Gly Lys Pro Val Glu Tyr Ala Ser Lys Leu Glu

995 1000 1005

Lys Arg Ala Gln Glu Arg Glu Ala Ser Arg Arg Asp Trp Glu Glu

1010 1015 1020

Val Glu Ala Ile Lys Asp Leu Lys Lys Gly Tyr Ile Ser Gln Val

1025 1030 1035

Ile Arg Asn Leu Ala Asp Leu Ile Ile Lys His Asn Ala Ile Ile

1040 1045 1050

Val Phe Glu Asp Leu Asn Met Arg Phe Lys Gln Ile Arg Gly Gly

1055 1060 1065

Ile Glu Lys Ser Ala Tyr Gln Gln Leu Glu Arg Ala Leu Ile Asp

1070 1075 1080

Lys Leu Ser Phe Leu Val Lys Lys Gly Glu Glu Asp Pro Lys Gln

1085 1090 1095

Thr Gly His Ile Leu Arg Ala Tyr Gln Leu Ala Ala Pro Val Ile

1100 1105 1110

Ala Phe Lys Asp Met Gly Lys Gln Thr Gly Leu Ile Phe Tyr Thr

1115 1120 1125

Gln Ala Gly Tyr Thr Ser Lys Thr Cys Pro Glu Cys Gly Tyr Arg

1130 1135 1140

Arg Asn Ile Lys Cys Leu Phe Glu Asn Ile Glu Gln Ala Lys Thr

1145 1150 1155

Leu Ile Glu Asn Leu Glu Ser Ile Asn Tyr Asn Lys Lys Glu Asp

1160 1165 1170

Val Phe Gln Ile Ser Tyr Ser Leu Glu Lys Leu Ser Ser Lys Asp

1175 1180 1185

Gln Lys Lys Glu Lys Lys Val Ser Asn Glu Leu Tyr Ala Lys Thr

1190 1195 1200

Leu Lys Lys Asp Ile Phe Ile Leu Thr Thr Lys Asn Ala Leu Arg

1205 1210 1215

Tyr Lys Trp Tyr Asp Arg Tyr Ser Glu Lys Ala Lys Val Ala Lys

1220 1225 1230

Arg Gly Ile Asp Glu Tyr Lys Gly Glu Val Asn Glu Ser Glu Thr

1235 1240 1245

Lys Lys Gly Val Val Lys Glu Phe Asn Leu Thr Glu Tyr Leu Lys

1250 1255 1260

Gly Leu Leu Lys Thr Tyr Glu Ile Asp Tyr Glu His Gly Gly Ile

1265 1270 1275

Arg Glu Gln Ile Leu Ser Val Ala Arg Gly Arg Glu Phe Tyr Lys

1280 1285 1290

Asp Phe Leu Tyr Ala Leu Phe Leu Leu Thr Glu Thr Arg His Ser

1295 1300 1305

Ile Ser Gly Arg Asn Thr Asp Tyr Ile Gln Cys Pro Glu Cys Glu

1310 1315 1320

Phe Asp Ser Arg Lys Gly Phe Lys Asp Ile Lys Glu Phe Asn Gly

1325 1330 1335

Asp Ala Asn Gly Ala Tyr Asn Ile Ala Arg Lys Gly Ile Met Ile

1340 1345 1350

Leu Glu Lys Ile Lys Gln Phe Lys Lys Asp Asn Asp Gly Asn Leu

1355 1360 1365

Glu Lys Met Gly Trp Gly Asp Leu Ser Ile Ser Ile Glu Glu Trp

1370 1375 1380

Asp Lys Phe Thr Gln Lys Glu

1385 1390

<210> 95

<211> 1333

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 95

Met Lys Asn Phe Gln Asp Phe Thr Asn Leu Tyr Glu Leu Ser Lys Thr

1 5 10 15

Leu Arg Phe Glu Leu Lys Pro Ile Gly Gly Thr Lys Lys Leu Ile Glu

20 25 30

Glu Lys Asn Ile Leu Lys Leu Asp Lys Lys Lys Arg Glu Asn Tyr Glu

35 40 45

Lys Val Lys Pro Tyr Phe Asn Lys Ile His Gln Glu Phe Ile Asn Phe

50 55 60

Ala Leu Arg Asn Pro Asn Phe Asp Phe Ser Gln Phe Glu Glu Lys Tyr

65 70 75 80

Leu Asn Trp Leu Lys Asp Lys Lys Asn Lys Asp Leu Leu Lys Glu Lys

85 90 95

Glu Ser Ile Asp Lys Ile Phe Leu Glu Lys Ile Gly Lys Leu Phe Glu

100 105 110

Asn Ser Val Lys Asp Phe Leu Lys Glu Asn Gly Phe Glu Ser Ile Val

115 120 125

Lys Glu Glu Asp Gln Asn Leu Lys Phe Phe Arg Arg Lys Glu Ile Phe
130 135 140

Glu Val Leu Gln Glu Lys Tyr Gly Ser Glu Leu Glu Thr Gln Met Val
145 150 155 160
Asn Lys Asp Gly Glu Ile Lys Ser Ile Phe Asn Gly Trp Glu Lys Trp
165 170 175
Leu Gly Tyr Phe Asp Lys Phe Phe Asn Thr Arg Asp Asn Phe Tyr Lys
180 185 190
Thr Asp Gly Thr Ser Thr Ala Ile Ala Thr Arg Ile Ile Lys Asp Asn
195 200 205

Leu Lys Ile Phe Leu Glu Asn Ile Val Ala Phe Gly Lys Ile Lys Asn
210 215 220
Lys Lys Ile Asp Phe Ser Glu Val Glu Lys Asn Phe Ser Val Ser Ile
225 230 235 240
Asp Thr Phe Phe Glu Ile Asn Asn Phe Asn Asn Cys Phe Leu Gln Asp
245 250 255
Gly Ile Asp Phe Tyr Asn Lys Val Ile Gly Gly Glu Thr Leu Glu Asn
260 265 270

Gly Glu Lys Leu Lys Gly Leu Asn Glu Ile Ile Asn Lys Tyr Arg Gln
275 280 285
Asp Thr Gly Glu Lys Ile Pro Tyr Phe Lys Lys Leu Gln Lys Gln Ile
290 295 300
Leu Ser Glu Lys Asp Gly Val Phe Ile Asp Lys Ile Glu Asp Asp Gly
305 310 315 320
Gly Phe Tyr Glu Val Leu Lys Asn Phe Tyr Lys Asn Ala Ala Glu Lys
325 330 335

Glu Gly Phe Leu Lys Asn Ile Phe Glu Asn Phe Tyr Thr Ile Ser Asp
340 345 350
Lys Asn Leu Glu Lys Ile Tyr Phe Asn Lys Ile Ala Phe Asn Thr Ile
355 360 365
Ser His Lys Phe Gly Ser Ala Leu Glu Phe Glu Arg Ile Leu Tyr Glu

370 375 380

Glu Met Lys Lys Glu Lys Ala Asp Gly Ile Lys Phe Glu Lys Lys Glu

385 390 395 400

Asn Lys Tyr Lys Phe Pro Asp Phe Ile Gln Ile Ile Phe Ile Lys Arg

405 410 415

Ser Leu Glu Asn Tyr Asp Ser Glu Asn Leu Phe Trp Lys Glu Arg Tyr

420 425 430

Tyr Lys Ser Glu Glu Asn Val Asp Gly Phe Leu Glu Lys Asn Asn Asn

435 440 445

Asn Leu Trp Gly Gln Phe Cys Lys Ile Leu Asn Phe Glu Phe Leu Asn

450 455 460

Ile Leu Lys Arg Arg Ile Ile Asp Glu Ala Gly Glu Glu Tyr Glu Val

465 470 475 480

Gly Phe Glu Ile Ser Lys Asn Ile Leu Gly Glu Lys Leu Glu Asn Phe

485 490 495

Glu Leu Asn Gln Glu Asn Lys Gly Ile Ile Lys Asp Phe Ala Asp Tyr

500 505 510

Ser Leu Ala Leu Tyr Ser Phe Gly Lys Tyr Phe Ala Val Glu Lys Gly

515 520 525

Arg Asn Trp Asp Leu Asn Ile Asp Ile Ser Asp Asp Phe Tyr Gly Gly

530 535 540

Glu Asp Gly Tyr Ile Glu Lys Phe Tyr Asn Thr Gly Tyr Asp Glu Ile

545 550 555 560

Val Lys Pro Tyr Asn Leu Met Arg Asn Tyr Ile Ser Lys Lys Pro Trp

565 570 575

Glu Asp Asn Lys Lys Trp Lys Ile Asn Phe Glu Thr Ser Ser Leu Leu

580 585 590

Ser Gly Trp Asp Lys Asn Leu Glu Ser Asn Gly Ser Tyr Ile Phe Gln

595 600 605

Lys Gly Asn Lys Tyr Tyr Leu Gly Ile Ile Asn Gly Ser Lys Pro Ala

610 615 620

Lys Glu Ile Leu Glu Lys Leu Tyr Ser Gly Asp Gly Glu Lys Ile Lys
625 630 635 640
Arg Phe Ile Tyr Asp Phe Gln Lys Pro Asp Asn Lys Asn Thr Pro Arg
645 650 655

Met Phe Ile Arg Ser Lys Lys Asp Ser Phe Ser Pro Ala Val Glu Lys
660 665 670
Tyr Asn Leu Pro Ile Asn Asp Ile Leu Glu Ile Tyr Asp Asn Gly Leu
675 680 685
Phe Lys Thr Glu Asn Lys Gly Asn Pro Asn Tyr Lys Glu Ser Leu Arg
690 695 700
Lys Leu Ile Asp Tyr Phe Lys Leu Gly Phe Ser Arg His Glu Ser Phe
705 710 715 720

Lys His Phe Asn Phe Val Trp Lys Asp Ser Lys Ser Tyr Glu Asn Ile
725 730 735
Ala Asp Phe Tyr Arg Asp Val Glu Lys Ser Cys Tyr Lys Ile Asp Phe
740 745 750
Glu Phe Leu Asn Phe Glu Glu Leu Lys Lys Leu Thr Phe Glu Lys His
755 760 765
Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Glu Leu Asp Glu Ser
770 775 780

Leu Gln Glu Lys Gly Tyr Asn Phe Lys Gly Glu Gly Gln Lys Asn Ile
785 790 795 800
His Thr Lys Tyr Phe Glu Ala Leu Phe Leu Glu Glu Asn Ile Ser Arg
805 810 815
Lys Ser Gly Ala Val Phe Lys Leu Ser Gly Gly Gly Glu Val Phe Phe
820 825 830
Arg Lys Lys Ser Ile Lys Ala Lys Lys Glu Lys Arg Asn Ser Val Glu
835 840 845

Val Ile Lys Asn Lys Arg Tyr Thr Glu Cys Lys Tyr Phe Leu His Phe
850 855 860
Pro Ile Gln Val Asn Phe Lys Glu Glu Ile Ser Gly Asn Phe Asn Gln

865 870 875 880

Glu Ile Asn Lys Phe Leu Ala Asn Asn Pro Asp Ile Asn Val Ile Gly

885 890 895

Ile Asp Arg Gly Glu Lys His Leu Ala Tyr Phe Ser Val Ile Asn Gln

900 905 910

Lys Gly Glu Ile Leu Glu Ser Gly Ser Phe Asn Lys Ile Glu Asn Tyr

915 920 925

Asn Lys Asn Gly Glu Lys Leu Leu Phe Pro Glu Arg Glu Ile Lys Glu

930 935 940

Ile His Lys Asp Gly Ser Leu Ile Asp Leu Glu Leu Val Glu Thr Gly

945 950 955 960

Arg Lys Val Asp Tyr Val Asp Tyr Lys Leu Leu Leu Glu Tyr Lys Glu

965 970 975

Arg Lys Arg Leu Leu Gln Arg Gln Ser Trp Lys Glu Val Glu Gln Ile

980 985 990

Lys Asp Leu Lys Lys Gly Tyr Ile Ser Ala Leu Val Arg Lys Ile Ala

995 1000 1005

Asp Leu Ile Ile Lys His Asn Ala Ile Val Ile Phe Glu Asp Leu

1010 1015 1020

Asn Phe Arg Phe Lys Gln Ile Arg Gly Gly Ile Glu Lys Ser Ile

1025 1030 1035

Tyr Gln Gln Leu Glu Lys Ala Leu Ile Asp Lys Leu Asn Phe Leu

1040 1045 1050

Val Asn Lys Asn Glu Ile Asn Leu Glu Lys Ala Gly Ser Ile Leu

1055 1060 1065

Lys Ala Tyr Gln Leu Thr Val Pro Val Asp Ser Leu Lys Glu Ile

1070 1075 1080

Gly Lys Gln Thr Gly Val Ile Phe Tyr Thr Glu Ala Ala Tyr Thr

1085 1090 1095

Ser Lys Ile Asp Pro Ile Thr Gly Trp Arg Pro Asn Leu Tyr Leu

1100 1105 1110

Lys Lys Asn Asn Ser Lys Ile Asn Lys Glu Asn Ile Leu Lys Phe
1115 1120 1125
Asp Asn Ile Val Phe Asn Ser Lys Glu Asn Arg Phe Glu Phe Thr
1130 1135 1140
Tyr Asp Leu Lys Lys Phe Phe Gly Lys Asp Ser Lys Phe Pro Ala
1145 1150 1155

Lys Thr Val Asn Thr Val Cys Ser Cys Val Glu Arg Phe Lys Trp
1160 1165 1170
Asn Arg Asn Leu Asn Asn Asn Lys Gly Gly Tyr Ile His Tyr Glu
1175 1180 1185
Asn Leu Thr Asp Gly Lys Leu Ala Asn Lys Glu Gln Lys Glu Asp
1190 1195 1200
Glu Phe Ser Asn Phe Lys Glu Leu Phe Glu Lys Tyr Phe Ile Asp
1205 1210 1215

Ile Asn Gly Asn Ile Leu Glu Gln Ile Lys Asn Leu Asp Thr Lys
1220 1225 1230
Asn Asn Glu Lys Phe Phe Ser Ser Phe Ile Asp Leu Phe Thr Leu
1235 1240 1245
Val Cys Gln Ile Arg Asn Thr Asn Gln Asn Ala Lys Gly Asp Glu
1250 1255 1260
Asn Asp Phe Ile Leu Ser Pro Val Glu Pro Phe Phe Asp Ser Arg
1265 1270 1275

Lys Ser Gln Asn Phe Gly Lys Ser Leu Pro Lys Asn Gly Asp Glu
1280 1285 1290
Asn Gly Ala Phe Asn Ile Ala Arg Lys Gly Leu Ile Ile Leu Asn
1295 1300 1305
Arg Ile Ser Glu Asn Pro Glu Lys Pro Asp Leu Leu Ile Phe Asn
1310 1315 1320
Ala Asp Trp Asp Asn Phe Ala Arg Asn Ile
1325 1330
<210> 96
<211> 1329

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 96

Met Ser Asn Asn Phe Gln Glu Phe Thr Gln Lys Tyr Ala Leu Ser Lys
1 5 10 15

Thr Leu Arg Phe Glu Leu Lys Pro Val Gly Lys Thr Lys Glu Ile Leu
20 25 30

Glu Lys Glu Met Pro Met Tyr Gln Ile Ile Asn Ala Asp Lys Asn Ile
35 40 45

Lys Ala Lys Tyr Ile Gln Thr Lys Pro Phe Phe Asp Gln Leu His Arg
50 55 60

Asp Phe Ile Lys Glu Ala Phe Glu Asn Val Glu Leu Ser Gly Leu Ser
65 70 75 80

Asp Phe Phe Glu Asn Trp Lys Ile Tyr Lys Gln Asp Lys Lys Ala Asn
85 90 95

Glu Lys Ile Tyr Lys Lys Ser Ala Glu Asn Leu Arg Lys Glu Val Val
100 105 110

Ser Phe Leu Asn Ala Lys Gly Lys Asp Trp Ala Glu Lys Tyr His Ser
115 120 125

Ser Gly Leu Lys Lys Ala Asp Ile Glu Ile Leu Phe Glu Glu Gly Ile
130 135 140

Phe Lys Val Leu Glu Ile Arg Tyr Gly Thr Asp Thr Asn Ser Phe Ile
145 150 155 160

Thr Asn Ala Thr Thr Gly Glu Ile Thr Ser Ile Phe Gln Gly Trp Lys
165 170 175

Gly Phe Thr Gly Tyr Phe Leu Lys Phe Trp Asn Thr Arg Glu Asn Tyr
180 185 190

Tyr Lys Thr Asp Gly Thr Ser Thr Ala Ile Ala Thr Arg Ile Val Asp
195 200 205

Gln Asn Leu Pro Gly Tyr Leu Glu Asn Leu Glu Ile Phe Glu Lys Met
210 215 220
Lys Gly Lys Ile Asp Phe Glu Ser Val Arg Gly Asp Phe Ser Asp Phe
225 230 235 240
Glu Lys Ile Gly Thr Val Glu Tyr Tyr Ser Thr Cys Leu Leu Gln Glu

245 250 255
Gly Ile Asp Gly Tyr Asn Arg Ile Ile Gly Gly Tyr Thr Tyr Glu Asn
260 265 270
Gly Glu Lys Ile Lys Gly Ile Asn Glu Ile Ile Asn Leu Tyr Arg Gln
275 280 285
Thr His Lys Asp Glu Lys Val Pro Phe Leu Lys Thr Leu Asp Lys Gln
290 295 300
Ile Gly Ser Glu Lys Ile Ala Phe Met Glu Thr Ile Asp Thr Pro Glu

305 310 315 320
Glu Phe Arg Lys Ile Phe Glu Glu Phe Val Leu Lys Ser Ser Glu Lys
325 330 335
Val Val Leu Leu Lys Gln Cys Leu Asn His Leu Phe Glu Asn Glu Leu
340 345 350
Thr Asp Gly Val Phe Leu Ser Lys Glu Ser Leu Asn Thr Ile Ser His
355 360 365
Lys Trp Ile Asp Ile Gly Asn Met Lys Leu Phe His Glu Ser Leu Phe

370 375 380
Thr Ile Leu Lys Lys Glu Gly Ala Lys Tyr Asp Ser Lys Glu Asp Glu
385 390 395 400
Tyr Lys Phe Pro Asp Phe Ile Arg Ile Ser Asp Ile Lys Thr Ala Leu
405 410 415
Val Lys Ile Thr Thr Glu Ser Phe Phe Trp Lys Asn Arg Tyr Leu Tyr
420 425 430
Glu Lys Asp Glu Asn Pro Thr Gly Phe Leu Thr Ser Asp Asn Ser Leu

435 440 445
Trp Glu Gly Phe Ile Gln Ile Phe Ser His Glu Phe Ser Ser Leu Phe

450 455 460

Glu Arg Thr Glu Lys Asp Glu Glu Gly Lys Asp Ile Gln Trp Gly Tyr

465 470 475 480

Asp Ile Ser Leu Leu Asn Ile Gln Lys Leu Leu Glu Asn Asn Glu Tyr

485 490 495

Asn Pro Asn Asp Glu Lys Asn Lys Ile Ile Ile Lys Ser Phe Ala Asp

500 505 510

Asp Ile Leu Arg Ile Tyr Gln Met Gly Lys Tyr Phe Ala Leu Glu Lys

515 520 525

Lys Arg Gln Trp Asn Pro Asp Asn Leu Glu Ile Gly Glu Phe Tyr Ser

530 535 540

His Pro Glu Ile Gly Tyr Asp Lys Phe Tyr Phe Asp Ser Tyr Lys Ile

545 550 555 560

Ile Val Gln Gly Tyr Asn Asp Ile Arg Asn Tyr Leu Thr Lys Asn Pro

565 570 575

Trp Ser Glu Glu Lys Trp Lys Leu Asn Phe Glu Asn Pro Thr Leu Ala

580 585 590

Asn Gly Trp Asp Lys Asn Lys Glu Thr Asp Asn Ser Cys Ile Phe Leu

595 600 605

Lys Arg Asp Asn Lys Phe Phe Leu Ala Leu Met Ser Arg Gly Asn Asn

610 615 620

Gln Val Phe Asp Glu Arg Asn Ile Gln Lys Phe Ala Gln Asn Ile Glu

625 630 635 640

Gln Gly Lys Tyr Glu Lys Met Val Tyr Lys Tyr Met Lys Asp Val Ala

645 650 655

Leu Gly Ile Pro Lys Ala Thr Thr Gln Leu Asn Ala Val Gln Glu His

660 665 670

Phe Phe Gln Ser Asp Lys Asp Tyr Ile Ile Thr Lys Gly Gly Ser Ser

675 680 685

Ile Gly Glu Phe Ile Lys Pro Leu Arg Val Thr Lys Arg Ile Phe Glu

690 695 700

Leu Asn Asn Arg Ile Tyr Pro Lys Asp Asn Leu Gly Ile Ser Phe Leu
705 710 715 720
Arg Asn Gln Val Asn Lys Lys Glu Gln Lys Asn Tyr Ile Lys Ile Phe
725 730 735
Gln Lys Glu Phe Ile Thr Leu Gly Gly Asp Glu Val Val Tyr Lys Lys
740 745 750
Ala Val His Asp Trp Ile Asp Phe Cys Lys Glu Tyr Thr Lys Ser Tyr

755 760 765
Pro Ser Cys Ala Tyr Phe Asp Tyr Ser Gly Leu Lys Asp Thr Lys Glu
770 775 780
Tyr Ser Ser Ile Asp Glu Phe Tyr Asn Asp Leu Asp Ser Phe Gly Tyr
785 790 795 800
Gln Ile Ser Trp Gln Asp Ile Ser Ser Ser Tyr Ile Asp Glu Leu Val
805 810 815
Glu Ser Gly Lys Leu Tyr Leu Phe Glu Ile Tyr Asn Gln Asp Phe Ser

820 825 830
Asn Gly Lys Thr Gly Ala Lys Asn Leu His Thr Leu Tyr Phe Glu His
835 840 845
Ile Phe Ser Lys Glu Asn Gln Glu Val Asn Phe Pro Leu Lys Leu Asn
850 855 860
Gly Gln Ala Glu Leu Phe Phe Arg Pro Lys Ser Ile Glu Ala Lys Gly
865 870 875 880
Glu Asn Arg Lys Phe Asn Arg Glu Ile Ile Ala Lys Lys Arg Tyr Thr

885 890 895
Glu Asp Lys Ile Phe Phe His Val Pro Leu Thr Leu Asn Arg Thr Glu
900 905 910
Gly Asp Ile Tyr Gly Phe Asn Thr Glu Ile Asn Asn Phe Leu Ala His
915 920 925
Asn Pro Asp Ile Asn Ile Ile Gly Ile Asp Arg Gly Glu Lys His Leu
930 935 940
Ala Tyr Tyr Ser Val Ile Asp Gln Lys Gly Asn Ile Ile Glu Ser Asp

945 950 955 960

Ser Leu Asn Thr Val Asn Glu Ile Asn Tyr Gly Glu Lys Leu Thr Asp

965 970 975

Thr Ala Glu Lys Arg Lys Gln Ala Arg Gln Asp Trp Gln Ala Val Glu

980 985 990

Gly Ile Lys Asn Leu Lys Lys Gly Tyr Ile Ser Ala Val Val His Lys

995 1000 1005

Leu Thr Asp Leu Ile Ile Lys Tyr Asn Ala Ile Val Ile Phe Glu

1010 1015 1020

Asp Leu Asn Met Arg Phe Lys Gln Ile Arg Gly Gly Ile Glu Lys

1025 1030 1035

Ser Val Tyr Gln Gln Leu Glu Lys Ala Leu Ile Glu Lys Leu Asn

1040 1045 1050

Tyr Leu Val Glu Lys Gly Glu Ile Asn Pro Glu Lys Ala Gly His

1055 1060 1065

Leu Leu Asn Ala Tyr Gln Leu Thr Ala Pro Phe Glu Thr Phe Lys

1070 1075 1080

Asp Met Gly Lys Gln Thr Gly Ile Val Phe Tyr Thr Gln Ala Ala

1085 1090 1095

Tyr Thr Ser Lys Ile Asp Pro Val Thr Gly Trp Arg Pro His Leu

1100 1105 1110

Tyr Leu Lys Tyr Ser Ser Ala Glu Gln Val Lys Lys Glu Ile Ala

1115 1120 1125

Lys Phe Ser Asn Ile Ile Trp Asn Asn Thr Glu Lys Arg Phe Asp

1130 1135 1140

Phe Met Tyr Asp Ile Arg Asn Phe Ser Thr Gln Lys Glu Tyr Pro

1145 1150 1155

Lys Asn Asn Ile Trp Thr Val Cys Ser Ser Val Glu Arg Tyr Arg

1160 1165 1170

Trp Asp Lys Thr Leu Asn Gln Asn Lys Gly Asp Tyr Val His Tyr

1175 1180 1185

Lys Ser Ile Thr Pro Glu Phe Glu Lys Leu Phe Ser Asp Phe Gln

1190 1195 1200

Ile Asp Gly Thr Lys Asn Ile Leu Glu Gln Ile Asn Arg Met Glu

1205 1210 1215

Thr Lys Gly Asn Glu Lys Phe Phe Lys Ser Phe Ile Phe Phe Phe

1220 1225 1230

Gly Leu Ile Cys Gln Ile Arg Asn Thr Asn Lys Ala Asp Ser Asp

1235 1240 1245

Glu Asn Lys Gln Asp Phe Ile Leu Ser Pro Val Val Pro Phe Phe

1250 1255 1260

Asp Ser Arg Asp Ser Glu Asn Thr Lys Asn Gly Leu Pro Arg Asn

1265 1270 1275

Gly Asp Glu Asn Gly Ala Tyr Asn Ile Ala Arg Lys Gly Leu Ile

1280 1285 1290

Ile Leu Gln Lys Ile Asn Glu Phe Ser Asp Glu Asn Gly Asn Cys

1295 1300 1305

Asp Lys Leu Gly Trp Lys Glu Leu Ser Ile Ser Gln Val Asp Trp

1310 1315 1320

Asp Asn Tyr Ile Lys Thr

1325

<210> 97

<211> 841

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 97

Met Glu Tyr Asp Glu His Ile Ser Leu Ile Glu Ser Glu Glu Lys Ala

1 5 10 15

Asp Glu Met Lys Lys Arg Leu Asp Met Tyr Met Asn Met Tyr His Trp

20 25 30

Ala Lys Ala Phe Ile Val Asp Glu Val Leu Asp Arg Asp Glu Met Phe

35 40 45

Tyr Ser Asp Ile Asp Asp Ile Tyr Asn Ile Leu Glu Asn Ile Val Pro

50 55 60

Leu Tyr Asn Arg Val Arg Asn Tyr Val Thr Gln Lys Pro Tyr Thr Ser

65 70 75 80

Lys Lys Ile Lys Leu Asn Phe Gln Ser Pro Thr Leu Ala Asn Gly Trp

85 90 95

Ser Gln Ser Lys Glu Phe Asp Asn Asn Ala Ile Ile Leu Ile Arg Asp

100 105 110

Asn Lys Tyr Tyr Leu Ala Ile Phe Asn Ala Lys Asn Lys Pro Asp Lys

115 120 125

Lys Ile Ile Gln Gly Asn Ser Asp Lys Lys Asn Asp Asn Asp Tyr Lys

130 135 140

Lys Met Val Tyr Asn Leu Leu Pro Gly Ala Asn Lys Met Leu Pro Lys

145 150 155 160

Val Phe Leu Ser Lys Lys Gly Ile Glu Thr Phe Lys Pro Ser Asp Tyr

165 170 175

Ile Ile Ser Gly Tyr Asn Ala His Lys His Ile Lys Thr Gly Glu Asn

180 185 190

Phe Asp Ile Ser Phe Cys Arg Asp Leu Ile Asp Tyr Phe Lys Asn Ser

195 200 205

Ile Glu Lys His Ala Glu Trp Arg Lys Tyr Glu Phe Lys Phe Ser Ala

210 215 220

Thr Asp Ser Tyr Asn Asp Ile Ser Glu Phe Tyr Arg Glu Val Glu Met

225 230 235 240

Gln Gly Tyr Arg Ile Asp Trp Thr Tyr Ile Ser Glu Ala Asp Ile Asn

245 250 255

Lys Leu Asp Glu Glu Gly Lys Ile Tyr Leu Phe Gln Ile Tyr Asn Lys

260 265 270

Asp Phe Ala Glu Asn Ser Thr Gly Lys Glu Asn Leu His Thr Met Tyr

275 280 285

Phe Lys Asn Ile Phe Ser Glu Glu Asn Leu Lys Asn Ile Val Ile Lys

290 295 300

Leu Asn Gly Gln Ala Glu Leu Phe Tyr Arg Lys Ala Ser Val Lys Asn

305 310 315 320

Pro Val Lys His Lys Lys Asp Ser Val Leu Val Asn Lys Thr Tyr Lys

325 330 335

Asn Gln Leu Asp Asn Gly Asp Val Val Arg Ile Pro Ile Pro Asp Asp

340 345 350

Ile Tyr Asn Glu Ile Tyr Lys Met Tyr Asn Gly Tyr Ile Lys Glu Ser

355 360 365

Asp Leu Ser Gly Ala Ala Lys Glu Tyr Leu Asp Lys Val Glu Val Arg

370 375 380

Thr Ala Gln Lys Glu Ile Val Lys Asp Tyr Arg Tyr Thr Val Asp Lys

385 390 395 400

Tyr Phe Ile His Thr Pro Ile Thr Ile Asn Tyr Lys Val Thr Ala Arg

405 410 415

Asn Asn Val Asn Asp Met Ala Val Lys Tyr Ile Ala Gln Asn Asp Asp

420 425 430

Ile His Val Ile Gly Ile Asp Arg Gly Glu Arg Asn Leu Ile Tyr Ile

435 440 445

Ser Val Ile Asp Ser His Gly Asn Ile Val Lys Gln Lys Ser Tyr Asn

450 455 460

Ile Leu Asn Asn Tyr Asp Tyr Lys Lys Lys Leu Val Glu Lys Glu Lys

465 470 475 480

Thr Arg Glu Tyr Ala Arg Lys Asn Trp Lys Ser Ile Gly Asn Ile Lys

485 490 495

Glu Leu Lys Glu Gly Tyr Ile Ser Gly Val Val His Glu Ile Ala Met

500 505 510

Leu Met Val Glu Tyr Asn Ala Ile Ile Ala Met Glu Asp Leu Asn Tyr

515 520 525

Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Arg Gln Val Tyr Gln Lys
530 535 540
Phe Glu Ser Met Leu Ile Asn Lys Leu Asn Tyr Phe Ala Ser Lys Gly

545 550 555 560
Lys Ser Val Asp Glu Pro Gly Gly Leu Leu Lys Gly Tyr Gln Leu Thr
565 570 575
Tyr Val Pro Asp Asn Ile Lys Asn Leu Gly Lys Gln Cys Gly Val Ile
580 585 590
Phe Tyr Val Pro Ala Ala Phe Thr Ser Lys Ile Asp Pro Ser Thr Gly
595 600 605
Phe Ile Ser Ala Phe Asn Phe Lys Ser Ile Ser Thr Asn Ala Ser Arg

610 615 620
Lys Gln Phe Phe Met Gln Phe Asp Glu Ile Arg Tyr Cys Ala Glu Lys
625 630 635 640
Asp Met Phe Ser Phe Gly Phe Asp Tyr Asn Asn Phe Asp Thr Tyr Asn
645 650 655
Ile Thr Met Gly Lys Thr Gln Trp Thr Val Tyr Thr Asn Gly Glu Arg
660 665 670
Leu Gln Ser Glu Phe Asn Asn Ala Arg Arg Thr Gly Lys Thr Lys Ser

675 680 685
Ile Asn Leu Thr Glu Thr Ile Lys Leu Leu Leu Lys Asp Asn Glu Ile
690 695 700
Asn Tyr Ala Asp Gly His Asp Val Arg Ile Asp Met Glu Lys Met Asp
705 710 715 720
Glu Asp Lys Asn Ser Glu Phe Phe Ala Gln Leu Leu Ser Leu Tyr Lys
725 730 735
Leu Thr Val Gln Met Arg Asn Ser Tyr Thr Glu Ala Glu Glu Gln Glu

740 745 750
Lys Gly Ile Ser Tyr Asp Lys Ile Ile Ser Pro Val Ile Asn Asp Glu
755 760 765
Gly Glu Phe Phe Asp Ser Asp Asn Tyr Lys Glu Ser Asp Asp Lys Glu

770 775 780

Cys Lys Met Pro Lys Asp Ala Asp Ala Asn Gly Ala Tyr Cys Ile Ala

785 790 795 800

Leu Lys Gly Leu Tyr Glu Val Leu Lys Ile Lys Ser Glu Trp Thr Glu

805 810 815

Asp Gly Phe Asp Arg Asn Cys Leu Lys Leu Pro His Ala Glu Trp Leu

820 825 830

Asp Phe Ile Gln Asn Lys Arg Tyr Glu

835 840

<210> 98

<211> 886

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 98

Met Phe Gly Asn Trp Gly Val Ile Gln Asn Ala Val Met Gln Asn Ile

1 5 10 15

Lys Arg Val Ala Pro Ala Arg Lys His Lys Glu Ser Glu Glu Asp Tyr

20 25 30

Glu Lys Arg Ile Ala Gly Ile Phe Lys Lys Ala Asp Ser Phe Ser Ile

35 40 45

Ser Tyr Ile Asn Asp Cys Leu Asn Glu Ala Asp Pro Asn Asn Ala Tyr

50 55 60

Phe Val Glu Asn Tyr Phe Ala Thr Phe Gly Ala Val Asn Thr Pro Thr

65 70 75 80

Met Gln Arg Glu Asn Leu Phe Ala Leu Val Gln Asn Ala Tyr Thr Glu

85 90 95

Ile Thr Ala Leu Leu His Ser Asp Tyr Pro Thr Glu Lys Asn Leu Ala

100 105 110

Gln Asp Lys Ala Asn Val Ala Lys Ile Lys Ala Leu Leu Asp Ala Ile

115 120 125

Lys Ser Leu Gln His Phe Val Lys Pro Leu Leu Gly Lys Gly Asp Glu
130 135 140

Ser Asp Lys Asp Glu Arg Phe Tyr Gly Glu Leu Ala Ser Leu Trp Ala
145 150 155 160
Glu Leu Asp Thr Met Thr Pro Leu Tyr Asn Met Ile Arg Asn Tyr Met
165 170 175
Thr Arg Lys Pro Tyr Ser Gln Lys Lys Ile Lys Leu Asn Phe Glu Asn
180 185 190
Pro Gln Leu Leu Gly Gly Trp Asp Ala Asn Lys Glu Lys Asp Tyr Ala
195 200 205

Thr Ile Ile Leu Arg Arg Asn Gly Leu Tyr Tyr Leu Ala Ile Met Asn
210 215 220
Lys Asp Ser Lys Lys Leu Leu Gly Lys Ala Met Pro Ser Asp Gly Glu
225 230 235 240
Cys Tyr Glu Lys Met Val Tyr Lys Leu Leu Pro Gly Ala Asn Lys Met
245 250 255
Leu Pro Lys Val Phe Phe Ala Lys Ser Arg Met Glu Asp Phe Lys Pro
260 265 270

Ser Lys Glu Leu Val Glu Lys Tyr Asn Asn Gly Thr His Lys Lys Gly
275 280 285
Lys Asn Phe Asn Ile Gln Asp Cys His Asn Leu Ile Asp Tyr Phe Lys
290 295 300
Gln Ser Ile Asp Lys His Glu Asp Trp Ser Lys Phe Gly Phe Lys Phe
305 310 315 320
Ser Asp Thr Ser Thr Tyr Glu Asp Leu Ser Gly Phe Tyr Arg Glu Val
325 330 335

Glu Gln Gln Gly Tyr Lys Leu Ser Phe Ala Arg Val Ser Val Ser Tyr
340 345 350
Ile Asn Gln Leu Val Glu Glu Gly Lys Met Tyr Leu Phe Gln Ile Tyr
355 360 365
Asn Lys Asp Phe Ser Glu Tyr Ser Lys Gly Thr Pro Asn Met His Thr

370 375 380

Leu Tyr Trp Lys Ala Leu Phe Asp Glu Arg Asn Leu Ala Asp Val Val

385 390 395 400

Tyr Lys Leu Asn Gly Gln Ala Glu Met Phe Tyr Arg Lys Lys Ser Ile

405 410 415

Glu Asn Thr His Pro Thr His Pro Ala Asn His Pro Ile Leu Asn Lys

420 425 430

Asn Lys Asp Asn Asn Lys Lys Glu Ser Leu Phe Glu Tyr Asp Leu Ile

435 440 445

Lys Asp Arg Arg Tyr Thr Val Asp Lys Phe Met Phe His Val Pro Ile

450 455 460

Thr Met Asn Phe Lys Ser Ser Gly Ser Glu Asn Ile Asn Gln Asp Val

465 470 475 480

Lys Ala Tyr Leu Cys His Ala Asp Asp Met His Ile Ile Gly Ile Asp

485 490 495

Arg Gly Glu Arg His Leu Leu Tyr Leu Val Val Ile Asp Leu Gln Gly

500 505 510

Asn Ile Lys Glu Gln Phe Ser Leu Asn Glu Ile Val Asn Asp Tyr Asn

515 520 525

Gly Asn Thr Tyr His Thr Asn Tyr His Asp Leu Leu Asp Val Arg Glu

530 535 540

Asp Glu Arg Leu Lys Ala Arg Gln Ser Trp Gln Thr Ile Glu Asn Ile

545 550 555 560

Lys Glu Leu Lys Glu Gly Tyr Leu Ser Gln Val Ile His Lys Ile Thr

565 570 575

Gln Leu Met Val Lys Tyr His Ala Ile Val Val Leu Glu Asp Leu Asn

580 585 590

Met Gly Phe Met Arg Gly Arg Gln Lys Val Glu Lys Gln Val Tyr Gln

595 600 605

Lys Phe Glu Lys Met Leu Ile Glu Lys Leu Asn Tyr Leu Val Asp Lys

610 615 620

Lys Ala Asp Ala Ser Val Ser Gly Gly Leu Leu Asn Ala Tyr Gln Leu
625 630 635 640
Thr Ser Lys Phe Asp Ser Phe Gln Lys Leu Gly Lys Gln Ser Gly Phe
645 650 655

Leu Phe Tyr Ile Pro Ala Trp Asn Thr Ser Lys Ile Asp Pro Val Thr
660 665 670
Gly Phe Val Asn Leu Leu Asp Thr Arg Tyr Gln Asn Val Glu Lys Ala
675 680 685
Lys Ser Phe Phe Ser Lys Phe Asp Ala Ile Arg Tyr Asn Lys Asp Lys
690 695 700
Glu Trp Phe Glu Phe Asn Leu Asp Tyr Asp Lys Phe Gly Lys Lys Ala
705 710 715 720

Glu Gly Thr Arg Thr Lys Trp Thr Leu Cys Thr Arg Gly Met Arg Ile
725 730 735
Asp Thr Phe Arg Asn Lys Glu Lys Asn Ser Gln Trp Asp Asn Gln Glu
740 745 750
Val Asp Leu Thr Ala Glu Met Lys Ser Leu Leu Glu His Tyr Tyr Ile
755 760 765
Asp Ile His Ser Asn Leu Lys Asp Ala Ile Ser Ala Gln Thr Asp Lys
770 775 780

Ala Phe Phe Thr Gly Leu Leu His Ile Leu Lys Leu Thr Leu Gln Met
785 790 795 800
Arg Asn Ser Ile Thr Gly Thr Glu Thr Asp Tyr Leu Val Ser Pro Val
805 810 815
Val Asp Glu Asn Gly Ile Phe Tyr Asp Ser Arg Ser Cys Gly Asp Glu
820 825 830
Leu Pro Glu Asn Ala Asp Ala Asn Gly Ala Tyr Asn Ile Ala Arg Lys
835 840 845

Gly Leu Met Met Ile Glu Gln Ile Lys Asp Ala Lys Asp Leu Asp Asn
850 855 860
Leu Lys Phe Asp Ile Ser Asn Lys Ala Trp Leu Asn Phe Ala Gln Gln

865 870 875 880

Lys Pro Tyr Lys Asn Gly

885

<210> 99

<211> 1228

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 99

Met Ser Asn Leu Tyr Ser Asn Leu His Asn Leu Tyr Gln Val Gln Lys

1 5 10 15

Thr Leu Arg Phe Glu Leu Lys Pro Gln Gly Lys Thr Lys Glu Asn Met

20 25 30

Glu Lys Val Gly Ile Leu Lys Ala Asp Glu His Arg Ala Glu Ile Tyr

35 40 45

Ser Lys Val Lys Lys Tyr Cys Asp Glu Tyr His Lys Leu Phe Ile Asp

50 55 60

Lys Ser Leu Ser Asn Ile Glu Leu Asn Gly Ile Asp Arg Tyr Tyr Glu

65 70 75 80

Leu Tyr Ser Ile Asn Asn Arg Asp Asp Lys Gln Lys Glu Glu Leu Asp

85 90 95

Gln Leu Glu Ala Ser Leu Arg Lys Gln Ile Ser Asp Ala Phe Lys Lys

100 105 110

Ser Ala Glu Tyr Lys Gly Leu Phe Gln Lys Asp Ile Ile Thr Ser Tyr

115 120 125

Leu Val Thr Met Tyr Lys Glu Asn Gln Glu Lys Met Gln Asp Ile Gly

130 135 140

Glu Phe Asn Arg Phe Thr Thr Tyr Phe Thr Gly Tyr Asn Lys Asn Arg

145 150 155 160

Glu Asn Met Tyr Ser Glu Glu Asp Lys Ser Thr Ala Ile Ser Tyr Arg

165 170 175

Leu Ile Asn Glu Asn Leu Pro Thr Phe Ile Asp Asn Ile Lys Ile Tyr
180 185 190
Lys Lys Ile Val Ser Leu Met Pro Glu Asp Ile Glu Lys Ile Tyr Lys
195 200 205

Asp Leu Glu Glu Tyr Ile Gln Val Asp Ser Ile Asp Glu Ile Phe Asn
210 215 220
Ile Ser Tyr Tyr Asn Asp Val Leu Thr Gln Arg Gly Ile Glu Cys Tyr
225 230 235 240
Asn Ile Leu Ile Ser Gly Arg Thr Lys Asn Asp Gly Asp Lys Ile Lys
245 250 255
Gly Leu Asn Glu Tyr Ile Asn Glu Phe Asn Gln Thr His Asn Glu Lys
260 265 270

Ile Pro Lys Leu Gln Glu Leu Tyr Lys Gln Ile Leu Ser Asp Ala Glu
275 280 285
Ser Ala Ser Phe Lys Ile Asp Val Ile Lys Asn Asp Lys Glu Leu Met
290 295 300
Asn Leu Ile Glu Val Tyr Tyr Ala Asn Ile Leu Pro Ile Leu Asn Lys
305 310 315 320
Ile Glu Asp Leu Phe Thr Arg Ile Ser Asn Tyr Asn Leu Glu Leu Ile
325 330 335

Leu Val Asn Asn Asp Gly Thr Leu Ser Thr Leu Ser Asn Met Val Phe
340 345 350
Asn Glu Trp Ser Tyr Ile Lys Gly Ala Ile Ser Glu Lys Tyr Asp Glu
355 360 365
Glu Tyr Ser Gly Lys Glu Lys Tyr Gly Thr Glu Lys Tyr Ala Gln Lys
370 375 380
Lys Gln Glu Tyr Leu Lys Lys Gln Lys Ile Tyr Ser Leu Lys Phe Leu
385 390 395 400

Asn Asp Cys Ile Gly Asn Asn Ala Ile Cys Glu Tyr Leu Lys Asn Tyr
405 410 415
Ile Ile Gln Asn Lys Asn Ile Glu Thr Ile Lys Glu Asp Tyr Asn Glu

420 425 430

Val Gln Asn Ile Lys Val Glu Asp Asp Thr Lys Glu Leu Ile Lys Asp

435 440 445

Glu Lys Ser Ile Glu Lys Ile Lys Lys Phe Leu Asp Asp Val Lys Ser

450 455 460

Leu Gln Glu Phe Val Lys Leu Val Ile Pro Lys Asp Arg Thr Val Glu

465 470 475 480

Lys Asp Ala Lys Phe Tyr Ser Glu Leu Thr Pro Tyr Tyr Glu Lys Ile

485 490 495

Lys Glu Ile Ile Pro Leu Tyr Asn Lys Val Arg Asn Tyr Val Thr Gln

500 505 510

Lys Pro Tyr Ser Thr Glu Lys Ile Lys Leu Asn Phe Glu Cys Pro Thr

515 520 525

Leu Leu Lys Gly Trp Asp Ala Asn Lys Glu Glu Ala Asn Leu Gly Val

530 535 540

Ile Leu Leu Lys Glu Gly Lys Tyr Tyr Leu Gly Ile Ile Asn Pro Tyr

545 550 555 560

Cys Lys Lys Ile Phe Glu Val Asp Glu Lys Asp Ser Asn Glu Gln Asn

565 570 575

Asn Tyr Lys Lys Met Glu Tyr Lys Leu Leu Pro Gly Pro Asn Lys Met

580 585 590

Leu Pro Lys Val Phe Phe Ser Asn Ser Arg Ile Glu Glu Phe Asn Pro

595 600 605

Ser Lys Glu Leu Gln Glu Lys Tyr Asn Lys Gly Tyr His Lys Lys Gly

610 615 620

Lys Asp Phe Asp Ile Asn Phe Cys His Glu Leu Ile Asp Phe Tyr Lys

625 630 635 640

Gln Ser Val Asn Lys His Glu Asp Trp Lys Lys Phe Asn Phe Lys Phe

645 650 655

Lys Asp Thr Ser Glu Tyr Asn Asp Ile Ser Glu Phe Tyr Arg Glu Val

660 665 670

Glu Lys Gln Gly Tyr Lys Ile Glu Tyr Thr Glu Tyr Ser Glu Lys Tyr
675 680 685
Ile Asn Glu Leu Val Asp Arg Gly Glu Leu Tyr Leu Phe Gln Ile Tyr
690 695 700
Asn Lys Asp Phe Ser Glu Tyr Ser Lys Gly Lys Glu Asn Leu His Thr
705 710 715 720

Leu Tyr Trp Lys Ala Val Phe Asp Pro Asp Asn Ile Met Asn Pro Val
725 730 735
Tyr Lys Leu Asn Gly Asn Ala Glu Val Phe Tyr Arg Lys Lys Ser Leu
740 745 750
Glu Met Lys Val Thr His Pro Ala Asn Gln Pro Ile Ala Asn Lys Asn
755 760 765
Ile Ser Thr Ile Glu Ala Gly Arg Ser Thr Ser Thr Phe Lys Tyr Asp
770 775 780

Leu Ile Lys Asp Lys Arg Tyr Thr Met Asp Lys Phe Gln Phe His Val
785 790 795 800
Pro Ile Thr Met Asn Phe Lys Ser Glu Arg Leu Phe Asn Ile Asn Gln
805 810 815
Ile Val Asn Lys Tyr Leu Lys Tyr Asn Asp Asp Ile His Val Ile Gly
820 825 830
Ile Asp Arg Gly Glu Arg Asn Leu Leu Tyr Val Cys Val Ile Asp Lys
835 840 845

Asn Glu Lys Ile Val Tyr Gln Lys Ser Leu Asn Glu Ile Val Ser Glu
850 855 860
Tyr Asn Asn Asn Arg Tyr Thr Thr Asp Tyr His Gly Leu Leu Asp Arg
865 870 875 880
Lys Glu Lys Glu Arg Glu Ile Ala Arg Glu Asp Trp Lys Asn Ile Glu
885 890 895
Asn Ile Lys Glu Leu Lys Glu Gly Tyr Met Ser Gln Val Ile His Ile
900 905 910

Leu Val Glu Leu Met Lys Lys Tyr Asn Ala Ile Ile Val Ile Glu Asp

915 920 925

Leu Asn Lys Gly Phe Lys Asn Ser Arg Ile Lys Val Glu Lys Gln Val

930 935 940

Tyr Gln Lys Phe Glu Lys Met Phe Ile Asp Lys Leu Asn Tyr Leu Val

945 950 955 960

Phe Lys Asp Glu Asp Lys Met Asn Glu Gly Gly Val Leu Asn Ala Tyr

965 970 975

Gln Leu Thr Asn Lys Phe Glu Ser Phe Thr Lys Leu Gly Lys Gln Ser

980 985 990

Gly Ile Leu Tyr Tyr Ile Pro Ala Trp Cys Thr Ser Lys Ile Asp Pro

995 1000 1005

Thr Thr Gly Phe Ile Asn Arg Phe Tyr Leu Lys Tyr Glu Asn Phe

1010 1015 1020

Asp Lys Ser Lys Glu Phe Val Asn Arg Ile Asp Asp Ile Arg Tyr

1025 1030 1035

Asn Glu Lys Glu Asn Leu Phe Glu Phe Asp Ile Asp Tyr Ser Lys

1040 1045 1050

Phe Thr Asp Arg Leu Asn Asp Thr Lys Asn Lys Trp Thr Leu Cys

1055 1060 1065

Ser Tyr Gly Glu Arg Ile Leu Thr Gln Lys Asn Ala Asn Gly Glu

1070 1075 1080

Trp Leu Asp Arg Arg Ile Gln Leu Ser Ile Glu Phe Lys Lys Leu

1085 1090 1095

Phe Glu Lys Tyr Gly Ile Asn Leu Asn Asn Ile Lys Asp Ser Ile

1100 1105 1110

Leu Lys Leu Asp Lys Asp Asn Leu Glu Phe Tyr Lys Gly Asn Gly

1115 1120 1125

Glu Ser Leu Gly Phe Ile Gln Leu Phe Lys Leu Met Val Gln Met

1130 1135 1140

Arg Asn Ser Leu Thr Gly Lys Glu Glu Asp Asn Leu Ile Ser Pro

1145 1150 1155

Val Lys Asn Gln His Gly Lys Phe Phe Asn Thr Ser Glu Lys Ile
1160 1165 1170

Glu Gly Leu Pro Ile Asp Ala Asp Ala Asn Gly Ala Tyr Asn Ile
1175 1180 1185

Ala Arg Lys Gly Phe Met Leu Val Glu Gln Met Lys Asn Val Glu
1190 1195 1200

Asp Glu Lys Leu Asn Lys Ile Lys Tyr Asn Ile Thr Glu Lys Glu
1205 1210 1215

Trp Leu Asn Tyr Val Gln Asn Arg Gly Met
1220 1225

<210> 100

<211> 1142

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas12 sequence

<400> 100

Met Ala Arg Ile Phe Glu Asp Phe Lys Arg Leu Tyr Pro Leu Ser Lys
1 5 10 15

Thr Leu Arg Phe Glu Ala Lys Pro Ile Gly Ala Thr Leu Asp Asn Ile
20 25 30

Val Lys Ser Gly Leu Leu Asp Glu Asp Glu His Arg Ala Glu Ser Tyr
35 40 45

Val Lys Val Lys Lys Leu Ile Asp Glu Tyr His Lys Val Phe Ile Asp
50 55 60

Arg Val Leu Asp Asn Gly Cys Leu Pro Leu Lys Asn Glu Gly His Asn
65 70 75 80

Asn Ser Leu Thr Glu Tyr Tyr Asp Ser Tyr Val Ser Lys Ser Gln Asn
85 90 95

Glu Asp Ala Lys Lys Ala Phe Glu Glu Asn Gln Gln Asn Leu Arg Ser
100 105 110

Ile Ile Ala Lys Lys Leu Thr Glu Asp Lys Ala Tyr Ala Asn Leu Phe

115 120 125

Gly Lys Asn Leu Ile Glu Ser Tyr Lys Asp Lys Thr Asp Lys Thr Lys

130 135 140

Ile Ile Asp Ser Asp Leu Ile Gln Phe Ile Asn Thr Ala Glu Ser Thr

145 150 155 160

Gln Leu Asn Ser Met Ser Gln Asp Glu Ala Lys Glu Leu Val Lys Glu

165 170 175

Phe Trp Gly Phe Thr Thr Tyr Phe Val Gly Phe Phe Asp Asn Cys Lys

180 185 190

Asn Met Tyr Thr Ala Glu Glu Lys Ser Thr Gly Ile Ala Tyr Arg Leu

195 200 205

Ile Asn Glu Asn Leu Pro Lys Phe Ile Asp Asn Met Glu Ala Phe Lys

210 215 220

Lys Ala Ile Ala Arg Pro Glu Ile Gln Ala Asn Met Glu Glu Leu Tyr

225 230 235 240

Ser Asn Phe Ser Glu Tyr Leu Asn Val Glu Ser Ile Gln Glu Met Phe

245 250 255

Leu Leu Asp Tyr Tyr Asn Met Leu Leu Thr Gln Lys Gln Ile Asp Val

260 265 270

Tyr Asn Ala Ile Ile Gly Gly Lys Thr Asp Asp Glu His Asp Val Lys

275 280 285

Ile Lys Gly Ile Asn Glu Tyr Ile Asn Leu Tyr Asn Gln Gln His Lys

290 295 300

Asp Asp Lys Leu Pro Lys Leu Lys Ala Leu Phe Lys Gln Ile Leu Ser

305 310 315 320

Asp Arg Asn Ala Ile Ser Trp Leu Pro Glu Glu Phe Asn Ser Asp Gln

325 330 335

Glu Val Leu Asn Ala Ile Lys Asp Cys Tyr Glu Arg Leu Ser Glu Asn

340 345 350

Val Leu Gly Asp Lys Val Leu Lys Ser Leu Leu Gly Ser Leu Ala Asp

355 360 365

Tyr Ser Leu Asp Gly Ile Phe Ile Arg Asn Asp Leu Gln Leu Thr Asp
370 375 380
Ile Ser Gln Lys Met Phe Gly Asn Trp Gly Val Ile Gln Asn Ala Ile
385 390 395 400
Met Gln Asn Ile Lys Arg Val Ala Pro Ala Arg Lys His Lys Glu Ser
405 410 415
Glu Glu Asp Tyr Glu Lys Arg Ile Ala Gly Ile Phe Lys Lys Ala Asp

420 425 430
Ser Phe Ser Ile Ser Tyr Ile Asn Asp Cys Leu Asn Glu Ala Asp Pro
435 440 445
Asn Asn Ala Tyr Phe Val Glu Asn Tyr Phe Ala Thr Phe Gly Ala Val
450 455 460
Asn Thr Pro Thr Met Gln Arg Glu Asn Leu Phe Ala Leu Val Gln Asn
465 470 475 480
Ala Tyr Thr Glu Val Ala Ser Leu Leu His Ser Tyr Tyr Pro Ala Glu

485 490 495
Lys Lys Leu Ala Gln Asp Lys Ala Asn Val Ala Lys Ile Lys Ala Leu
500 505 510
Leu Asp Ala Ile Lys Ser Leu Gln His Phe Val Lys Pro Leu Leu Gly
515 520 525
Lys Gly Asp Glu Ser Asp Lys Asp Glu Arg Phe Tyr Gly Glu Leu Ala
530 535 540
Ser Leu Trp Ala Glu Leu Asp Thr Val Thr Pro Leu Tyr Asn Met Ile

545 550 555 560
Arg Asn Tyr Ile Thr Arg Lys Pro Tyr Ser Gln Lys Lys Ile Lys Leu
565 570 575
Asn Phe Glu Asn Pro Gln Leu Leu Gly Gly Trp Asp Ala Asn Lys Glu
580 585 590
Lys Asp Tyr Ala Thr Ile Ile Leu Arg Arg Asn Gly Leu Tyr Tyr Leu
595 600 605
Ala Ile Met Asp Lys Asp Ser Arg Lys Leu Leu Gly Lys Ala Met Pro

610 615 620

Ser Asp Gly Glu Cys Tyr Glu Lys Met Val Tyr Lys Leu Leu Pro Gly

625 630 635 640

Ala Asn Lys Met Leu Pro Lys Val Phe Phe Ala Lys Ser Arg Met Asp

645 650 655

Asp Phe Lys Pro Ser Lys Glu Leu Ile Glu Lys Tyr Asn Asn Gly Thr

660 665 670

His Lys Lys Gly Lys Asn Phe Asp Ile Gln Asp Cys His Asn Leu Ile

675 680 685

Asp Tyr Phe Lys Gln Ser Ile Asp Lys His Glu Asp Trp Ser Lys Phe

690 695 700

Gly Phe Asn Phe Ser Asp Thr Ser Thr Tyr Glu Asp Leu Ser Gly Phe

705 710 715 720

Tyr Arg Glu Val Glu Gln Gln Gly Tyr Lys Leu Ser Phe Ala Arg Val

725 730 735

Ser Val Ser Tyr Ile Asn Gln Leu Val Glu Glu Gly Lys Met Tyr Leu

740 745 750

Phe Gln Ile Tyr Asn Lys Asp Phe Ser Glu Tyr Ser Lys Gly Thr Pro

755 760 765

Asn Met His Thr Leu Tyr Trp Lys Ala Leu Phe Asp Glu Arg Asn Leu

770 775 780

Ala Asp Val Val Tyr Lys Leu Asn Gly Gln Ala Glu Met Phe Tyr Arg

785 790 795 800

Lys Lys Ser Ile Glu Asn Thr His Pro Thr His Pro Ala Asn His Pro

805 810 815

Ile Leu Asn Lys Asn Lys Asp Asn Lys Lys Lys Glu Ser Leu Phe Glu

820 825 830

Tyr Asp Leu Ile Lys Asp Arg Arg Tyr Thr Val Asp Lys Phe Met Phe

835 840 845

His Val Pro Ile Thr Met Asn Phe Lys Ser Val Gly Ser Glu Asn Ile

850 855 860

Asn Gln Gly Val Lys Glu Tyr Leu His His Ala Asp Asp Met His Ile

865 870 875 880

Ile Gly Ile Asp Arg Gly Glu Arg His Leu Leu Tyr Leu Val Val Ile

885 890 895

Asp Leu Gln Gly Asn Ile Lys Glu Gln Tyr Ser Leu Asn Glu Ile Val

900 905 910

Asn Glu Tyr Asn Gly Asn Thr Tyr His Thr Asn Tyr His Asp Leu Leu

915 920 925

Asp Ala Arg Glu Asp Glu Arg Leu Lys Ala Arg Gln Ser Trp Gln Thr

930 935 940

Ile Glu Asn Ile Lys Glu Leu Lys Glu Gly Tyr Leu Ser Gln Val Ile

945 950 955 960

His Lys Ile Thr Gln Leu Met Val Lys Tyr His Ala Ile Val Val Leu

965 970 975

Glu Asp Leu Asn Met Gly Phe Met Arg Gly Arg Gln Lys Val Glu Lys

980 985 990

Gln Val Tyr Gln Lys Phe Glu Lys Met Leu Ile Asp Lys Leu Asn Tyr

995 1000 1005

Leu Val Asp Lys Lys Ala Asp Ala Ser Val Ser Gly Gly Leu Leu

1010 1015 1020

Asn Ala Tyr Gln Leu Thr Ser Lys Phe Asp Ser Phe Gln Lys Leu

1025 1030 1035

Gly Lys Gln Ser Gly Phe Leu Phe Tyr Ile Pro Ala Trp Asn Thr

1040 1045 1050

Ser Lys Ile Asp Pro Val Thr Gly Phe Val Asn Leu Leu Asp Ala

1055 1060 1065

Arg Tyr Gln Asn Val Glu Lys Ala Lys Ala Phe Phe Ser Lys Phe

1070 1075 1080

Asp Ala Ile Arg Tyr Lys Arg Ile Arg Thr Gly Leu Ser Leu Ile

1085 1090 1095

Ser Thr Met Thr Ser Leu Val Lys Lys Gln Lys Val Gln Gly Leu

1100 1105 1110

Ser Gly Phe Tyr Ala Pro Glu Glu Cys Val Leu Ile Leu Ser Glu

1115 1120 1125

Ile Lys Lys Lys Thr His Asn Gly Ile Ile Arg Lys Leu Thr

1130 1135 1140

<210> 101

<211> 1250

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 101

Met Ile Ser Leu Asn Tyr Phe Gln Asn Gln Tyr Ala Val Ala Lys Thr

1 5 10 15

Leu Cys Leu Glu Leu Arg Pro Ile Glu Lys Thr Met Glu Tyr Ile Ile

20 25 30

Ser Ser Gly Ile Leu Lys Glu Asp Glu His Arg Asn Glu Ser Tyr Lys

35 40 45

Leu Val Lys Lys Ile Ile Asp Asp Tyr His Lys Ala Tyr Ile Glu Leu

50 55 60

Ser Leu Ser Arg Phe Glu Leu Lys Ile Thr Ser Cys Ser Lys Asn Asp

65 70 75 80

Ala Leu Glu Asp Phe Tyr Cys Gln Tyr Leu Ala Asn Ser Gln Glu Glu

85 90 95

Lys Asp Lys Asn Ile Phe Lys Lys Thr Gln Asp Asn Leu Arg Lys Gln

100 105 110

Ile Ala Lys His Leu Thr Gln Gly Glu Ala Tyr Lys Arg Ile Asp Lys

115 120 125

Lys Glu Leu Ile Gln Glu Asp Leu Leu Glu Phe Val Ala Ala Asp Pro

130 135 140

Asp Ala Ala Asn Lys Lys Ile Leu Ile Asn Glu Phe Arg Asp Phe Thr

145 150 155 160

Thr Tyr Phe Thr Gly Phe Tyr Glu Asn Arg Lys Asn Met Tyr Ser Glu

165 170 175

Glu Ala Gln Ser Thr Ala Ile Ala Tyr Arg Ile Ile His Glu Asn Leu

180 185 190

Pro Lys Phe Ile Asp Asn Met Gly Thr Phe Lys Gln Leu Met Gln Ser

195 200 205

Ser Ile Thr Asp Ile Leu Pro Gln Ile Phe Asp Asn Phe Lys Lys Asp

210 215 220

Leu Glu Val Ser Ser Ile Gln Glu Ile Phe Asp Leu Asn Tyr Phe Asn

225 230 235 240

Lys Val Leu Thr Gln Lys Gln Ile Asp Ile Tyr Asn Ala Ile Ile Gly

245 250 255

Gly Lys Ser Leu Asn Glu Asn Ser Arg Ile Gln Gly Leu Asn Glu Tyr

260 265 270

Ile Asn Leu Tyr Asn Gln Gln His Lys Glu Asn Lys Leu Pro Leu Leu

275 280 285

Lys Leu Leu Phe Lys Gln Ile Leu Ser Asp Arg Asn Ser Leu Ser Trp

290 295 300

Leu Pro Glu Ala Phe Glu Thr Asp Lys Gln Val Leu His Ala Val Arg

305 310 315 320

Lys Cys Tyr Ala Asn Leu Lys Glu Ser Val Leu His Glu Ala Gly Leu

325 330 335

Val Gln Leu Leu Ser Ser Leu Pro Ser Tyr Asp Ser Thr Arg Ile Tyr

340 345 350

Ile Arg Asn Asp Gln Ala Leu Thr Thr Ile Ser Gln Lys Leu Phe Gly

355 360 365

Asp Trp Gly Ile Ile Pro His Ala Ile Lys Glu Arg Leu Lys Lys Asp

370 375 380

Ile Ser Ala Lys Arg Lys Glu Thr Glu Glu Ala Tyr Leu Glu Arg Ile

385 390 395 400

Glu Lys Ala Phe Lys Gln Ala Asp Ser Tyr Thr Ile Ala Tyr Ile Asn

405 410 415

Asp Ser Leu Lys Glu Ile Gly Val Asp Lys Lys Asn Ile Glu Asp Tyr

420 425 430

Phe Ile His Leu Gly Ala Ile Cys Thr Glu Gly Gln Glu Gln Glu Asn

435 440 445

Ile Leu Gln Arg Ile Ala Ser Ala Tyr Ser Gln Ala Gln Pro Leu Leu

450 455 460

Glu Glu Lys Val Pro Val His Lys Asn Leu Met Gln Asp Lys Asp Ser

465 470 475 480

Val Glu Leu Ile Lys Ser Leu Leu Asp Glu Leu Lys Asn Leu Gln His

485 490 495

Phe Ile Lys Pro Leu Leu Gly Lys Gly Ser Glu Ser Asp Lys Asp Glu

500 505 510

Arg Phe Tyr Gly Glu Phe Val Gly Leu Trp Asn Glu Leu Asp Gln Ile

515 520 525

Thr Thr Leu Tyr Asn Lys Val Arg Asn Tyr Val Thr Arg Lys Pro Tyr

530 535 540

Ser Ile Glu Lys Phe Lys Ile Asn Phe Gln Asn Ala Thr Leu Leu Lys

545 550 555 560

Gly Trp Asp Arg Asn Lys Glu Arg Asp Asn Thr Ser Ile Ile Leu Arg

565 570 575

Lys Asn Gly Leu Tyr Tyr Leu Ala Ile Met Arg Lys Glu Tyr Asn Lys

580 585 590

Val Phe Glu Lys Tyr Pro Ala Gly Thr Glu Glu Asn Cys Tyr Glu Lys

595 600 605

Met Glu Tyr Lys Leu Leu Pro Gly Ala Asn Lys Met Leu Pro Lys Val

610 615 620

Phe Phe Ser Lys Ser Arg Ile Asn Glu Phe Asn Pro Ser Pro Gln Leu

625 630 635 640

Leu Gln Asn Tyr Gln Met Gly Thr His Lys Lys Gly Asp Gln Phe Lys

645 650 655

Lys Glu Asp Cys His Ala Leu Ile Asp Phe Phe Lys Thr Ser Ile Glu

660 665 670

Lys His Glu Asp Trp Lys Asn Phe Asn Phe Gln Phe Ser Pro Thr Ser

675 680 685

Val Tyr Glu Asp Met Ser Gly Phe Tyr Arg Glu Val Glu Gln Gln Gly

690 695 700

Tyr Lys Leu Val Phe Arg Ser Ile Asp Ala Glu Tyr Ile Asp Lys Leu

705 710 715 720

Val Glu Glu Gly Lys Ile Phe Leu Phe Gln Ile Tyr Asn Lys Asp Phe

725 730 735

Ser Pro Phe Ser Lys Gly Thr Pro Asn Leu His Thr Leu Tyr Trp Lys

740 745 750

Met Leu Phe Asp Glu Arg Asn Leu Asn Asn Val Val Tyr Lys Leu Asn

755 760 765

Gly Glu Ala Glu Ile Phe Phe Arg Lys Lys Ser Ile Thr Tyr Thr His

770 775 780

Pro Thr His Pro Ala Glu Ile Pro Ile Lys Asn Lys Asn Val Gln Asn

785 790 795 800

Lys Lys Lys Glu Ser Val Phe Gln Tyr Asp Leu Ile Lys Asn His Arg

805 810 815

Phe Thr Ile Asp Ser Phe Gln Phe His Val Pro Ile Thr Met Asn Phe

820 825 830

Lys Asn Ala Gly Leu Ser Asn Leu Asn Glu Gln Val Tyr Thr Tyr Leu

835 840 845

Arg Glu Asn Lys Asp Ala His Ile Ile Gly Ile Asp Arg Gly Glu Arg

850 855 860

His Leu Leu Tyr Leu Val Val Ile Asp Arg Tyr Gly Arg Ile Val Lys

865 870 875 880

Gln Phe Ser Leu Asn Glu Ile Val Asn Glu Tyr His Gly Asn Thr Tyr

885 890 895

Thr Thr Asn Tyr His Asp Leu Leu Asp Lys Arg Glu Glu Ala Arg Gln

900 905 910

Gln Ala Arg Gln Ser Trp Gln Ser Ile Glu Asn Ile Lys Glu Leu Lys

915 920 925

Glu Gly Tyr Leu Ser Gln Val Val His Lys Ile Ala Asn Leu Met Val

930 935 940

Glu Tyr His Ala Ile Val Val Leu Glu Asp Leu Asn Ile Gly Phe Met

945 950 955 960

Arg Gly Arg Gln Lys Val Glu Lys Gln Val Tyr Gln Lys Phe Glu Lys

965 970 975

Met Leu Ile Asp Lys Leu Asn Tyr Leu Val Asp Lys Lys Lys Ala Pro

980 985 990

Glu Ala Asp Gly Gly Leu Leu Lys Ala Phe Gln Leu Thr Asn Gln Phe

995 1000 1005

Glu Ser Phe Gln Lys Leu Gly Lys Gln Ser Gly Phe Leu Phe Tyr

1010 1015 1020

Val Pro Ala Trp Asn Thr Ser Lys Ile Asp Pro Cys Thr Gly Phe

1025 1030 1035

Thr Asn Leu Leu Asp Thr Arg Tyr Glu Asn Ile Ala Lys Ala Gln

1040 1045 1050

Lys Phe Phe Arg Thr Phe Asp Ala Ile Arg Tyr Asn Ala Val Lys

1055 1060 1065

Asp Tyr Phe Glu Leu Glu Leu Asp Tyr Asp Lys Phe His Lys Arg

1070 1075 1080

Ala Glu Gly Thr Gln Thr Lys Trp Thr Leu Cys Thr Tyr Gly Thr

1085 1090 1095

Arg Ile Lys Thr Phe Arg Asn Pro Glu Asn Asn Asn Gln Trp Asp

1100 1105 1110

Asn Val Glu Ile Asn Leu Thr Glu Glu Phe Lys Lys Leu Phe Lys

1115 1120 1125

Gln Phe Gly Ile Asn Leu Ser Gly Asp Leu Gln Gln Ala Ile Cys

1130 1135 1140

Ala Gln Thr Glu Lys Ser Phe Phe Glu Ser Leu Leu Arg Leu Leu

1145 1150 1155

Lys Leu Thr Leu Gln Met Arg Asn Ser Ile Thr Gly Thr Asp Val

1160 1165 1170

Asp Tyr Leu Leu Ser Pro Val Gln Asn Ala Glu Gly Tyr Phe Tyr

1175 1180 1185

Asp Ser Arg Lys Gly Asp Lys Ser Leu Pro Ala Asn Ala Asp Ala

1190 1195 1200

Asn Gly Ala Tyr Asn Ile Ala Arg Lys Gly Leu Trp Val Ile Gln

1205 1210 1215

Gln Ile Lys Gln Thr Pro Gln Gly Gln Lys Ala Lys Leu Ser Ile

1220 1225 1230

Ser Asn Lys Glu Trp Leu Lys Phe Ala Gln Glu Lys Pro Tyr Leu

1235 1240 1245

Lys Asp

1250

<210> 102

<211> 1193

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 102

Met Lys Thr Phe Glu Asn Phe Thr Asn Leu Tyr Ser Leu Pro Arg Thr

1 5 10 15

Leu Arg Phe Glu Leu Lys Pro Leu Tyr Lys Thr Lys Glu Leu Ile Asp

20 25 30

Ser Lys Gln Glu Leu Phe Pro Lys Asp Lys Arg Ile Asp Glu Ile Tyr

35 40 45

Gln Asn Ile Ile Lys Pro Cys Leu Asn Glu Leu His Ser Asp Phe Ile

50 55 60

Glu Lys Ser Met Glu Asn Lys Asp Phe Gln Asn Ile Pro Asp Asn Ile
65 70 75 80
Leu Lys Ile Tyr Ser Asn Glu Lys Asn Ile Asp Asp Phe Lys Asn Ile

85 90 95
Glu Lys Asp Leu Ile Lys Gln Ile Asn Trp Phe Leu Lys Ser Asn Lys
100 105 110
Thr Phe Phe Ala Glu Asn Tyr Ser Asp Leu Leu Gly Lys Asn Ser Ile
115 120 125
Asp Ile Ile Ile Lys Val Phe Trp Glu Lys Ile Tyr Lys Lys Asp Asp
130 135 140
Ser Trp Lys Ile Phe Leu Tyr Asn Asp Leu Leu Trp Lys Ser Tyr Glu

145 150 155 160
Glu Leu Ile Asn Ile Tyr Phe Lys Trp Phe Ser Thr Tyr Leu Ser Asn
165 170 175
Phe Asn Lys Asn Arg Glu Asn Leu Tyr Asp Lys Lys Asn Glu Ala Lys
180 185 190
Val Trp Ser Val Ser Gly Arg Thr Ile Trp Glu Asn Phe Pro Arg Phe
195 200 205
Leu Gln Asn Cys Ile Asn Phe Arg Asp Lys Leu Glu Lys Leu Asn Leu

210 215 220
Ser Ile Glu Gln Lys Asp Ile Phe Ile Thr Asn Asn Phe Trp Lys Cys
225 230 235 240
Ile Ser Gln Lys Gln Ile Asp Tyr Tyr Asn Lys Ile Ile Trp Gln Ile
245 250 255
Asn Ser Lys Thr Asn Glu Phe Asn Gln Lys Asn Gly Leu Lys Trp Asn
260 265 270
Lys Lys Leu Pro Lys Leu Leu Leu Leu His Lys Gln Ile Leu Trp Lys

275 280 285
Ser Glu Asn Glu Asn Ile Leu Asn Phe Ile Asn Asn Ile Ile Gln Thr
290 295 300
Asp Phe Glu Leu Glu Gln Glu Ile Lys Ile Ile Asn Lys Asp Ile Phe

305 310 315 320

Gln Arg Ile Asp Phe Ile Lys Lys Ser Ile Val Ser Asn Ile Glu Asp

325 330 335

Phe Glu Leu Glu Lys Ile Phe Ile Lys Lys Asn Arg Leu Lys Asp Ile

340 345 350

Ser Ser Leu Leu Met Asp Asn Tyr Ser Val Leu Glu Lys Leu Leu Pro

355 360 365

Glu Phe Asn Glu Glu Trp Lys Ile Ile Lys Glu Asn Glu Leu Val Asn

370 375 380

Leu Ser Lys Ile Lys Lys Ser Phe Glu Asn Ile Asp Leu Lys Asp Leu

385 390 395 400

Lys Asn Ile Phe Lys Lys Glu Tyr Phe Asp Glu Ser Lys Asp Trp Phe

405 410 415

Lys Leu Phe Leu Asn Trp Ile Tyr Asn His Phe Ser Asp Leu Glu Asn

420 425 430

Asn Ile Lys His Thr His Lys Leu Val Gln Asp Lys Leu Ile Ser Trp

435 440 445

Asn Phe Ser Glu Asn Ile Gln Lys Ser Glu Lys Asn Ile Asn Leu Arg

450 455 460

Asp Glu Ile Phe Val Ser Ser Lys Trp Leu Leu Lys Ala Tyr Leu Asp

465 470 475 480

Ser Ile Leu Ala Leu Asp Arg Phe Val His Met Phe Asp Tyr Trp Glu

485 490 495

Gln Lys Asp Phe Asp Ser Asn Phe Tyr Asn Asn Ile Glu Glu Tyr Ser

500 505 510

Ile Asn Phe Ser Pro Phe Lys Thr Tyr Asn Ala Val Arg Asn Tyr Leu

515 520 525

Thr Lys Lys Asn Tyr Ser Thr Asp Lys Ile Lys Leu Asn Phe Asp Tyr

530 535 540

Pro Asp Phe Leu Gly Ser Asn Ser Leu Trp Lys Tyr Ala Phe Ile Tyr

545 550 555 560

Lys Asp Ser Lys Trp Phe Tyr Tyr Leu Trp Val Leu Asp His Ser Asn
565 570 575
Ser Gln Ser Lys Tyr Lys Pro Gln Ile Leu Lys Asn Asn Thr Glu Phe
580 585 590
Tyr Gln Leu Glu Tyr Lys Gln Ile Lys Phe Asn Thr Leu Ala Trp Lys

595 600 605
Trp Tyr Ile Arg Asp Phe Trp Val Lys Tyr Ser Glu Asp Glu Asn Cys
610 615 620
Ile Ile Asn Leu Lys Thr Leu Ile Lys Lys Gln Tyr Leu Glu Arg Tyr
625 630 635 640
Pro Val Leu Lys Glu Ile Val Asp Phe Gln Thr Asp Asp Lys Lys Ile
645 650 655
Phe Asp Ala Lys Val Lys Thr Ile Leu Glu Gln Ala Tyr Ser Ile Asn

660 665 670
Phe Val Asn Ile Asp Lys Asn Tyr Ile Leu Glu Glu Asn Asn Asn Trp
675 680 685
Asn Leu His Phe Phe Gln Ile Tyr Asn Lys Asp Phe Ser Glu Asn Lys
690 695 700
Lys Ile Asn Ser Met Glu Asn Leu His Thr Met Tyr Phe Lys Ala Leu
705 710 715 720
Phe Glu Lys Glu Asn Phe Asn Trp Trp Ala Cys Phe Lys Leu Asn Ser

725 730 735
Gln Trp Ala Glu Ile Phe Phe Arg Glu Lys Ser Ile Asn Glu Lys Lys
740 745 750
Val Lys Asp Leu Lys Thr Arg Asn Glu Asn Ala Ile Glu Lys Lys Arg
755 760 765
Tyr Thr Glu Asn Lys Val Phe Leu His Leu Pro Ile Thr Leu Asn Phe
770 775 780
Ile Asn Lys Trp Tyr Ser Lys Tyr Ser Phe Trp Tyr Ile Asn Asp Ser

785 790 795 800
Val Lys Lys Tyr Ile Lys Glu Asn Lys Ile Ser Ile Ile Trp Ile Asp

805 810 815

Arg Trp Glu Lys Asn Leu Ile Tyr Phe Ser Met Ile Asn Glu Asn Leu

820 825 830

Glu Ile Ile Glu Leu Lys Ser Leu Asn Ser Leu Ile Leu Lys Val Ser

835 840 845

Asp Leu Glu Glu Lys Glu Val Asn Tyr Phe Glu Lys Leu Ser Lys Lys

850 855 860

Glu Trp Asn Arg Asn Lys Glu Arg Lys Asp Trp Asp Glu Ile Glu Thr

865 870 875 880

Ile Lys Glu Leu Lys Glu Trp Tyr Ile Ser Gln Ile Val Asp Asn Leu

885 890 895

Val Lys Leu Ile Val Lys His Asn Ala Ile Val Val Met Glu Asp Leu

900 905 910

Asn Ser Gly Phe Lys Arg Trp Arg Gln Lys Ile Glu Lys Gln Ile Tyr

915 920 925

Gln Lys Phe Glu Leu Ala Leu Ala Lys Lys Leu Asn Phe Thr Val Asp

930 935 940

Lys Asn Lys Lys His Asp Glu Leu Trp Trp Ile Tyr Lys Ala Tyr Gln

945 950 955 960

Leu Thr Pro Gln Ile Glu Asn Phe Gln Asp Ile Tyr Ser Gln Thr Trp

965 970 975

Ile Ile Phe Tyr Thr Gln Ala Ala Tyr Thr Ser Val Thr Cys Pro Asn

980 985 990

Cys Ser Phe Arg Lys Asn Ile Tyr Gln Lys Tyr Glu Asn Glu Ser Lys

995 1000 1005

Phe Lys Glu Phe Phe Lys Lys Tyr Ile Leu Glu Ile Lys Phe Glu

1010 1015 1020

Asp Asn Cys Phe Ile Ile Lys Tyr Lys Ile Asp Glu Lys Ile Asp

1025 1030 1035

Lys Lys Lys Asn Lys Leu Lys Lys Leu Glu Phe Gln Val Asn Thr

1040 1045 1050

Lys Asn Gln Ile Arg Leu Lys Phe Glu Lys Ser Leu Lys Trp Lys

1055 1060 1065

Trp Trp Glu Thr Lys Glu Phe Asn Ile Thr Glu Lys Phe Lys Glu

1070 1075 1080

Ile Phe Glu Lys His Lys Leu Asp Leu Trp Asn Leu Lys Glu Glu

1085 1090 1095

Leu Leu Ala Trp Asn Trp Glu Ile Gln Leu Tyr Lys Asp Phe Met

1100 1105 1110

Phe Tyr Phe Asn Leu Leu Leu Gln Leu Arg Asn Ser Lys Glu Asn

1115 1120 1125

Asp Asn Trp Trp Tyr Ile Ser Cys Pro Ser Cys Trp Phe His Ser

1130 1135 1140

Gly Asn Trp Phe Gln Trp Phe Ser Tyr Asn Trp Asp Ala Asn Trp

1145 1150 1155

Ala Tyr Asn Ile Ala Arg Lys Trp Arg Ile Ile Leu Asp Lys Ile

1160 1165 1170

Lys Lys Asp Glu Lys Asn Leu Trp Ile Thr Asn Val Glu Trp Asp

1175 1180 1185

Asn Tyr Tyr Gln Lys

1190

<210> 103

<211> 1202

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 103

Met Ala Val Arg Ser Val Lys Leu Lys Leu Leu Val Pro Arg Asp Gly

1 5 10 15

Ser Ala Glu Ser Val Arg Lys Arg Lys Ala Leu Trp Ala Thr His Gln

20 25 30

Phe Val Asn Asp Ala Ala Ala Ala Tyr Ala Glu Leu Leu Leu Glu Met

35 40 45

Arg Gln Glu Asp Val Cys Arg Gly Thr Asp Asp His Gly Lys Asp Val

50 55 60

Ile Glu Pro Ala Ala His Trp Gln Ala Lys Leu Arg Ala Arg Leu Ala

65 70 75 80

Ala Lys Gln Leu Pro Pro Val Ala Val Ala Glu Ala Leu Pro Leu Leu

85 90 95

Lys Ala Phe Tyr Gly Ser Arg Leu Ile Lys Ser Phe Val Ala Asn Asp

100 105 110

Lys Gly Val Ala Gly Thr Gly Asn Ala Thr Asp Leu Asn Thr Trp Leu

115 120 125

Ser Gly Leu Val Asp Pro Ala Ser Val Ala Gly Glu Lys Thr Glu Leu

130 135 140

Arg Lys Gln Leu Leu Ala Glu Leu Pro Leu Cys Glu Ala Ala Asp Ala

145 150 155 160

Asp Phe Glu Gly Ala Ala Arg Lys Met Leu Ala Lys Ser Asp Ala Arg

165 170 175

Glu Ala Leu Leu Glu Gly Pro Gly Thr Gly Val Gly Trp Pro Ala Ala

180 185 190

Tyr Asn Ala Asn Pro Thr Asp Ser Val Trp Leu Asp Met Leu His Lys

195 200 205

Ala Ala Ala Lys Ala Arg Leu Glu Leu Ala Asp Thr Thr Val Ser Glu

210 215 220

Leu Lys Lys Leu Gly Val Phe Pro Leu Leu Gln Ala Ala Ser Ser Asn

225 230 235 240

Arg Val Phe Gly Ser Gly Val Leu Asn Pro Phe Glu Arg Met Ala Ala

245 250 255

Ala Gln Ala Ala Ala Ala Leu Leu Pro Trp Glu Thr Lys Arg His Glu

260 265 270

Met Arg Lys Arg Arg Asp Lys Phe Ala Asp Gln Leu Asn Gln Trp Asp

275 280 285

Thr Glu Phe Gly Ala Ser His Ala Thr Ala Leu Ala Ala Ile Arg Ala
290 295 300
Phe Glu Ala Glu Glu Ser Glu Arg Ala Arg Arg Glu Ser Leu Gly Asn
305 310 315 320
Glu Gly Thr Gly Tyr Arg Ile Gly Gly Arg Glu Leu Arg Asp Ala Trp
325 330 335
Thr Leu Leu Arg Asp Trp Leu Lys Gly His Ser Thr Ala Thr Ala Ala

340 345 350
Ala Arg Glu Asp Lys Val Arg Glu Leu Gln Ala Lys Gln Gly Arg Ser
355 360 365
Phe Gly Ser His Arg Leu Leu Ser Trp Leu Ala Lys Pro Ala Gln Gln
370 375 380
Trp Leu Ala Asp His Ser Ala Gly Asp Val Val Thr Arg Ile Ala Val
385 390 395 400
Arg Asn Ala Arg Gln Arg Lys Leu Asp Thr Ala Arg Thr Leu Pro Ile

405 410 415
Trp Thr Gly Ala Asp Ala Val Lys His Pro Arg Phe Ala Asn Phe Asp
420 425 430
Pro Pro Asn Asn Thr Asn Gln Pro Gly Phe Asp Leu Arg Ala Gly Thr
435 440 445
Gln Lys Gly Arg Leu Thr Leu Arg Leu Ser Leu Leu Thr Glu Arg Ala
450 455 460
Asp Gly Leu Leu Leu Ala Gln Asp His Asp Phe Gln Leu Val Pro Ser

465 470 475 480
Arg Gln Met Ala Glu Ile Val Leu His Lys Asp Gly Lys Glu Arg Ala
485 490 495
Leu Ser Trp Gln Ser Gln Asp Gly Ile Gly Arg Gln Val Gly Asp Val
500 505 510
Gly Gly Ser Ala Leu Leu Phe Ser Arg Asp His Ala Glu Cys Leu Leu
515 520 525
Glu Arg Lys Gln Ile Thr Arg Leu Glu Arg Gly Ala Trp Pro Ala Ala

530 535 540

Leu Pro Val Trp Phe Lys Leu Ser Leu Asp Ile Gly Ala Glu His Lys

545 550 555 560

Ala Leu Leu Lys Gln Arg Phe Lys Trp Gly Val Trp Leu Asn Ser Ala

565 570 575

Leu Val Thr Arg Asn Ala Lys Asp Ala Lys Gly Val Pro Pro Pro Val

580 585 590

Gly Thr Arg Val Leu Ala Val Asp Leu Gly Leu Arg Ser Ala Ala Thr

595 600 605

Val Ser Val Trp Gln Val Val Asp Ala Ala Thr Pro Val Val Ala Gly

610 615 620

Lys Trp Arg Val Pro Leu Ser Asp Thr Leu Ser Ala Val His Glu Arg

625 630 635 640

Ser Ala Met Leu Ala Leu Pro Gly Glu His Val Asp Ala Gly Val Leu

645 650 655

Ala Ala Arg Arg Ala Ala Asn Glu Lys Leu Ala Gly Leu Leu Ala Ala

660 665 670

Thr Ser His Leu Ser Thr Val Phe Lys Leu Gly Arg Ala Glu Gln Gly

675 680 685

Asp Arg Arg Arg Glu Leu Leu Glu Arg Leu Gly Glu Gly Asp Asp Arg

690 695 700

Arg Ala Arg Ala Ala Val Ala Thr Thr Ala Ala Glu Arg Asp Gly Leu

705 710 715 720

Arg Ala Val Leu Gly Ala Thr Gln Asp Ala Trp Ala Gly Ala Val Ala

725 730 735

Ala Val Trp Arg Arg Leu Glu Thr Asp Leu Ala Gly Ala Ile Ala Ala

740 745 750

Tyr Arg Lys Gln Gln Arg Glu Asp Val Gln Leu Arg Arg Glu Ala Arg

755 760 765

His Gly Pro Gly Ala Ser Gln Leu Pro Lys Gln Ala Ala Ala Glu Arg

770 775 780

Leu Leu Gly Gly Lys Ser Ala Trp Gln Ile Glu Tyr Lys Glu Arg Val

785 790 795 800

Arg Lys Leu Leu Thr Arg Trp Ile Met Arg Gln Arg Pro Gly Asp Thr

805 810 815

Ala Val Arg Arg Leu Ala Arg Lys Asp Leu Gly Lys Tyr Cys Gly Gly

820 825 830

Leu Leu Asp His Leu Thr Ala Leu Lys Glu Asp Arg Ala Lys Thr Thr

835 840 845

Ala Asp Leu Ile Val Gln Ala Ala Arg Gly Arg Val Arg Ala His Lys

850 855 860

Asp Ala His Gly Arg Gln Gln Asp Arg Glu Leu Trp Leu Ala Lys Tyr

865 870 875 880

Ala Pro Cys Asp Leu Ile Val Met Glu Asp Leu Gly Arg Tyr Arg Phe

885 890 895

Ala Thr Asp Arg Pro Pro Ser Glu Asn Arg Gln Leu Met Gln Trp Thr

900 905 910

His Arg Glu Val Phe Arg Leu Val Gln Met Gln Ala Glu Val Glu Gly

915 920 925

Ile Gln Val Leu Glu Thr Gly Ala Glu Phe Ser Ser Lys Phe Asp Ala

930 935 940

Arg Thr Trp Ala Pro Gly Val Arg Cys Glu Pro Ile Thr Lys Leu Trp

945 950 955 960

Val Glu Arg Tyr Arg Asn Gly Glu Met Pro Trp Leu Ala Asp Lys Ala

965 970 975

Asp Glu Trp Arg Arg Glu Gly Ile Glu Leu Ala Gln Leu Val Pro Gly

980 985 990

Gln Leu Leu Pro Thr Gly Ser Gly Glu Gln Phe Val Ala Val Ser Ala

995 1000 1005

Thr Gly Gly Leu Arg Val Arg His Ala Asp Leu Asn Ala Ala Gln

1010 1015 1020

Cys Ile Ala Leu Arg Ala Leu Thr Gly His Gly Thr Ala Phe Arg

1025 1030 1035

Leu Thr Ala Arg Arg Leu Gly Asp Val Phe Val Ser Ala Lys Gly

1040 1045 1050

Leu Gly Lys Arg Pro Gln Gly Ala Leu Trp Arg Glu Phe Gly Ser

1055 1060 1065

Ala Leu Pro Pro Ala Val Val Val Leu Arg Pro Ala Gly Glu Val

1070 1075 1080

Arg Tyr Ala Leu Arg Pro Phe Ala Ser Ala Arg Asp Ala Ala Ala

1085 1090 1095

Ala Leu Gly Leu Gln Leu Gly Ala Leu Arg Asn Val Asp Ala Thr

1100 1105 1110

Asp Ala Glu Ser Asp Ala Glu Asp Gly Asp Leu Ala Glu Leu Leu

1115 1120 1125

Ala Gly Ala Asp Pro Asp Arg Ala Thr Phe Phe Arg Asp Pro Ser

1130 1135 1140

Gly Asp Val His Gly Gly Ala Trp Val Gln Ala Lys Val Phe Trp

1145 1150 1155

Ala Glu Val Arg Arg His Val Arg Leu Gly Leu Gln Ala Gln Gly

1160 1165 1170

Leu Leu Pro Ala Ala Ala Arg Ser Ser Glu Pro Arg Gln Met Gln

1175 1180 1185

Leu Pro Leu Ala Gly Ala Leu Pro Gly Asp Asp Ile Pro Leu

1190 1195 1200

<210> 104

<211> 669

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 104

Met Leu Asp Lys Phe Ala Ser Leu Tyr Pro Val Thr Lys Thr Leu Arg

1 5 10 15

Phe Arg Leu Leu Pro Gln Gly Arg Thr Glu Glu Asn Met Gln Val Ala
20 25 30
Lys Val Leu Glu Asn Asp Leu Glu Arg Ser Glu Ala Ala Ala Val Val
35 40 45
Lys Gly Leu Ile Lys Lys Tyr His Leu Gln Phe Ile Ser Asp Thr Leu
50 55 60
Ser Gly Ser Thr Leu Ser Trp Gln Ala Leu Thr Glu Thr Leu Asp Lys
65 70 75 80

Phe Lys Ala Asp His Thr Ala Thr Ala Glu Leu Asp Ser Ala Leu Ala
85 90 95
Ala Tyr Arg Cys Lys Leu Ala Glu Leu Phe Thr Lys Ser Pro Lys Tyr
100 105 110
Lys Val Met Ala Thr Pro Val Ser Ile Ile Lys Glu Ile Leu Lys Thr
115 120 125
Glu Thr Asp Pro Glu Asn Ile Ala Ala Leu Asn Lys Leu Asn Gly Tyr
130 135 140

Thr Tyr Ile Ile Phe Asp Tyr Val Ser Thr Arg Met Leu Thr Tyr Ser
145 150 155 160
Ala Asp Ala Lys Ala Thr Ser Leu Ala Tyr Arg Leu Val Asp Glu Asn
165 170 175
Tyr Leu Arg Phe Tyr Gln Asp Ile Ser Ala Ala Ala Glu Ile Ser Ala
180 185 190
Val Leu Glu Glu Ala Gly Phe Asp Asn Ala Glu Val Glu Ala Phe Ile
195 200 205

Arg Thr Asp Tyr Asn Thr Cys Leu Thr Ser Glu Gly Ile Ala Ser Phe
210 215 220
Asn Ala Ala Ala Gly Ser Ile Asn Gln Phe Val Asn Val Leu Leu Gln
225 230 235 240
Gln Asn Pro Val Leu Gln Ser Glu Pro Ala Leu Arg Arg His Leu Gln
245 250 255

Pro Leu Tyr Lys Met Leu Leu Asp Glu Ala Glu Ser Lys Ile Ile Lys
260 265 270

Phe Glu Asp Tyr Gly Gln Leu Arg Asp Ala Val Glu Asn Phe Arg Arg
275 280 285

Asn Phe Gln Asp Leu Pro Gln Ser Leu Ile Asp Ile Phe Ala Gly Arg
290 295 300

Tyr Asp Tyr Ser Lys Ile Tyr Val Gly Tyr Lys Tyr Leu Asn Glu Ala
305 310 315 320

Ser Ser Gln Ile Ala Gly Gly Tyr Asn Trp Lys Leu Leu Glu Asn Ala
325 330 335

Leu Glu Asp Phe Tyr Ser Lys Pro Tyr Leu Val Asn Gly Lys Leu Pro
340 345 350

Val Lys Tyr Lys Thr Val Val Asn Lys Lys Met Asn Gln Leu Ala Tyr
355 360 365

Ser Phe Thr Glu Leu Gln Glu Ala Leu Asp Ala Gly Asp Ser Gly Ser
370 375 380

Ser Ile Thr Asp Leu Phe Gly Lys Tyr Ala Glu Leu His Ala Ala Tyr
385 390 395 400

Ala Ala Ala Asp Gly Asn Val Phe Tyr Lys Glu Tyr Asp Arg Lys Ser
405 410 415

Ile Ala Ser Leu Lys Asn Tyr Leu Asp Ala Val Asn Ala Ile Ala Arg
420 425 430

Phe Ile Lys Ile Phe Ala Ala Pro Glu Val Tyr Val Lys Asp Glu Gly
435 440 445

Phe Tyr Gly Ile Val Asp Gly Ala Ala Asp Lys Leu Arg Asp Phe Asp
450 455 460

Leu Leu Tyr Asn Met Val Arg Asn Tyr Ile Thr Lys Lys Pro Tyr Lys
465 470 475 480

Lys Ser Lys Val Ala Leu Thr Phe Asn Ser Ser Ser Phe Gly Arg Gly
485 490 495

Trp Asp Glu Asn Lys Ile Tyr Asp Glu Leu Thr Thr Ile Phe Thr Tyr

500 505 510

Asn Gly Lys Tyr Tyr Leu Gly Val Ile Asn Lys Asn Asp Lys Pro Asp

515 520 525

Leu Ala Ala Ala Val Ser Lys Asp Glu Gly Gly Tyr Lys Arg Met Val

530 535 540

Tyr Lys Thr Phe Asp Ile Val Lys Gln Leu Pro Arg Leu Ser Phe Thr

545 550 555 560

Lys Ala Val Lys Ala His Phe Ala Glu Ser Asp Glu Asp Phe Ile Phe

565 570 575

Asp Gly Pro Lys Phe Ala Lys Pro Leu Arg Val Pro Lys Glu Ile Tyr

580 585 590

Leu Gln Ser Phe Thr Asp Asn Gly Asp Lys Leu Ala Asp Ser Ala Lys

595 600 605

Lys Tyr Thr Lys Ala Tyr Leu Asp Met Ser Gly Asp Tyr Lys Gly Tyr

610 615 620

Tyr Glu Ala Ile Ile Lys Arg Ile Asp Tyr Thr Lys Glu Phe Leu Ser

625 630 635 640

Ala Tyr Lys Ser Thr Ser Ile Tyr Asp Leu Ala Phe Leu Lys Pro Ala

645 650 655

Gly Lys Ala Ala Gly Ser Leu Cys Trp Thr Arg His Ile

660 665

<210> 105

<211> 1193

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 105

Met Lys Thr Phe Glu Asn Phe Thr Asn Leu Tyr Ser Leu Pro Arg Thr

1 5 10 15

Leu Arg Phe Glu Leu Lys Pro Leu Tyr Lys Thr Lys Glu Leu Ile Asp

20 25 30

Ser Lys Gln Glu Leu Phe Pro Lys Asp Lys Arg Ile Asp Glu Ile Tyr

35 40 45

Gln Asn Ile Ile Lys Pro Cys Leu Asn Glu Leu His Ser Asp Phe Ile

50 55 60

Glu Lys Ser Met Glu Asn Lys Asp Phe Gln Asn Ile Pro Asp Asn Ile

65 70 75 80

Leu Lys Ile Tyr Ser Asn Glu Lys Asn Ile Asp Asp Phe Lys Asn Ile

85 90 95

Glu Lys Asp Leu Ile Lys Gln Ile Asn Trp Phe Leu Lys Ser Asn Lys

100 105 110

Thr Phe Phe Ala Glu Asn Tyr Ser Asp Leu Leu Gly Lys Asn Ser Ile

115 120 125

Asp Ile Ile Ile Lys Val Phe Trp Glu Lys Ile Tyr Lys Lys Asp Asp

130 135 140

Ser Trp Lys Ile Phe Leu Tyr Asn Asp Leu Leu Trp Lys Ser Tyr Glu

145 150 155 160

Glu Leu Ile Asn Ile Tyr Phe Lys Trp Phe Ser Thr Tyr Leu Ser Asn

165 170 175

Phe Asn Lys Asn Arg Glu Asn Leu Tyr Asp Lys Lys Asn Glu Ala Lys

180 185 190

Val Trp Ser Val Ser Gly Arg Thr Ile Trp Glu Asn Phe Pro Arg Phe

195 200 205

Leu Gln Asn Cys Ile Asn Phe Arg Asp Lys Leu Glu Lys Leu Asn Leu

210 215 220

Ser Ile Glu Gln Lys Asp Ile Phe Ile Thr Asn Asn Phe Trp Lys Cys

225 230 235 240

Ile Ser Gln Lys Gln Ile Asp Tyr Tyr Asn Lys Ile Ile Trp Gln Ile

245 250 255

Asn Ser Lys Thr Asn Glu Phe Asn Gln Lys Asn Gly Leu Lys Trp Asn

260 265 270

Lys Lys Leu Pro Lys Leu Leu Leu Leu His Lys Gln Ile Leu Trp Lys

275 280 285

Ser Glu Asn Glu Asn Ile Leu Asn Phe Ile Asn Asn Ile Ile Gln Thr

290 295 300

Asp Phe Glu Leu Glu Gln Glu Ile Lys Ile Ile Asn Lys Asp Ile Phe

305 310 315 320

Gln Arg Ile Asp Phe Ile Lys Lys Ser Ile Val Ser Asn Ile Glu Asp

325 330 335

Phe Glu Leu Glu Lys Ile Phe Ile Lys Lys Asn Arg Leu Lys Asp Ile

340 345 350

Ser Ser Leu Leu Met Asp Asn Tyr Ser Val Leu Glu Lys Leu Leu Pro

355 360 365

Glu Phe Asn Glu Glu Trp Lys Ile Ile Lys Glu Asn Glu Leu Val Asn

370 375 380

Leu Ser Lys Ile Lys Lys Ser Phe Glu Asn Ile Asp Leu Lys Asp Leu

385 390 395 400

Lys Asn Ile Phe Lys Lys Glu Tyr Phe Asp Glu Ser Lys Asp Trp Phe

405 410 415

Lys Leu Phe Leu Asn Trp Ile Tyr Asn His Phe Ser Asp Leu Glu Asn

420 425 430

Asn Ile Lys His Thr His Lys Leu Val Gln Asp Lys Leu Ile Ser Trp

435 440 445

Asn Phe Ser Glu Asn Ile Gln Lys Ser Glu Lys Asn Ile Asn Leu Arg

450 455 460

Asp Glu Ile Phe Val Ser Ser Lys Trp Leu Leu Lys Ala Tyr Leu Asp

465 470 475 480

Ser Ile Leu Ala Leu Asp Arg Phe Val His Met Phe Asp Tyr Trp Glu

485 490 495

Gln Lys Asp Phe Asp Ser Asn Phe Tyr Asn Asn Ile Glu Glu Tyr Ser

500 505 510

Ile Asn Phe Ser Pro Phe Lys Thr Tyr Asn Ala Val Arg Asn Tyr Leu

515 520 525

Thr Lys Lys Asn Tyr Ser Thr Asp Lys Ile Lys Leu Asn Phe Asp Tyr
530 535 540
Pro Asp Phe Leu Gly Ser Asn Ser Leu Trp Lys Tyr Ala Phe Ile Tyr

545 550 555 560
Lys Asp Ser Lys Trp Phe Tyr Tyr Leu Trp Val Leu Asp His Ser Asn
565 570 575
Ser Gln Ser Lys Tyr Lys Pro Gln Ile Leu Lys Asn Asn Thr Glu Phe
580 585 590
Tyr Gln Leu Glu Tyr Lys Gln Ile Lys Phe Asn Thr Leu Ala Trp Lys
595 600 605
Trp Tyr Ile Arg Asp Phe Trp Val Lys Tyr Ser Glu Asp Glu Asn Cys

610 615 620
Ile Ile Asn Leu Lys Thr Leu Ile Lys Lys Gln Tyr Leu Glu Arg Tyr
625 630 635 640
Pro Val Leu Lys Glu Ile Val Asp Phe Gln Thr Asp Asp Lys Lys Ile
645 650 655
Phe Asp Ala Lys Val Lys Thr Ile Leu Glu Gln Ala Tyr Ser Ile Asn
660 665 670
Phe Val Asn Ile Asp Lys Asn Tyr Ile Leu Glu Glu Asn Asn Asn Trp

675 680 685
Asn Leu His Phe Phe Gln Ile Tyr Asn Lys Asp Phe Ser Glu Asn Lys
690 695 700
Lys Ile Asn Ser Met Glu Asn Leu His Thr Met Tyr Phe Lys Ala Leu
705 710 715 720
Phe Glu Lys Glu Asn Phe Asn Trp Trp Ala Cys Phe Lys Leu Asn Ser
725 730 735
Gln Trp Ala Glu Ile Phe Phe Arg Glu Lys Ser Ile Asn Glu Lys Lys

740 745 750
Val Lys Asp Leu Lys Thr Arg Asn Glu Asn Ala Ile Glu Lys Lys Arg
755 760 765
Tyr Thr Glu Asn Lys Val Phe Leu His Leu Pro Ile Thr Leu Asn Phe

770 775 780

Ile Asn Lys Trp Tyr Ser Lys Tyr Ser Phe Trp Tyr Ile Asn Asp Ser

785 790 795 800

Val Lys Lys Tyr Ile Lys Glu Asn Lys Ile Ser Ile Ile Trp Ile Asp

805 810 815

Arg Trp Glu Lys Asn Leu Ile Tyr Phe Ser Met Ile Asn Glu Asn Leu

820 825 830

Glu Ile Ile Glu Leu Lys Ser Leu Asn Ser Leu Ile Leu Lys Val Ser

835 840 845

Asp Leu Glu Glu Lys Glu Val Asn Tyr Phe Glu Lys Leu Ser Lys Lys

850 855 860

Glu Trp Asn Arg Asn Lys Glu Arg Lys Asp Trp Asp Glu Ile Glu Thr

865 870 875 880

Ile Lys Glu Leu Lys Glu Trp Tyr Ile Ser Gln Ile Val Asp Asn Leu

885 890 895

Val Lys Leu Ile Val Lys His Asn Ala Ile Val Val Met Glu Asp Leu

900 905 910

Asn Ser Gly Phe Lys Arg Trp Arg Gln Lys Ile Glu Lys Gln Ile Tyr

915 920 925

Gln Lys Phe Glu Leu Ala Leu Ala Lys Lys Leu Asn Phe Thr Val Asp

930 935 940

Lys Asn Lys Lys His Asp Glu Leu Trp Trp Ile Tyr Lys Ala Tyr Gln

945 950 955 960

Leu Thr Pro Gln Ile Glu Asn Phe Gln Asp Ile Tyr Ser Gln Thr Trp

965 970 975

Ile Ile Phe Tyr Thr Gln Ala Ala Tyr Thr Ser Val Thr Cys Pro Asn

980 985 990

Cys Ser Phe Arg Lys Asn Ile Tyr Gln Lys Tyr Glu Asn Glu Ser Lys

995 1000 1005

Phe Lys Glu Phe Phe Lys Lys Tyr Ile Leu Glu Ile Lys Phe Glu

1010 1015 1020

Asp Asn Cys Phe Ile Ile Lys Tyr Lys Ile Asp Glu Lys Ile Asp

1025 1030 1035

Lys Lys Lys Asn Lys Leu Lys Lys Leu Glu Phe Gln Val Asn Thr

1040 1045 1050

Lys Asn Gln Ile Arg Leu Lys Phe Glu Lys Ser Leu Lys Trp Lys

1055 1060 1065

Trp Trp Glu Thr Lys Glu Phe Asn Ile Thr Glu Lys Phe Lys Glu

1070 1075 1080

Ile Phe Glu Lys His Lys Leu Asp Leu Trp Asn Leu Lys Glu Glu

1085 1090 1095

Leu Leu Ala Trp Asn Trp Glu Ile Gln Leu Tyr Lys Asp Phe Met

1100 1105 1110

Phe Tyr Phe Asn Leu Leu Leu Gln Leu Arg Asn Ser Lys Glu Asn

1115 1120 1125

Asp Asn Trp Trp Tyr Ile Ser Cys Pro Ser Cys Trp Phe His Ser

1130 1135 1140

Gly Asn Trp Phe Gln Trp Phe Ser Tyr Asn Trp Asp Ala Asn Trp

1145 1150 1155

Ala Tyr Asn Ile Ala Arg Lys Trp Arg Ile Ile Leu Asp Lys Ile

1160 1165 1170

Lys Lys Asp Glu Lys Asn Leu Trp Ile Thr Asn Val Glu Trp Asp

1175 1180 1185

Asn Tyr Tyr Gln Lys

1190

<210> 106

<211> 1583

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 106

Met Ser Phe Leu Val Pro His Leu Pro Thr Val Val Ser His Arg Leu

1 5 10 15

Gly Gly Tyr Ser Ser Ala Met Asp Gln Thr Pro Thr Arg Leu Thr Pro

20 25 30

Ala Val Lys Asn Thr Ala Ala Ala Thr Pro Lys Pro Glu Val Pro Leu

35 40 45

Thr Gln Arg Ala Tyr Thr Leu Arg Leu Arg Gly Ala Asn Asp Gly Asp

50 55 60

Gln Ser Trp Arg Glu Ala Val Trp Ala Thr His Glu Ala Val Asn Met

65 70 75 80

Gly Ala Lys Val Phe Gly Asp Trp Leu Leu Thr Leu Arg Gly Gly Leu

85 90 95

Asp Arg Glu Leu Ala Asp Ala Lys Val Lys Ala Gly Asn Asn Asn Pro

100 105 110

Asp Arg Asn Pro Thr Pro Glu Glu Arg Arg Gly Arg Arg Val Leu Leu

115 120 125

Ala Leu Ser Trp Leu Ser Val Glu Ser Ala Pro Lys Lys Gly Asp Ala

130 135 140

Tyr Glu Lys Phe Val Ile Ala Ser Gly Lys Lys Asp Ser Gln Ser Ile

145 150 155 160

Arg Asp Glu Lys Val Val Arg Ala Leu Arg Glu Ile Leu Ala Lys Arg

165 170 175

Gly Val Ala Asn Gln Asp Leu Glu Gly Trp Ile Val Asp Cys Glu Pro

180 185 190

Ser Leu Ser Ala Ala Ile Arg Asp Asp Ala Val Trp Val Asn Arg Ser

195 200 205

Ala Ala Phe Asp Ala Ala Gln Cys Arg Val Gly Thr Ser Leu Thr Arg

210 215 220

Glu Glu Ile Trp Asp Leu Leu Lys Pro Phe Phe Gly Ser Cys Glu Ser

225 230 235 240

Tyr Leu Ala Ser Leu Thr Thr Asp Glu Asp Ser Asp Thr Glu Ala Ala

245 250 255

Ala Thr Asp Asp Lys Ala Lys Asp Leu Val Gln Lys Ala Gly Gln Trp
260 265 270
Leu Ser Ser Arg Phe Gly Thr Gly Lys Gly Ala Asp Phe Ala Ala Met
275 280 285
Ser Lys Val Tyr Ser Glu Thr Ala Phe Trp Ala Gly Arg Ala Ser Pro

290 295 300
Phe Arg Ser Gly Ala Glu Ala Leu Arg Leu Ile Ala Glu Ser Leu Lys
305 310 315 320
Ser Phe Cys Pro Lys Ser Phe Asp Ala Asp Gly Ile Leu Gly Leu Ile
325 330 335
Ser Gly Pro Gly Tyr Lys Ser Ala Thr Arg Asn Ile Ile Lys Ala Trp
340 345 350
Ser Lys Arg Ala Gly Pro Val Thr Ala Asp Asp Leu Ala Asn Leu Ser

355 360 365
Ala Val Ala Ala Glu Asp Ala Asn Lys Cys Ser Ala Asn Thr Gly Ser
370 375 380
Lys Gly His Arg Pro Trp Ser Asp Ala Ile Leu Cys Glu Val Glu Asn
385 390 395 400
Ala Cys Gly Phe Thr Tyr Leu Gln Pro Asp Gly Pro Ala Leu His Ser
405 410 415
Glu Phe Ala Val Met Leu Asp His Ala Ala Arg Arg Val Ser Ile Gly

420 425 430
His Ser Trp Ile Lys Arg Ala Glu Ala Glu Arg Asp Arg Phe Thr Lys
435 440 445
Asp Ala Leu Arg Ile Lys Glu Val Pro Asp Pro Ile Arg Val Cys Leu
450 455 460
Asp Arg Phe Cys Ala Asp Arg Ala Gly Thr Ser Gly Ala Ile Asp Gly
465 470 475 480
Tyr Arg Ile Arg Lys Arg Ala Val Ser Ala Trp Lys Glu Val Ile Thr

485 490 495
Arg Trp Gly Gln Ala Ala Cys Lys Thr Ala Glu Asp Arg Val Ile Ala

500 505 510

Val Arg Glu Thr Gln Ala Asp Pro Asp Ile Asp Lys Phe Gly Asp Ile

515 520 525

Gln Leu Phe Glu Ala Leu Ala Val Asp Asp Ala Glu Cys Val Trp Arg

530 535 540

Val Asn Gly Glu Val Thr Pro Gln Pro Leu Ile Asp Tyr Ala Ala Ala

545 550 555 560

Thr Asp Ala Glu Ala Lys Gln Lys Arg Phe Lys Val Pro Ala Tyr Arg

565 570 575

His Pro Asp Pro Leu Ser His Pro Val Phe Cys Asp Phe Gly Asn Ser

580 585 590

Arg Trp Lys Ile Arg Phe Ala Ala His Asp Ala Val Thr Lys Leu Ala

595 600 605

Asn Ala Arg Thr Ser Leu Asp Arg Arg Glu Ala Asp Leu Ala Lys Ala

610 615 620

Lys Glu Arg Leu Asp Lys Ala Thr Ala Pro Glu Glu Gln Thr Glu Gly

625 630 635 640

Lys Glu Ser Leu Glu Glu Ala Glu Arg His Leu Arg Asp Ala Arg Asp

645 650 655

Arg Val Ala Trp Leu Ser Ser Met His Ala Phe Ser Met Arg Leu Trp

660 665 670

Gly Ala Gly Arg Val Gly Asp Gly Gln Arg Leu Phe Trp Ser Cys Lys

675 680 685

Arg Leu Thr Asp Asp Met Ala Leu Arg Gln Asn Ser Gly Gln Ala Pro

690 695 700

Thr Ile Ala Val Thr Arg Ala Asp Arg Leu Gly Arg Ala Ala Ala Gly

705 710 715 720

Ala Asp Thr Ala Asp Ser Val Asp Ile Leu Gly Val Phe Thr Glu Glu

725 730 735

His Trp Asn Gly Arg Leu Gln Ala Pro Arg Ala Gln Leu Asp Val Ile

740 745 750

Ala Ala His Val Ala Lys Asn Gln Trp Asp Ala Lys Ala Lys Lys Met
755 760 765
Arg Asp Arg Ile Arg Trp Leu Val Ser Phe Ser Ala Lys Leu Gln Pro
770 775 780
Val Gly Pro Trp Ile Glu Tyr Ser Ala Thr Phe Pro Glu Ala Ala Leu
785 790 795 800
Ala Lys Pro Phe Val Ser Arg Lys Gly Glu Tyr Ala Val Arg His Val

805 810 815
Ser Asn Asp Asp Arg Ala Gly Leu Gly Lys Leu Val Leu Ser Arg Leu
820 825 830
Pro Gly Leu Arg Val Leu Ser Val Asp Leu Gly His Arg Tyr Ala Ala
835 840 845
Ala Cys Ala Val Trp Glu Thr Val Ser Ile Ala Gln Thr Asn Ala Ala
850 855 860
Cys Asp Ala Ala Gly His Glu Leu Pro Thr Glu Ser Asp Leu Phe Leu

865 870 875 880
Gln Leu Ser Thr Thr Asp Leu Thr Gly Lys Asn Arg Thr Thr Ile Tyr
885 890 895
Arg Arg Ile Gly Ala Asp Met Ile Thr Asp Pro Lys Thr Gly Glu Lys
900 905 910
Thr Pro His Pro Ala Pro Trp Ala Arg Leu Glu Arg Gln Phe Leu Val
915 920 925
Lys Leu Pro Gly Glu Asp Ile Pro Ala Arg Lys Ala Ser Pro Ala Glu

930 935 940
Phe Asp Ala Ile Arg Arg Leu Glu Glu Ala Phe Gly Arg Thr Arg Thr
945 950 955 960
Ala Asp Asp Pro Leu Leu Val Arg Val Asp Glu Leu Leu Ala Ala Thr
965 970 975
Val Asp Ser Ala Arg Leu Ala Leu Arg Arg His Gly Asp Ala Ala Arg
980 985 990
Ile Ala Tyr Ala Phe Lys Pro Ser Ala Glu Lys Leu Thr Pro Gly Gly

995 1000 1005

Gly Arg Glu Val Met Ser Pro Glu Ala Arg Lys Ala Met Ile Leu

1010 1015 1020

Asp Ala Leu Leu Leu Trp His Gly Leu Trp His Gly Asp Arg Trp

1025 1030 1035

Ala Asp Val Trp Ala Ser Gln Gln Trp Asp Ala Tyr Ile Lys Pro

1040 1045 1050

Glu Leu Gly Met Asp Leu Pro Pro Trp Ser Glu Thr Ser Gly Glu

1055 1060 1065

Pro Arg Cys Gln Tyr Arg Ser Lys Val Glu Gly Leu Leu Lys Arg

1070 1075 1080

Val Ala Glu Ser Leu Ala Ala Arg Asp Gly Ala Gly Leu His Leu

1085 1090 1095

Leu Trp Ala Glu Gln Trp Arg Thr Arg Asn Ala Lys Trp Leu Gly

1100 1105 1110

Asn Thr Gly His Leu Arg Thr Leu Arg Ser Leu Leu Leu Pro Arg

1115 1120 1125

Gly Leu Thr Thr Ser Thr Pro Ala Ala Trp Asn Val Gly Gly Leu

1130 1135 1140

Ser Leu Thr Arg Ile Ala Thr Leu Lys Ser Leu Tyr Gln Leu His

1145 1150 1155

Lys Ala Tyr His Met Arg Pro Glu Pro Glu Asp Pro Arg Lys Asn

1160 1165 1170

Val Pro Ala Lys Gly Glu Glu Glu Leu Arg Asp Phe Gly Arg Gly

1175 1180 1185

Met Leu Asp Val Met Glu Arg Leu Arg Glu Gln Arg Val Lys Gln

1190 1195 1200

Leu Ala Ser Arg Leu Ala Glu Ala Ala Leu Gly Ile Gly Arg Met

1205 1210 1215

Lys Ala Ser Glu Gly Lys Arg Asp Arg Lys Arg Pro Arg Ala Gln

1220 1225 1230

Ile Asp Gln Pro Cys His Ala Val Val Ile Glu Asn Leu Lys Asn

1235 1240 1245

Tyr Arg Pro Glu Glu Thr Arg Thr Arg Arg Glu Asn Arg Gln Leu

1250 1255 1260

Met Ser Trp Ser Ser Ser Lys Val Lys Lys Tyr Leu Ser Glu Ala

1265 1270 1275

Cys Gln Leu Asn Gly Leu His Leu Arg Glu Val Gln Ala Ser Tyr

1280 1285 1290

Thr Ser Arg Gln Asp Ser Arg Thr Gly Ala Pro Gly Ile Arg Cys

1295 1300 1305

Ala Asp Val Pro Val Gln Asp Phe Phe Thr Lys Pro Trp Trp Arg

1310 1315 1320

Arg Gln Val Ser Ile Ala Val Gly Arg Val Asn Gln Gly Arg Gly

1325 1330 1335

Asp Ala Arg Glu Arg Phe Leu Ala Asp Leu Asp Ala Lys Trp Ser

1340 1345 1350

Ala Ala Glu Lys Ser Glu Arg Ile Thr Ala Pro Pro Leu Arg Ile

1355 1360 1365

Pro Val Asn Gly Gly Glu Leu Phe Val Ser Ala Asp Leu His Ser

1370 1375 1380

Pro Ala Ala Leu Gly Leu Gln Ala Asp Leu Asn Ala Ala Ala Asn

1385 1390 1395

Ile Gly Leu Lys Ala Leu Leu Asp Pro Asp Trp Pro Gly Lys Trp

1400 1405 1410

Trp Phe Val Pro Ala Ser Leu Asp Ala Asp Gly Trp Arg Val Pro

1415 1420 1425

Ala Ala Lys Ser Cys Ala Gly Ala Glu Trp Val Lys Asn Trp Lys

1430 1435 1440

Val Gly Gln Leu Gly Asp Ser Tyr Ala Pro Asn Gly Lys Pro Leu

1445 1450 1455

Gln Pro Thr Asp Asp Glu Gly Val Lys Lys Ala Glu Asp Gly Val

1460 1465 1470

Lys Leu Ala Lys Ala Ser Leu Asp Asp Ala Glu Gln Ala Leu Lys

1475 1480 1485

Ala Ala Lys Lys Thr Lys Arg Lys Ala Glu Ile Asp Val Ala Ser

1490 1495 1500

Ala Arg Ala Gln Glu Ala Lys Lys Asn Val Asp Asp Met Lys Lys

1505 1510 1515

Ala Leu Val Ala Ala Lys Lys Gly Ala Ser Ala Lys Glu Ile Ile

1520 1525 1530

Asn Leu Trp Arg Asp Pro Val Gly Val Asp Pro Ala Asp Phe Ala

1535 1540 1545

Ser Gly Glu Pro Trp Arg Ala Tyr Thr Val Tyr Lys Gln Arg Val

1550 1555 1560

Glu Tyr His Val Ile Asn Asp Val Leu Arg Gly Arg Ala Gly Pro

1565 1570 1575

Arg Ser Asp Arg Pro

1580

<210> 107

<211> 1254

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 107

Met Ser Ile Thr Arg Ser Ile Lys Val Lys Leu Ile Val Pro Arg Asp

1 5 10 15

Ala Ser Leu Glu Ala Arg Gln Leu Arg Glu Gly Leu Trp Ala Thr His

20 25 30

Leu Phe Val Asn Asp Gly Cys His Tyr Tyr Glu Arg Leu Leu Leu Glu

35 40 45

Phe Arg Gln Arg Asp Val Cys Val Gly Lys Asp Asp Ala Gly Lys Asp

50 55 60

Val Ile Val Pro Ala Ala Glu Trp Ala Asp Arg Leu Arg Ala Arg Leu

65 70 75 80

Gly Arg Asn Gly Met Val Pro Ser His Ile Glu Ala Ala Leu Pro Ile

85 90 95

Phe Arg Glu Leu Tyr Glu Asn Met Val Pro Ser Ala Leu Lys Ala Lys

100 105 110

Ser Gly Thr Gly Gln Ala Gly Arg Ser Trp His Ser Lys Leu Val Ser

115 120 125

Pro Thr Ser Arg Gly Gly Glu Ala Ser Ala Ala Arg Ile Asp Val Leu

130 135 140

Arg Pro Leu Leu Pro Val Ser Gly Asp Asp Pro Ala Phe Glu Pro Ala

145 150 155 160

Ala Arg Ala Leu Ile Glu Glu Ala Gly Asp Glu Leu Leu Thr Ser Thr

165 170 175

Gly Arg Cys Pro Ala Trp Val Thr Ala Tyr Arg Lys Gly Pro Glu Gly

180 185 190

Ser Ala Trp Val Glu Lys Leu Arg Ile Gln Leu Arg Glu Ala Val Glu

195 200 205

Ala Gly Asp Phe Asp Pro Pro Ser Asp Pro Gln Ile Leu Ala Ala Gly

210 215 220

Ala Val Pro Ala Ala Pro Pro Leu Gly Ala Gly Ile Asp Ala Leu Arg

225 230 235 240

Pro Leu Leu Pro Leu Leu Gly Gly Asp Pro Ala Phe Glu Pro Ala Ala

245 250 255

Arg Ala Leu Val Glu Asp Ile Gly Asp Glu Leu Phe Thr Ser Thr Gly

260 265 270

Arg Pro Pro Thr Trp Val Thr Ala His Pro Thr Trp Val Arg Ala His

275 280 285

Arg Lys Asp Ala Glu Cys Leu Glu Ala Ala Asp Asp Phe Lys Trp Val

290 295 300

Glu Arg Leu Arg Gln Arg Leu Arg Asp Asp Ala Lys Ala Gly Lys Phe

305 310 315 320

Glu Gln Pro Leu His Glu Arg Leu Gly Ala Leu Gly Ala Leu Pro Val

325 330 335

Ala Lys Pro Ile Gly Ala Gly Arg Val Val Ser Arg Ala Asp Leu Thr

340 345 350

Val Phe Glu Arg Gly Ala Met Glu Leu Ala Ile Glu His Leu Ile Gly

355 360 365

Trp Glu Ser Ala Gly His Arg Ala Arg Ala Gln Tyr Val Glu Arg Lys

370 375 380

Lys Arg His Asp Asp Leu Leu Gln Trp Ile Glu Ala Glu Ala Pro Asp

385 390 395 400

Ala Leu Leu Ala Val Arg Ala Tyr Glu Ala Ala Arg Thr Ile His Leu

405 410 415

Ala Thr Leu Gly Glu Leu Gly Ala Ala Pro Gln Tyr Thr Leu Arg Leu

420 425 430

Arg Glu Ile Arg Pro Trp Arg Lys Leu Arg Glu Trp Leu Leu Gln Asn

435 440 445

Pro Asp Ala Thr Ile Asp Glu Arg Arg Arg Arg Leu Ala Thr Met Gln

450 455 460

Thr Asn Asp Pro Arg Gly Tyr Gly Gly Glu Ala Leu Ala Trp Leu Ala

465 470 475 480

Ala Pro Glu Arg Arg Ala Leu Val Glu His Pro Ala Gly Asp Val Val

485 490 495

Thr Arg Ile Ala Val Leu Asn Ile Arg Lys Ser Ile Leu Asp Arg Ser

500 505 510

Arg Leu Phe Pro Thr Cys Thr Leu Ala Asp Pro Val Glu His Pro Arg

515 520 525

Phe Ala Lys Phe Gly Lys Pro Gly Asp Lys Asn Ser Ala Gly Tyr Ala

530 535 540

Leu Ala Val Asp Gly Val Arg Arg Glu Ala Ile Ile Lys Ile Leu Val

545 550 555 560

Pro Arg Gln Asp Gly Leu Leu Val Pro Thr Asp Leu Arg Val Pro Phe
565 570 575
Ala Pro Ser Gly Gln Met Arg Asp Leu Arg Ala Ser Gly Leu Asp Ile

580 585 590
Ser Tyr Glu Arg Gln Asp Gly Arg Gly Arg Gln Ala Ala Lys Leu Gln
595 600 605
Gly Gly Asn Leu Met Phe Asp Arg Thr His Phe Ala Arg Cys Gly Ala
610 615 620
Pro Gly Pro Glu Ala Leu Gly Ser Val Trp Ile Lys Val Ala Leu Asp
625 630 635 640
Leu Ser Ser Pro Ala Ala Ser Leu Ala Met Lys Thr Ala Thr Pro Val

645 650 655
Arg Thr Tyr Leu Ser Thr Ala Val Arg Gly Arg Pro Glu Ser Thr Lys
660 665 670
Tyr Glu Lys Ala Ala Pro Pro Glu Gly Phe Arg Val Leu Ser Val His
675 680 685
Met Gly Leu Arg Thr Ala Ala Thr Ala Ser Met Leu Arg Phe Gly Ala
690 695 700
Pro Glu Glu Gly Gly His Glu Val Pro Val Ser Gly Leu Ala Gly Glu

705 710 715 720
Thr Leu Val Ala Phe His Glu Arg Thr Val Thr Met Lys Leu Pro Gly
725 730 735
Glu Asp Pro Asp Thr Arg Thr Glu Ala Asn Arg Gly Val Ala Lys Arg
740 745 750
Glu Leu Arg Gly Leu Gly Arg Gly Ile Gly Cys Leu Lys Ala Ile Arg
755 760 765
Arg Ala Ser Ala Ser Ala Thr Pro Glu Asp Arg Ala Glu Ala Leu Val

770 775 780
Ile Ile Glu Thr His Val Gly Gln Gly Asp Arg His Gly Trp Ala Pro
785 790 795 800
Ala Glu Ala Val Gly Arg Leu Asp Pro His Gly Asp Pro Asp Asp Trp

805 810 815

Lys Thr Ala Cys Ala Ala Leu Tyr Ala Ala Val Glu Ala Asp Leu Gly

820 825 830

Val Ala Ile Ser Ser Trp Arg Lys Ala Ala Arg Ala Gly Gly Ala Thr

835 840 845

Gly Met Leu Gly Gly Lys Ser Leu Trp Ala Val Asp His Leu Glu Arg

850 855 860

Ser Phe Arg Phe Leu Arg Ser Trp Asp Leu Arg Ala Arg Pro His Asp

865 870 875 880

Gly Asp Pro Arg Arg Pro Arg Pro Gly Tyr Ala Ser Lys Leu Leu His

885 890 895

His Ile Asp Gly Val Lys Asp Asp Arg Val Lys Thr Thr Ala Asp Arg

900 905 910

Ile Val Gln Ala Ala Cys Gly Arg Ala Trp Ile Gly Gly Pro Thr Val

915 920 925

Lys Arg Gly Thr Gln Asp Val Arg Leu Pro Gly Arg Trp Glu Gln Arg

930 935 940

Gly Pro Arg Ala Asp Leu Ile Leu Leu Pro Asp Leu Thr His Phe Arg

945 950 955 960

Phe Arg Ser Asp Arg Pro Arg Ala Glu Asn Ser Arg Leu Met Arg Trp

965 970 975

Ala His Arg Gln Leu Ala Ile Tyr Val Arg Met Gln Ala Glu Val Glu

980 985 990

Gly Ile Leu Val Ala Asp Thr Gly Ala Ala Phe Thr Thr Arg Phe Asp

995 1000 1005

Ala Trp Thr Gly Ala Pro Gly Val Arg Cys Glu Pro Val Thr Ala

1010 1015 1020

Asp His Leu Arg Gly Ile Ala Lys Arg Glu Asp Tyr Trp Leu Ala

1025 1030 1035

Arg Leu Leu Arg Glu Gly Ala Leu Lys His Leu Arg Ile Asp Pro

1040 1045 1050

Ala Ser Leu Arg Val Asp Asp Leu Val Pro Met Asp His Gly Lys

1055 1060 1065

Ile Leu Val Ala Leu Asp Gly Val Asp Leu Pro Gly Leu Arg Ile

1070 1075 1080

Leu Asp Thr Asp Val Asn Ala Ser Gln Gly Leu Gly Arg Arg Tyr

1085 1090 1095

Ile Glu Gly His Gly Leu Ala Tyr Arg Leu Pro Gly Ala Arg Val

1100 1105 1110

Pro Arg Gly Glu Gly Glu Arg Glu Ala Ala Val Val His Ile Lys

1115 1120 1125

Gly Lys Arg Leu Ala Ser Ala Met Gly Gly Thr Val Val Val Leu

1130 1135 1140

Arg Ala Ser Glu Gly Pro Gly Asp Ile Thr Trp Thr Ala Glu Val

1145 1150 1155

Tyr Asp Arg Pro Gln Gly Ala Arg Lys Ala Leu Gly Leu Ser Leu

1160 1165 1170

Ala Ala Phe Asn Ser Ile Ala Thr Ala Ala Val Asp Asp Glu Gly

1175 1180 1185

Pro Ala Pro Glu Asn Asp Asp Glu Ala Leu Glu Glu Glu Ala Glu

1190 1195 1200

Glu Ala Leu Gly Ile Ala Thr Gly Glu Arg Ile Val Phe Phe Arg

1205 1210 1215

Asp Pro Ser Gly Ala Val Ala Gly Gly Gly Trp Leu Glu Ala Ser

1220 1225 1230

Ala Phe Trp Gly Ile Ala Asn Arg Met Val Thr Asp Arg Leu Arg

1235 1240 1245

Glu Leu Gly Arg Leu Gly

1250

<210> 108

<211> 1468

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 108

Met Ala Thr Ala Val Asp Thr Ser Thr Thr Arg Ala Tyr Thr Leu Arg

1 5 10 15

Leu Ser Gly Gly Asn Asn Trp Arg Glu Leu Leu Trp Gln Thr His Val

20 25 30

Ala Val Asn Arg Gly Ala Trp Val Trp Gly Asp Trp Leu Leu Thr Leu

35 40 45

Arg Gly Gly Leu Pro Ala Ser Leu Ala Asp Gly Asp Ala Glu Arg Arg

50 55 60

Val Val Leu Ala Leu Ser Trp Leu Ser Val Glu Ser Pro Ala Ser Leu

65 70 75 80

Ala Pro Gln Ala His Ile Val Ala Tyr Gly Ser Asp Ala Arg Asp Glu

85 90 95

Arg Asn Arg Lys Val Thr Glu Arg Phe Arg Asp Ile Leu Arg Arg Met

100 105 110

Gly Ile Lys Gln Gln Gln Glu Gln Glu Trp Leu Asp Ala Cys Leu Pro

115 120 125

Ala Leu Met Ala Ser Ile Arg Glu Asp Ala Val Trp Val Asp Arg Ser

130 135 140

Ala Cys Phe Ala Glu Ala Gln Gln Cys Tyr Arg Gly Leu Ser Ser Glu

145 150 155 160

Trp Ala Arg Lys Thr Leu Phe Asp Phe Leu Gly Gly Glu Asp Asp Tyr

165 170 175

Phe Lys Pro Ser Ala Lys Glu Gly Ala Ser Ser Lys Ala Lys Asp Phe

180 185 190

Val Gln Lys Ala Gly Arg Trp Leu Ser Arg His Trp Gly Ala Gly Lys

195 200 205

Lys Ser Asp Pro Arg Asp Ile Ser Thr Arg Leu Gly Lys Leu Ala Gly

210 215 220

Val Asp Pro Lys Ala Ile Asp Gly His Thr Gly Arg Ala Ala Leu Glu
225 230 235 240
Asp Leu Leu Arg Thr Leu Gly Ser Arg Pro Ala Gln Asn Ala Asp Ala
245 250 255
Glu Lys Leu Tyr Arg Gln Leu Lys Arg Ala Val Gly Trp Lys Gly Arg

260 265 270
Pro Ser Lys Gly Ala Val Ala Leu Lys Lys Ile Arg Asp Ala Glu Arg
275 280 285
Val Pro Asn Asp Leu Trp Lys Glu Ile Ala Ser Thr Leu Arg Glu Glu
290 295 300
Ala Ala Val Gln Ser Ser Gln Thr Ser Asp His Ala Ala Val Pro Asp
305 310 315 320
Trp Arg Ser His Trp Pro Ala Glu Ile Thr Gly Leu Pro Met Pro Tyr

325 330 335
Arg Val Asp Arg Asp Tyr Ile Trp Glu His Gly Val Met Leu Asp His
340 345 350
Ala Leu Arg Arg Val Ser Ser Ala His Thr Trp Ile Lys Arg Ala Glu
355 360 365
Ala Glu Arg Arg Arg Phe Gln Gln Asp Ala Ala Lys Met Gly Ser Ile
370 375 380
Pro Glu Glu Ala Arg Asn Trp Leu Asp Ala Phe Arg Glu Arg Arg Ser

385 390 395 400
Ser Ser Ser Gly Ala Thr Gly Asp Tyr Leu Ile Arg Glu Arg Ala Ile
405 410 415
Asn Gly Trp Asp Lys Val Val Gln Ala Trp Glu Thr Leu Gly Pro Asn
420 425 430
Ser Thr Arg Asp Gln Arg Ile Ala Ala Ala Arg Asp Val Gln Ala Asn
435 440 445
Leu Asp Glu Asp Glu Lys Phe Gly Asp Ile Gln Leu Phe Ala Gly Phe

450 455 460
Gly Asp Glu His Val Asp Asp Pro Glu Arg Cys Leu Ala Asp Asp Arg

465 470 475 480

Ala Thr Cys Val Trp Arg Asn Ser Ser Gly Arg Ala Asp Gly Arg Ile

485 490 495

Leu Lys Asp Tyr Val Ala Ala Thr Val Ala Glu His Asn Gln Arg Arg

500 505 510

Phe Lys Val Pro Ala Tyr Arg His Pro Asp Pro Leu Arg His Pro Val

515 520 525

Phe Val Asp Tyr Gly Lys Ser Arg Trp Ser Ile Asn Tyr Ser Ala Leu

530 535 540

Thr Ala Ala Gln Gln Arg Arg Lys Thr Thr Gln Lys Leu Ala Gln Ala

545 550 555 560

Lys Thr Asp Asn Thr Arg Ala Lys Leu Gln Gln Gln Leu Ala Ser Thr

565 570 575

Ala Asp Leu Arg Ser Val Thr Leu Gly Val Trp Asp Gly Asn Arg Ile

580 585 590

Val Lys Ile Ser Gln Arg Trp Arg Ser Lys Arg Phe Trp Arg Asp Leu

595 600 605

Asp Leu Asp His Phe Gly Ser His Pro Ser Ala Ala Val Ser Arg Ala

610 615 620

Asp Arg Leu Gly Arg Val Ala Ala Arg Gln Asp Pro Gly Ala Ala Val

625 630 635 640

Tyr Val Ala Lys Val Phe Glu Gln Gln Asp Trp Asn Gly Arg Leu Gln

645 650 655

Val Pro Arg Arg Glu Leu Asn Arg Leu Ala Asp Val Val Tyr Gly Lys

660 665 670

Gly Ala Asp Pro Asp Phe Gly Lys Leu Glu Arg Leu Asp Pro Arg Ala

675 680 685

Arg Arg Leu Trp Glu Arg Leu Ser Trp Phe Leu Thr Thr Ser Ala Thr

690 695 700

Val Gln Pro Gln Gly Pro Trp Leu Asp Tyr Val Ala Ala Gly Leu Pro

705 710 715 720

Ser Gly Ile Gln Tyr Thr Lys Ser Arg Ala Gly Tyr Tyr Leu Asn Tyr
725 730 735
Asp Ala Asn His Gly Arg Lys Gly Arg Ala Arg Leu Cys Leu Ala Arg
740 745 750
Leu Pro Gly Leu Arg Val Leu Ser Leu Asp Leu Gly His Arg Tyr Ala
755 760 765
Ala Ala Cys Ala Val Trp Gln Thr Leu Thr Ile Glu Gln Met Thr Asn

770 775 780
Glu Cys Arg Gln Ala Ala His Pro Ala Pro Ser Asn Asp Asp Leu Phe
785 790 795 800
Ile His Leu Arg His Pro Thr His Lys Pro Gln Lys Ser Gly Arg Lys
805 810 815
Lys Gly Arg Pro Val Thr Lys Thr Thr Ile Tyr Arg Arg Ile Gly Pro
820 825 830
Asp Lys Leu Pro Asp Gly Thr Asp His Pro Ala Pro Trp Ala Arg Leu

835 840 845
Glu Arg Gln Phe Leu Ile Lys Leu Gln Gly Glu Asp Arg Pro Ala Arg
850 855 860
Tyr Ala Ser Gln Lys Glu Ile Asp Glu Val Asn Gln Phe Arg Asn Phe
865 870 875 880
Val Gly Leu Glu Pro Ile Val Asp Arg Pro Arg Val Asp Asp Leu His
885 890 895
Ser Asp Ala Val Arg Val Ala Arg Leu Gly Leu Arg Arg Leu Ala Asp

900 905 910
Ala Ala Arg Ile Ala Phe Ala Met Thr Ala Ala Lys Lys Pro Ile Ser
915 920 925
Gly Gly His Glu Val Glu Leu Thr Thr Ala Gln Arg Ile Glu Phe Leu
930 935 940
Gln Asp Ala Leu Leu Leu Trp Gln Ser Leu Ala Ala Ser Arg Arg Tyr
945 950 955 960
Arg Asp Asp Trp Ala Glu Lys Leu Trp Gln Ser Trp Val Val Glu Lys

965 970 975

Leu Gly Gly Pro Gln Pro Ala Glu Ile Ala Asp Asp Leu Pro Arg Ser

980 985 990

Gln Arg Ala Ala Ser Leu Lys Thr Ala Arg Gln Ser Leu Arg Lys Val

995 1000 1005

Ala Glu Lys Leu Ser Asp Gly Gln Ser Pro Ser Ala Ala Glu Leu

1010 1015 1020

His Arg Leu Trp Ala Glu Arg Trp Gln Gln Arg Gln Thr Glu Trp

1025 1030 1035

Arg Arg His Leu Arg Trp Leu Arg Arg Leu Ile Leu Pro Arg Arg

1040 1045 1050

Lys Asp His Gln Gln Glu Asp Arg Pro Leu Gln Arg Val Gly Gly

1055 1060 1065

Leu Ser Val Lys Arg Ile Gln Thr Ile Arg Gln Leu Tyr Gln Val

1070 1075 1080

Leu Lys Ala Phe Arg Met Arg Pro Glu Pro Ser Asp Leu Arg Lys

1085 1090 1095

Asn Ile Pro Ala Pro Gly Asp Arg Ser Leu Ala Ser Phe Gly Arg

1100 1105 1110

Arg Ile Leu Asn His Leu Glu Arg Leu Arg Glu Gln Arg Ile Lys

1115 1120 1125

Gln Leu Ala Ser Arg Val Val Glu Ala Ala Leu Gly Ala Gly Arg

1130 1135 1140

Ile Ser Lys Pro Pro Gly Arg Asp Arg Arg Arg Pro Gln Gln Pro

1145 1150 1155

Val Asp Arg Pro Cys His Ala Val Val Ile Glu Asn Leu Gln His

1160 1165 1170

Tyr Lys Pro Glu Asp Ser Arg Leu Arg Arg Glu Asn Arg Gln Leu

1175 1180 1185

Met Asp Trp Gln Ala Arg Asn Leu Arg Lys Tyr Ile Val Glu Gly

1190 1195 1200

Cys Glu Leu His Gly Leu Leu Phe Val Glu Val Ser Pro Ala Tyr

1205 1210 1215

Thr Ser Arg Gln Asp Ser Arg Thr Gly Ala Pro Gly Leu Arg Cys

1220 1225 1230

Glu Asp Val Ser Arg Thr Ala Leu Gln Glu Ala Ala Arg Arg Met

1235 1240 1245

His Ala Ser His Ser Arg Pro Ser Asn Ser Ser Pro Gly Gly Ser

1250 1255 1260

Gln Thr Gln Phe Glu Arg Glu Val Cys Arg Trp Ile Asn Glu Phe

1265 1270 1275

Lys Arg Val Glu Gly Ser Ser Ser Ser Leu Ser Ala Arg Gln Ala

1280 1285 1290

Val Leu Lys Ala Phe Leu His His Gln Ala Ser Ile Pro Thr Ser

1295 1300 1305

Leu Ser Thr Ile Leu Leu Pro Arg Arg Gly Gly Glu Leu Phe Val

1310 1315 1320

Ser Ala Asp Pro Asp Ser Pro Leu Ala Cys Gly Leu Gln Ala Asp

1325 1330 1335

Leu Asn Ala Ala Ala Asn Ile Gly Leu Lys Ala Leu Thr Asp Pro

1340 1345 1350

Asp Trp Met Gly Ala Trp Trp Phe Val Leu Val Asp Arg Ala Ser

1355 1360 1365

Gly Gln Pro Val Glu Glu Gln Val Gln Gly Cys Pro Ile Trp Leu

1370 1375 1380

Ser Cys Gly Pro Leu Ser Asn Ser Asn Pro Ala Thr Ile Asp Pro

1385 1390 1395

Ser Asp Ser Pro Thr Ala Ala Arg Arg Ser Asn Gly Thr Gly Ala

1400 1405 1410

Lys Gly Arg Ala Arg Ala Asn Glu Tyr Trp Trp Ser Ser Leu Ser

1415 1420 1425

Ala Thr Thr Leu Pro Asp His Lys Ala Trp Gln Pro Thr Gln Asp

1430 1435 1440

Tyr Trp Arg Asp Ile Glu Gln Arg Val Val Lys Arg Leu Leu Arg

1445 1450 1455

Leu Leu Asp Gly Ser Glu Trp Ser Glu Asp

1460 1465

<210> 109

<211> 669

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 109

Met Leu Asp Lys Phe Ala Ser Leu Tyr Pro Val Thr Lys Thr Leu Arg

1 5 10 15

Phe Arg Leu Leu Pro Gln Gly Arg Thr Glu Glu Asn Met Gln Val Ala

20 25 30

Lys Val Leu Glu Asn Asp Leu Glu Arg Ser Glu Ala Ala Ala Val Val

35 40 45

Lys Gly Leu Ile Lys Lys Tyr His Leu Gln Phe Ile Ser Asp Thr Leu

50 55 60

Ser Gly Ser Thr Leu Ser Trp Gln Ala Leu Thr Glu Thr Leu Asp Lys

65 70 75 80

Phe Lys Ala Asp His Thr Ala Thr Ala Glu Leu Asp Ser Ala Leu Ala

85 90 95

Ala Tyr Arg Cys Lys Leu Ala Glu Leu Phe Thr Lys Ser Pro Lys Tyr

100 105 110

Lys Val Met Ala Thr Pro Val Ser Ile Ile Lys Glu Ile Leu Lys Thr

115 120 125

Glu Thr Asp Pro Glu Asn Ile Ala Ala Leu Asn Lys Leu Asn Gly Tyr

130 135 140

Thr Tyr Ile Ile Phe Asp Tyr Val Ser Thr Arg Met Leu Thr Tyr Ser

145 150 155 160

Ala Asp Ala Lys Ala Thr Ser Leu Ala Tyr Arg Leu Val Asp Glu Asn
165 170 175
Tyr Leu Arg Phe Tyr Gln Asp Ile Ser Ala Ala Ala Glu Ile Ser Ala
180 185 190
Val Leu Glu Glu Ala Gly Phe Asp Asn Ala Glu Val Glu Ala Phe Ile
195 200 205
Arg Thr Asp Tyr Asn Thr Cys Leu Thr Ser Glu Gly Ile Ala Ser Phe
210 215 220

Asn Ala Ala Ala Gly Ser Ile Asn Gln Phe Val Asn Val Leu Leu Gln
225 230 235 240
Gln Asn Pro Val Leu Gln Ser Glu Pro Ala Leu Arg Arg His Leu Gln
245 250 255
Pro Leu Tyr Lys Met Leu Leu Asp Glu Ala Glu Ser Lys Ile Ile Lys
260 265 270
Phe Glu Asp Tyr Gly Gln Leu Arg Asp Ala Val Glu Asn Phe Arg Arg
275 280 285

Asn Phe Gln Asp Leu Pro Gln Ser Leu Ile Asp Ile Phe Ala Gly Arg
290 295 300
Tyr Asp Tyr Ser Lys Ile Tyr Val Gly Tyr Lys Tyr Leu Asn Glu Ala
305 310 315 320
Ser Ser Gln Ile Ala Gly Gly Tyr Asn Trp Lys Leu Leu Glu Asn Ala
325 330 335
Leu Glu Asp Phe Tyr Ser Lys Pro Tyr Leu Val Asn Gly Lys Leu Pro
340 345 350

Val Lys Tyr Lys Thr Val Val Asn Lys Lys Met Asn Gln Leu Ala Tyr
355 360 365
Ser Phe Thr Glu Leu Gln Glu Ala Leu Asp Ala Gly Asp Ser Gly Ser
370 375 380
Ser Ile Thr Asp Leu Phe Gly Lys Tyr Ala Glu Leu His Ala Ala Tyr
385 390 395 400

Ala Ala Ala Asp Gly Asn Val Phe Tyr Lys Glu Tyr Asp Arg Lys Ser
405 410 415

Ile Ala Ser Leu Lys Asn Tyr Leu Asp Ala Val Asn Ala Ile Ala Arg
420 425 430

Phe Ile Lys Ile Phe Ala Ala Pro Glu Val Tyr Val Lys Asp Glu Gly
435 440 445

Phe Tyr Gly Ile Val Asp Gly Ala Ala Asp Lys Leu Arg Asp Phe Asp
450 455 460

Leu Leu Tyr Asn Met Val Arg Asn Tyr Ile Thr Lys Lys Pro Tyr Lys
465 470 475 480

Lys Ser Lys Val Ala Leu Thr Phe Asn Ser Ser Ser Phe Gly Arg Gly
485 490 495

Trp Asp Glu Asn Lys Ile Tyr Asp Glu Leu Thr Thr Ile Phe Thr Tyr
500 505 510

Asn Gly Lys Tyr Tyr Leu Gly Val Ile Asn Lys Asn Asp Lys Pro Asp
515 520 525

Leu Ala Ala Ala Val Ser Lys Asp Glu Gly Gly Tyr Lys Arg Met Val
530 535 540

Tyr Lys Thr Phe Asp Ile Val Lys Gln Leu Pro Arg Leu Ser Phe Thr
545 550 555 560

Lys Ala Val Lys Ala His Phe Ala Glu Ser Asp Glu Asp Phe Ile Phe
565 570 575

Asp Gly Pro Lys Phe Ala Lys Pro Leu Arg Val Pro Lys Glu Ile Tyr
580 585 590

Leu Gln Ser Phe Thr Asp Asn Gly Asp Lys Leu Ala Asp Ser Ala Lys
595 600 605

Lys Tyr Thr Lys Ala Tyr Leu Asp Met Ser Gly Asp Tyr Lys Gly Tyr
610 615 620

Tyr Glu Ala Ile Ile Lys Arg Ile Asp Tyr Thr Lys Glu Phe Leu Ser
625 630 635 640

Ala Tyr Lys Ser Thr Ser Ile Tyr Asp Leu Ala Phe Leu Lys Pro Ala

645 650 655

Gly Lys Ala Ala Gly Ser Leu Cys Trp Thr Arg His Ile

660 665

<210> 110

<211> 677

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<220><221> MOD_RES

<222> (19)..(339)

<223> Any amino acid

<400> 110

Met Cys Ile Arg Asp Arg Asp Leu Ala Val Ala Ala Leu Asn Arg Gly

1 5 10 15

Asp Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

210 215 220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

245 250 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

260 265 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

275 280 285

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

290 295 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

305 310 315 320

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

325 330 335

Xaa Xaa Xaa Gly Gln Leu Asn Ala Ile Arg Asn Phe Leu Ala Ser Asp

340 345 350

Gly Tyr Gly Ala His Asp Leu Val Pro Val Asn Tyr Asn Gly Ser Asn

355 360 365

Asp Arg Gly Ala Glu Val Gln Val Gly Asn Gln Lys Asn Trp Thr Val

370 375 380

Thr Ser Ser Ala Pro Val Val Val Gln Tyr Asn Asn Ala Asp Thr Thr

385 390 395 400

Leu Thr Val Gln Gly His Thr Asp Arg Leu Ile Val Thr Gly Ser Gly
405 410 415
Asn Asp Thr Ile Thr Leu Lys Asp Ser Gly Asp Asp Lys Val Leu Leu
420 425 430

Gly Asp Gly Asn Asn Thr Val Val Ala Gly Ser Gly Ala Asp Thr Ile
435 440 445
Val Gly Gly Ala Gly Asn Asp Val Leu Ile Gly Thr Asn Gly Gly Tyr
450 455 460
Gly Thr Glu Leu Leu Gly Gly Ala Gly Asn Asp Val Leu Arg Asn Ala
465 470 475 480
Gly Ser His Gly Ile Tyr Met Asp Gly Gly Ala Gly Asn Asp Thr Phe
485 490 495

Tyr Gly Gly Thr Gly Pro Asp Thr Met Glu Gly Gly Asp Gly Asn Asp
500 505 510
Leu Met Tyr Ala Asn Gly Arg Gly Ser Ser Ile Asp Gly Gly Ala Gly
515 520 525
Asn Asp Thr Ile Tyr Gly Gly Pro Gly Gly Asp Thr Leu Thr Gly Gly
530 535 540
Asp Gly Asn Asp Leu Leu Arg Ser Asp Ser Ala Phe Gly Thr Lys Gly
545 550 555 560

Ser Gly Asn Leu Leu Val Gly Gly Ala Gly Asn Asp Thr Leu Trp Ala
565 570 575
Gly Ala Gly Tyr Asp Thr Leu Lys Ala Gly Ser Gly Ser Asp Thr Leu
580 585 590
Ile Ser Gly Thr Gly Ser Ser Gln Met Ile Gly Gly Ser Ser Gly Asn
595 600 605
Thr Thr Phe Glu Val Ala Tyr His Thr Gly Asn Asp Thr Ile Thr Gly
610 615 620

Ser Gly Ser Gly Asn Thr Val Tyr Leu Asp Gly Arg Asp Phe Ser Asp
625 630 635 640
Ala Thr Ile Ser Asn His Ser Gly Val Thr Thr Val Ser Phe Ser Asp

645 650 655

Gly Gln Val Leu Lys Ile Ser Gly Val Gln Asp Ile Val Phe Ser Asp

660 665 670

His Asp Tyr Lys Val

675

<210> 111

<211> 1254

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 111

Met Ser Ile Thr Arg Ser Ile Lys Val Lys Leu Ile Val Pro Arg Asp

1 5 10 15

Ala Ser Leu Glu Ala Arg Gln Leu Arg Glu Gly Leu Trp Ala Thr His

20 25 30

Leu Phe Val Asn Asp Gly Cys His Tyr Tyr Glu Arg Leu Leu Leu Glu

35 40 45

Phe Arg Gln Arg Asp Val Cys Val Gly Lys Asp Asp Ala Gly Lys Asp

50 55 60

Val Ile Val Pro Ala Ala Glu Trp Ala Asp Arg Leu Arg Ala Arg Leu

65 70 75 80

Gly Arg Asn Gly Met Val Pro Ser His Ile Glu Ala Ala Leu Pro Ile

85 90 95

Phe Arg Glu Leu Tyr Glu Asn Met Val Pro Ser Ala Leu Lys Ala Lys

100 105 110

Ser Gly Thr Gly Gln Ala Gly Arg Ser Trp His Ser Lys Leu Val Ser

115 120 125

Pro Thr Ser Arg Gly Gly Glu Ala Ser Ala Ala Arg Ile Asp Val Leu

130 135 140

Arg Pro Leu Leu Pro Val Ser Gly Asp Asp Pro Ala Phe Glu Pro Ala

145 150 155 160

Ala Arg Ala Leu Ile Glu Glu Ala Gly Asp Glu Leu Leu Thr Ser Thr
165 170 175
Gly Arg Cys Pro Ala Trp Val Thr Ala Tyr Arg Lys Gly Pro Glu Gly
180 185 190

Ser Ala Trp Val Glu Lys Leu Arg Ile Gln Leu Arg Glu Ala Val Glu
195 200 205
Ala Gly Asp Phe Asp Pro Pro Ser Asp Pro Gln Ile Leu Ala Ala Gly
210 215 220
Ala Val Pro Ala Ala Pro Pro Leu Gly Ala Gly Ile Asp Ala Leu Arg
225 230 235 240
Pro Leu Leu Pro Leu Leu Gly Gly Asp Pro Ala Phe Glu Pro Ala Ala
245 250 255

Arg Ala Leu Val Glu Asp Ile Gly Asp Glu Leu Phe Thr Ser Thr Gly
260 265 270
Arg Pro Pro Thr Trp Val Thr Ala His Pro Thr Trp Val Arg Ala His
275 280 285
Arg Lys Asp Ala Glu Cys Leu Glu Ala Ala Asp Asp Phe Lys Trp Val
290 295 300
Glu Arg Leu Arg Gln Arg Leu Arg Asp Asp Ala Lys Ala Gly Lys Phe
305 310 315 320

Glu Gln Pro Leu His Glu Arg Leu Gly Ala Leu Gly Ala Leu Pro Val
325 330 335
Ala Lys Pro Ile Gly Ala Gly Arg Val Val Ser Arg Ala Asp Leu Thr
340 345 350
Val Phe Glu Arg Gly Ala Met Glu Leu Ala Ile Glu His Leu Ile Gly
355 360 365
Trp Glu Ser Ala Gly His Arg Ala Arg Ala Gln Tyr Val Glu Arg Lys
370 375 380

Lys Arg His Asp Asp Leu Leu Gln Trp Ile Glu Ala Glu Ala Pro Asp
385 390 395 400
Ala Leu Leu Ala Val Arg Ala Tyr Glu Ala Ala Arg Thr Ile His Leu

405 410 415

Ala Thr Leu Gly Glu Leu Gly Ala Ala Pro Gln Tyr Thr Leu Arg Leu

420 425 430

Arg Glu Ile Arg Pro Trp Arg Lys Leu Arg Glu Trp Leu Leu Gln Asn

435 440 445

Pro Asp Ala Thr Ile Asp Glu Arg Arg Arg Arg Leu Ala Thr Met Gln

450 455 460

Thr Asn Asp Pro Arg Gly Tyr Gly Gly Glu Ala Leu Ala Trp Leu Ala

465 470 475 480

Ala Pro Glu Arg Arg Ala Leu Val Glu His Pro Ala Gly Asp Val Val

485 490 495

Thr Arg Ile Ala Val Leu Asn Ile Arg Lys Ser Ile Leu Asp Arg Ser

500 505 510

Arg Leu Phe Pro Thr Cys Thr Leu Ala Asp Pro Val Glu His Pro Arg

515 520 525

Phe Ala Lys Phe Gly Lys Pro Gly Asp Lys Asn Ser Ala Gly Tyr Ala

530 535 540

Leu Ala Val Asp Gly Val Arg Arg Glu Ala Ile Ile Lys Ile Leu Val

545 550 555 560

Pro Arg Gln Asp Gly Leu Leu Val Pro Thr Asp Leu Arg Val Pro Phe

565 570 575

Ala Pro Ser Gly Gln Met Arg Asp Leu Arg Ala Ser Gly Leu Asp Ile

580 585 590

Ser Tyr Glu Arg Gln Asp Gly Arg Gly Arg Gln Ala Ala Lys Leu Gln

595 600 605

Gly Gly Asn Leu Met Phe Asp Arg Thr His Phe Ala Arg Cys Gly Ala

610 615 620

Pro Gly Pro Glu Ala Leu Gly Ser Val Trp Ile Lys Val Ala Leu Asp

625 630 635 640

Leu Ser Ser Pro Ala Ala Ser Leu Ala Met Lys Thr Ala Thr Pro Val

645 650 655

Arg Thr Tyr Leu Ser Thr Ala Val Arg Gly Arg Pro Glu Ser Thr Lys
660 665 670
Tyr Glu Lys Ala Ala Pro Pro Glu Gly Phe Arg Val Leu Ser Val His
675 680 685
Met Gly Leu Arg Thr Ala Ala Thr Ala Ser Met Leu Arg Phe Gly Ala
690 695 700

Pro Glu Glu Gly Gly His Glu Val Pro Val Ser Gly Leu Ala Gly Glu
705 710 715 720
Thr Leu Val Ala Phe His Glu Arg Thr Val Thr Met Lys Leu Pro Gly
725 730 735
Glu Asp Pro Asp Thr Arg Thr Glu Ala Asn Arg Gly Val Ala Lys Arg
740 745 750
Glu Leu Arg Gly Leu Gly Arg Gly Ile Gly Cys Leu Lys Ala Ile Arg
755 760 765

Arg Ala Ser Ala Ser Ala Thr Pro Glu Asp Arg Ala Glu Ala Leu Val
770 775 780
Ile Ile Glu Thr His Val Gly Gln Gly Asp Arg His Gly Trp Ala Pro
785 790 795 800
Ala Glu Ala Val Gly Arg Leu Asp Pro His Gly Asp Pro Asp Asp Trp
805 810 815
Lys Thr Ala Cys Ala Ala Leu Tyr Ala Ala Val Glu Ala Asp Leu Gly
820 825 830

Val Ala Ile Ser Ser Trp Arg Lys Ala Ala Arg Ala Gly Gly Ala Thr
835 840 845
Gly Met Leu Gly Gly Lys Ser Leu Trp Ala Val Asp His Leu Glu Arg
850 855 860
Ser Phe Arg Phe Leu Arg Ser Trp Asp Leu Arg Ala Arg Pro His Asp
865 870 875 880
Gly Asp Pro Arg Arg Pro Arg Pro Gly Tyr Ala Ser Lys Leu Leu His
885 890 895

His Ile Asp Gly Val Lys Asp Asp Arg Val Lys Thr Thr Ala Asp Arg

900 905 910

Ile Val Gln Ala Ala Cys Gly Arg Ala Trp Ile Gly Gly Pro Thr Val

915 920 925

Lys Arg Gly Thr Gln Asp Val Arg Leu Pro Gly Arg Trp Glu Gln Arg

930 935 940

Gly Pro Arg Ala Asp Leu Ile Leu Leu Pro Asp Leu Thr His Phe Arg

945 950 955 960

Phe Arg Ser Asp Arg Pro Arg Ala Glu Asn Ser Arg Leu Met Arg Trp

965 970 975

Ala His Arg Gln Leu Ala Ile Tyr Val Arg Met Gln Ala Glu Val Glu

980 985 990

Gly Ile Leu Val Ala Asp Thr Gly Ala Ala Phe Thr Thr Arg Phe Asp

995 1000 1005

Ala Trp Thr Gly Ala Pro Gly Val Arg Cys Glu Pro Val Thr Ala

1010 1015 1020

Asp His Leu Arg Gly Ile Ala Lys Arg Glu Asp Tyr Trp Leu Ala

1025 1030 1035

Arg Leu Leu Arg Glu Gly Ala Leu Lys His Leu Arg Ile Asp Pro

1040 1045 1050

Ala Ser Leu Arg Val Asp Asp Leu Val Pro Met Asp His Gly Lys

1055 1060 1065

Ile Leu Val Ala Leu Asp Gly Val Asp Leu Pro Gly Leu Arg Ile

1070 1075 1080

Leu Asp Thr Asp Val Asn Ala Ser Gln Gly Leu Gly Arg Arg Tyr

1085 1090 1095

Ile Glu Gly His Gly Leu Ala Tyr Arg Leu Pro Gly Ala Arg Val

1100 1105 1110

Pro Arg Gly Glu Gly Glu Arg Glu Ala Ala Val Val His Ile Lys

1115 1120 1125

Gly Lys Arg Leu Ala Ser Ala Met Gly Gly Thr Val Val Val Leu

1130 1135 1140

Arg Ala Ser Glu Gly Pro Gly Asp Ile Thr Trp Thr Ala Glu Val
1145 1150 1155
Tyr Asp Arg Pro Gln Gly Ala Arg Lys Ala Leu Gly Leu Ser Leu
1160 1165 1170
Ala Ala Phe Asn Ser Ile Ala Thr Ala Ala Val Asp Asp Glu Gly
1175 1180 1185
Pro Ala Pro Glu Asn Asp Asp Glu Ala Leu Glu Glu Glu Ala Glu
1190 1195 1200

Glu Ala Leu Gly Ile Ala Thr Gly Glu Arg Ile Val Phe Phe Arg
1205 1210 1215
Asp Pro Ser Gly Ala Val Ala Gly Gly Gly Trp Leu Glu Ala Ser
1220 1225 1230
Ala Phe Trp Gly Ile Ala Asn Arg Met Val Thr Asp Arg Leu Arg
1235 1240 1245
Glu Leu Gly Arg Leu Gly
1250

<210> 112
<211> 767
<212> PRT
<213> Unknown
<220><223> Description of Unknown:

Cas12 sequence

<400> 112
Met Ala Gln Ala Ser Ser Thr Pro Ala Val Ser Pro Arg Pro Arg Pro
1 5 10 15
Arg Tyr Arg Glu Glu Arg Thr Leu Val Arg Lys Leu Leu Pro Arg Pro
20 25 30
Gly Gln Ser Lys Gln Glu Phe Arg Glu Asn Val Lys Lys Leu Arg Lys
35 40 45
Ala Phe Leu Gln Phe Asn Ala Asp Val Ser Gly Val Cys Gln Trp Ala
50 55 60

Ile Gln Phe Arg Pro Arg Tyr Gly Lys Pro Ala Glu Pro Thr Glu Thr

65 70 75 80

Phe Trp Lys Phe Phe Leu Glu Pro Glu Thr Ser Leu Pro Pro Asn Asp
85 90 95

Ser Arg Ser Pro Glu Phe Arg Arg Leu Gln Ala Phe Glu Ala Ala Ala
100 105 110

Gly Ile Asn Gly Ala Ala Ala Leu Asp Asp Pro Ala Phe Thr Asn Glu
115 120 125

Leu Arg Asp Ser Ile Leu Ala Val Ala Ser Arg Pro Lys Thr Lys Glu
130 135 140

Ala Gln Arg Leu Phe Ser Arg Leu Lys Asp Tyr Gln Pro Ala His Arg
145 150 155 160

Met Ile Leu Ala Lys Val Ala Ala Glu Trp Ile Glu Ser Arg Tyr Arg
165 170 175

Arg Ala His Gln Asn Trp Glu Arg Asn Tyr Glu Glu Trp Lys Lys Glu
180 185 190

Lys Gln Glu Trp Glu Gln Asn His Pro Glu Leu Thr Pro Glu Ile Arg
195 200 205

Glu Ala Phe Asn Gln Ile Phe Gln Gln Leu Glu Val Lys Glu Lys Arg
210 215 220

Val Arg Ile Cys Pro Ala Ala Arg Leu Leu Gln Asn Lys Asp Asn Cys
225 230 235 240

Gln Tyr Ala Gly Lys Asn Lys His Ser Val Leu Cys Asn Gln Phe Asn
245 250 255

Glu Phe Lys Lys Asn His Leu Gln Gly Lys Ala Ile Lys Phe Phe Tyr
260 265 270

Lys Asp Ala Glu Lys Tyr Leu Arg Cys Gly Leu Gln Ser Leu Lys Pro
275 280 285

Asn Val Gln Gly Pro Phe Arg Glu Asp Trp Asn Lys Tyr Leu Arg Tyr
290 295 300

Met Asn Leu Lys Glu Glu Thr Leu Arg Gly Lys Asn Gly Gly Arg Leu
305 310 315 320

Pro His Cys Lys Asn Leu Gly Gln Glu Cys Glu Phe Asn Pro His Thr
325 330 335
Ala Leu Cys Lys Gln Tyr Gln Gln Leu Ser Ser Arg Pro Asp Leu
340 345 350
Val Gln His Asp Glu Leu Tyr Arg Lys Trp Arg Arg Glu Tyr Trp Arg
355 360 365
Glu Pro Arg Lys Pro Val Phe Arg Tyr Pro Ser Val Lys Arg His Ser
370 375 380

Ile Ala Lys Ile Phe Gly Glu Asn Tyr Phe Gln Ala Asp Phe Lys Asn
385 390 395 400
Ser Val Val Gly Leu Arg Leu Asp Ser Met Pro Ala Gly Gln Tyr Leu
405 410 415
Glu Phe Ala Phe Ala Pro Trp Pro Arg Asn Tyr Arg Pro Gln Pro Gly
420 425 430
Glu Thr Glu Ile Ser Ser Val His Leu His Phe Val Gly Thr Arg Pro
435 440 445

Arg Ile Gly Phe Arg Phe Arg Val Pro His Lys Arg Ser Arg Phe Asp
450 455 460
Cys Thr Gln Glu Glu Leu Asp Glu Leu Arg Ser Arg Thr Phe Pro Arg
465 470 475 480
Lys Ala Gln Asp Gln Lys Phe Leu Glu Ala Ala Arg Lys Arg Leu Leu
485 490 495
Glu Thr Phe Pro Gly Asn Ala Glu Gln Glu Leu Arg Leu Leu Ala Val
500 505 510

Asp Leu Gly Thr Asp Ser Ala Arg Ala Ala Phe Phe Ile Gly Lys Thr
515 520 525
Phe Gln Gln Ala Phe Pro Leu Lys Ile Val Lys Ile Glu Lys Leu Tyr
530 535 540
Glu Gln Trp Pro Asn Gln Lys Gln Ala Gly Asp Arg Arg Asp Ala Ser
545 550 555 560
Ser Lys Gln Pro Arg Pro Gly Leu Ser Arg Asp His Val Gly Arg His

565 570 575

Leu Gln Lys Met Arg Ala Gln Ala Ser Glu Ile Ala Gln Lys Arg Gln
580 585 590
Glu Leu Thr Gly Thr Pro Ala Pro Glu Thr Thr Thr Asp Gln Ala Ala
595 600 605
Lys Lys Ala Thr Leu Gln Pro Phe Asp Leu Arg Gly Leu Thr Val His
610 615 620
Thr Ala Arg Met Ile Arg Asp Trp Ala Arg Leu Asn Ala Arg Gln Ile
625 630 635 640

Ile Gln Leu Ala Glu Glu Asn Gln Val Asp Leu Ile Val Leu Glu Ser
645 650 655
Leu Arg Gly Phe Arg Pro Pro Gly Tyr Glu Asn Leu Asp Gln Glu Lys
660 665 670
Lys Arg Arg Val Ala Phe Phe Ala His Gly Arg Ile Arg Arg Lys Val
675 680 685
Thr Glu Lys Ala Val Glu Arg Gly Met Arg Val Val Thr Val Pro Tyr
690 695 700

Leu Ala Ser Ser Lys Val Cys Ala Glu Cys Arg Lys Lys Gln Lys Asp
705 710 715 720
Asn Lys Gln Trp Glu Lys Asn Lys Lys Arg Gly Leu Phe Lys Cys Glu
725 730 735
Gly Cys Gly Ser Gln Ala Gln Val Asp Glu Asn Ala Ala Arg Val Leu
740 745 750
Gly Arg Val Phe Trp Gly Glu Ile Glu Leu Pro Thr Ala Ile Pro
755 760 765

<210> 113
<211> 1210
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence

<400> 113

Met Asn Ile Ile Met Glu Asn Phe Glu Lys Phe Val Asn Leu Tyr Glu
1 5 10 15

Leu Ser Lys Thr Leu Arg Phe Glu Leu Ile Pro Phe Ser Gln Thr Lys
20 25 30

Val Glu Leu Glu Lys Asp Trp Ile Ile Glu Lys Asp Arg Glu Ile Glu
35 40 45

Glu Lys Tyr His Ile Ile Lys Glu Lys Leu Asp Thr Leu His Ile Lys
50 55 60

Phe Val Trp Gln Ala Leu Glu Trp Val Asp Leu Ser Leu Leu Glu Glu
65 70 75 80

Tyr Ala Glu Leu Tyr Phe Ala Cys Lys Lys Asp Thr Lys Asn Lys Lys
85 90 95

Leu Lys Ser Lys Phe Glu Lys Leu Glu Lys Lys Ile Arg Gln Glu Ile
100 105 110

Thr Ser Phe Phe Asp Ala Glu Trp Asn Lys Trp Lys Glu Lys Tyr Gly
115 120 125

Phe Leu Lys Lys Trp Trp Thr Ser Phe Leu Thr Glu Lys Glu Ile Leu
130 135 140

Asp Val Leu Ile Asp Ile Phe Pro Glu Asn Lys Asp Asp Phe Glu Ile
145 150 155 160

Phe Lys Trp Phe Phe Thr Tyr Phe Ser Asn Phe Asn Glu Ser Arg Lys
165 170 175

Asn Phe Tyr Lys Asp Glu Trp Lys Ala Gly Gln Ile Ala Thr Arg Ala
180 185 190

Ile Asp Glu Asn Leu Thr Thr Phe Leu Glu Asn Ile Ile Lys Tyr Lys
195 200 205

Asn Phe Lys Lys Glu Asn Pro Asp Phe Phe Thr Glu Asn Glu Glu Lys
210 215 220

Val Phe Glu Leu Asp Phe Tyr Asn Phe Cys Leu Thr Gln Lys Trp Ile
225 230 235 240

Asp Asn Tyr Asn Glu Ile Ile Trp Ala Lys Ser Leu Glu Glu Trp Lys
245 250 255
Asn Thr Gln Gly Val Asn Gln Arg Ile Asn Leu Leu Lys Gln Lys Asn
260 265 270
Glu Lys Ser Asn Lys Lys Asn Leu Ser Tyr Pro Lys Phe Asp Ile Leu
275 280 285
Tyr Lys Gln Ile Leu Ser Glu Lys Ser Glu Asn Asp Phe Ile Pro Asn
290 295 300

Ile Glu Asn Thr Glu Glu Leu Phe Thr Val Ile Gln Lys Ser Ile Lys
305 310 315 320
Glu Asn Asp Lys Lys Ile Thr Glu Ile Asp Lys Leu Phe Lys Lys Phe
325 330 335
Phe Leu Glu Glu Asn Asn Ile Asp Ile Trp Lys Val Tyr Ile Ser Lys
340 345 350
Gln Ala Val Asn Thr Ile Ser Ser Lys Tyr Phe Glu Asn Trp Ser Ser
355 360 365

Leu Trp Trp Tyr Leu Trp Glu Asn Ser Lys Lys Lys Tyr Phe Ser Leu
370 375 380
Trp Glu Ile Lys Glu Ala Leu Glu Asp Ile Lys Glu Lys Asn Ile Phe
385 390 395 400
Lys Gly Glu Tyr Tyr Asn Asn Lys Ile Ala Phe Glu Asn Lys Ser Asn
405 410 415
Phe Glu Asn Phe Leu Ala Ile Phe Tyr Tyr Glu Phe Gln Thr Asn Leu
420 425 430

Ser Leu Leu Asn Trp Asn Gln Asn Asn Leu Glu Ser Leu Gln Glu Lys
435 440 445
Glu Phe Lys Lys Glu Glu Lys Gln Val Asp Ile Ile Lys Lys Tyr Phe
450 455 460
Asp Ser Val Met Asp Leu Tyr Ala Met Ser Lys Tyr Phe Phe Val Asp
465 470 475 480
Leu Lys Gln Ala Lys Asn Phe Pro Lys Asp Ile Glu Phe Tyr Asn Asp

485 490 495

Phe Asp Leu Tyr Phe Ser Asp Tyr Glu Pro Trp Lys Val Tyr Asn Leu
500 505 510
Val Arg Asn Phe Leu Thr Lys Lys Glu Val Lys Thr Asp Lys Phe Lys
515 520 525
Leu Asn Phe Ser Asn Ser Gln Phe Leu Thr Gly Trp Asp Lys Asp Lys
530 535 540
Glu Lys Glu Arg Phe Trp Val Ile Leu Arg Lys Asn Glu Lys Tyr Phe
545 550 555 560

Leu Ala Ile Leu Lys Lys Asn Asn Asn Lys Ile Phe Glu Asn Tyr Arg
565 570 575
Glu Asn Asn Pro Thr Asp Phe Tyr Glu Lys Met Glu Tyr Lys Gln Leu
580 585 590
Asn Asn Val Tyr Arg Gln Ile Pro Arg Leu Gly Phe Pro Leu Gln Lys
595 600 605
Lys Leu Asp Ser Leu Lys Trp Lys Glu Leu Glu Glu Tyr Leu Glu Lys
610 615 620

Tyr Lys Asn Asn Phe Trp Tyr Asn Lys Glu Ile Ala Phe Ile Lys Glu
625 630 635 640
Glu Phe Asp Ile Phe Gln Lys Asn Lys Glu Lys Trp Glu Lys Phe Asp
645 650 655
Arg Glu Lys Leu Lys Lys Leu Ile Asp Tyr Tyr Lys Lys Val Val Leu
660 665 670
Glu Lys Tyr Ser Asp Leu Tyr Asp Leu Lys Lys Leu Glu Asn Thr Asp
675 680 685

Tyr Asp Glu Leu Val Asn Phe Tyr Asp Asp Val Glu Lys Ser Met Tyr
690 695 700
Ser Leu His Phe Thr Lys Ile Glu Thr Glu Phe Leu Glu Asn Leu Glu
705 710 715 720
Lys Asn Trp Glu Ile Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser
725 730 735

Asp Tyr Lys Lys Glu Asn Thr Lys Glu Asn Ile His Thr Lys Tyr Phe
740 745 750

Lys His Leu Phe Ser Glu Glu Asn Leu Glu Asn Leu Lys Ile Lys Leu
755 760 765

Ser Gly Trp Ala Glu Ile Phe Phe Arg Asp Lys Thr His Asn Leu Lys
770 775 780

Gln Lys Leu Asp Lys Asn Trp Lys Lys Met Phe Tyr Trp Glu Asn Lys
785 790 795 800

Asp Lys Lys Val Leu Glu His Arg Arg Tyr Ala Lys Asp Ser Tyr Gly
805 810 815

Phe His Ile Ser Ile Thr Leu Trp Ala Asn Asn Trp Asp Met Tyr Lys
820 825 830

Phe Asn Gln Phe Phe Asn Lys Asn Phe Thr Pro Lys His Ile Ile Gly
835 840 845

Ile Asp Arg Trp Glu Lys His Leu Ala Tyr Tyr Ser Val Ile Asp Leu
850 855 860

Glu Gly Asn Leu Val Glu Thr Asp Thr Leu Asn Ile Val Asn Gly Ile
865 870 875 880

Asn Tyr Leu Glu Lys Leu Glu Asn Ile Glu Lys Ser Arg Met Gln Glu
885 890 895

Arg Lys Ser Trp Trp Glu Ile Glu Asn Ile Lys Asn Leu Lys Asp Gly
900 905 910

Tyr Ile Ser Ala Val Val Ser Lys Leu Thr Glu Leu Ile Glu Lys Tyr
915 920 925

Gln Ala Ile Ile Val Phe Glu Asp Leu Asn Leu Gly Phe Lys Arg Trp
930 935 940

Arg Glu Lys Ile Glu Arg Gln Val Tyr Gln Lys Leu Glu Leu Ala Leu
945 950 955 960

Ala Lys Lys Leu Asn Tyr Leu Thr Phe Lys Asn Lys Lys Asp Cys Glu
965 970 975

Ile Trp Gly Val Leu Asn Gly Ile Gln Leu Val Pro Arg Val Lys Asp

980 985 990

Tyr Gln Asp Ile Ala Asn Tyr Lys Gln Ser Gly Ile Ile Phe Tyr Thr

995 1000 1005

Asn Pro Ala Tyr Thr Ser Thr Thr Cys Pro Glu Cys Gly Trp Arg

1010 1015 1020

Lys Thr Leu Lys Phe Pro Ser Lys Ile Thr Lys Thr Ser Ile Leu

1025 1030 1035

Glu Phe Phe Lys Glu Ile Gln Met Ser Phe Tyr Trp Glu Lys Phe

1040 1045 1050

Ser Phe Thr Tyr Glu Asn Ile Leu Trp Lys Ser Glu Thr Leu Phe

1055 1060 1065

Ser Asn Val Lys Arg Thr Gln Trp Asn Asn Lys Ser Arg Lys Ile

1070 1075 1080

Glu His Lys Glu Asn Ile Thr Gln Glu Leu Lys Ser Val Phe Glu

1085 1090 1095

Lys Tyr Asn Ile Asn Leu Trp Glu Asn Ile Ser Glu Lys Leu Gln

1100 1105 1110

Gln Thr Asp Met Leu Leu Glu Asp Leu Lys Val Leu Phe Tyr Asn

1115 1120 1125

Phe Lys Leu Ile Asn Asn Ile Arg Asn Ser Asp Ser Lys Leu Glu

1130 1135 1140

Glu Asp Ile Ile Ser Cys Pro Cys Cys Leu Phe Asn Ser Glu Asn

1145 1150 1155

Trp Phe Lys Gly Ala Tyr Phe Asn Gly Asp Ala Asn Gly Ala Tyr

1160 1165 1170

Asn Thr Ala Arg Lys Gly Ile Ile Met Leu Glu Asn Ile Lys Val

1175 1180 1185

Asn Pro Glu Arg Ser Asn Leu Phe Val Arg Asn Glu Glu Trp Asp

1190 1195 1200

Glu Phe Leu Arg Glu Glu Phe

1205 1210

<210> 114

<211> 1187

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 114

Met Ser Lys Leu Phe Glu Asn Met Thr Asn Leu Tyr Ser Leu Asn Lys
1 5 10 15

Thr Leu Arg Phe Glu Leu Lys Pro Val Gly Asn Thr Arg Glu Leu Ile

20 25 30

Glu Ser Lys Asp Phe Phe Lys Asn Asp Glu Glu Lys Ala Glu Asn Tyr
35 40 45

Gln Phe Met Lys Glu Lys Met Asp Lys Ile His Arg Asn Tyr Ile Gln
50 55 60

Lys Ser Leu Glu Thr Ile Lys Met Leu Pro Ile Leu Asp Gln Thr Glu
65 70 75 80

Gln Lys Arg Leu Lys Lys Glu Asp Ile Lys Asn Glu Leu Lys Ser Leu

85 90 95

Arg Ser Phe Ile Ser Ala Ala Phe Val Ser Val Lys Asp Leu Leu Ser
100 105 110

Asn Lys Ile Ile Glu Trp Leu Ile Ser Glu Ala Ser Ile Glu Glu Lys
115 120 125

Glu Lys Ile Lys Lys Phe Asp Lys Phe Phe Gly Tyr Phe Lys Thr Tyr
130 135 140

Val Gln Asn Arg Gly Asn Leu Tyr Lys Ala Glu Asp Lys Ala Gly Gln

145 150 155 160

Ile Ala Phe Arg Leu Ile Asp Glu Asn Leu Pro Arg Phe Phe Lys Ala

165 170 175

Lys Gln Ile Ile Glu Glu Ile Ile Lys Lys Thr Pro Asp Phe Val Val
180 185 190

Lys Glu Arg Asn Glu Lys Gln Glu Glu Thr Glu Lys Lys Ile Thr Glu

195 200 205

Tyr Leu Ser Ile Phe Tyr Leu Asn Ser Tyr Cys His Tyr Leu Ser Gln

210 215 220

Ser Gly Ile Asp Leu Phe Asn Glu Ile Val Gly His Ile Asn Leu Ser

225 230 235 240

Ile Asn Leu Tyr Lys Gln Lys Thr Gly Val Lys Phe Ser Leu Ile Pro

245 250 255

Leu Leu Tyr Lys Leu Pro Leu Ala Pro Arg Lys Gln Ile Ser Arg Leu

260 265 270

Pro Lys Gln Ile Glu Asn Pro Glu Glu Leu Glu Leu Ile Val Lys Ser

275 280 285

Val Leu Asp Arg Ile Asp Gln Lys Ile Asn Pro Phe Ile Asn Asn Ile

290 295 300

Leu Gln Thr Val Leu Glu Glu Asn Ser Val Tyr Asp Leu Asn Trp Ile

305 310 315 320

Tyr Ile Ser Ile Lys Thr Thr Glu Gln Trp Trp Ser Ile Gly Leu Ser

325 330 335

Gly Arg Asn Ser Leu Arg Glu Leu Gly Tyr Asn Gln Ser Lys Asn Trp

340 345 350

Glu Glu Pro Val Leu Lys Ala Glu Lys Asn Lys Phe Pro Phe Ile Ser

355 360 365

Leu Gly Glu Ile Lys Ser Phe Leu Asp Ala Lys Gln Leu Ala Trp Asp

370 375 380

Asp Ile Lys Ser Val Phe Trp Glu Gly Lys Ser Gln Ser Leu Met Asn

385 390 395 400

Trp Ser Trp Ser Asn Ile Phe Phe His Leu Ile Gly Lys Glu Ile Ser

405 410 415

Ser Leu Ile Glu Lys Tyr Leu His Ser Arg Lys Asn Tyr Gln Ile Ser

420 425 430

Gln Ser Lys Glu Asn Gln Lys His Val Leu Asp Asn Ser Leu Ser Leu

435 440 445

Trp Arg Leu Leu Gly Trp Phe Val Leu Met His Lys Lys Thr His Leu
450 455 460
Thr Pro Glu Ile Lys Glu Ser Phe Phe Tyr Asp Trp Glu Asn Gly Leu

465 470 475 480
Asp Ala Ile Val Phe Asp Glu Asn Ser Asp Pro Ile His Thr Ile Tyr
485 490 495
Asp Lys Val Arg Asn Cys Leu Thr Lys Lys Pro Tyr Ser Asn Lys Asp
500 505 510
Lys Ile Lys Val Asn Phe Asp Cys Pro Tyr Leu Leu Trp Gly Trp Asp
515 520 525
Gln Asn Tyr Asp Ala Phe Gly Trp Leu Ile Phe His Asp Trp Lys Lys

530 535 540
Tyr Phe Leu Trp Leu Ile Lys Gly Ser Trp Leu Asn Met Glu Glu Lys
545 550 555 560
Asn Lys Leu Tyr Glu Trp Ile Asn Pro Met Asn Ser Ile Thr Lys Ile
565 570 575
Ile Tyr Asp Tyr Gln Lys Pro Asp Phe Lys Asn Val Pro Arg Leu Phe
580 585 590
Ile Arg Ser Lys Trp Asp Thr Phe Ala Pro Met Val Arg Glu Tyr Trp

595 600 605
Leu Pro Val Asn Asp Ile Leu Tyr Leu Tyr Asp Asn Glu Leu Tyr Lys
610 615 620
Pro Asp Lys Lys Asn Pro Trp Lys His Lys Ser Tyr Leu Arg Arg Leu
625 630 635 640
Ile Asp Tyr Phe Lys Leu Trp Leu Ser Lys His Lys Ser Phe Lys His
645 650 655
Tyr Ile Phe Lys Arg Lys Glu Ser Asp Gln Tyr Glu Asn Leu Ala Glu

660 665 670
Phe Tyr Ser Asp Val Glu Phe Ser Cys Tyr Ala Ile Lys Lys Glu Lys
675 680 685
Val Asn Phe Asp Gln Val Lys Ala Leu Cys Glu Ser Glu Arg Leu Tyr

690 695 700

Leu Phe Glu Ile Tyr Asn Lys Asp Tyr Asn Gln Phe Ser Lys Trp Lys

705 710 715 720

Asn Lys Asn Leu His Thr Gln Tyr Phe Glu Ala Leu Phe Glu Glu Arg

725 730 735

Asp Asn Asn Leu Phe Met Leu Ser Gly Gly Trp Ser Ile Phe Trp Arg

740 745 750

Glu Ser Asn Trp Lys Ile Val Glu Lys Ile Arg Ser Tyr Ser Pro Lys

755 760 765

Tyr Asn Ile Glu Ile Ile Asp Lys Arg Arg Tyr Thr Lys Asn Lys Leu

770 775 780

Met Ile His Ile Pro Ile Val Leu Asn Phe Cys Arg Asn Gln Glu Trp

785 790 795 800

Arg Val Asn Asp Met Ile Lys Ser Leu Ile Gln Ser Gln Ser Asn Asn

805 810 815

Phe Thr Ile Leu Gly Ile Asp Arg Trp Glu Lys His Leu Leu Tyr Tyr

820 825 830

Ser Leu Ile Arg Gln Asp Trp Thr Ile Ile Lys Thr Gly Ser Arg Asn

835 840 845

Thr Ile Thr Asn Lys Ile Lys Ile Val Asp Tyr His Lys Lys Leu Asp

850 855 860

Asp Arg Glu Lys Lys Arg Asp Glu Ala Gln Ala Asn Trp Glu Gln Gln

865 870 875 880

Glu Gln Ile Lys Asp Leu Lys Lys Trp Tyr Ile Ser Gln Val Ile Asn

885 890 895

Glu Ile Ser Lys Met Ile Ile Glu His Asn Ala Ile Ile Val Leu Glu

900 905 910

Asp Leu Asn Gly Trp Phe Lys Arg Trp Arg Gln Lys Val Glu Lys Ser

915 920 925

Ile Tyr Gln Gln Phe Glu Leu Ala Leu Ala Lys Lys Leu Asn His Leu

930 935 940

Val Phe Lys Asn Arg Trp Asp Thr Glu Ser Trp Gly Thr Met Lys Ala
945 950 955 960
Tyr Gln Leu Thr Pro Leu Val Ala Gln Phe Gln Asp Leu Ser Phe Gln
965 970 975
Thr Trp Val Val Phe Tyr Thr Pro Ala Trp Tyr Thr Ser Thr Thr Cys

980 985 990
Pro Cys Cys Gly Trp Arg Lys Asn Ile Tyr Phe Lys Tyr Glu Asn Glu
995 1000 1005
Lys Gln Ala Lys Ile Glu Leu Glu Lys Leu Asn Ile Val Arg Glu
1010 1015 1020
Asn Asn Tyr Phe Ser Ile Thr Tyr Thr Ala Glu Trp Trp Asn Lys
1025 1030 1035
Lys Trp Lys Ile Thr Trp Ser Val Leu Asn Lys Thr Asp Arg Ile

1040 1045 1050
Leu Thr Thr Lys Trp Gln Thr Arg Leu Gln Tyr Asp Arg Ala Ser
1055 1060 1065
Lys Asn Thr Lys Glu Tyr Asp Ile Thr Thr Asp Phe Asn Ser Val
1070 1075 1080
Phe Thr Ala Lys Phe Leu Asp Tyr Lys Ile Arg Leu Glu Asn Ala
1085 1090 1095
Gly Ser Lys Gln Cys Arg Asn Leu Ile Asn Ser Ile Asn Leu Leu

1100 1105 1110
Leu Lys Ile Arg Asn Ala Lys Ser Gly Thr Asp Ile Asp Thr Ile
1115 1120 1125
Gln Cys Pro Ala Cys Glu Phe His Ser Gln Trp Trp Phe Gln Trp
1130 1135 1140
Asn Glu Phe Asn Trp Asp Ala Asn Trp Ala Tyr Asn Ile Ala Arg
1145 1150 1155
Lys Gly Lys Val Ile Ile Asp Lys Ile Val Lys Gly Glu Lys Asn

1160 1165 1170
Thr Thr Val Ser Gln Ile Glu Phe Asp Asn Glu Ile Gln Lys

1175 1180 1185

<210> 115

<211> 938

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 115

Pro Ala Tyr Arg His Pro Asp Pro Leu Leu His Pro Val Phe Cys Asp
1 5 10 15
Phe Gly Cys Ser Arg Trp Gln Ile Cys Phe Asp Val Arg Lys Asn Val
20 25 30

Arg Thr Thr Ser Pro Arg Arg Leu Cys Leu Thr Leu Phe Thr Gly Ser
35 40 45
Gly Met Glu Leu Val Pro Phe Ser Trp Gln Ser Lys Arg Leu Ala Arg
50 55 60
Asp Leu Ala Leu Glu Gln Arg His Arg Asn Pro Glu Ala Ser Glu Val
65 70 75 80
Thr Arg Ala Asp Arg Leu Gly Arg Ala Ala Ala Gly Val Ser Ala Gly
85 90 95

Gly Ala Val Ser Ile Lys Asn Ile Phe Asn Glu Glu Asn Trp Asn Gly
100 105 110
Arg Leu Gln Ala Pro Arg Ser Gln Leu Ala Ala Ile Ala Ala Arg Val
115 120 125
Asp Lys His Gly Trp Asp Ala Lys Ala Leu Arg Met Leu Asp Arg Leu
130 135 140
Arg Trp Leu Ile Thr Phe Ser Pro Arg Leu Glu Pro Thr Gly Pro Trp
145 150 155 160

Ile Glu Tyr Ala Leu Arg Ile Pro Asp Asp Ala Ala Ala Lys Pro Phe
165 170 175
Leu Ser Arg Lys Asn Gly Phe Ala Val Leu His Arg Ser Asn Asp Asp
180 185 190

Arg Lys Gly Leu Ala Lys Leu Ile Leu Ser Arg Leu Pro Gly Leu Arg
195 200 205

Val Leu Ser Val Asp Leu Gly His Arg Tyr Ala Ala Ala Cys Ala Val
210 215 220

Trp Glu Thr Leu Ser Ala Asp Gln Val Arg Glu Ala Cys Gln Ala Ala
225 230 235 240

Gly His Asp Gly Pro Thr Glu Cys Asp Leu Tyr Leu His Leu Lys Lys
245 250 255

Asp Gly Arg Thr Val Ile Tyr Arg Arg Ile Gly Ala Asp Thr Leu Ser
260 265 270

Asp Gly Thr Pro His Pro Ala Pro Trp Ala Arg Leu Asp Arg Gln Phe
275 280 285

Leu Ile Lys Leu Gln Gly Glu Glu His Lys Ala Arg Glu Ala Ser Asn
290 295 300

Ala Glu Ile Trp Ala Val His Gln Met Glu Ala Ala Leu Gly Arg Ser
305 310 315 320

Val Pro Leu Ile Asp Arg Leu Val Ala Ser Gly Trp Gly Gln Arg Thr
325 330 335

Glu Gly Gln Arg Ala Arg Leu Glu Ala Leu Lys Gln Leu Gly Trp Arg
340 345 350

Pro Val Ala Glu Lys Leu Asp Ser Asp Asp Glu Pro Gly Val Met Glu
355 360 365

Glu Ser Pro Ala Ile Lys Pro Ser Leu Ser Ile Asp Glu Leu Met Ser
370 375 380

Ser Ala Val Arg Thr Met Arg Leu Ala Leu Lys Arg His Gly Asp Arg
385 390 395 400

Ala Arg Ile Ala His Tyr Leu Ile Thr Asp Glu Lys Thr Lys Pro Gly
405 410 415

Asn Val Lys Glu Gln Leu Asp Glu Asn Gly Arg Ile Glu Leu Leu Gln
420 425 430

Asp Ala Leu Val Leu Trp His Asp Leu Phe Ser Ser Lys Gly Trp Gln

435 440 445

Asp Asn Lys Ala Lys Glu Leu Trp Tyr Val His Ile Ala Thr Leu Pro

450 455 460

Glu Tyr Lys Ala Phe Gln Ser Ser Gly Glu Gly His Ala Gly Pro Glu

465 470 475 480

Arg Arg Gly Lys Pro Glu Glu Asp Arg Glu Lys Leu Gly Val Val Ala

485 490 495

Gln Ala Leu Ala Pro Asn Val Thr Leu Arg Glu Ala Leu His Asn Ala

500 505 510

Trp Lys Lys Arg Trp Glu Glu Asp Asp Ala Arg Trp Lys Ala Leu Leu

515 520 525

Arg Trp Cys Lys Asp Trp Ile Leu Pro Arg Gly Glu Ala Ala Asn Ser

530 535 540

Pro Ala Ile Arg Lys Val Gly Gly Leu Ser Leu Ile Arg Leu Ala Thr

545 550 555 560

Leu Thr Glu Phe Arg Arg Lys Val Gln Val Gly Phe Phe Ala Arg Leu

565 570 575

Arg Pro Asp Gly Lys Lys Ala Glu Thr Gly Glu Lys Phe Gly Arg Lys

580 585 590

Thr Leu Asp Ala Leu Glu Glu Leu Arg Glu Gln Arg Val Lys Gln Leu

595 600 605

Ala Ser Arg Ile Ala Glu Ala Ala Leu Gly Ile Gly Lys Glu His Val

610 615 620

Phe Pro Thr Ala Lys Glu Pro Gln Lys Lys Cys Trp Cys Gly Ser Val

625 630 635 640

His Arg Lys Lys Asp Pro Lys Arg Pro Arg Glu Arg Val His Ser Pro

645 650 655

Cys His Ala Val Val Ile Glu Asn Leu Thr His Tyr Arg Pro Glu Glu

660 665 670

Thr Arg Thr Arg Arg Glu Asn Arg Gln Leu Met Ser Trp Ser Ser Gly

675 680 685

Lys Val Lys Lys Tyr Leu Ala Glu Ala Cys Gln Leu Asn Gly Leu His
690 695 700
Leu Arg Glu Val Asn Ala Ala Tyr Thr Ser Arg Gln Asp Ser Arg Thr
705 710 715 720
Gly Ala Pro Gly Ile Arg Cys Gln Asp Val Pro Val Lys Glu Phe Met
725 730 735

Arg Ser Pro Phe Trp Arg Glu Gln Val Ala Gln Ala Lys Lys Lys Gln
740 745 750
Ala Glu Gly Lys Gly Asp Ala Arg Glu Arg Phe Leu Cys Asp Leu Asp
755 760 765
Glu Gln Trp Lys Asn Arg Ser Glu Asp Glu Trp Lys Lys Ala Gly Pro
770 775 780
Val Arg Val Pro Leu Arg Gly Gly Glu Ile Phe Val Ser Ala Asp Gly
785 790 795 800

Thr Ser Pro Thr Ala Lys Gly Leu His Ala Asp Leu Asn Ala Ala Ala
805 810 815
Asn Ile Gly Leu Cys Ala Leu Thr Asp Pro Asp Trp Pro Gly Arg Trp
820 825 830
Trp Tyr Val Pro Cys Asp Pro Ala Ser Phe Lys Pro Ile Met Asp Lys
835 840 845
Val Glu Gly Ser Ala Ala Val Gln Pro Asp Gln Ala Leu Arg Gln Pro
850 855 860

Ala Gln Ala Gln Arg Gly Asp Ala Ala Arg Asp Arg Lys Lys Arg Gly
865 870 875 880
Lys Val Gly Gly Arg Ser Arg Glu Val Val Asn Leu Trp Arg Asp Val
885 890 895
Ser Ser Arg Pro Ile Ser Pro Asn Asp Ser Trp Gln Glu Phe Thr Pro
900 905 910
Tyr Trp Asn Asp Val Gln Ala Arg Val Val Asn Ile Leu Arg Gln Ser
915 920 925

Ala Gly Leu Thr Arg Gly Gln Gly Glu Pro

930 935

<210> 116

<211> 1140

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 116

Met Pro Leu Arg Ser Ile Asn Ile Lys Met Arg Leu Lys Arg Ala Ala
1 5 10 15
Glu Gly Arg Ala Leu Arg Gln Ser Leu Trp Leu Thr His Ser Val Val
20 25 30
Asn Cys Ala Val Ala Glu Ile Glu Arg Val Leu Leu Leu Cys Arg Gly

35 40 45
Arg Gly Tyr Trp Thr Gly Asp Asp Glu Pro Val Ser Ala Glu Thr Val
50 55 60
Gln Gln Gln Ala Leu Ala Phe Ala Arg Glu Thr Gln Ala Arg Asn Gly
65 70 75 80
Gln Pro Gly Ile Gly Gly Asp Ala Glu Ile Leu Ala Ala Leu Arg Gly
85 90 95
Leu Tyr Glu Ala Ile Val Pro Ser Val Asn Arg Asp Glu Gln Gly Arg

100 105 110
Pro Leu Glu Gly Asn Ala Gln Ala Ala Gly Gly Phe Ala Gly Pro Met
115 120 125
Met Asp Ala Glu Ser Glu Gly Phe Gln Ser Val Phe Asp Lys Ile Leu
130 135 140
Glu Pro Leu Pro Ser Trp Val Ala Lys Met Thr Gly Gly Thr Arg Gly
145 150 155 160
Trp Glu Gln Glu Ser Val Gln Trp Leu Lys Ser Pro Glu Ser Glu Arg

165 170 175
Leu Gln His Ala Ser Gly Ser Pro Pro Ala Trp Val Arg Arg Leu Arg
180 185 190

Thr Gly Glu Pro Trp Gln Glu Ala Phe Val Gln Asp Gln Glu Asn Lys
195 200 205
Arg Lys Glu Val Lys Gly Val Pro Ser Leu Ile Gln Arg Leu Lys Lys
210 215 220
Glu Leu Gly Leu Leu Pro Leu Met Arg Pro Pro Ile Thr Leu Gln Phe

225 230 235 240
Glu Asp Lys Arg Ser Gly Leu Thr Pro Trp Asp Arg Leu Thr Leu Arg
245 250 255
Leu Ala Val Ala His Leu Leu Ser Trp Glu Ser Trp Asn His Arg Ala
260 265 270
Ala Asp Glu His Gly Arg Val Thr Glu Arg Leu Ala Arg Leu Glu Thr
275 280 285
Glu Ala Ala Pro Leu Ala Ser Leu Ile Glu Gly Leu Arg Glu Tyr Glu

290 295 300
Lys Ile Arg His Glu Glu Leu Lys Arg Val Ala Gln Ala Asn Asp Glu
305 310 315 320
Asn Pro Phe Arg Ile Gly Ala Arg Gly Val Arg Gly Trp Asp Arg Val
325 330 335
Arg Glu Ala Trp Leu Gly Ala Thr Asp Asp Thr Lys Glu Gly Arg Phe
340 345 350
Thr Ser Val Ala Ala Leu Gln Thr Lys Leu Gly Gly Arg Phe Gly Asp

355 360 365
Pro Asp Leu Phe Arg Trp Leu Ala Glu Glu Gly Arg Glu His Leu Trp
370 375 380
Gly Glu His Asp Pro Leu Pro Ile Leu Ala Arg Leu Asn Ala Leu Ser
385 390 395 400
Arg Leu Leu Arg Arg Lys Lys Asp His Ala Ile Tyr Thr Ala Pro Asp
405 410 415
Ala Arg Leu His Pro Arg Trp Thr Ala Tyr Glu Ala Pro Gly Gly Gly

420 425 430
Asn Leu Arg Asn Tyr Ser Phe Glu Ile Ser Gly Asn Asp Leu Ala Leu

435 440 445

Arg Leu Pro Leu Leu Arg Arg Val Glu Ser Gly Leu Glu Glu Asp Ser

450 455 460

Gln Arg Ala Glu Ile Ala Leu Ala Pro Ser Gly Gln Phe Gln Ser Ala

465 470 475 480

Ser Trp Lys Gly Asp Gly Lys Pro Asn Arg His Leu Thr Tyr Tyr Ser

485 490 495

Ala His Glu Gln Phe Ser Ala Glu Leu Gly Gly Ala Glu Ile Leu Tyr

500 505 510

Arg Arg Arg His Leu Glu Asn Arg Lys Val Lys Glu Leu Glu Gln Gly

515 520 525

Asp Ile Gly Pro Val Trp Leu Lys Leu Val Leu Asp Val Gln Pro Asn

530 535 540

Ala Pro Glu Gly Trp Phe Thr Pro Arg Gly Arg Val Val Thr Pro Pro

545 550 555 560

Thr Val His His Phe Asn Thr Ala Leu Val Asn Arg Ser Lys His Ala

565 570 575

Pro Asp Leu Val Pro Gly Leu Arg Val Leu Ala Val Asp Leu Gly Val

580 585 590

Arg Thr Phe Ala Ala Cys Ser Val Phe Glu Leu Val Gln Gly Glu Pro

595 600 605

Gly Asn Gly Met Ala Phe Leu Ala Asp Gln Glu Arg Asp Leu Trp Ala

610 615 620

Arg His Glu Arg Ser Phe Leu Leu Pro Leu Pro Gly Glu Ala Val Asp

625 630 635 640

Ser Gln Leu Leu Ala Ala Arg Arg Ala Ala Tyr Asn Gln Leu Gly Leu

645 650 655

Leu Arg Arg Asp Leu Gly Arg Leu Lys Gly Ile Leu Arg Leu Ser Val

660 665 670

Lys Glu Thr Ala Glu Asn Arg Cys Gly Ser Leu Glu Glu Leu Leu Ala

675 680 685

Ser Leu Glu Asp Glu Trp Asn Arg Gly Asn Ala Pro Ala Ile Asp Val
690 695 700
Ala Ala Leu Leu Ser Ala Lys Gly Cys Leu Glu Met Pro Gln Pro Ala
705 710 715 720
Trp Glu Ala Ala Ile Ala Gly Thr Tyr Gln Ala Ala Glu Arg Glu Leu
725 730 735
Gly Asn Arg Val Arg Asp Trp Arg Arg Thr Thr Arg Pro Arg Thr Thr

740 745 750
Gly Glu Asp Asp Arg Arg Gln Arg Arg Gly Tyr Ser Gly Gly Lys Ser
755 760 765
Ala Trp Ala Val Glu Tyr Leu Asp Gln Val Arg Arg Leu Leu Gln Gly
770 775 780
Trp Ser Leu His Gly Arg Ser Tyr Ala Gln Ile Arg Arg Leu Asp Arg
785 790 795 800
Glu Lys Met Gly Thr Phe Ala Ala Gly Leu Leu Asp His Ile Asn Ala

805 810 815
Leu Lys Gln Asp Arg Val Lys Thr Gly Ser Asp Leu Ile Val Gln Ala
820 825 830
Ala Arg Gly Tyr Leu Pro Thr Gly Lys Lys Gly Trp Ile Lys Gln Tyr
835 840 845
Glu Pro Cys Arg Leu Ile Leu Phe Glu Asp Leu Ala Arg Tyr Arg Phe
850 855 860
Arg Thr Asp Arg Pro Arg Arg Glu Asn Ala Arg Leu Met Arg Trp Asn

865 870 875 880
His Arg Gln Ile Leu Thr Glu Thr Glu Leu Gln Ala Glu Ile Phe Gly
885 890 895
Leu Leu Ile Gly Thr Thr Gly Ala Gly Phe Ser Ser Arg Phe His Ala
900 905 910
Arg Ser Gly Ala Pro Gly Cys Arg Thr Arg Leu Leu Thr Ala Glu Asp
915 920 925
Leu Arg Ser Pro Thr Leu Ala Lys Gln Leu Glu Leu Leu Ala Glu Thr

930 935 940

Gln Gly Ile Asp Pro Lys Cys Phe Arg Pro Gly Met Gln Ile Pro Trp

945 950 955 960

Asp Ser Gly Ala Asp Phe Val Thr Leu Asp Ser Glu Gly Lys Leu Val

965 970 975

Gln Ile His Ala Asp Val Asn Ala Ala Gln Asn Leu Gln Arg Arg Phe

980 985 990

Trp Thr Arg Phe Arg Asp Ala Tyr Arg Ile Ser Ala Val Glu Ile Lys

995 1000 1005

Gln Asp Gly Arg Thr Ser Trp Tyr Pro Asp Arg Glu Gly Val Arg

1010 1015 1020

Leu Arg Gly Ala Leu Ser Thr Ile Val Gly Gly Asp Gly Tyr Ala

1025 1030 1035

Arg Leu Val Ala Ala Asp Asp Asp Asp Gly Phe Val Leu Glu Lys

1040 1045 1050

Val Thr Arg Pro His Trp Arg Arg Ala Ala Gly Ala Gln Ala Glu

1055 1060 1065

Ser Gly Asp Asp Val Gly Leu Asp Glu Val Ala Leu Glu Met Ala

1070 1075 1080

Glu Ala Met Asp Thr Asp Leu Glu Arg Gly Glu Gly Arg Leu Val

1085 1090 1095

Phe Phe Arg Asp Pro Ser Gly Ser Val Ile Arg Ala Asp Arg Trp

1100 1105 1110

Tyr Gln Ala Lys Ala Phe Trp Gly Gln Val Arg Ser Arg Val Thr

1115 1120 1125

Arg Ala Leu Gly Leu Arg Arg Pro Gly Ala Ser Ser

1130 1135 1140

<210> 117

<211> 669

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 117

```
Met Leu Asp Lys Phe Ala Ser Leu Tyr Pro Val Thr Lys Thr Leu Arg
1               5                  10                  15
Phe Arg Leu Leu Pro Gln Gly Arg Thr Glu Glu Asn Met Gln Val Ala
            20                  25                  30

Lys Val Leu Glu Asn Asp Leu Glu Arg Ser Glu Ala Ala Ala Val Val
        35                  40                  45
Lys Gly Leu Ile Lys Lys Tyr His Leu Gln Phe Ile Ser Asp Thr Leu
    50                  55                  60
Ser Gly Ser Thr Leu Ser Trp Gln Ala Leu Thr Glu Thr Leu Asp Lys
65                  70                  75                  80
Phe Lys Ala Asp His Thr Ala Thr Ala Glu Leu Asp Ser Ala Leu Ala
                85                  90                  95

Ala Tyr Arg Cys Lys Leu Ala Glu Leu Phe Thr Lys Ser Pro Lys Tyr
            100                 105                 110
Lys Val Met Ala Thr Pro Val Ser Ile Ile Lys Glu Ile Leu Lys Thr
        115                 120                 125
Glu Thr Asp Pro Glu Asn Ile Ala Ala Leu Asn Lys Leu Asn Gly Tyr
    130                 135                 140
Thr Tyr Ile Ile Phe Asp Tyr Val Ser Thr Arg Met Leu Thr Tyr Ser
145                 150                 155                 160

Ala Asp Ala Lys Ala Thr Ser Leu Ala Tyr Arg Leu Val Asp Glu Asn
                165                 170                 175
Tyr Leu Arg Phe Tyr Gln Asp Ile Ser Ala Ala Ala Glu Ile Ser Ala
            180                 185                 190
Val Leu Glu Glu Ala Gly Phe Asp Asn Ala Glu Val Glu Ala Phe Ile
        195                 200                 205
Arg Thr Asp Tyr Asn Thr Cys Leu Thr Ser Glu Gly Ile Ala Ser Phe
    210                 215                 220

Asn Ala Ala Ala Gly Ser Ile Asn Gln Phe Val Asn Val Leu Leu Gln
```

225 230 235 240

Gln Asn Pro Val Leu Gln Ser Glu Pro Ala Leu Arg Arg His Leu Gln

245 250 255

Pro Leu Tyr Lys Met Leu Leu Asp Glu Ala Glu Ser Lys Ile Ile Lys

260 265 270

Phe Glu Asp Tyr Gly Gln Leu Arg Asp Ala Val Glu Asn Phe Arg Arg

275 280 285

Asn Phe Gln Asp Leu Pro Gln Ser Leu Ile Asp Ile Phe Ala Gly Arg

290 295 300

Tyr Asp Tyr Ser Lys Ile Tyr Val Gly Tyr Lys Tyr Leu Asn Glu Ala

305 310 315 320

Ser Ser Gln Ile Ala Gly Gly Tyr Asn Trp Lys Leu Leu Glu Asn Ala

325 330 335

Leu Glu Asp Phe Tyr Ser Lys Pro Tyr Leu Val Asn Gly Lys Leu Pro

340 345 350

Val Lys Tyr Lys Thr Val Val Asn Lys Lys Met Asn Gln Leu Ala Tyr

355 360 365

Ser Phe Thr Glu Leu Gln Glu Ala Leu Asp Ala Gly Asp Ser Gly Ser

370 375 380

Ser Ile Thr Asp Leu Phe Gly Lys Tyr Ala Glu Leu His Ala Ala Tyr

385 390 395 400

Ala Ala Ala Asp Gly Asn Val Phe Tyr Lys Glu Tyr Asp Arg Lys Ser

405 410 415

Ile Ala Ser Leu Lys Asn Tyr Leu Asp Ala Val Asn Ala Ile Ala Arg

420 425 430

Phe Ile Lys Ile Phe Ala Ala Pro Glu Val Tyr Val Lys Asp Glu Gly

435 440 445

Phe Tyr Gly Ile Val Asp Gly Ala Ala Asp Lys Leu Arg Asp Phe Asp

450 455 460

Leu Leu Tyr Asn Met Val Arg Asn Tyr Ile Thr Lys Lys Pro Tyr Lys

465 470 475 480

Lys Ser Lys Val Ala Leu Thr Phe Asn Ser Ser Ser Phe Gly Arg Gly
485 490 495
Trp Asp Glu Asn Lys Ile Tyr Asp Glu Leu Thr Thr Ile Phe Thr Tyr
500 505 510
Asn Gly Lys Tyr Tyr Leu Gly Val Ile Asn Lys Asn Asp Lys Pro Asp
515 520 525
Leu Ala Ala Ala Val Ser Lys Asp Glu Gly Gly Tyr Lys Arg Met Val
530 535 540

Tyr Lys Thr Phe Asp Ile Val Lys Gln Leu Pro Arg Leu Ser Phe Thr
545 550 555 560
Lys Ala Val Lys Ala His Phe Ala Glu Ser Asp Glu Asp Phe Ile Phe
565 570 575
Asp Gly Pro Lys Phe Ala Lys Pro Leu Arg Val Pro Lys Glu Ile Tyr
580 585 590
Leu Gln Ser Phe Thr Asp Asn Gly Asp Lys Leu Ala Asp Ser Ala Lys
595 600 605

Lys Tyr Thr Lys Ala Tyr Leu Asp Met Ser Gly Asp Tyr Lys Gly Tyr
610 615 620
Tyr Glu Ala Ile Ile Lys Arg Ile Asp Tyr Thr Lys Glu Phe Leu Ser
625 630 635 640
Ala Tyr Lys Ser Thr Ser Ile Tyr Asp Leu Ala Phe Leu Lys Pro Ala
645 650 655
Gly Lys Ala Ala Gly Ser Leu Cys Trp Thr Arg His Ile
660 665

<210> 118

<211> 1236

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 118

Met Ser Arg Ser Ile Phe Ser Pro Phe Thr Asn Leu Tyr Pro Ile Gln

1 5 10 15

Lys Thr Leu Arg Arg Glu Leu Lys Pro Leu Asn Glu Asn Phe Gln His

20 25 30

Asp Pro Ala Leu Ser Ala Leu Arg Asn Ser Glu Ile Pro Gln Arg Asp

35 40 45

Glu Gln Arg Glu Lys Asp Tyr Gln Ala Ile Lys Pro Leu Leu Asp Glu

50 55 60

Phe His Asn Gln Phe Ile Thr Glu Ser Leu His Ser Leu Glu Pro Gln

65 70 75 80

Asp Arg Ser Asp Phe Ile Leu Phe Tyr Gln Thr Tyr Gln Lys Lys Lys

85 90 95

Lys Asn Lys Ala Glu Ile Ser Glu Lys Glu Leu Lys Ser Leu Asp Glu

100 105 110

Glu Phe Glu Ser Arg Thr Lys Ala Leu Arg Asn Ala Ile Gly Thr Ser

115 120 125

Phe Ser Val Thr Ala Glu Leu Arg Lys Ser Asn Pro Asp Tyr Val Ser

130 135 140

Glu Lys Gly Lys Pro Phe Leu Thr Gln Lys Ser Tyr Lys Ile Leu Thr

145 150 155 160

Glu Ala Gly Val Leu Trp Leu Leu Glu Lys Lys Tyr Thr Ser Asp Pro

165 170 175

Glu Lys Leu Ala Leu Ile Arg Arg Phe Gly Asn Phe Phe Thr Tyr Phe

180 185 190

Thr Gly Phe Asn Gln Asn Arg Glu Asn Tyr Tyr Ala Thr Asp Glu Lys

195 200 205

Ser Thr Ala Val Ala Tyr Arg Ala Ile Asn Glu Asn Leu Leu Thr Phe

210 215 220

Ala Asn Asn Cys Glu Leu Phe Glu Lys Leu Ser Val Leu Ser Leu Ser

225 230 235 240

Glu Leu Glu Lys Lys Thr Phe Asn Pro Asp Ser Tyr Ser Glu Tyr Leu

245 250 255

Thr Gln Ser Gly Ile Val Phe Tyr Asn Glu Met Leu Ala Asn Ile Arg
260 265 270
Ser Lys Ala Asn Leu Tyr Thr Gln Glu His Lys Ala Lys Leu Pro Gln
275 280 285
Pro Lys Leu Leu Tyr Lys Gln Ile Trp Ser Pro Arg Gly Asp Thr Ile
290 295 300
Pro Phe Asp Leu Ile Ala Ser Glu Ala Glu Phe Gln Glu Thr Leu His

305 310 315 320
Thr Met Ile Arg Glu Thr Asp Gln Arg Ile Pro Glu Phe Asn Lys Leu
325 330 335
Leu Glu Gln Ile Phe Glu Glu Lys Val Asp Leu Ser Gln Ile Phe Phe
340 345 350
Ser Lys Thr Ser Leu Asn Ile Ile Ser Asn Arg Tyr Phe Ser Ser Trp
355 360 365
His Thr Leu Leu Glu Lys Gly Val Glu Leu Lys Leu Phe Lys Phe Lys

370 375 380
Lys Asn Asp Glu Glu Ser Phe Lys Leu Pro Ala Tyr Leu Ser Leu Ala
385 390 395 400
Glu Leu Lys Glu Leu Leu Glu Ser Ala Pro Phe Gln Met Ala Glu Lys
405 410 415
Ala Asp Ala Asp Glu Glu Lys His His Gln Ala Ser Leu Phe Lys Leu
420 425 430
Gln Arg Glu Asn Leu His Leu Glu Lys Ser His Ser Asn Trp Glu Leu

435 440 445
Leu Leu Lys Ser Met Lys Ser Asp Phe Glu Ser Phe Trp Thr Trp Glu
450 455 460
Gly Glu Phe Trp Ser Tyr Thr Leu Ala Lys Lys Ala Leu Gln Ser Leu
465 470 475 480
Ser Ala Leu Glu Ser Thr Asn Gln Glu His Lys Asn Leu Ile Lys Met
485 490 495
Leu Leu Asp Asn Ala Leu Tyr Ala Tyr Arg Met Leu Lys Trp Phe Lys

500 505 510

Val Asp Thr Ser Lys Leu Gly Phe Val Pro Glu Gly Glu Phe Tyr Pro

515 520 525

Ser Leu Asp Gln Leu Leu Gln Asp Tyr Pro Leu Pro Lys Trp Tyr Asp

530 535 540

Met Ile Arg Asn Tyr Leu Thr Arg Lys Thr Tyr Ser Gln Ala Lys Leu

545 550 555 560

Lys Leu Asn Phe Asp Cys Ser Thr Leu Leu Asn Gly Arg Asp Lys Asn

565 570 575

Lys Glu Ile Gln Asn Leu Ser Val Ile Leu Arg Lys Asp Gly Lys Phe

580 585 590

Tyr Leu Ala Ile Met Lys Lys Asp Gln Asn Lys Phe Phe Glu Asn Ser

595 600 605

Ala Leu Tyr Glu Gly Asn Leu Gly Thr Met Glu Lys Met Asp Tyr Lys

610 615 620

Leu Leu Pro Trp Ala Asn Lys Met Leu Pro Lys Cys Leu Met Pro Gly

625 630 635 640

Ser Asp Lys Lys Lys Tyr Gly Ala Ser Asp Gln Val Leu Glu Leu Tyr

645 650 655

Ala Lys Gly Ser Phe Lys Lys Ser Glu Lys Ser Phe Asn Leu Ala Asp

660 665 670

Leu His Thr Leu Ile Asp Phe Tyr Lys Leu Ala Leu Pro Lys Tyr Glu

675 680 685

Asp Trp Lys Val Phe Asn Phe Gln Phe Gln Ala Thr Glu Asn Tyr Gln

690 695 700

Asp Ile Ser Gln Phe Tyr Arg Glu Val Glu Gln Gln Gly Tyr Leu Leu

705 710 715 720

Asn Trp Arg Lys Val Asn Glu Lys Leu Ile Lys Gln Gly Ile Lys Asp

725 730 735

Trp Ser Leu Phe Leu Phe Gln Ile Ser Ser Lys Asp Phe Glu Gly Lys

740 745 750

Ser Lys Thr Pro Asp Leu Gln Thr Leu Tyr Trp Gln Gln Leu Phe Glu

755 760 765

Phe Ser Thr Asn Val Lys Leu Asn Gly Glu Ala Glu Ile Phe Phe Arg

770 775 780

Pro Trp Ser Met Lys Lys Glu Lys Lys Lys Leu Lys Val Asp Asn Tyr

785 790 795 800

Asp Val Phe Lys His Lys Arg Tyr Thr Glu Asp Lys Ile Leu Phe His

805 810 815

Val Pro Ile Thr Leu Trp Phe Gly Asn Asn Glu Val Ser Pro Ser Ala

820 825 830

Pro Ser Lys Phe Asn Gln Lys Leu Asn Gln Glu Leu Ile Ile Pro His

835 840 845

Phe Asp Asp Leu His Val Ile Gly Val Asp Arg Trp Glu Lys His Leu

850 855 860

Ala Phe Tyr Ser Val Val Ser Val Lys Thr Gly Lys Ile Val Lys Gln

865 870 875 880

Gly Thr Leu Asn Leu Leu Asn Gly Thr Asp Tyr Glu Ala Lys Leu Ser

885 890 895

Gln Lys Ala Glu Asn Arg Leu His Ala Arg Gln Asn Arg Asp Thr Ile

900 905 910

Glu Lys Ile Ala Asp Leu Lys Asn Gly Tyr Ile Ser Gln Val Val Asn

915 920 925

Lys Leu Val Glu Leu Val Leu Glu Tyr Asn Ala Val Ile Val Phe Glu

930 935 940

Asp Leu Asn Ala Gly Phe Lys Arg Gly Arg Gln Lys Ile Glu Gln Ser

945 950 955 960

Val Tyr Gln Lys Leu Glu Leu Ala Leu Ala Lys Lys Leu Asn Phe Ile

965 970 975

Val Lys Lys Glu Lys Ala Val Gly Glu Pro Trp Ser Val Thr Ser Ala

980 985 990

Tyr Gln Leu Ala Pro Gln Ile Asn Thr Phe Trp Asp Ile Lys Trp Lys

995 1000 1005

Gln Arg Gly Ile Met Leu Tyr Thr Arg Ala Asn Tyr Thr Ser Val

1010 1015 1020

Thr Asp Pro Leu Thr Gly Trp Arg Lys Gln Tyr Tyr Phe Lys Lys

1025 1030 1035

Gly Ser Ser Glu Glu Met Lys Ala Gln Phe Phe Lys Ser Phe Lys

1040 1045 1050

Asn Leu Thr Arg Asp Ala Gly Gln Glu Ala Tyr Ile Phe Asp Asp

1055 1060 1065

Gly Thr Trp Leu Leu Tyr Ser Asn Val Glu Arg Arg Arg Gly Lys

1070 1075 1080

Arg Gly Asp His Arg Glu Arg Thr Gln Ile Lys Tyr Asp Pro Ser

1085 1090 1095

Leu Glu Leu Asp Thr Leu Phe Ser Lys Tyr Gln Ile Glu Lys Ser

1100 1105 1110

Asp Ser Leu Phe Asp Gln Leu Lys Asn Arg Glu Leu Pro Gln Thr

1115 1120 1125

Phe Trp Thr Ser Phe Phe Arg Ile Ile Asp Leu Ile Met Gln Ile

1130 1135 1140

Arg Asn Thr Asp Asp Glu Gly Arg Asp Ile Ile Leu Ser Pro Ile

1145 1150 1155

Gly Asn Pro Gln Glu Arg Phe Asp Ser Arg Lys Arg Tyr Asn Gln

1160 1165 1170

Leu Pro Arg Asp Glu Lys Gly Gly Ile Ile Glu Glu Ser Ala Phe

1175 1180 1185

Glu Tyr Pro Thr Ser Trp Asp Ala Asn Gly Ala Tyr Asn Ile Ala

1190 1195 1200

Arg Lys Gly Val Met Met Leu Glu Arg Ile Lys Glu Asn Pro Glu

1205 1210 1215

Lys Pro Asp Leu Leu Ile Arg Asp Ala Glu Trp Asp Lys Lys Ile

1220 1225 1230

Thr Arg Lys

1235

<210> 119

<211> 1333

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 119

Met Lys Asn Phe Gln Asp Phe Thr Asn Leu Tyr Glu Leu Ser Lys Thr

1 5 10 15

Leu Arg Phe Glu Leu Lys Pro Ile Trp Gly Thr Lys Lys Leu Ile Glu

20 25 30

Glu Lys Asn Ile Leu Lys Leu Asp Lys Lys Lys Arg Glu Asn Tyr Glu

35 40 45

Lys Val Lys Pro Tyr Phe Asn Lys Ile His Gln Glu Phe Ile Asn Phe

50 55 60

Ala Leu Arg Asn Pro Asn Phe Asp Phe Ser Gln Phe Glu Glu Lys Tyr

65 70 75 80

Leu Asn Trp Leu Lys Asp Lys Lys Asn Lys Asp Leu Leu Lys Glu Lys

85 90 95

Glu Ser Ile Asp Lys Ile Phe Leu Glu Lys Ile Trp Lys Leu Phe Glu

100 105 110

Asn Ser Val Lys Asp Phe Leu Lys Glu Asn Gly Phe Glu Ser Ile Val

115 120 125

Lys Ser Glu Asp Gln Asn Leu Lys Phe Phe Arg Arg Lys Glu Ile Phe

130 135 140

Glu Val Leu Gln Glu Lys Tyr Gly Ser Glu Leu Glu Thr Gln Met Val

145 150 155 160

Asn Lys Asp Trp Glu Ile Lys Ser Ile Phe Asn Gly Trp Glu Lys Trp

165 170 175

Leu Trp Tyr Phe Asp Lys Phe Phe Asn Thr Arg Asp Asn Phe Tyr Lys

180 185 190

Thr Asp Trp Thr Ser Thr Ala Ile Ala Thr Arg Ile Ile Lys Asp Asn

195 200 205

Leu Lys Ile Phe Leu Glu Asn Thr Ile Ile Phe Glu Lys Val Lys Asn

210 215 220

Lys Lys Ile Asp Phe Ser Glu Val Glu Lys Asn Phe Ser Val Ser Ile

225 230 235 240

Asp Thr Phe Phe Glu Ile Asn Asn Phe Asn Asn Cys Phe Leu Gln Asp

245 250 255

Trp Ile Asp Phe Tyr Asn Lys Val Ile Trp Gly Glu Thr Leu Glu Asn

260 265 270

Trp Glu Lys Leu Lys Trp Leu Asn Glu Ile Ile Asn Lys Tyr Arg Gln

275 280 285

Asp Thr Gly Glu Lys Ile Pro Tyr Phe Lys Lys Leu Gln Lys Gln Ile

290 295 300

Leu Ser Glu Lys Asp Trp Val Phe Ile Asp Lys Ile Glu Asp Asp Gly

305 310 315 320

Gly Phe Tyr Glu Val Leu Lys Asn Phe Tyr Lys Asn Ala Ala Glu Lys

325 330 335

Glu Trp Phe Leu Lys Asn Ile Phe Glu Asn Phe Tyr Thr Ile Ser Asp

340 345 350

Lys Asn Leu Glu Lys Ile Tyr Phe Asn Lys Ile Ala Phe Asn Thr Ile

355 360 365

Ser His Lys Phe Trp Ser Ala Leu Glu Phe Glu Arg Ile Leu Tyr Glu

370 375 380

Glu Met Lys Lys Glu Lys Ala Asp Trp Ile Lys Phe Glu Lys Lys Glu

385 390 395 400

Asn Lys Tyr Lys Phe Pro Asp Phe Ile Gln Ile Ile Phe Ile Lys Arg

405 410 415

Ser Leu Glu Asn Tyr Asp Ser Glu Asn Leu Phe Trp Lys Glu Arg Tyr

420 425 430

Tyr Lys Ser Glu Glu Asn Val Asp Trp Phe Leu Glu Lys Asn Asn Asn
435 440 445
Asn Ile Trp Glu Gln Phe Cys Lys Ile Leu Asn Phe Glu Phe Leu Asn

450 455 460
Ile Leu Lys Arg Arg Ile Ile Asp Glu Ala Trp Glu Glu Tyr Glu Val
465 470 475 480
Trp Phe Glu Ile Ser Lys Asn Ile Leu Trp Glu Lys Leu Glu Asn Phe
485 490 495
Glu Leu Asn Gln Glu Asn Lys Trp Ile Ile Lys Asp Phe Ala Asp Tyr
500 505 510
Ser Leu Ala Leu Tyr Ser Phe Trp Lys Tyr Phe Ala Val Glu Lys Trp

515 520 525
Arg Asn Trp Asp Leu Asn Ile Asp Ile Ser Asp Asp Phe Tyr Gly Trp
530 535 540
Glu Asp Trp Tyr Ile Glu Lys Phe Tyr Asn Thr Gly Tyr Asp Glu Ile
545 550 555 560
Val Lys Pro Tyr Asn Leu Met Arg Asn Tyr Ile Ser Lys Lys Pro Trp
565 570 575
Glu Asp Ser Lys Lys Trp Lys Ile Asn Phe Glu Thr Ser Ser Leu Leu

580 585 590
Ser Trp Trp Asp Lys Asn Leu Glu Ser Asn Trp Ser Tyr Ile Phe Gln
595 600 605
Lys Trp Asn Lys Tyr Tyr Ile Trp Ile Ile Asn Trp Ser Lys Pro Ala
610 615 620
Lys Glu Val Leu Glu Lys Leu Tyr Ser Trp Asn Gly Glu Lys Ile Lys
625 630 635 640
Arg Phe Ile Tyr Asp Phe Gln Lys Pro Asp Asn Lys Asn Thr Pro Arg

645 650 655
Met Phe Ile Arg Ser Lys Lys Asp Ser Phe Ser Pro Ala Val Gly Lys
660 665 670
Tyr Asn Leu Pro Val Glu Asp Ile Leu Glu Ile Tyr Asp Asn Trp Leu

675 680 685

Phe Lys Thr Glu Asn Lys Asp Asn Ser Asn Tyr Lys Glu Ser Leu Ser

690 695 700

Lys Leu Ile Asp Tyr Phe Lys Leu Gly Phe Ser Lys His Glu Ser Phe

705 710 715 720

Lys His Phe Asn Phe Val Trp Lys Asp Ser Lys Glu Tyr Glu Asn Ile

725 730 735

Ala Asp Phe Tyr Arg Asp Val Glu Lys Ser Cys Tyr Gln Ile Thr Ser

740 745 750

Glu Phe Leu Asp Phe Glu Glu Leu Lys Lys Leu Thr Phe Lys Lys His

755 760 765

Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Glu Leu Asp Glu Ser

770 775 780

Leu Gln Lys Asn Trp Tyr Asn Phe Arg Asp Glu Trp Gln Lys Asn Ile

785 790 795 800

His Thr Lys Tyr Phe Glu Ala Leu Phe Leu Glu Glu Asn Ile Leu Arg

805 810 815

Lys Ser Trp Ala Val Phe Lys Leu Ser Trp Gly Trp Glu Val Phe Phe

820 825 830

Arg Lys Glu Ser Ile Lys Ala Glu Lys Glu Lys Arg Lys Asn Ile Glu

835 840 845

Val Thr Lys Asn Arg Arg Tyr Thr Glu Glu Lys Tyr Phe Leu His Phe

850 855 860

Pro Ile Gln Val Asn Phe Lys Asn Glu Ile Ser Trp Asn Phe Asn Gln

865 870 875 880

Glu Ile Asn Lys Phe Leu Ala Asn Asn Pro Asp Ile Asn Val Ile Trp

885 890 895

Ile Asp Arg Trp Glu Lys His Leu Ala Tyr Phe Ser Val Ile Asn Gln

900 905 910

Lys Trp Glu Ile Leu Glu Ser Trp Ser Phe Asn Lys Ile Glu Asn Tyr

915 920 925

Asn Lys Asn Trp Glu Lys Leu Leu Phe Pro Glu Arg Glu Ile Lys Glu
930 935 940
Ile His Lys Asp Trp Ser Leu Ile Asp Leu Glu Leu Val Glu Thr Trp
945 950 955 960
Arg Lys Val Asp Tyr Val Asp Tyr Lys Leu Leu Leu Glu Tyr Lys Glu

965 970 975
Arg Lys Arg Leu Leu Gln Arg Gln Ser Trp Lys Glu Val Glu Gln Ile
980 985 990
Lys Asp Leu Lys Lys Trp Tyr Ile Ser Ala Leu Val Arg Lys Ile Ala
995 1000 1005
Asp Leu Ile Ile Lys His Asn Ala Ile Val Ile Phe Glu Asp Leu
1010 1015 1020
Asn Phe Arg Phe Lys Gln Ile Arg Gly Trp Ile Glu Lys Ser Ile

1025 1030 1035
Tyr Gln Gln Leu Glu Lys Ala Leu Ile Asp Lys Leu Asn Phe Leu
1040 1045 1050
Val Asn Lys Asn Glu Ile Asn Leu Glu Lys Ala Gly Ser Ile Leu
1055 1060 1065
Lys Ala Tyr Gln Leu Thr Val Pro Val Asp Ser Leu Lys Glu Ile
1070 1075 1080
Trp Lys Gln Thr Trp Val Ile Phe Tyr Thr Glu Ala Ala Tyr Thr

1085 1090 1095
Ser Lys Ile Asp Pro Ile Lys Trp Trp Arg Pro Asn Leu Tyr Leu
1100 1105 1110
Lys Lys Gln Asn Ala Glu Ile Asn Lys Glu Asn Ile Leu Lys Phe
1115 1120 1125
Asp Asn Ile Ile Phe Asn Ser Lys Glu Asn Arg Phe Glu Phe Thr
1130 1135 1140
Tyr Asp Leu Lys Lys Phe Phe Trp Lys Asp Ser Lys Phe Pro Ala

1145 1150 1155
Lys Thr Val Asn Thr Val Cys Ser Cys Val Glu Arg Phe Lys Trp

1160 1165 1170

Asn Arg Asn Leu Asn Asn Asn Lys Trp Gly Tyr Ile His Tyr Glu

1175 1180 1185

Asn Leu Thr Asp Trp Lys Leu Ala Asn Lys Glu Gln Lys Glu Asp

1190 1195 1200

Glu Phe Ser Asn Phe Lys Glu Leu Phe Glu Lys Tyr Phe Ile Asp

1205 1210 1215

Ile Asn Trp Asn Ile Leu Glu Gln Ile Lys Asn Leu Asp Thr Lys

1220 1225 1230

Asn Asn Glu Lys Phe Phe Ser Ser Phe Ile Asp Leu Phe Thr Leu

1235 1240 1245

Val Cys Gln Ile Arg Asn Thr Asn Gln Asn Ala Lys Trp Asp Glu

1250 1255 1260

Asn Asp Phe Ile Leu Ser Pro Val Glu Pro Phe Phe Asp Ser Arg

1265 1270 1275

Lys Ser Gln Asn Phe Trp Lys Ser Leu Pro Lys Asn Trp Asp Glu

1280 1285 1290

Asn Trp Ala Phe Asn Ile Ala Arg Lys Gly Leu Ile Ile Leu Asn

1295 1300 1305

Arg Ile Ser Glu Asn Pro Glu Lys Pro Asp Leu Leu Ile Phe Asn

1310 1315 1320

Ala Asp Trp Asp Asn Phe Ala Arg Asn Ile

1325 1330

<210> 120

<211> 926

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 120

Arg Pro Gly Ala Ser Ala Ala Leu Ser Leu Thr Pro Leu Lys Thr Leu

1 5 10 15

Phe Ser Glu Asn Phe Ser Ser Phe Met Cys Gly Asn Trp Gln Ile Ile
20 25 30
Asn Asp Ser Leu Lys Thr Tyr Tyr Asn Glu Asn Ile Lys Ser Lys Gly
35 40 45

Lys Ala Lys Glu Glu Lys Val Lys Lys Ala Ile Lys Ala Ile Glu Tyr
50 55 60
Lys Ser Leu Ala Asp Ile Asn Gln Leu Val Glu Arg Tyr Asn Asn Asp
65 70 75 80
Glu Leu Asn Arg Lys Ala Glu Glu Tyr Ile Ser Ala Ile Asn Glu Lys
85 90 95
Ile Lys Asp Leu Asp Val Asn Glu Ile Glu Tyr Asp Glu Lys Ile Asn
100 105 110

Leu Ile Glu Asn Glu Thr Lys Ser Glu Glu Ile Lys Ser Lys Leu Asp
115 120 125
Ser Ile Met Glu Ile Met His Trp Thr Lys Met Phe Ile Ile Glu Glu
130 135 140
Glu Ile Glu Lys Asp Val Asn Phe Tyr Asn Glu Ile Glu Glu Ile Tyr
145 150 155 160
Asp Glu Leu Gln Pro Leu Val Thr Ile Tyr Asn Arg Ile Arg Asn Tyr
165 170 175

Val Thr Gln Lys Pro Tyr Ser Glu Glu Lys Ile Lys Leu Asn Phe Gly
180 185 190
Ile Pro Thr Leu Ala Asn Gly Trp Ser Lys Thr Lys Glu Tyr Asp Asn
195 200 205
Asn Ala Ile Ile Met Ile Arg Asp Gly Lys Tyr Tyr Leu Gly Ile Phe
210 215 220
Asn Ala Lys Asn Lys Pro Asp Lys Lys Ile Met Glu Gly His Gln Ser
225 230 235 240

Glu Glu Asn Gly Asp Tyr Lys Lys Met Ile Tyr Arg Leu Leu Pro Gly
245 250 255
Pro Asn Lys Met Leu Pro Lys Val Phe Met Ser Lys Thr Gly Ile Ala

260 265 270

Glu Tyr Lys Pro Ser Gln Tyr Ile Leu Glu Cys Tyr Glu Gln Asn Lys

275 280 285

His Ile Lys Ser Asp Lys Asn Phe Asp Ile Lys Phe Cys Arg Asp Leu

290 295 300

Ile Asp Phe Phe Lys Thr Ser Ile Asn Arg His Pro Glu Trp Ser Lys

305 310 315 320

Phe Asn Phe Lys Phe Ser Glu Thr Ser Glu Tyr Glu Asp Ile Ser Thr

325 330 335

Phe Tyr Arg Glu Val Glu Lys Gln Gly Tyr Lys Ile Glu Trp Thr Tyr

340 345 350

Ile Ser Glu Lys Glu Ile Lys Glu Leu Asp Glu Asn Gly Gln Leu Tyr

355 360 365

Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Glu Lys Ser Lys Gly Lys

370 375 380

Glu Asn Leu His Thr Met Tyr Leu Lys Asn Leu Phe Ser Glu Glu Asn

385 390 395 400

Leu Lys Asn Ile Val Leu Lys Leu Asn Gly Glu Ala Glu Val Phe Phe

405 410 415

Arg Lys Ser Ser Ile Lys Lys Pro Ile Ile His Lys Lys Gly Ser Val

420 425 430

Leu Val Asn Lys Thr Tyr Asn Glu Asn Gly Glu Arg Lys Ser Ile Pro

435 440 445

Glu Glu Gln Tyr Thr Glu Ile Tyr Lys Tyr Leu Asn Ser Ile Gly Thr

450 455 460

Asn Glu Leu Ser Glu Lys Ser Lys Lys Leu Met Glu Glu Gly Lys Val

465 470 475 480

Glu Tyr Tyr Lys Ala Asn Tyr Asp Ile Val Lys Asp Tyr Arg Tyr Ser

485 490 495

Val Asp Lys Phe Phe Ile His Leu Pro Met Thr Ile Asn Phe Lys Ala

500 505 510

Ala Gly Phe Ser Pro Ile Asn Asn Ile Ala Leu Lys Asn Ile Ala Leu
515 520 525

Lys Asp Asp Met His Ile Ile Gly Ile Asp Arg Gly Glu Arg Asn Leu
530 535 540

Ile Tyr Val Ser Val Ile Asp Thr Lys Gly Asn Ile Val Glu Gln Arg
545 550 555 560

Asn Phe Asn Ile Val Asn Gly Ile Asp Tyr Lys Glu Lys Leu Lys Gln
565 570 575

Lys Glu Leu Asp Arg Asp Asn Ala Arg Lys Asn Trp Lys Glu Ile Gly
580 585 590

Lys Ile Lys Asp Leu Lys Glu Gly Tyr Leu Ser Leu Val Val His Glu
595 600 605

Ile Ala Lys Leu Val Val Lys Tyr Asn Ala Ile Ile Thr Met Glu Asp
610 615 620

Leu Asn Gln Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Arg Gln Val
625 630 635 640

Tyr Gln Lys Phe Glu Thr Met Leu Ile Asn Lys Leu Asn Tyr Leu Val
645 650 655

Asp Lys Asp Leu Ala Val Asp Gln Glu Gly Gly Leu Leu Arg Gly Tyr
660 665 670

Gln Leu Thr Tyr Ile Pro Glu Ser Leu Lys Val Leu Gly Arg Gln Cys
675 680 685

Gly Tyr Ile Phe Tyr Val Pro Ala Ala Tyr Thr Ser Lys Ile Asp Pro
690 695 700

Thr Thr Gly Phe Val Ala Ile Phe Asn Tyr Lys Gly Met Thr Asp Lys
705 710 715 720

Asp Phe Val Thr Ser Phe Asp Ser Ile Lys Tyr Asp Asp Glu Arg Gly
725 730 735

Leu Phe Ala Phe Glu Phe Asp Tyr Glu Asn Phe Val Thr His Lys Val
740 745 750

Glu Met Ala Arg Asn Lys Trp Thr Val Tyr Thr Tyr Gly Glu Arg Ile

755 760 765

Lys Arg Lys Phe Lys Asn Gly Ser Trp Asp Thr Ala Glu Lys Val Asp

770 775 780

Leu Thr Tyr Gln Met Arg Ser Ile Leu Glu Lys Tyr Glu Ile Glu Tyr

785 790 795 800

Asn Lys Gly Gln Asp Ile Leu Glu Gln Ile Glu Glu Leu Asp Glu Lys

805 810 815

Ala Gln Asn Gly Ile Cys Lys Glu Ile Lys Tyr Leu Val Lys Asp Ile

820 825 830

Val Gln Met Arg Asn Ser Leu Pro Asp Asn Ala Ala Glu Asp Tyr Asp

835 840 845

Ala Ile Ile Ser Pro Val Ile Asn Asn Asn Gly Glu Phe Phe Asp Ser

850 855 860

Thr Arg Gly Asp Glu Asp Lys Pro Leu Asp Ala Asp Ala Asn Gly Ala

865 870 875 880

Tyr Cys Ile Ala Leu Lys Gly Leu Tyr Glu Val Met Gln Ile Lys Lys

885 890 895

Asn Trp Asn Glu Glu Thr Glu Phe Pro Arg Lys Glu Leu Lys Ile Arg

900 905 910

His Gln Asp Trp Leu Asp Phe Ile Gln Asn Lys Arg Tyr Leu

915 920 925

<210> 121

<211> 1466

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 121

Met Gln Cys Gly Ser Leu Arg His Asn Ser Lys Ser Leu Asp Ser Ala

1 5 10 15

Leu Ala Tyr Pro Ala Arg Leu Thr Thr Gly Gly Asn Glu Gly Lys Thr

20 25 30

Ser Glu Ala His Ile Glu Asn Asp Ser Leu Pro Glu Ile Thr Arg Arg

35 40 45

Pro Ser Arg Leu Ala Arg Asp Phe Ala Pro Ser Asn Pro Phe Pro Phe

50 55 60

Met Lys Arg Ile Tyr Gln Gly Gln Ile Thr Gly Met Gln Phe His Gly

65 70 75 80

Ala Ala Gly Glu Gln Ala Val Pro Ala Asn Gln Asn Trp Glu Gln Ala

85 90 95

Leu Trp Asp His His Gly Leu Phe His Asp Ala Val Asn Tyr Tyr Leu

100 105 110

Val Cys Leu Leu Ala Leu Ala Arg Pro Gly Asn Pro Val Tyr Ala Ile

115 120 125

Arg Glu Lys Leu Asp Ala His Asn Gly Ala Glu Pro Asp Glu Leu Met

130 135 140

Val Trp Arg Thr Phe Arg Arg Arg Gly Cys Asn Arg Pro Gly Leu Arg

145 150 155 160

Asp Ser Val Ala Lys Tyr Leu Thr Pro Gly Asn Asp Glu Pro Thr Thr

165 170 175

Glu Glu Cys Phe Ala Ala Val Leu Ala Gly Asn Pro Leu Gly Ala Thr

180 185 190

Glu Glu Gly Arg Ala Ile Leu Asn Glu Gly Leu Ala Gln Leu Leu Gly

195 200 205

Lys Cys Thr Gly Glu Ser Gly Cys Arg Asn Ser Ala Lys Glu Tyr Leu

210 215 220

Pro Arg Phe Thr Lys Pro Asp Phe Lys Gly Asn Phe Glu Glu Asp Thr

225 230 235 240

Ala Arg Leu Asn Arg Ala Glu Ala Ser Lys Arg Leu Pro Phe Tyr Leu

245 250 255

His Asp Pro Ala Thr Thr Pro Asn Ser Pro Ala Leu Asp Glu Phe Gly

260 265 270

Val Leu Ser Ile Ala Leu Pro Asn Pro Lys Arg Ala Glu Leu Thr Gly

275 280 285

Ala Glu Ala Arg Asp Lys Leu Leu Glu Phe Ser Arg Glu Trp Ser Ala

290 295 300

Arg Leu Pro Asp Gly Ser Ala Asp Trp Arg Arg Leu Glu Ala Lys Ile

305 310 315 320

Thr Ala Leu Gly Asp Ser Leu Ala Ile Pro Gly Tyr Thr Ser Gly Ser

325 330 335

Ala Lys Gly Glu Asn Arg Phe Gln Leu Tyr Ala Met Phe Leu Phe Cys

340 345 350

Phe Val Glu Lys Ser Asp Phe Thr Leu Gly Leu Leu Arg Gln Thr Thr

355 360 365

Arg Arg Pro Val Glu Gly Glu Glu Pro Pro Pro Arg Ser Asn His Ser

370 375 380

Ala Thr Ala Gly Asp Pro Ile Arg Ile Ala Arg Gly Gly Arg Gly Tyr

385 390 395 400

Val Phe Arg Ala Phe Thr Ser Leu Lys Gln Trp Gly Gly Asp Thr Gly

405 410 415

Gly Asp Leu Lys Trp Pro Lys Phe Asp Met Ala Ala Phe Cys Glu Ala

420 425 430

Leu Lys Ala Leu His Gln Val Glu Ala Lys Ala Lys Gln Arg Ala Glu

435 440 445

Glu Arg Ser Lys Lys Gln Ala Leu Leu Asp Tyr Gln Arg Gly Arg Ile

450 455 460

Arg Arg Phe Lys Pro Thr Ala Asn Ser Glu Asp Ala Thr Pro Pro Pro

465 470 475 480

Val Leu Ala Gly Asp Pro Arg Ile Ser Arg Leu Glu Gln Leu Leu Asn

485 490 495

Thr Asp Leu Gln Asp Glu Tyr Glu Met Ser Glu Gly Val Ala Val Ala

500 505 510

Tyr Gly Leu His Pro Arg Thr Ile Arg Gly Phe Arg Glu Ile Arg Lys

515 520 525

Arg Trp Ile Ser Ala Val Gly Asn Ala Pro Phe Ser Glu Ala Ala Arg
530 535 540
Ala Thr Leu Ile Ala Cys Val Arg Ser Phe Gln Ser Glu Asn Pro Gly
545 550 555 560
Thr Val Gly Ser Ala Arg Leu Phe Glu Ala Leu Ala Glu Glu Ser Asn
565 570 575
Trp Ile Ile Trp Arg Glu Pro Ser Ala Ala Glu Gln Gln Ser Trp Arg

580 585 590
Glu Asn Ala Asp Leu Pro Glu Ser Ala Glu Phe Ala Leu Asp Pro Leu
595 600 605
Gln Ala Leu Thr Asp Glu Arg Glu Leu Lys Asp Glu Ile Glu Arg Leu
610 615 620
Ser Gly Pro Ile Arg Phe Thr Pro Ala Asp Ala Glu His Ser Arg Arg
625 630 635 640
Gln Phe Tyr Phe Ser Asp Val Ser Gln Ile Asp Lys Arg Asn Arg Phe

645 650 655
Arg Pro Arg Leu Asn Glu Val Glu Val Glu Leu Ala Val Arg Pro Asn
660 665 670
Gly His Trp Thr Asn Val Trp Val Thr Leu Gln Tyr Ser Ala Pro Arg
675 680 685
Leu Leu Arg Asp Gln Leu Pro Thr Ala Asp Glu Ala Gly Gly Gly Trp
690 695 700
Gln Gln Ala Met Met Ala Ala Leu Asn Leu Arg Ala Pro Leu Lys Lys

705 710 715 720
Gly Gly Glu Ala Val Ser Phe Ala Asp Cys Ala Ala Leu Ser Leu Met
725 730 735
Pro Asp Ile Ser Pro Asp Gly Glu Lys Arg Leu Leu Leu Asn Phe Pro
740 745 750
Val Glu Leu Asp Gly Glu Ala Ile Ala Asn Gln Leu Gly Arg Ser Lys
755 760 765
Arg Trp Glu Thr Leu Gln Phe Gly Gly Ala Asp Asp Glu Ser Tyr Trp

770 775 780

Leu Arg Trp Pro Lys Thr Trp Ile Asp Glu Thr Lys Val Arg Arg Lys

785 790 795 800

Ala Ala Pro Pro Lys Trp Trp Leu Ser Lys Glu Pro Phe Ser Val Leu

805 810 815

Gly Val Asp Leu Gly Gln Arg Asp Ala Ala Ala Cys Ala Leu Val Gln

820 825 830

Val Ser Pro Gly Asn Cys Pro Thr Gly Val Cys Arg His Val Gly Ser

835 840 845

Ala Asp Gly Val Asp Trp Trp Ala Thr Val Arg Ser Met Asn Met Leu

850 855 860

Arg Leu Pro Gly Glu Asn Ala Lys Val Met Arg Asp Gly Arg Phe Gln

865 870 875 880

Glu Glu Leu Ser Gly Ser Arg Gly Arg Ser Ala Ser Ile Asp Glu Leu

885 890 895

Lys Glu Ala Gly Asp Ile Cys Ala Arg Leu Gly Phe Val Ala Asp Thr

900 905 910

Ile Leu Gly Ala Asn Gly Arg Ala Leu Ser Phe Pro Glu Leu Asn Asp

915 920 925

Arg Leu Leu Phe Ser Leu Arg Ser Ala Gln Ser Arg Leu Ala Arg Leu

930 935 940

Gln Ser Trp Ser Cys Val Ala His Ala Asp Val Pro Pro Ala Arg Arg

945 950 955 960

Glu Gly Ile Leu Arg Asp Ile Ser Glu Ala Lys Asp Asp Pro Leu Gly

965 970 975

Leu Lys Pro Leu Ala Thr Ala Gly Asn Leu Glu Ala Ile Ala Ser Thr

980 985 990

Leu Arg Glu Val Ile Leu Gln Glu Arg Thr Ser Ile Ser Ala Gln Leu

995 1000 1005

Val Arg Val Ala Asp Arg Ile Leu Pro Leu Arg Gly Arg Arg Trp

1010 1015 1020

Glu Trp Val Ala Arg Pro Glu Ser Pro Ser Asn His Met Leu Arg

1025 1030 1035

Ala Thr Ala Pro Asp Thr Asp Pro Arg Arg Lys Leu Val Ala Gly

1040 1045 1050

Gln Arg Gly Leu Ser Leu Ala Arg Val Glu Gln Leu Glu Ser Leu

1055 1060 1065

Arg Gln Arg Cys Gln Ser Leu Asn Arg Ala Leu Met Gln Val Pro

1070 1075 1080

Gly Thr Pro Ser Lys Leu Gly Arg Arg Ser Arg Gly Val Glu Leu

1085 1090 1095

Pro Asp Pro Cys Pro Asp Leu Leu Asp Arg Leu Asp Ala Leu Lys

1100 1105 1110

Glu Gln Arg Val Asn Gln Thr Ala His Leu Ile Leu Ala Gln Ala

1115 1120 1125

Leu Gly Val Arg Leu Arg Ile His Gln Val Ser Gly Pro Gln Arg

1130 1135 1140

Thr Arg Ser Asp Ser His Gly Glu Tyr Glu Arg Ile Pro Gly Arg

1145 1150 1155

Glu Pro Val Asp Phe Leu Val Leu Glu Asn Leu Asp Arg Tyr Leu

1160 1165 1170

Ala Ser Gln Gly Arg Ser Arg Ser Glu Asn Ser Arg Leu Met Lys

1175 1180 1185

Trp Cys His Arg Ala Ile Leu Leu Lys Leu Lys Gln Leu Cys Glu

1190 1195 1200

Pro Tyr Gly Leu Arg Val Leu Glu Thr Pro Ala Ala Tyr Ser Ser

1205 1210 1215

Lys Phe Ser Ser Arg Asp Gly Thr Ala Gly Phe Arg Ala Val Glu

1220 1225 1230

Val Thr Pro Asp Asp Leu Gly Ser His Arg Trp Arg Lys His Ser

1235 1240 1245

Glu Arg Leu Ala Asp Pro Gly Ala Ser Leu Ser Arg Asp Glu Arg

1250 1255 1260

Glu Glu Ser Thr Arg Leu Met Ala Phe Ala Glu Arg Leu Lys Ala

1265 1270 1275

Leu Asn Gln Asp Leu Ile Ala Arg Gln Glu Ala Ala Arg Ser Ser

1280 1285 1290

Asn Gln Pro Phe Arg Pro Lys Trp Arg Thr Leu Leu Ala Pro Gln

1295 1300 1305

Gln Leu Gly Pro Ile Phe Val Pro Ala Val Gly Lys Pro Leu Gln

1310 1315 1320

Ala Asp Ile Asn Ala Ala Ile Asn Ile Ala Leu Arg Ala Ile Ala

1325 1330 1335

Ser Pro Asp Val Asp Asp Ile His Leu Arg Ile Arg Ala Ala Arg

1340 1345 1350

Ser Gly Asp Lys Phe Val Val Arg Ala Glu Asn Thr Arg Glu Arg

1355 1360 1365

Ala Arg Trp Gly Ser Ala Glu Ala Glu Ile Gly Leu Pro Thr Gly

1370 1375 1380

Ala Gly Ala Lys Glu Ile Glu Glu Arg Arg Ser Leu Leu Thr Glu

1385 1390 1395

Ala Arg Val Asn Phe Phe Phe Asp Pro Ala Ser Val Ala Ala Phe

1400 1405 1410

Asp His Gly Lys Val Arg Asp Ala Lys Leu Ala Val Thr Ser Gly

1415 1420 1425

Arg Gly Leu Trp Gly Thr Leu Arg Arg Glu Glu Trp Ala Ile Val

1430 1435 1440

Gly Lys Ile Asn Asn Asp Arg Leu Ala Ala His Gly Leu Gly Arg

1445 1450 1455

Pro Phe Ala Glu Arg Val Asp Leu

1460 1465

<210> 122

<211> 1464

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 122

Met Ser Gln Arg Asp Pro Leu Pro Ser Pro Thr Pro Arg Ala Tyr Thr
1 5 10 15

Leu Arg Leu Ser Thr Pro Asp Ala Asp Asn Gly Ala Trp Arg Glu Arg
20 25 30

Leu Trp Lys Thr His Glu Val Val Asn Ser Gly Ala Glu Ala Phe Gly
35 40 45

Asp Trp Leu Leu Ser Leu Arg Gly Gly Leu Asp His Arg Leu Val Ala
50 55 60

Val Lys Val Arg Val Gly Arg Gly Ala Ser Lys Thr Glu Arg Glu Pro
65 70 75 80

Thr Glu Asp Glu Arg Arg Glu Arg Arg Ile Val Leu Ala Leu Cys Trp
85 90 95

Leu Ser Val Glu Ser Lys Lys Gly Ala Pro Gln Gly Arg Val Val Glu
100 105 110

Asp Pro Val Asp Ala Leu Lys Arg Ile Leu Gly Gln Arg Gly Leu Ser
115 120 125

Glu Ala Asp Ala Glu Gln Trp Val Phe Asp Cys Arg Asp Ser Leu Ser
130 135 140

Ala Thr Ile Arg Asp Asp Ala Thr Trp Val Asp Arg Ser Ala Ala Phe
145 150 155 160

Asp Glu Thr Val Gln Arg Leu Gly Ser Ser Leu Thr Arg Glu His Ala
165 170 175

Glu Gln Val Ile Ile Glu Phe Phe Gly Asp Ile His Asp Tyr Leu Ala
180 185 190

Leu Pro Lys Asn Met Glu Glu Asp Gly Val Thr Ser Pro Arg Gly Gly
195 200 205

Ser Gly Lys Glu Phe Arg Thr Gln Ala Arg Ser Trp Leu Ser Glu Asn

210 215 220

Trp Gly Ala Gly Gln Lys Gly Asp Lys Ala Gln Ile Val Asp Ala Leu
225 230 235 240
Arg Lys Cys Ser Arg Cys Ile Ala Gln Glu Lys Pro Ser Thr Gly Ser
245 250 255
Asp Leu Leu Arg Val Leu Val Arg Ser Leu Gly Gly Ser Pro Glu Glu
260 265 270
Thr Leu Arg Phe Asp Glu Leu Arg Lys Leu Val Gly Trp Arg Thr Gly
275 280 285

Arg Arg Ser Thr Gly Ala Phe Ala Leu Gln Arg Thr Val Asp Met Asp
290 295 300
Arg Leu Ser Glu Ser Asp Leu Glu Ser Leu Glu Ala Lys Leu Thr Val
305 310 315 320
Glu Ile Asp Ala Lys Ser Pro Glu Ala Ser Arg Ser Val Pro Gln Trp
325 330 335
Val Glu Ser Met Arg Thr Ala Val Glu Arg Glu Val Gly Met Pro Phe
340 345 350

Arg Ser Thr Arg Asp Leu Ile Gly Glu Phe Gly Val Met Leu Asp His
355 360 365
Ala Ala Arg Arg Val Ser Ala Thr His Ser Trp Ile Lys Arg Ala Glu
370 375 380
Ala Glu Arg Arg Lys Phe Glu Gly Asp Ala Ala Lys Leu Ala Gln Ile
385 390 395 400
Pro Glu Glu Ala Arg Gln Trp Leu Asp Gln Phe Cys Glu Asp Arg Ser
405 410 415

Gln Glu Leu Asn Ala Leu Glu Pro Tyr Arg Ile Arg Arg Arg Ala Val
420 425 430
Glu Gly Trp Glu Ser Val Val Arg Thr Trp Ala Lys Ala Asp Cys Lys
435 440 445
Ala Glu Gly Asp Arg Val Lys Ala Val Arg Ala Leu Gln Pro Glu Ile
450 455 460

Glu Lys Phe Gly Asp Ala Ala Leu Phe Glu Ala Leu Ala Ala Glu Asp
465 470 475 480

Ala Leu Cys Val Trp Leu Leu Asp Gly Lys Ala Thr Pro Arg Pro Leu
485 490 495

Leu Asp Tyr Ser Ala Ala Thr Asp Ala Gln Tyr Arg Lys Arg Arg Phe
500 505 510

Lys Val Pro Ala Tyr Arg His Pro Asp Ala Leu Leu His Pro Val Phe
515 520 525

Cys Asp Phe Gly Glu Ser Arg Trp Thr Ile Glu Phe Ser Ala His Arg
530 535 540

Ala Leu Gly Arg Arg Arg Lys Ala Gln Gln Leu Val Asp Asn Lys Thr
545 550 555 560

Val Ala Leu Gln Lys Ala Gln Glu Arg Leu Arg Lys Ala Lys Ala Glu
565 570 575

Ser Ser Arg Ser Arg Ala Glu Glu Lys Val Arg Ala Ala Glu His Ala
580 585 590

Leu Glu Ala Ala Arg Lys Lys Leu Ala Phe Leu Gln Tyr Arg Arg Ala
595 600 605

Leu Ala Val Cys Leu Trp Thr Gly Lys Gly Val Glu Ser Thr Ser Leu
610 615 620

Arg Trp His Ser Lys Arg Phe Ala Lys Asp Phe Ala Ile Gly Ser Ser
625 630 635 640

Pro Glu Asp Gly Ala Ser Thr Gly Val Pro Val Ala Arg Ala Asp Arg
645 650 655

Leu Gly Arg Ala Ser Ala Asn Val Pro Arg Gly Ala Ser Val Thr Ile
660 665 670

Ser Gly Val Phe Glu Gln Lys Glu Trp Asn Gly Arg Leu Gln Ala Pro
675 680 685

Arg Asp Ala Leu Asn Ala Ile Ala Lys Val Arg Asp Asp Glu Thr Leu
690 695 700

Pro Ala Ala Asp Arg Ser Arg Arg Val Gln Gln Met Leu Ser Arg Leu

705 710 715 720

Pro Trp Phe Val Thr Phe Ser Ala Arg Leu Val Pro Gln Gly Pro Trp

725 730 735

Leu Asp Tyr Ala Ser Glu His Ser Ala Leu Gly Leu Arg Val Asp Pro

740 745 750

Lys Tyr Trp Pro His Ala Glu Glu Asn Arg Gln Arg Lys Gly Met Ala

755 760 765

Arg Leu Ile Leu Ser Arg Leu Pro Ser Leu Arg Val Leu Ser Val Asp

770 775 780

Leu Gly His Arg Tyr Ala Ala Ala Cys Ala Val Trp Glu Thr Leu Ser

785 790 795 800

Ala Gln Glu Met Gln Arg Ile Cys Arg Glu Met Gly Ser Ala Pro Pro

805 810 815

Ser Pro Asp Asp Leu Tyr Leu His Leu Arg Arg Ala Asp Gly Asn Gly

820 825 830

Lys Gln Arg Thr Thr Val Tyr Arg Arg Ile Gly Pro Asp Thr Leu Pro

835 840 845

Asp Gly Gly Gln His Pro Ala Pro Trp Ala Arg Leu Asp Arg Gln Phe

850 855 860

Leu Ile Lys Leu Gln Gly Glu Asp Glu Ser Ala Arg Lys Ala Ser Asp

865 870 875 880

Ser Glu Ile Ala Val Val Lys Lys Phe Glu Ala Asp Leu Gly Arg Pro

885 890 895

Ala Met Gln Arg Arg Ser Leu Arg Val Asp Asp Leu Met Ser Ala Ala

900 905 910

Val Arg Thr Ala Arg Leu Ala Leu Arg Arg His Gly Asp Arg Ala Arg

915 920 925

Ile Ala Phe Asn Leu Ile Ala Asp Arg Arg Phe Arg Pro Gly Gly Ala

930 935 940

Glu Glu Pro Leu Thr Asp Glu Thr Arg Val Asp Leu Leu Ala Asp Thr

945 950 955 960

Leu Ala Thr Trp His Gly Leu Phe Ser Gly Gly Gln Cys His Asp Glu
965 970 975
Arg Ala Glu Glu Gln Trp Asn Glu His Ile Ala Pro Leu Leu Ala Ser
980 985 990

Ser Gly Ala Ser Leu Ser Val Pro Ser Asp Gly Asp Ala Val Ala Ala
995 1000 1005
Thr Pro Ala Arg Arg Arg Arg Lys Glu Val Arg Gly Lys Leu Val
1010 1015 1020
Pro Ala Ala Met Glu Leu Ala Arg Arg Asp Leu Ser Gln Leu Ser
1025 1030 1035
Val Leu Trp Val Ala Arg Trp His Gln Asp Asp Glu Ser Trp Arg
1040 1045 1050

Ala Arg Leu Arg Trp Leu Arg Asp Trp Ile Leu Pro Arg Gly Ala
1055 1060 1065
Lys Ala Asp Ser Gly Ala Ile Arg His Val Gly Gly Leu Ser Val
1070 1075 1080
Thr Arg Leu Ala Thr Ile Arg Ser Leu Trp Gln Leu Gln Lys Ala
1085 1090 1095
Tyr Arg Thr Gln Pro Glu Pro Glu Asp Pro Arg Lys Asn Val Pro
1100 1105 1110

Lys Lys Gly Asp Thr Ser Leu Asp Asp Phe Gly Arg Thr Ile Leu
1115 1120 1125
Asp Asp Leu Glu His Leu Arg Glu Asn Arg Val Lys Gln Leu Ala
1130 1135 1140
Ser Arg Ile Cys Glu Ala Ala Leu Gly Val Gly Val Glu Gln Pro
1145 1150 1155
Asn Gly Gly Ala Lys Asp Pro Lys Arg Pro Gln Glu Arg Arg Phe
1160 1165 1170

Ser Pro Cys Gln Ala Val Val Ile Glu Asn Leu Thr Arg Tyr Arg
1175 1180 1185
Pro Glu Glu Thr Arg Thr Arg Arg Glu Asn Arg Gln Leu Leu Asn

1190 1195 1200

Trp Ser Ala Gly Lys Val Lys Gln Tyr Leu Ser Glu Ala Cys Glu

1205 1210 1215

Leu His Gly Leu His Leu Arg Glu Val Ser Ala Ala Tyr Thr Ser

1220 1225 1230

Arg Gln Asp Ser Arg Thr Gly Ala Pro Gly Ile Arg Cys Gln Asp

1235 1240 1245

Ile Pro Val Val Asp Phe Val Arg Glu Asn Gly Pro Cys Trp Gly

1250 1255 1260

Arg Leu Arg Ser Ala Gln Gln Ser Ser Gly Gly Thr Ala Glu Asp

1265 1270 1275

Gln Leu Leu Leu Ala Leu Tyr Glu Arg Trp Ser Glu Lys Glu Arg

1280 1285 1290

Thr Trp Arg Asp Gln Ser Gly Asn Val Trp Ala Met Asp Gly Glu

1295 1300 1305

Gly Arg Trp Val Ala Arg Asn Gly Thr Gln Leu Pro Gln Gly Ser

1310 1315 1320

Gly Leu Thr Pro His Pro Ile Arg Val Pro Gln Arg Gly Gly Asp

1325 1330 1335

Ile Phe Val Ser Ala Ala Pro Arg Ser Pro Ala Ala Asn Gly Ile

1340 1345 1350

Gln Ala Asp Leu Asn Ala Ala Ala Asn Ile Gly Leu Trp Ala Leu

1355 1360 1365

Leu Asp Pro Asp Trp Glu Gly Arg Trp Trp Arg Leu Pro Cys Ser

1370 1375 1380

Ala Met Asp Leu Lys Pro Val Lys Gly Ser Val Asn Gly Ser Ala

1385 1390 1395

Val Ile His Leu Asp Ala Pro Leu Lys Ala Ala Ala Thr Lys Gly

1400 1405 1410

Ala Ala Lys Lys Asp Val Val Asn Leu Trp Arg Asp Ile Ser Val

1415 1420 1425

Arg Ser Leu Thr Glu Gly Val Trp Arg Gly Tyr Asp Ala Tyr Trp
1430 1435 1440
Asn Leu Ala Arg Tyr Arg Val Val Gln Thr Leu Arg Pro Gln Val
1445 1450 1455
Gly Ile Gly Ser Asp Glu
1460

<210> 123
<211> 1247
<212> PRT
<213> Unknown
<220><223> Description of Unknown:

Cas12 sequence

<400> 123
Met Phe Lys Gly Asp Ala Phe Thr Gly Leu Tyr Glu Val Gln Lys Thr
1 5 10 15
Leu Arg Phe Glu Leu Val Pro Ile Gly Leu Thr Gln Ser Tyr Leu Glu
20 25 30
Asn Asp Trp Val Ile Gln Lys Asp Lys Glu Val Glu Glu Asn Tyr Gly
35 40 45
Lys Ile Lys Ala Tyr Phe Asp Leu Ile His Lys Glu Phe Val Arg Gln
50 55 60

Ser Leu Glu Asn Ala Trp Leu Cys Gln Leu Asp Asp Phe Tyr Glu Lys
65 70 75 80
Tyr Ile Glu Leu His Asn Ser Leu Glu Thr Arg Lys Asp Lys Asn Leu
85 90 95
Ala Lys Gln Phe Glu Lys Val Met Lys Ser Leu Lys Lys Glu Phe Val
100 105 110
Ser Phe Phe Asp Ala Lys Trp Asn Glu Trp Lys Gln Lys Phe Ser Phe
115 120 125

Leu Lys Lys Trp Trp Ile Asp Val Leu Asn Glu Lys Glu Val Leu Asp
130 135 140
Leu Met Ala Glu Phe Tyr Pro Asp Glu Lys Glu Leu Phe Asp Lys Phe

145 150 155 160

Asp Lys Phe Phe Thr Tyr Phe Ser Asn Phe Lys Glu Ser Arg Lys Asn

165 170 175

Phe Tyr Ala Asp Asp Gly Arg Ala Trp Ala Ile Ala Thr Arg Ala Ile

180 185 190

Asp Glu Asn Leu Ile Thr Phe Ile Lys Asn Ile Glu Asp Phe Lys Lys

195 200 205

Leu Asn Ser Ser Phe Arg Glu Phe Val Asn Asp Asn Phe Ser Glu Glu

210 215 220

Asp Lys Gln Ile Phe Glu Ile Asp Phe Tyr Asn Asn Cys Leu Leu Gln

225 230 235 240

Pro Trp Ile Asp Lys Tyr Asn Lys Ile Val Trp Trp Tyr Ser Leu Glu

245 250 255

Asn Trp Glu Lys Val Gln Trp Leu Asn Glu Lys Ile Asn Asn Phe Lys

260 265 270

Gln Asn Gln Asn Lys Ser Asn Ser Lys Asp Leu Lys Phe Pro Arg Met

275 280 285

Lys Leu Leu Tyr Lys Gln Ile Leu Gly Asp Lys Glu Lys Lys Val Tyr

290 295 300

Ile Asp Glu Ile Arg Asp Asp Lys Asn Leu Ile Asp Leu Ile Asp Asn

305 310 315 320

Ser Lys Arg Arg Asn Gln Ile Lys Ile Asp Asn Ala Asn Asp Ile Ile

325 330 335

Asn Asp Phe Ile Asn Asn Asn Ala Lys Phe Glu Leu Asp Lys Ile Tyr

340 345 350

Leu Thr Arg Gln Ser Ile Asn Thr Ile Ser Ser Lys Tyr Phe Ser Ser

355 360 365

Trp Asp Tyr Ile Arg Trp Tyr Phe Trp Thr Gly Glu Leu Gln Glu Phe

370 375 380

Val Ser Phe Tyr Asp Leu Lys Glu Thr Phe Trp Lys Ile Glu Tyr Glu

385 390 395 400

Thr Leu Glu Asn Ile Phe Lys Asp Cys Tyr Val Lys Gly Ile Asn Thr
405 410 415

Glu Ser Gln Asn Asn Ile Val Phe Glu Thr Gln Gly Ile Tyr Glu Asn
420 425 430

Phe Leu Asn Ile Phe Lys Phe Glu Phe Asn Gln Asn Ile Ser Gln Ile
435 440 445

Ser Leu Leu Glu Trp Glu Leu Asp Lys Ile Gln Asn Glu Asp Ile Lys
450 455 460

Lys Asn Glu Lys Gln Val Glu Val Ile Lys Asn Tyr Phe Asp Ser Val
465 470 475 480

Met Ser Val Tyr Lys Met Thr Lys Tyr Phe Ser Leu Glu Lys Trp Lys
485 490 495

Lys Arg Val Glu Leu Asp Thr Asp Asn Asn Phe Tyr Asn Asp Phe Asn
500 505 510

Glu Tyr Leu Glu Gly Phe Glu Ile Trp Lys Asp Tyr Asn Leu Val Arg
515 520 525

Asn Tyr Ile Thr Lys Lys Gln Val Asn Thr Asp Lys Ile Lys Leu Asn
530 535 540

Phe Asp Asn Ser Gln Phe Leu Thr Trp Trp Asp Lys Asp Lys Glu Asn
545 550 555 560

Glu Arg Leu Gly Ile Ile Leu Arg Arg Glu Trp Lys Tyr Tyr Leu Trp
565 570 575

Ile Leu Lys Lys Trp Asn Thr Leu Asn Phe Gly Asp Tyr Leu Gln Lys
580 585 590

Glu Trp Glu Ile Phe Tyr Glu Lys Met Asn Tyr Lys Gln Leu Asn Asn
595 600 605

Val Tyr Arg Gln Leu Pro Arg Leu Leu Phe Pro Leu Thr Lys Lys Leu
610 615 620

Asn Glu Leu Lys Trp Asp Glu Leu Lys Lys Tyr Leu Ser Lys Tyr Ile
625 630 635 640

Gln Asn Phe Trp Tyr Asn Glu Glu Ile Ala Gln Ile Lys Ile Glu Phe

645 650 655

Asp Ile Phe Gln Glu Ser Lys Glu Lys Trp Glu Lys Phe Asp Ile Asp

660 665 670

Lys Leu Arg Lys Leu Ile Glu Tyr Tyr Lys Lys Trp Val Leu Ala Leu

675 680 685

Tyr Ser Asp Leu Tyr Asp Leu Glu Phe Ile Lys Tyr Lys Asn Tyr Asp

690 695 700

Asp Leu Ser Ile Phe Tyr Ser Asp Val Glu Lys Lys Met Tyr Asn Leu

705 710 715 720

Asn Phe Thr Lys Ile Asp Lys Ser Leu Ile Asp Gly Lys Val Lys Ser

725 730 735

Trp Glu Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Glu Ser

740 745 750

Lys Lys Glu Trp Ser Thr Glu Asn Ile His Thr Lys Tyr Phe Lys Leu

755 760 765

Leu Phe Asn Glu Lys Asn Leu Gln Asn Leu Val Val Lys Leu Ser Trp

770 775 780

Trp Ala Asp Ile Phe Phe Arg Asp Lys Thr Glu Asn Leu Lys Phe Lys

785 790 795 800

Lys Asp Lys Asn Gly Gln Glu Ile Leu Asp His Arg Arg Phe Ser Gln

805 810 815

Asp Lys Ile Met Phe His Ile Ser Ile Thr Leu Asn Ala Asn Cys Trp

820 825 830

Asp Lys Tyr Trp Phe Asn Gln Tyr Val Asn Glu Tyr Met Asn Lys Glu

835 840 845

Arg Asp Ile Lys Ile Ile Trp Ile Asp Arg Trp Glu Lys His Leu Ala

850 855 860

Tyr Tyr Cys Val Ile Asp Lys Ser Trp Lys Ile Phe Asn Asn Glu Ile

865 870 875 880

Trp Thr Leu Asn Glu Leu Asn Trp Val Asn Tyr Leu Glu Lys Leu Glu

885 890 895

Lys Ile Glu Ser Ser Arg Lys Asp Ser Arg Ile Ser Trp Trp Glu Ile
900 905 910

Glu Asn Ile Lys Glu Leu Lys Asn Gly Tyr Ile Ser Gln Val Ile Asn
915 920 925

Lys Leu Thr Glu Leu Ile Val Lys Tyr Asn Ala Ile Ile Val Phe Glu
930 935 940

Asp Leu Asn Ile Trp Phe Lys Arg Trp Arg Gln Lys Ile Glu Lys Gln
945 950 955 960

Ile Tyr Gln Lys Leu Glu Leu Ala Leu Ala Lys Lys Leu Asn Tyr Leu
965 970 975

Thr Gln Lys Asp Lys Lys Asp Asp Glu Ile Leu Trp Asn Leu Lys Ala
980 985 990

Leu Gln Leu Val Pro Lys Val Asn Asp Tyr Gln Asp Ile Trp Asn Tyr
995 1000 1005

Lys Gln Ser Trp Ile Met Phe Tyr Val Arg Ala Asn Tyr Thr Ser
1010 1015 1020

Val Thr Cys Pro Asn Cys Trp Leu Arg Lys Asn Leu Tyr Ile Ser
1025 1030 1035

Asn Ser Ala Thr Lys Glu Asn Gln Lys Lys Ser Leu Asn Ser Ile
1040 1045 1050

Ala Ile Lys Tyr Asn Asp Trp Lys Phe Ser Phe Ser Tyr Glu Ile
1055 1060 1065

Asp Asp Lys Ser Trp Lys Gln Lys Gln Ser Leu Asn Lys Lys Lys
1070 1075 1080

Phe Ile Val Tyr Ser Asp Ile Glu Arg Phe Val Tyr Ser Pro Leu
1085 1090 1095

Glu Lys Leu Thr Lys Val Ile Asp Val Asn Lys Lys Leu Leu Glu
1100 1105 1110

Leu Phe Arg Asp Phe Asn Leu Ser Leu Asp Ile Asn Lys Gln Ile
1115 1120 1125

Gln Glu Lys Asp Leu Asp Ser Val Phe Phe Lys Ser Leu Thr His

1130 1135 1140

Leu Phe Asn Leu Ile Leu Gln Leu Arg Asn Ser Asp Ser Lys Asp
1145 1150 1155
Asn Lys Asp Tyr Ile Ser Cys Pro Ser Cys Tyr Tyr His Ser Asn
1160 1165 1170
Asn Trp Leu Gln Trp Phe Glu Phe Asn Trp Asp Ala Asn Trp Ala
1175 1180 1185
Tyr Asn Ile Ala Arg Lys Gly Ile Ile Leu Leu Asp Arg Ile Arg
1190 1195 1200

Lys Asn Gln Glu Lys Pro Asp Leu Tyr Val Ser Asp Ile Asp Trp
1205 1210 1215
Asp Asn Phe Val Gln Ser Asn Gln Phe Pro Asn Thr Ile Ile Pro
1220 1225 1230
Ile Gln Asn Ile Glu Lys Gln Val Pro Leu Asn Ile Lys Ile
1235 1240 1245

<210> 124
<211> 1250
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 124

Met Leu Ser Phe Asn Trp Val Leu Phe Phe Phe Phe Ser Lys Met Ser

1 5 10 15
Arg Ser Ile Phe Ser Pro Phe Thr Asn Leu Tyr Pro Ile Gln Lys Thr
20 25 30
Leu Arg Arg Glu Leu Lys Pro Leu Asn Glu Asn Phe Gln His Asp Pro
35 40 45
Ala Leu Ser Ala Leu Arg Asn Ser Glu Ile Pro Gln Arg Asp Glu Gln
50 55 60
Arg Glu Lys Asp Tyr Gln Ala Ile Lys Pro Leu Leu Asp Glu Phe His

65 70 75 80

Asn Gln Phe Ile Thr Glu Ser Leu His Ser Leu Glu Pro Gln Asp Arg

85 90 95

Ser Asp Phe Ile Leu Phe Tyr Gln Thr Tyr Gln Lys Lys Lys Lys Asn

100 105 110

Lys Ala Glu Ile Ser Glu Lys Glu Leu Lys Ser Leu Asp Glu Glu Phe

115 120 125

Glu Ser Arg Thr Lys Ala Leu Arg Asn Ala Ile Gly Thr Ser Phe Ser

130 135 140

Val Thr Ala Glu Leu Arg Lys Ser Asn Pro Asp Tyr Val Ser Glu Lys

145 150 155 160

Gly Lys Pro Phe Leu Thr Gln Lys Ser Tyr Lys Ile Leu Thr Glu Ala

165 170 175

Gly Val Leu Trp Leu Leu Glu Lys Lys Tyr Thr Ser Asp Pro Glu Lys

180 185 190

Leu Ala Leu Ile Arg Arg Phe Gly Asn Phe Phe Thr Tyr Phe Thr Gly

195 200 205

Phe Asn Gln Asn Arg Glu Asn Tyr Tyr Ala Thr Asp Glu Lys Ser Thr

210 215 220

Ala Val Ala Tyr Arg Ala Ile Asn Glu Asn Leu Leu Thr Phe Ala Asn

225 230 235 240

Asn Cys Glu Leu Phe Glu Lys Leu Ser Val Leu Ser Leu Ser Glu Leu

245 250 255

Glu Lys Lys Thr Phe Asn Pro Asp Ser Tyr Ser Glu Tyr Leu Thr Gln

260 265 270

Ser Gly Ile Val Phe Tyr Asn Glu Met Leu Ala Asn Ile Arg Ser Lys

275 280 285

Ala Asn Leu Tyr Thr Gln Glu His Lys Ala Lys Leu Pro Gln Pro Lys

290 295 300

Leu Leu Tyr Lys Gln Ile Trp Ser Pro Arg Gly Asp Thr Ile Pro Phe

305 310 315 320

Asp Leu Ile Ala Ser Glu Ala Glu Phe Gln Glu Thr Leu His Thr Met

325 330 335

Ile Arg Glu Thr Asp Gln Arg Ile Pro Glu Phe Asn Lys Leu Leu Glu

340 345 350

Gln Ile Phe Glu Glu Lys Val Asp Leu Ser Gln Ile Phe Phe Ser Lys

355 360 365

Thr Ser Leu Asn Ile Ile Ser Asn Arg Tyr Phe Ser Ser Trp His Thr

370 375 380

Leu Leu Glu Lys Gly Val Glu Leu Lys Leu Phe Lys Phe Lys Lys Asn

385 390 395 400

Asp Glu Glu Ser Phe Lys Leu Pro Ala Tyr Leu Ser Leu Ala Glu Leu

405 410 415

Lys Glu Leu Leu Glu Ser Ala Pro Phe Gln Met Ala Glu Lys Ala Asp

420 425 430

Ala Asp Glu Glu Lys His His Gln Ala Ser Leu Phe Lys Leu Gln Arg

435 440 445

Glu Asn Leu His Leu Glu Lys Ser His Ser Asn Trp Glu Leu Leu Leu

450 455 460

Lys Ser Met Lys Ser Asp Phe Glu Ser Phe Trp Thr Trp Glu Gly Glu

465 470 475 480

Phe Trp Ser Tyr Thr Leu Ala Lys Lys Ala Leu Gln Ser Leu Ser Ala

485 490 495

Leu Glu Ser Thr Asn Gln Glu His Lys Asn Leu Ile Lys Met Leu Leu

500 505 510

Asp Asn Ala Leu Tyr Ala Tyr Arg Met Leu Lys Trp Phe Lys Val Asp

515 520 525

Thr Ser Lys Leu Gly Phe Val Pro Glu Gly Glu Phe Tyr Pro Ser Leu

530 535 540

Asp Gln Leu Leu Gln Asp Tyr Pro Leu Pro Lys Trp Tyr Asp Met Ile

545 550 555 560

Arg Asn Tyr Leu Thr Arg Lys Thr Tyr Ser Gln Ala Lys Leu Lys Leu

565 570 575

Asn Phe Asp Cys Ser Thr Leu Leu Asn Gly Arg Asp Lys Asn Lys Glu

580 585 590

Ile Gln Asn Leu Ser Val Ile Leu Arg Lys Asp Gly Lys Phe Tyr Leu

595 600 605

Ala Ile Met Lys Lys Asp Gln Asn Lys Phe Phe Glu Asn Ser Ala Leu

610 615 620

Tyr Glu Gly Asn Leu Gly Thr Met Glu Lys Met Asp Tyr Lys Leu Leu

625 630 635 640

Pro Trp Ala Asn Lys Met Leu Pro Lys Cys Leu Met Pro Gly Ser Asp

645 650 655

Lys Lys Lys Tyr Gly Ala Ser Asp Gln Val Leu Glu Leu Tyr Ala Lys

660 665 670

Gly Ser Phe Lys Lys Ser Glu Lys Ser Phe Asn Leu Ala Asp Leu His

675 680 685

Thr Leu Ile Asp Phe Tyr Lys Leu Ala Leu Pro Lys Tyr Glu Asp Trp

690 695 700

Lys Val Phe Asn Phe Gln Phe Gln Ala Thr Glu Asn Tyr Gln Asp Ile

705 710 715 720

Ser Gln Phe Tyr Arg Glu Val Glu Gln Gln Gly Tyr Leu Leu Asn Trp

725 730 735

Arg Lys Val Asn Glu Lys Leu Ile Lys Gln Gly Ile Lys Asp Trp Ser

740 745 750

Leu Phe Leu Phe Gln Ile Ser Ser Lys Asp Phe Glu Gly Lys Ser Lys

755 760 765

Thr Pro Asp Leu Gln Thr Leu Tyr Trp Gln Gln Leu Phe Glu Phe Ser

770 775 780

Thr Asn Val Lys Leu Asn Gly Glu Ala Glu Ile Phe Phe Arg Pro Trp

785 790 795 800

Ser Met Lys Lys Glu Lys Lys Lys Leu Lys Val Asp Asn Tyr Asp Val

805 810 815

Phe Lys His Lys Arg Tyr Thr Glu Asp Lys Ile Leu Phe His Val Pro
820 825 830
Ile Thr Leu Trp Phe Gly Asn Asn Glu Val Ser Pro Ser Ala Pro Ser

835 840 845
Lys Phe Asn Gln Lys Leu Asn Gln Glu Leu Ile Ile Pro His Phe Asp
850 855 860
Asp Leu His Val Ile Gly Val Asp Arg Trp Glu Lys His Leu Ala Phe
865 870 875 880
Tyr Ser Val Val Ser Val Lys Thr Gly Lys Ile Val Lys Gln Gly Thr
885 890 895
Leu Asn Leu Leu Asn Gly Thr Asp Tyr Glu Ala Lys Leu Ser Gln Lys

900 905 910
Ala Glu Asn Arg Leu Tyr Ala Arg Gln Asn Arg Asp Thr Ile Glu Lys
915 920 925
Ile Ala Asp Leu Lys Asn Gly Tyr Ile Ser Gln Val Val Asn Lys Leu
930 935 940
Val Glu Leu Val Leu Glu Tyr Asn Ala Val Ile Val Phe Glu Asp Leu
945 950 955 960
Asn Ala Gly Phe Lys Arg Gly Arg Gln Lys Ile Glu Gln Ser Val Tyr

965 970 975
Gln Lys Leu Glu Leu Ala Leu Ala Lys Lys Leu Asn Phe Ile Val Lys
980 985 990
Lys Glu Lys Ala Val Gly Glu Pro Trp Ser Val Thr Ser Ala Tyr Gln
995 1000 1005
Leu Ala Pro Gln Ile Asn Thr Phe Trp Asp Ile Lys Trp Lys Gln
1010 1015 1020
Arg Gly Ile Met Leu Tyr Thr Arg Ala Asn Tyr Thr Ser Val Thr

1025 1030 1035
Asp Pro Leu Thr Gly Trp Arg Lys Gln Tyr Tyr Phe Lys Lys Gly
1040 1045 1050
Ser Ser Glu Glu Met Lys Ala Gln Phe Phe Lys Ser Phe Lys Asn

1055 1060 1065

Leu Thr Arg Asp Ala Gly Gln Glu Ala Tyr Ile Phe Asp Asp Gly

1070 1075 1080

Thr Trp Leu Leu Tyr Ser Asn Val Glu Arg Arg Arg Gly Lys Arg

1085 1090 1095

Gly Asp His Arg Glu Arg Thr Gln Ile Lys Tyr Asp Pro Ser Leu

1100 1105 1110

Glu Leu Asp Thr Leu Phe Ser Lys Tyr Gln Ile Glu Lys Ser Asp

1115 1120 1125

Ser Leu Phe Asp Gln Leu Lys Asn Arg Glu Leu Pro Gln Thr Phe

1130 1135 1140

Trp Thr Ser Phe Phe Arg Ile Ile Asp Leu Ile Met Gln Ile Arg

1145 1150 1155

Asn Thr Asp Asp Glu Gly Arg Asp Ile Ile Leu Ser Pro Ile Gly

1160 1165 1170

Asn Pro Gln Glu Arg Phe Asp Ser Arg Lys Arg Tyr Asn Gln Leu

1175 1180 1185

Pro Arg Asp Glu Lys Gly Gly Ile Ile Glu Glu Ser Ala Phe Glu

1190 1195 1200

Tyr Pro Thr Ser Trp Asp Ala Asn Gly Ala Tyr Asn Ile Ala Arg

1205 1210 1215

Lys Gly Val Met Met Leu Glu Arg Ile Lys Glu Asn Pro Glu Lys

1220 1225 1230

Pro Asp Leu Leu Ile Arg Asp Ala Glu Trp Asp Lys Lys Ile Thr

1235 1240 1245

Arg Lys

1250

<210> 125

<211> 669

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 125

Met Leu Asp Lys Phe Ala Ser Leu Tyr Pro Val Thr Lys Thr Leu Arg

1 5 10 15

Phe Arg Leu Leu Pro Gln Gly Arg Thr Glu Glu Asn Met Gln Val Ala

20 25 30

Lys Val Leu Glu Asn Asp Leu Glu Arg Ser Glu Ala Ala Ala Val Val

35 40 45

Lys Gly Leu Ile Lys Lys Tyr His Leu Gln Phe Ile Ser Asp Thr Leu

50 55 60

Ser Gly Ser Thr Leu Ser Trp Gln Ala Leu Thr Glu Thr Leu Asp Lys

65 70 75 80

Phe Lys Ala Asp His Thr Ala Thr Ala Glu Leu Asp Ser Ala Leu Ala

85 90 95

Ala Tyr Arg Cys Lys Leu Ala Glu Leu Phe Thr Lys Ser Pro Lys Tyr

100 105 110

Lys Val Met Ala Thr Pro Val Ser Ile Ile Lys Glu Ile Leu Lys Thr

115 120 125

Glu Thr Asp Pro Glu Asn Ile Ala Ala Leu Asn Lys Leu Asn Gly Tyr

130 135 140

Thr Tyr Ile Ile Phe Asp Tyr Val Ser Thr Arg Met Leu Thr Tyr Ser

145 150 155 160

Ala Asp Ala Lys Ala Thr Ser Leu Ala Tyr Arg Leu Val Asp Glu Asn

165 170 175

Tyr Leu Arg Phe Tyr Gln Asp Ile Ser Ala Ala Ala Glu Ile Ser Ala

180 185 190

Val Leu Glu Glu Ala Gly Phe Asp Asn Ala Glu Val Glu Ala Phe Ile

195 200 205

Arg Thr Asp Tyr Asn Thr Cys Leu Thr Ser Glu Gly Ile Ala Ser Phe

210 215 220

Asn Ala Ala Ala Gly Ser Ile Asn Gln Phe Val Asn Val Leu Leu Gln

225 230 235 240

Gln Asn Pro Val Leu Gln Ser Glu Pro Ala Leu Arg Arg His Leu Gln

245 250 255

Pro Leu Tyr Lys Met Leu Leu Asp Glu Ala Glu Ser Lys Ile Ile Lys

260 265 270

Phe Glu Asp Tyr Gly Gln Leu Arg Asp Ala Val Glu Asn Phe Arg Arg

275 280 285

Asn Phe Gln Asp Leu Pro Gln Ser Leu Ile Asp Ile Phe Ala Gly Arg

290 295 300

Tyr Asp Tyr Ser Lys Ile Tyr Val Gly Tyr Lys Tyr Leu Asn Glu Ala

305 310 315 320

Ser Ser Gln Ile Ala Gly Gly Tyr Asn Trp Lys Leu Leu Glu Asn Ala

325 330 335

Leu Glu Asp Phe Tyr Ser Lys Pro Tyr Leu Val Asn Gly Lys Leu Pro

340 345 350

Val Lys Tyr Lys Thr Val Val Asn Lys Lys Met Asn Gln Leu Ala Tyr

355 360 365

Ser Phe Thr Glu Leu Gln Glu Ala Leu Asp Ala Gly Asp Ser Gly Ser

370 375 380

Ser Ile Thr Asp Leu Phe Gly Lys Tyr Ala Glu Leu His Ala Ala Tyr

385 390 395 400

Ala Ala Ala Asp Gly Asn Val Phe Tyr Lys Glu Tyr Asp Arg Lys Ser

405 410 415

Ile Ala Ser Leu Lys Asn Tyr Leu Asp Ala Val Asn Ala Ile Ala Arg

420 425 430

Phe Ile Lys Ile Phe Ala Ala Pro Glu Val Tyr Val Lys Asp Glu Gly

435 440 445

Phe Tyr Gly Ile Val Asp Gly Ala Ala Asp Lys Leu Arg Asp Phe Asp

450 455 460

Leu Leu Tyr Asn Met Val Arg Asn Tyr Ile Thr Lys Lys Pro Tyr Lys

465 470 475 480

Lys Ser Lys Val Ala Leu Thr Phe Asn Ser Ser Ser Phe Gly Arg Gly
485 490 495
Trp Asp Glu Asn Lys Ile Tyr Asp Glu Leu Thr Thr Ile Phe Thr Tyr
500 505 510
Asn Gly Lys Tyr Tyr Leu Gly Val Ile Asn Lys Asn Asp Lys Pro Asp

515 520 525
Leu Ala Ala Ala Val Ser Lys Asp Glu Gly Gly Tyr Lys Arg Met Val
530 535 540
Tyr Lys Thr Phe Asp Ile Val Lys Gln Leu Pro Arg Leu Ser Phe Thr
545 550 555 560
Lys Ala Val Lys Ala His Phe Ala Glu Ser Asp Glu Asp Phe Ile Phe
565 570 575
Asp Gly Pro Lys Phe Ala Lys Pro Leu Arg Val Pro Lys Glu Ile Tyr

580 585 590
Leu Gln Ser Phe Thr Asp Asn Gly Asp Lys Leu Ala Asp Ser Ala Lys
595 600 605
Lys Tyr Thr Lys Ala Tyr Leu Asp Met Ser Gly Asp Tyr Lys Gly Tyr
610 615 620
Tyr Glu Ala Ile Ile Lys Arg Ile Asp Tyr Thr Lys Glu Phe Leu Ser
625 630 635 640
Ala Tyr Lys Ser Thr Ser Ile Tyr Asp Leu Ala Phe Leu Lys Pro Ala

645 650 655
Gly Lys Ala Ala Gly Ser Leu Cys Trp Thr Arg His Ile
660 665

<210> 126
<211> 1367
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 126
Met Asn Arg Ile Tyr Gln Gly Arg Val Thr Lys Val Glu Ile Leu Asn

1 5 10 15

Gly Lys Asn Ala Asp Gly Gln Pro Gln Glu Leu Pro Asn Trp Gln Thr

20 25 30

Ala Leu Trp Gln His His Glu Leu Phe Gln Asp Ala Val Asn Tyr Tyr

35 40 45

Leu Phe Cys Leu Ala Ala Leu Ala Ser Ser Ala Ser Ser Pro Met Gly

50 55 60

Lys Leu Arg Asn Gln Leu Gly Ser Val Trp Glu Pro Phe Gly Arg Thr

65 70 75 80

Gly Arg Arg Phe Lys Gly Leu Arg Asp Ser Val Gly Pro Tyr Leu Leu

85 90 95

Pro Asp Arg Pro Thr Pro Ser Ile Glu Glu Ala Phe Ala Ala Ala Leu

100 105 110

Ala Gly Asn Asn Ser Gln Pro Glu Leu Leu Gln Leu Ala Val Asp Ala

115 120 125

Leu Val Glu Asp Leu Gly Gly Asp Ala Ala Ile Gln Gln Glu Gly Arg

130 135 140

Gly Tyr Leu Pro Arg Leu Cys Ser Pro Ala Tyr Asn Gly Gln Phe Pro

145 150 155 160

Arg Gly Ala Asn Ser Leu Gln Lys Glu Ala Ala Lys Ile Arg Leu Pro

165 170 175

Thr Leu Leu His Asn Val Ala Thr Ser Arg Asn Leu Asp Ala Leu Ala

180 185 190

Ala Glu Leu Glu Phe Gly Phe Phe Ala Asn Pro Val Pro Asn Ala Gly

195 200 205

Pro Ile Ala Gly Gln Glu Ala Arg Asn Lys Leu Leu Glu Ala Leu Ala

210 215 220

Trp Leu Lys Ala Lys Asp Thr Arg Leu Thr His Ser Ala Asn Glu Leu

225 230 235 240

Glu Lys Arg Ile Gly Val Leu Pro Asp Ser Val Ser Phe Pro Thr Tyr

245 250 255

Ser Gly Gly Ser Ile Asn Lys Glu Ala Leu Lys His Arg Phe Phe Ala
260 265 270
Tyr Leu Leu Phe Gln His Val Glu Arg Ser Leu Val Thr Phe Glu Ile
275 280 285

Leu Arg Asp Ser Tyr Pro Thr Pro Lys Pro Ser Ala Arg Lys Ser Ser
290 295 300
Lys Ala Thr Pro Asp Thr Met Ala Gln Leu Thr Gln Phe Gly Asp Asp
305 310 315 320
Pro Val Lys Leu Ala Arg Gly Thr Arg Gly Tyr Val Phe Arg Ala Phe
325 330 335
Thr Ser Leu Pro Cys Trp Gly Ala Lys Ala Pro Ser Asp Ile Leu Trp
340 345 350

Ser Glu Phe Asp Ile Ala Ala Phe Lys Glu Ala Leu Lys Thr Ala Asn
355 360 365
Gln Phe Arg Leu Lys Thr Lys Glu Arg Leu Asp Lys Ala Asp Glu Leu
370 375 380
Ala Gly Glu Leu Ala Trp Met Asn Gly Glu Lys Ser Lys Phe Lys Pro
385 390 395 400
Ser Glu His Ser Glu Gln Glu Pro Pro Ala Val Leu Lys Gly Asp Pro
405 410 415

Arg Phe Glu Val Leu Lys Gln Leu Phe Glu Val Glu Leu Ala Glu Glu
420 425 430
His Tyr Leu Ala Glu Gly Glu Ser Val Ile Tyr Gly Leu His Pro Arg
435 440 445
Thr Leu Arg Cys Tyr Arg Glu Leu Val Glu Arg Trp Asn Lys Thr Val
450 455 460
Gln Pro Gly Glu Val Phe Thr Glu Ala Thr Ser Lys Lys Leu Val Ala
465 470 475 480

Ser Thr Asp Lys Phe Gln Ala Glu Asn Lys Glu Arg Ile Gly Ser Val
485 490 495
Thr Leu Phe Lys Lys Leu Leu Glu Arg Asp Tyr Trp Cys Leu Trp Gln

500 505 510

Thr Pro Asp Val Gln Thr Val Ala Ala Arg Gln Lys Ala Gly Phe Ser

515 520 525

Ser Asn Ile Ile Glu Asp Tyr Gln Arg Tyr Leu Glu Leu Gln Thr Asp

530 535 540

Ile Ala Arg Leu Lys Glu Pro Ile Arg Phe Thr Pro Ala Asp Ala Glu

545 550 555 560

Gln Ser Arg Arg Leu Phe Met Phe Ser Asp Leu Ala Gly Lys Ser Lys

565 570 575

His Lys His Leu Pro Asn Ala Thr Pro Tyr Gly Phe Ala Val Asp Val

580 585 590

Ala Leu Ala Ala Ser Glu Gly Gly Val Trp Lys Glu Thr Arg Val Arg

595 600 605

Leu His Tyr Ser Ala Pro Arg Leu Arg Arg Asp Gly Leu Arg Lys Gly

610 615 620

Val Gly Glu Asp Leu Lys Arg Thr Ala Trp Leu Gln Pro Met Val Ala

625 630 635 640

Ala Leu Asn Leu Ser Glu Pro Ala Pro Gln Asp Phe Ser Lys Cys Ala

645 650 655

Val Ser Leu Met Pro Asp Lys Ser Trp Lys Gly Leu Arg His Leu Leu

660 665 670

Asn Phe Pro Val Thr Leu Asp Pro Thr Val Val Gln Lys Ala Ile Gly

675 680 685

Ser Gln Ala Arg Trp Ala Asn Gln Phe Val Ala Phe Gly Lys Gly Ala

690 695 700

Thr Glu Gln Lys Phe Phe Leu Arg Trp Pro Glu Glu Val Ser Ala Ser

705 710 715 720

Gln Lys Lys Ala Gly Pro Trp Trp Asp Ala Leu Arg Ala Phe Ser Cys

725 730 735

Leu Ser Val Asp Leu Gly Gln Arg Asp Ala Gly Ala Phe Ala Leu Leu

740 745 750

Asp Val Arg Ala Asn Ala Asp Trp Gly Lys Lys Pro Ser Arg Phe Ile
755 760 765

Gly Glu Ala Asp Gly Arg Asn Trp Arg Ala Ala Leu Ala Ala Ala Gly
770 775 780

Leu Leu Arg Leu Pro Gly Glu Asp Ala Leu Val Trp Arg Asp Gly Lys
785 790 795 800

Trp Gln Glu Glu Leu Tyr Gly Glu Lys Gly Arg Leu Ala Thr Lys Glu
805 810 815

Glu Trp Leu Glu Thr Asn Ala Ile Phe Ser Ala Leu Glu Gln Asn Ser
820 825 830

Glu Glu Trp Ile Gly Ala Asp Pro Lys Arg Arg Ser Phe Pro Glu Leu
835 840 845

Asn Ser Lys Leu Leu Val Val Ala Arg Arg Gly Gln Ser Trp Leu Ala
850 855 860

Arg Leu His Arg Trp Leu Trp Met Leu Gly Asp Glu Asn Lys Arg Glu
865 870 875 880

Arg Ala Leu Arg Glu Leu Leu Glu Gln Glu Arg Gln Glu Ala Trp Arg
885 890 895

Lys Arg Ala Glu Gly Lys Asp Leu Leu Ala Leu Lys Gln Ser Leu Thr
900 905 910

Ala Glu Ile Gln Arg Leu Asn Gly Leu Leu Pro Glu Gln Leu Val Phe
915 920 925

Leu Ala Asn Arg Cys Leu Pro Leu Arg Asn Arg Lys Trp Ala Trp Asn
930 935 940

Gln His Pro Asp Lys Ala Phe Ala Glu Lys Gly Cys His Leu Leu Glu
945 950 955 960

Met Val Glu Ala Pro Ser His Leu Pro Leu Leu Ala Gly Gln Arg Gly
965 970 975

Ile Ser Phe Glu Arg Ile Gly Gln Leu Glu Glu Leu Arg Arg Arg Phe
980 985 990

Gln Ser Leu Asn Arg Val Leu Gln Arg Glu Leu Gly Ala Pro Pro Lys

995 1000 1005

Ser Gly Arg Glu Leu Arg Asp Asp Leu Val Pro Asp Cys Cys Pro

1010 1015 1020

Asp Ile Leu Ala Lys Leu Asp Arg Val Lys Glu Gln Arg Val Asn

1025 1030 1035

Gln Thr Ala His Leu Ile Val Ala Gln Val Leu Gly Val Gln Leu

1040 1045 1050

Arg Lys His Gln Thr Pro Glu Ser Glu Arg Thr Glu Arg Asp Leu

1055 1060 1065

His Gly Glu Tyr Glu Ile Met Pro Gly Arg Lys Pro Val Asp Phe

1070 1075 1080

Ile Val Leu Glu Asp Leu Ser Lys Tyr Leu Ser Ser Gln Ala Arg

1085 1090 1095

Gly Arg Gly Glu Asn Val Arg Leu Met Lys Trp Cys His Arg Gln

1100 1105 1110

Val Thr Ala Lys Val Lys Glu Leu Cys Glu Pro Phe Gly Leu Pro

1115 1120 1125

Val Leu Glu Thr Pro Ala Ala Tyr Ser Ser Lys Phe Cys Ser Arg

1130 1135 1140

Thr Gly Val Ala Gly Phe Arg Gly Val Glu Val Thr Leu Lys Asp

1145 1150 1155

Arg Gln Ser Phe Pro Trp Ser Lys Arg Leu Glu Glu Asp Ser Ala

1160 1165 1170

Glu Val Ala Glu Leu Phe Gly Trp Leu Glu Thr Ala Ser Ala Gly

1175 1180 1185

His Lys Thr Lys Gln Pro Arg Cys Leu Leu Ala Pro Met Ser Leu

1190 1195 1200

Gly Pro Leu Phe Ile Pro Val Thr Ser Gln Ala Pro Ile Met Gln

1205 1210 1215

Ala Asp Ile Asn Ala Ala Ile Asn Leu Gly Leu Arg Ala Met Ala

1220 1225 1230

Ala Pro Ser Val His Glu Ile His Val Arg Ile Arg Ser Glu Ala
1235 1240 1245
Lys Asp Gly Gln Phe Arg Val Arg Ala Gln Ser Lys Arg Glu Lys
1250 1255 1260
Ala Arg Trp Gly Asn Glu Pro Pro Pro Ile Lys Met Leu Val Glu
1265 1270 1275
Thr Gln Arg Val Ala Leu Ala Arg Glu Gly Gly His Pro Asn Phe
1280 1285 1290

Phe Val Asp Pro Leu Lys Ala Ala Thr Phe Asp Arg Ala Glu Val
1295 1300 1305
Glu Gly Leu Gly Leu Pro Val Ala Ser Gly Arg Gly Leu Trp Lys
1310 1315 1320
Ser Val Arg Asp Ala Glu Trp Lys Arg Cys Arg Glu Ile Asn Leu
1325 1330 1335
Glu Arg Met Arg Arg Trp Gly Phe Ile Met Glu Ala Pro Arg Thr
1340 1345 1350

Leu Gln Val Ser Arg Lys Glu Asp Glu Asp Asp Leu Thr Phe
1355 1360 1365
<210> 127
<211> 1202
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 127
Met Ala Val Arg Ser Val Lys Leu Lys Leu Leu Val Pro Arg Asp Gly
1 5 10 15
Ser Ala Glu Ser Val Arg Lys Arg Lys Ala Leu Trp Ala Thr His Gln
20 25 30

Phe Val Asn Asp Ala Ala Ala Ala Tyr Ala Glu Leu Leu Leu Glu Met
35 40 45
Arg Gln Glu Asp Val Cys Arg Gly Thr Asp Asp His Gly Lys Asp Val

50 55 60

Ile Glu Pro Ala Ala His Trp Gln Ala Lys Leu Arg Ala Arg Leu Ala
65 70 75 80

Ala Lys Gln Leu Pro Pro Val Ala Val Ala Glu Ala Leu Pro Leu Leu
85 90 95

Lys Ala Phe Tyr Gly Ser Arg Leu Ile Lys Ser Phe Val Ala Asn Asp
100 105 110

Lys Gly Val Ala Gly Thr Gly Asn Ala Thr Asp Leu Asn Thr Trp Leu
115 120 125

Ser Gly Leu Val Asp Pro Ala Ser Val Ala Gly Glu Lys Thr Glu Leu
130 135 140

Arg Lys Gln Leu Leu Ala Glu Leu Pro Leu Cys Glu Ala Ala Asp Ala
145 150 155 160

Asp Phe Glu Gly Ala Ala Arg Lys Met Leu Ala Lys Ser Asp Ala Arg
165 170 175

Glu Ala Leu Leu Glu Gly Pro Gly Thr Gly Val Gly Trp Pro Ala Ala
180 185 190

Tyr Asn Ala Asn Pro Thr Asp Ser Val Trp Leu Asp Met Leu His Lys
195 200 205

Ala Ala Ala Lys Ala Arg Leu Glu Leu Ala Asp Thr Thr Val Ser Glu
210 215 220

Leu Lys Lys Leu Gly Val Phe Pro Leu Leu Gln Ala Ala Ser Ser Asn
225 230 235 240

Arg Val Phe Gly Ser Gly Val Leu Asn Pro Phe Glu Arg Met Ala Ala
245 250 255

Ala Gln Ala Ala Ala Ala Leu Leu Pro Trp Glu Thr Lys Arg His Glu
260 265 270

Met Arg Lys Arg Arg Asp Lys Phe Ala Asp Gln Leu Asn Gln Trp Asp
275 280 285

Thr Glu Phe Gly Ala Ser His Ala Thr Ala Leu Ala Ala Ile Arg Ala
290 295 300

Phe Glu Ala Glu Glu Ser Glu Arg Ala Arg Arg Glu Ser Leu Gly Asn
305 310 315 320
Glu Gly Thr Gly Tyr Arg Ile Gly Gly Arg Glu Leu Arg Asp Ala Trp
325 330 335
Thr Leu Leu Arg Asp Trp Leu Lys Gly His Ser Thr Ala Thr Ala Ala
340 345 350

Ala Arg Glu Asp Lys Val Arg Glu Leu Gln Ala Lys Gln Gly Arg Ser
355 360 365
Phe Gly Ser His Arg Leu Leu Ser Trp Leu Ala Lys Pro Ala Gln Gln
370 375 380
Trp Leu Ala Asp His Ser Ala Gly Asp Val Val Thr Arg Ile Ala Val
385 390 395 400
Arg Asn Ala Arg Gln Arg Lys Leu Asp Thr Ala Arg Thr Leu Pro Ile
405 410 415

Trp Thr Gly Ala Asp Ala Val Lys His Pro Arg Phe Ala Asn Phe Asp
420 425 430
Pro Pro Asn Asn Thr Asn Gln Pro Gly Phe Asp Leu Arg Ala Gly Thr
435 440 445
Gln Lys Gly Arg Leu Thr Leu Arg Leu Ser Leu Leu Thr Glu Arg Ala
450 455 460
Asp Gly Leu Leu Leu Ala Gln Asp His Asp Phe Gln Leu Val Pro Ser
465 470 475 480

Arg Gln Met Ala Glu Ile Val Leu His Lys Asp Gly Lys Glu Arg Ala
485 490 495
Leu Ser Trp Gln Ser Gln Asp Gly Ile Gly Arg Gln Val Gly Asp Val
500 505 510
Gly Gly Ser Ala Leu Leu Phe Ser Arg Asp His Ala Glu Cys Leu Leu
515 520 525
Glu Arg Lys Gln Ile Thr Arg Leu Glu Arg Gly Ala Trp Pro Ala Ala
530 535 540

Leu Pro Val Trp Phe Lys Leu Ser Leu Asp Ile Gly Ala Glu His Lys

545 550 555 560

Ala Leu Leu Lys Gln Arg Phe Lys Trp Gly Val Trp Leu Asn Ser Ala

565 570 575

Leu Val Thr Arg Asn Ala Lys Asp Ala Lys Gly Val Pro Pro Pro Val

580 585 590

Gly Thr Arg Val Leu Ala Val Asp Leu Gly Leu Arg Ser Ala Ala Thr

595 600 605

Val Ser Val Trp Gln Val Val Asp Ala Ala Thr Pro Val Val Ala Gly

610 615 620

Lys Trp Arg Val Pro Leu Ser Asp Thr Leu Ser Ala Val His Glu Arg

625 630 635 640

Ser Ala Met Leu Ala Leu Pro Gly Glu His Val Asp Ala Gly Val Leu

645 650 655

Ala Ala Arg Arg Ala Ala Asn Glu Lys Leu Ala Gly Leu Leu Ala Ala

660 665 670

Thr Ser His Leu Ser Thr Val Phe Lys Leu Gly Arg Ala Glu Gln Gly

675 680 685

Asp Arg Arg Arg Glu Leu Leu Glu Arg Leu Gly Glu Gly Asp Asp Arg

690 695 700

Arg Ala Arg Ala Ala Val Ala Thr Thr Ala Ala Glu Arg Asp Gly Leu

705 710 715 720

Arg Ala Val Leu Gly Ala Thr Gln Asp Ala Trp Ala Gly Ala Val Ala

725 730 735

Ala Val Trp Arg Arg Leu Glu Thr Asp Leu Ala Gly Ala Ile Ala Ala

740 745 750

Tyr Arg Lys Gln Gln Arg Glu Asp Val Gln Leu Arg Arg Glu Ala Arg

755 760 765

His Gly Pro Gly Ala Ser Gln Leu Pro Lys Gln Ala Ala Ala Glu Arg

770 775 780

Leu Leu Gly Gly Lys Ser Ala Trp Gln Ile Glu Tyr Lys Glu Arg Val

785 790 795 800

Arg Lys Leu Leu Thr Arg Trp Ile Met Arg Gln Arg Pro Gly Asp Thr
805 810 815
Ala Val Arg Arg Leu Ala Arg Lys Asp Leu Gly Lys Tyr Cys Gly Gly
820 825 830
Leu Leu Asp His Leu Thr Ala Leu Lys Glu Asp Arg Ala Lys Thr Thr
835 840 845
Ala Asp Leu Ile Val Gln Ala Ala Arg Gly Arg Val Arg Ala His Lys
850 855 860

Asp Ala His Gly Arg Gln Gln Asp Arg Glu Leu Trp Leu Ala Lys Tyr
865 870 875 880
Ala Pro Cys Asp Leu Ile Val Met Glu Asp Leu Gly Arg Tyr Arg Phe
885 890 895
Ala Thr Asp Arg Pro Pro Ser Glu Asn Arg Gln Leu Met Gln Trp Thr
900 905 910
His Arg Glu Val Phe Arg Leu Val Gln Met Gln Ala Glu Val Glu Gly
915 920 925

Ile Gln Val Leu Glu Thr Gly Ala Glu Phe Ser Ser Lys Phe Asp Ala
930 935 940
Arg Thr Trp Ala Pro Gly Val Arg Cys Glu Pro Ile Thr Lys Leu Trp
945 950 955 960
Val Glu Arg Tyr Arg Asn Gly Glu Met Pro Trp Leu Ala Asp Lys Ala
965 970 975
Asp Glu Trp Arg Arg Glu Gly Ile Glu Leu Ala Gln Leu Val Pro Gly
980 985 990

Gln Leu Leu Pro Thr Gly Ser Gly Glu Gln Phe Val Ala Val Ser Ala
995 1000 1005
Thr Gly Gly Leu Arg Val Arg His Ala Asp Leu Asn Ala Ala Gln
1010 1015 1020
Cys Ile Ala Leu Arg Ala Leu Thr Gly His Gly Thr Ala Phe Arg
1025 1030 1035
Leu Thr Ala Arg Arg Leu Gly Asp Val Phe Val Ser Ala Lys Gly

1040 1045 1050

Leu Gly Lys Arg Pro Gln Gly Ala Leu Trp Arg Glu Phe Gly Ser
1055 1060 1065
Ala Leu Pro Pro Ala Val Val Val Leu Arg Pro Ala Gly Glu Val
1070 1075 1080
Arg Tyr Ala Leu Arg Pro Phe Ala Ser Ala Arg Asp Ala Ala Ala
1085 1090 1095
Ala Leu Gly Leu Gln Leu Gly Ala Leu Arg Asn Val Asp Ala Thr
1100 1105 1110

Asp Ala Glu Ser Asp Ala Glu Asp Gly Asp Leu Ala Glu Leu Leu
1115 1120 1125
Ala Gly Ala Asp Pro Asp Arg Ala Thr Phe Phe Arg Asp Pro Ser
1130 1135 1140
Gly Asp Val His Gly Gly Ala Trp Val Gln Ala Lys Val Phe Trp
1145 1150 1155
Ala Glu Val Arg Arg His Val Arg Leu Gly Leu Gln Ala Gln Gly
1160 1165 1170

Leu Leu Pro Ala Ala Ala Arg Ser Ser Glu Pro Arg Gln Met Gln
1175 1180 1185
Leu Pro Leu Ala Gly Ala Leu Pro Gly Asp Asp Ile Pro Leu
1190 1195 1200

<210> 128
<211> 1352
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 128
Met Ser Thr Gln Lys Asn Pro Phe Asn Gln Phe Thr Asn Leu Tyr Glu
1 5 10 15
Leu Gln Lys Thr Leu Arg Phe Glu Leu Arg Pro Val Pro Glu Thr Lys

20 25 30

Lys Leu Leu Glu Lys Gly Glu Gly Lys Asn Leu Ile Gln Met Asp Leu

35 40 45

Glu Ile Asp Arg Leu Tyr Glu Lys Glu Met Lys Pro Met Phe Asn Ile

50 55 60

Leu His Glu Lys Phe Ile Asn Glu Ser Leu Gly Leu Val Lys Leu Asp

65 70 75 80

Cys Lys Lys Leu Lys Lys Leu Glu Asn Leu Leu Ala Glu Ala Asp Lys

85 90 95

Leu Arg Lys Gln Ile Lys Glu Gly Arg Lys Asn Lys Asn Asn Ile Ser

100 105 110

Glu Val Glu Lys Arg Leu Lys Ile Ile Ile Gly Asp Asn Ser Gln Gly

115 120 125

Lys Asn Lys Asn Gly Glu Ile Ala Val Leu Gln Asp Glu Leu Arg Val

130 135 140

Leu Ile Val Lys Ala Phe Asn Leu Thr Ala Asp Lys Trp Lys Lys Glu

145 150 155 160

Leu Asn Asn Lys Glu Thr Leu Leu Pro Glu Lys Lys Gly Lys Arg Lys

165 170 175

Ile Lys Ile Lys Lys Ser Gly Pro Lys Ile Leu Gln Glu Glu Asn Val

180 185 190

Leu Ala Ile Leu Ala Tyr Phe Asn Pro Asp Lys Ala Asp Ile Ile Lys

195 200 205

Lys Phe Ala Gly Phe Phe Thr Tyr Phe Ser Gly Phe Asn Gln Asn Arg

210 215 220

Ala Asn Tyr Tyr Thr Val Lys Ala Leu Ala Thr Gly Val Ala Asn Arg

225 230 235 240

Ala Ile Asn Arg Asn Phe Leu Ile Phe Leu Ala Asn Arg Lys Asp Phe

245 250 255

Ala Arg Phe Lys Glu Arg Leu Pro Arg Leu Ala Glu Phe Asp Asn Tyr

260 265 270

Phe Glu Leu Glu Asn Tyr Glu Lys Tyr Leu Ser Gln Thr Gly Ile Glu

275 280 285

Glu Tyr Asn Asp Gln Ile Gly Lys Ile Lys Gln Ile Val Asn Leu Glu

290 295 300

His Asn Gln Gln Gln Lys Asp Asn Lys Phe Gln Leu Lys Gly Leu Ala

305 310 315 320

Thr Leu Glu Lys Gln Ile Gly Cys Arg Thr Lys Lys Gln Arg Glu Glu

325 330 335

Gly Gly Asp Lys Ser Ala Pro Lys Phe Leu Glu Lys Val Gly Leu Gly

340 345 350

Phe Gln Val Ser Gln Asp Asp Asp Gly Glu Tyr Leu Ile Trp Glu Cys

355 360 365

Leu Asn Tyr Ile Asn Lys Glu Leu Ala Gly Lys Leu Lys Ser Ile Lys

370 375 380

Asp Asn Tyr Gln Lys Phe Phe Ala Asp Trp Arg Thr Gly Ala Tyr Asp

385 390 395 400

Leu Glu Lys Ile Trp Phe Arg Lys Glu Ala Leu Asn Thr Ile Ser Gly

405 410 415

Arg Trp Phe Gly Gly Asn Asn Trp Phe Ile Ile Gly Lys Ala Leu Ala

420 425 430

Leu Thr Gly Val Gly Lys Phe Asp Lys Arg Glu Asn Thr Tyr Lys Ile

435 440 445

Pro Glu Phe Val Ser Leu Ala Glu Ile Lys Thr Ala Phe Glu Met Leu

450 455 460

Glu Asn Gly Val Asn Tyr Asp Phe Lys Lys Ser Lys Lys Lys Lys Glu

465 470 475 480

Gly Asp Asp Thr Asp Val Val Lys Tyr Ser Ala Asp Asn Leu Phe Lys

485 490 495

Glu Glu Tyr Lys Lys Lys Gly Leu Ile Lys Asn Ser Leu Phe Glu Thr

500 505 510

Met Leu Ala Val Trp Gln Ser Glu Ile Lys Arg Lys Phe Glu Gln Ile

515 520 525

Phe Asp Gly Tyr Lys Leu Glu Lys Asp Asp Val Phe Gly Arg Lys Lys

530 535 540

Gly Glu Trp Val Glu Pro Phe Ile Glu Asn Phe Gln Lys Val Ser Gln

545 550 555 560

Glu Lys Phe Asp Arg Gly Val Lys Asp Glu Asn Gly Arg Ser Ile His

565 570 575

Thr Glu Val Val Lys Asn Leu Ile Glu Glu Gly Tyr Leu Arg Leu Phe

580 585 590

Gln Leu Thr Lys Tyr His Asn Leu Asp Lys Lys Gly Glu Arg Asp Pro

595 600 605

Arg Pro Phe Asp Gly Asn Phe Tyr Ala Thr Leu Asp Glu Phe Trp Lys

610 615 620

Asp Asn Ile Val Val Val Tyr His Lys Ala Leu Gln Ser Thr Leu Thr

625 630 635 640

Lys Lys Pro Tyr Ser Glu Asp Lys Ile Lys Leu Asn Phe Glu Asn Gly

645 650 655

Ser Leu Leu Gly Gly Phe Ser Asp Gly Gln Glu Arg Ser Lys Ala Gly

660 665 670

Val Val Leu Lys Asn Lys Asn Lys Phe Tyr Leu Gly Ile Leu Ile Asp

675 680 685

Arg Gly Phe Phe Arg Thr Asp Lys Ala Asn Pro Val Tyr Asp Asn Ala

690 695 700

Gln Asn Asn Glu Trp Glu Arg Leu Ile Leu Thr Asn Leu Lys Phe Gln

705 710 715 720

Thr Leu Ala Gly Lys Gly Phe Leu Gly Lys His Gly Val Ser Tyr Gly

725 730 735

Glu Met Gly Lys Asp Asn Pro Met Met Ala Val Glu Tyr Leu Gln Lys

740 745 750

Phe Ile Lys Leu Lys Tyr Leu Asp Lys Tyr Pro Ala Leu Asn Glu Val

755 760 765

Ala His Lys Lys Tyr Thr Ile Lys Lys Glu Phe Asp Ala Asp Val Lys

770 775 780

Asn Ala Leu Lys Asp Cys Phe Thr Met Asn Phe Lys Pro Val Asp Phe

785 790 795 800

Gly Met Ile Arg Gln Gly Leu Thr Glu Ser Leu Phe Tyr Leu Phe Glu

805 810 815

Ile Val Asn Lys Asp Ile Ser Ser Gln Ala Lys Asn Gly Lys Asn Val

820 825 830

His Thr Leu Tyr Trp Glu Ala Leu Phe Gly Asp Gln Asn Leu Lys Lys

835 840 845

Pro Ile Leu Ala Leu Asn Gly Gly Ala Glu Ile Phe Tyr Arg Glu Ser

850 855 860

Gln Arg Glu Lys Leu Glu Lys Lys Leu Asp Lys Ser Gly Lys Glu Val

865 870 875 880

Leu Asp His Lys Arg Tyr Gly Gln Asp Lys Tyr Phe Leu His Ala Ser

885 890 895

Ile Thr Ile Asn Tyr Gly Gln Pro Lys Asn Ile Lys Phe Lys Glu Val

900 905 910

Ile Asn Glu Lys Ile Ser Gln Asn Ala Asp Arg Val Asn Ile Ile Gly

915 920 925

Ile Asp Arg Gly Glu Lys His Leu Leu Tyr Tyr Ser Val Val Ser Pro

930 935 940

Glu Gly Val Leu Leu Glu Gln Gly Ser Phe Asn Gln Ile Glu Thr Lys

945 950 955 960

Asn Lys Val Asp Ile Lys Ala Val Lys Ala Glu Tyr Gly Glu Arg Gly

965 970 975

Glu Leu Lys Lys Val Glu Leu Val Pro Thr Gly Lys Lys Val Lys Tyr

980 985 990

Val Asp Tyr Gln Ile Leu Leu Asp Tyr Tyr Glu Lys Lys Arg Asn Leu

995 1000 1005

Ala Arg Arg Asp Trp Gln Thr Ile Gly Lys Ile Lys Asp Leu Lys

1010 1015 1020

Asp Gly Tyr Leu Ser Gln Thr Val His Arg Ile Tyr Gln Leu Ile

1025 1030 1035

Leu Lys Tyr Asn Ala Val Val Ala Met Glu Asp Leu Asn Val Glu

1040 1045 1050

Phe Lys Ala Lys Arg Ala Ala Lys Val Glu Lys Ser Val Tyr Lys

1055 1060 1065

Asn Phe Glu Met Ala Leu Ala Lys Lys Leu Asn His Leu Ile Leu

1070 1075 1080

Lys Asp Arg Arg Ala Asp Glu Ile Gly Gly Ala Leu Arg Ala Tyr

1085 1090 1095

Gln Leu Thr Pro Ala Ile Pro Ala Asn Asp Val Gly Lys Phe Asp

1100 1105 1110

Lys Ala Lys Gln Trp Gly Ile Met Phe Tyr Val Arg Ala Asn Tyr

1115 1120 1125

Thr Ser Thr Thr Asp Pro Leu Thr Gly Trp Arg Lys His Lys Tyr

1130 1135 1140

Ile Ser Asn Ser Glu Lys Ile Asp Asn Ile Gln Lys Phe Phe Ser

1145 1150 1155

Pro Gly Asp Gly Ile Gln Ile Asp Tyr Asp Thr Glu Lys Gln Cys

1160 1165 1170

Phe Lys Phe Ser Tyr Asp His Glu Leu Glu Gly Gly Ala Lys Lys

1175 1180 1185

His Trp Glu Leu Phe Ala Cys Asp Gly Leu Glu Arg Phe Tyr Trp

1190 1195 1200

Asp Asn Arg Glu Arg Gln Ile Lys Lys Tyr Asn Leu Tyr Glu Glu

1205 1210 1215

Phe Glu Lys Leu Leu Gly Gly Leu Arg Lys Glu Glu Asn Ile Asn

1220 1225 1230

Ile Gln Ile Asp Gly Val Ser Glu Phe Arg Trp Lys Asp Leu Val

1235 1240 1245

Phe Phe Trp Asn Leu Leu Asn Gln Ile Arg Asn Thr Asp Arg Ser

1250 1255 1260

Ala Gln Gly Asp Glu Asn Asp Phe Leu Gln Ser Pro Val Trp Ser

1265 1270 1275

Glu Lys Tyr Asn Cys Phe Tyr Asp Ser Arg Lys Ala Pro Asn Asn

1280 1285 1290

Met Pro Asn Asn Gly Asp Ala Asn Gly Ala Phe Asn Ile Ala Arg

1295 1300 1305

Lys Gly Gln Leu Ile Leu Glu Arg Ile Lys Lys Cys Ser Asp Ile

1310 1315 1320

Pro Lys Phe Gly Asn Asp Asn Asn Gly Lys Asn Pro Glu Asn Asn

1325 1330 1335

Tyr Phe Ile Ser Asp Ala Asp Trp Asp Lys Phe Ala Gln Lys

1340 1345 1350

<210> 129

<211> 1129

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 129

Met Ala Val Lys Ser Ile Lys Val Lys Leu Arg Leu Asp Asp Met Pro

1 5 10 15

Glu Ile Arg Ala Gly Leu Trp Lys Leu His Lys Glu Val Asn Ala Gly

20 25 30

Val Arg Tyr Tyr Thr Glu Trp Leu Ser Leu Leu Arg Gln Glu Asn Leu

35 40 45

Tyr Arg Arg Ser Pro Asn Gly Asp Gly Glu Gln Glu Cys Asp Lys Thr

50 55 60

Ala Glu Glu Cys Lys Ala Glu Leu Leu Glu Arg Leu Arg Ala Arg Gln

65 70 75 80

Val Glu Asn Gly His Arg Gly Pro Ala Gly Ser Asp Asp Glu Leu Leu

85 90 95

Gln Leu Ala Arg Gln Leu Tyr Glu Leu Leu Val Pro Gln Ala Ile Gly

100 105 110

Ala Lys Gly Asp Ala Gln Gln Ile Ala Arg Lys Phe Leu Ser Pro Leu

115 120 125

Ala Asp Lys Asp Ala Val Gly Gly Leu Gly Ile Ala Lys Ala Gly Asn

130 135 140

Lys Pro Arg Trp Val Arg Met Arg Glu Ala Gly Glu Pro Gly Trp Glu

145 150 155 160

Glu Glu Lys Glu Lys Ala Glu Thr Arg Lys Ser Ala Asp Arg Thr Ala

165 170 175

Asp Val Leu Arg Ala Leu Ala Asp Phe Gly Leu Lys Pro Leu Met Arg

180 185 190

Val Tyr Thr Asp Ser Glu Met Ser Ser Val Glu Trp Lys Pro Leu Arg

195 200 205

Lys Gly Gln Ala Val Arg Thr Trp Asp Arg Asp Met Phe Gln Gln Ala

210 215 220

Ile Glu Arg Met Met Ser Trp Glu Ser Trp Asn Gln Arg Val Gly Gln

225 230 235 240

Glu Tyr Ala Lys Leu Val Glu Gln Lys Asn Arg Phe Glu Gln Lys Asn

245 250 255

Phe Val Gly Gln Glu His Leu Val His Leu Val Asn Gln Leu Gln Gln

260 265 270

Asp Met Lys Glu Ala Ser Pro Gly Leu Glu Ser Lys Glu Gln Thr Ala

275 280 285

His Tyr Val Thr Gly Arg Ala Leu Arg Gly Ser Asp Lys Val Phe Glu

290 295 300

Lys Trp Gly Lys Leu Ala Pro Asp Ala Pro Phe Asp Leu Tyr Asp Ala

305 310 315 320

Glu Ile Lys Asn Val Gln Arg Arg Asn Thr Arg Arg Phe Gly Ser His

325 330 335

Asp Leu Phe Ala Lys Leu Ala Glu Pro Glu Tyr Gln Ala Leu Trp Arg

340 345 350

Glu Asp Ala Ser Phe Leu Thr Arg Tyr Ala Val Tyr Asn Ser Ile Leu

355 360 365

Arg Lys Leu Asn His Ala Lys Met Phe Ala Thr Phe Thr Leu Pro Asp

370 375 380

Ala Thr Ala His Pro Ile Trp Thr Arg Phe Asp Lys Leu Gly Gly Asn

385 390 395 400

Leu His Gln Tyr Thr Phe Leu Phe Asn Glu Phe Gly Glu Arg Arg His

405 410 415

Ala Ile Arg Phe His Lys Leu Leu Lys Val Glu Asn Gly Val Ala Arg

420 425 430

Glu Val Asp Asp Val Thr Val Pro Ile Ser Met Ser Glu Gln Leu Asp

435 440 445

Asn Leu Leu Pro Arg Asp Pro Asn Glu Pro Ile Ala Leu Tyr Phe Arg

450 455 460

Asp Tyr Gly Ala Glu Gln His Phe Thr Gly Glu Phe Gly Gly Ala Lys

465 470 475 480

Ile Gln Cys Arg Arg Asp Gln Leu Ala His Met His Arg Arg Arg Gly

485 490 495

Ala Arg Asp Val Tyr Leu Asn Val Ser Val Arg Val Gln Ser Gln Ser

500 505 510

Glu Ala Arg Gly Glu Arg Arg Pro Pro Tyr Ala Ala Val Phe Arg Leu

515 520 525

Val Gly Asp Asn His Arg Ala Phe Val His Phe Asp Lys Leu Ser Asp

530 535 540

Tyr Leu Ala Glu His Pro Asp Asp Gly Lys Leu Gly Ser Glu Gly Leu

545 550 555 560

Leu Ser Gly Leu Arg Val Met Ser Val Asp Leu Gly Leu Arg Thr Ser

565 570 575

Ala Ser Ile Ser Val Phe Arg Val Ala Arg Lys Asp Glu Leu Lys Pro

580 585 590

Asn Ser Lys Gly Arg Val Pro Phe Phe Phe Pro Ile Lys Gly Asn Asp

595 600 605

Asn Leu Val Ala Val His Glu Arg Ser Gln Leu Leu Lys Leu Pro Gly

610 615 620

Glu Thr Glu Ser Lys Asp Leu Arg Ala Ile Arg Glu Glu Arg Gln Arg

625 630 635 640

Thr Leu Arg Gln Leu Arg Thr Gln Leu Ala Tyr Leu Arg Leu Leu Val

645 650 655

Arg Cys Gly Ser Glu Asp Val Gly Arg Arg Glu Arg Ser Trp Ala Lys

660 665 670

Leu Ile Glu Gln Pro Val Asp Ala Ala Asn His Met Thr Pro Asp Trp

675 680 685

Arg Glu Ala Phe Glu Asn Glu Leu Gln Lys Leu Lys Ser Leu His Gly

690 695 700

Ile Cys Ser Asp Lys Glu Trp Met Asp Ala Val Tyr Glu Ser Val Arg

705 710 715 720

Arg Val Trp Arg His Met Gly Lys Gln Val Arg Asp Trp Arg Lys Asp

725 730 735

Val Arg Ser Gly Glu Arg Pro Lys Ile Arg Gly Tyr Ala Lys Asp Val

740 745 750

Val Gly Gly Asn Ser Ile Glu Gln Ile Glu Tyr Leu Glu Arg Gln Tyr

755 760 765

Lys Phe Leu Lys Ser Trp Ser Phe Phe Gly Lys Val Ser Gly Gln Val

770 775 780

Ile Arg Ala Glu Lys Gly Ser Arg Phe Ala Ile Thr Leu Arg Glu His

785 790 795 800

Ile Asp His Ala Lys Glu Asp Arg Leu Lys Lys Leu Ala Asp Arg Ile

805 810 815

Ile Met Glu Ala Leu Gly Tyr Val Tyr Ala Leu Asp Glu Arg Gly Lys

820 825 830

Gly Lys Trp Val Ala Lys Tyr Pro Pro Cys Gln Leu Ile Leu Leu Glu

835 840 845

Glu Leu Ser Glu Tyr Gln Phe Asn Asn Asp Arg Pro Pro Ser Glu Asn

850 855 860

Asn Gln Leu Met Gln Trp Ser His Arg Gly Val Phe Gln Glu Leu Ile

865 870 875 880

Asn Gln Ala Gln Val His Asp Leu Leu Val Gly Thr Met Tyr Ala Ala

885 890 895

Phe Ser Ser Arg Phe Asp Ala Arg Thr Gly Ala Pro Gly Ile Arg Cys

900 905 910

Arg Arg Val Pro Ala Arg Cys Thr Gln Glu His Asn Pro Glu Pro Phe

915 920 925

Pro Trp Trp Leu Asn Lys Phe Val Val Glu His Thr Leu Asp Ala Cys

930 935 940

Pro Leu Arg Ala Asp Asp Leu Ile Pro Thr Gly Glu Gly Glu Ile Phe

945 950 955 960

Val Ser Pro Phe Ser Ala Glu Glu Gly Asp Phe His Gln Ile His Ala

965 970 975

Asp Leu Asn Ala Ala Gln Asn Leu Gln Gln Arg Leu Trp Ser Asp Phe

980 985 990

Asp Ile Ser Gln Ile Arg Leu Arg Cys Asp Trp Gly Glu Val Asp Gly

995 1000 1005

Glu Leu Val Leu Ile Pro Arg Leu Thr Gly Lys Arg Thr Ala Asp

1010 1015 1020

Ser Tyr Ser Asn Lys Val Phe Tyr Thr Asn Thr Gly Val Thr Tyr

1025 1030 1035

Tyr Glu Arg Glu Arg Gly Lys Lys Arg Arg Lys Val Phe Ala Gln

1040 1045 1050

Glu Lys Leu Ser Glu Glu Glu Ala Glu Leu Leu Val Glu Ala Asp

1055 1060 1065

Glu Ala Arg Glu Lys Ser Val Val Leu Met Arg Asp Pro Ser Gly

1070 1075 1080

Ile Ile Asn Arg Gly Asn Trp Thr Arg Gln Lys Glu Phe Trp Ser

1085 1090 1095

Met Val Asn Gln Arg Ile Glu Gly Tyr Leu Val Lys Gln Ile Arg

1100 1105 1110

Ser Arg Val Pro Leu Gln Asp Ser Ala Cys Glu Asn Thr Gly Asp

1115 1120 1125

Ile

<210> 130

<211> 1352

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 130

Met Ser Thr Gln Lys Asn Pro Phe Asn Gln Phe Thr Asn Leu Tyr Glu

1 5 10 15

Leu Gln Lys Thr Leu Arg Phe Glu Leu Arg Pro Val Pro Glu Thr Lys

20 25 30

Lys Leu Leu Glu Lys Gly Glu Gly Lys Asn Leu Ile Gln Met Asp Leu

35 40 45

Glu Ile Asp Arg Leu Tyr Glu Lys Glu Met Lys Pro Met Phe Asn Ile

50 55 60

Leu His Glu Lys Phe Ile Asn Glu Ser Leu Gly Leu Val Lys Leu Asp

65 70 75 80

Cys Lys Lys Leu Lys Lys Leu Glu Asn Leu Leu Ala Glu Ala Asp Lys

85 90 95

Leu Arg Lys Gln Ile Lys Glu Gly Arg Lys Asn Lys Asn Asn Ile Ser

100 105 110

Glu Val Glu Lys Arg Leu Lys Ile Ile Ile Gly Asp Asn Ser Gln Gly

115 120 125

Lys Asn Lys Asn Gly Glu Ile Ala Val Leu Gln Asp Glu Leu Arg Val
130 135 140
Leu Ile Val Lys Ala Phe Asn Leu Thr Ala Asp Lys Trp Lys Lys Glu
145 150 155 160
Leu Asn Asn Lys Glu Thr Leu Leu Pro Glu Lys Lys Gly Lys Arg Lys

165 170 175
Ile Lys Ile Lys Lys Ser Gly Pro Lys Ile Leu Gln Glu Glu Asn Val
180 185 190
Leu Ala Ile Leu Ala Tyr Phe Asn Pro Asp Lys Ala Asp Ile Ile Lys
195 200 205
Lys Phe Ala Gly Phe Phe Thr Tyr Phe Ser Gly Phe Asn Gln Asn Arg
210 215 220
Ala Asn Tyr Tyr Thr Val Lys Ala Leu Ala Thr Gly Val Ala Asn Arg

225 230 235 240
Ala Ile Asn Arg Asn Phe Leu Ile Phe Leu Ala Asn Arg Lys Asp Phe
245 250 255
Ala Arg Phe Lys Glu Arg Leu Pro Arg Leu Ala Glu Phe Asp Asn Tyr
260 265 270
Phe Glu Leu Glu Asn Tyr Glu Lys Tyr Leu Ser Gln Thr Gly Ile Glu
275 280 285
Glu Tyr Asn Asp Gln Ile Gly Lys Ile Lys Gln Ile Val Asn Leu Glu

290 295 300
His Asn Gln Gln Gln Lys Asp Asn Lys Phe Gln Leu Lys Gly Leu Ala
305 310 315 320
Thr Leu Glu Lys Gln Ile Gly Cys Arg Thr Lys Lys Gln Arg Glu Glu
325 330 335
Gly Gly Asp Lys Ser Ala Pro Lys Phe Leu Glu Lys Val Gly Leu Gly
340 345 350
Phe Gln Val Ser Gln Asp Asp Asp Gly Glu Tyr Leu Ile Trp Glu Cys

355 360 365
Leu Asn Tyr Ile Asn Lys Glu Leu Ala Gly Lys Leu Lys Ser Ile Lys

370 375 380

Asp Asn Tyr Gln Lys Phe Phe Ala Asp Trp Arg Thr Gly Ala Tyr Asp

385 390 395 400

Leu Glu Lys Ile Trp Phe Arg Lys Glu Ala Leu Asn Thr Ile Ser Gly

405 410 415

Arg Trp Phe Gly Gly Asn Asn Trp Phe Ile Ile Gly Lys Ala Leu Ala

420 425 430

Leu Thr Gly Val Gly Lys Phe Asp Lys Arg Glu Asn Thr Tyr Lys Ile

435 440 445

Pro Glu Phe Val Ser Leu Ala Glu Ile Lys Thr Ala Phe Glu Met Leu

450 455 460

Glu Asn Gly Val Asn Tyr Asp Phe Lys Lys Ser Lys Lys Lys Lys Glu

465 470 475 480

Gly Asp Asp Thr Asp Val Val Lys Tyr Ser Ala Asp Asn Leu Phe Lys

485 490 495

Glu Glu Tyr Lys Lys Lys Gly Leu Ile Lys Asn Ser Leu Phe Glu Thr

500 505 510

Met Leu Ala Val Trp Gln Ser Glu Ile Lys Arg Lys Phe Glu Gln Ile

515 520 525

Phe Asp Gly Tyr Lys Leu Glu Lys Asp Asp Val Phe Gly Arg Lys Lys

530 535 540

Gly Glu Trp Val Glu Pro Phe Ile Glu Asn Phe Gln Lys Val Ser Gln

545 550 555 560

Glu Lys Phe Asp Arg Gly Val Lys Asp Glu Asn Gly Arg Ser Ile His

565 570 575

Thr Glu Val Val Lys Asn Leu Ile Glu Glu Gly Tyr Leu Arg Leu Phe

580 585 590

Gln Leu Thr Lys Tyr His Asn Leu Asp Lys Lys Gly Glu Arg Asp Pro

595 600 605

Arg Pro Phe Asp Gly Asn Phe Tyr Ala Thr Leu Asp Glu Phe Trp Lys

610 615 620

Asp Asn Ile Val Val Val Tyr His Lys Ala Leu Gln Ser Thr Leu Thr
625 630 635 640
Lys Lys Pro Tyr Ser Glu Asp Lys Ile Lys Leu Asn Phe Glu Asn Gly
645 650 655
Ser Leu Leu Gly Gly Phe Ser Asp Gly Gln Glu Arg Ser Lys Ala Gly
660 665 670
Val Val Leu Lys Asn Lys Asn Lys Phe Tyr Leu Gly Ile Leu Ile Asp

675 680 685
Arg Gly Phe Phe Arg Thr Asp Lys Ala Asn Pro Val Tyr Asp Asn Ala
690 695 700
Gln Asn Asn Glu Trp Glu Arg Leu Ile Leu Thr Asn Leu Lys Phe Gln
705 710 715 720
Thr Leu Ala Gly Lys Gly Phe Leu Gly Lys His Gly Val Ser Tyr Gly
725 730 735
Glu Met Gly Lys Asp Asn Pro Met Met Ala Val Glu Tyr Leu Gln Lys

740 745 750
Phe Ile Lys Leu Lys Tyr Leu Asp Lys Tyr Pro Ala Leu Asn Glu Val
755 760 765
Ala His Lys Lys Tyr Thr Ile Lys Lys Glu Phe Asp Ala Asp Val Lys
770 775 780
Asn Ala Leu Lys Asp Cys Phe Thr Met Asn Phe Lys Pro Val Asp Phe
785 790 795 800
Gly Met Ile Arg Gln Gly Leu Thr Glu Ser Leu Phe Tyr Leu Phe Glu

805 810 815
Ile Val Asn Lys Asp Ile Ser Ser Gln Ala Lys Asn Gly Lys Asn Val
820 825 830
His Thr Leu Tyr Trp Glu Ala Leu Phe Gly Asp Gln Asn Leu Lys Lys
835 840 845
Pro Ile Leu Ala Leu Asn Gly Gly Ala Glu Ile Phe Tyr Arg Glu Ser
850 855 860
Gln Arg Glu Lys Leu Glu Lys Lys Leu Asp Lys Ser Gly Lys Glu Val

865 870 875 880

Leu Asp His Lys Arg Tyr Gly Gln Asp Lys Tyr Phe Leu His Ala Ser

885 890 895

Ile Thr Ile Asn Tyr Gly Gln Pro Lys Asn Ile Lys Phe Lys Glu Val

900 905 910

Ile Asn Glu Lys Ile Ser Gln Asn Ala Asp Arg Val Asn Ile Ile Gly

915 920 925

Ile Asp Arg Gly Glu Lys His Leu Leu Tyr Tyr Ser Val Val Ser Pro

930 935 940

Glu Gly Val Leu Leu Glu Gln Gly Ser Phe Asn Gln Ile Glu Thr Lys

945 950 955 960

Asn Lys Val Asp Ile Lys Ala Val Lys Ala Glu Tyr Gly Glu Arg Gly

965 970 975

Glu Leu Lys Lys Val Glu Leu Val Pro Thr Gly Lys Lys Val Lys Tyr

980 985 990

Val Asp Tyr Gln Ile Leu Leu Asp Tyr Tyr Glu Lys Lys Arg Asn Leu

995 1000 1005

Ala Arg Arg Asp Trp Gln Thr Ile Gly Lys Ile Lys Asp Leu Lys

1010 1015 1020

Asp Gly Tyr Leu Ser Gln Thr Val His Arg Ile Tyr Gln Leu Ile

1025 1030 1035

Leu Lys Tyr Asn Ala Val Val Ala Met Glu Asp Leu Asn Val Glu

1040 1045 1050

Phe Lys Ala Lys Arg Ala Ala Lys Val Glu Lys Ser Val Tyr Lys

1055 1060 1065

Asn Phe Glu Met Ala Leu Ala Lys Lys Leu Asn His Leu Ile Leu

1070 1075 1080

Lys Asp Arg Arg Ala Asp Glu Ile Gly Gly Ala Leu Arg Ala Tyr

1085 1090 1095

Gln Leu Thr Pro Ala Ile Pro Ala Asn Asp Val Gly Lys Phe Asp

1100 1105 1110

Lys Ala Lys Gln Trp Gly Ile Met Phe Tyr Val Arg Ala Asn Tyr

1115 1120 1125

Thr Ser Thr Thr Asp Pro Leu Thr Gly Trp Arg Lys His Lys Tyr

1130 1135 1140

Ile Ser Asn Ser Glu Lys Ile Asp Asn Ile Gln Lys Phe Phe Ser

1145 1150 1155

Pro Gly Asp Gly Ile Gln Ile Asp Tyr Asp Thr Glu Lys Gln Cys

1160 1165 1170

Phe Lys Phe Ser Tyr Asp His Glu Leu Glu Gly Gly Ala Lys Lys

1175 1180 1185

His Trp Glu Leu Phe Ala Cys Asp Gly Leu Glu Arg Phe Tyr Trp

1190 1195 1200

Asp Asn Arg Glu Arg Gln Ile Lys Lys Tyr Asn Leu Tyr Glu Glu

1205 1210 1215

Phe Glu Lys Leu Leu Gly Gly Leu Arg Lys Glu Glu Asn Ile Asn

1220 1225 1230

Ile Gln Ile Asp Gly Val Ser Glu Phe Arg Trp Lys Asp Leu Val

1235 1240 1245

Phe Phe Trp Asn Leu Leu Asn Gln Ile Arg Asn Thr Asp Arg Ser

1250 1255 1260

Ala Gln Gly Asp Glu Asn Asp Phe Leu Gln Ser Pro Val Trp Ser

1265 1270 1275

Glu Lys Tyr Asn Cys Phe Tyr Asp Ser Arg Lys Ala Pro Asn Asn

1280 1285 1290

Met Pro Asn Asn Gly Asp Ala Asn Gly Ala Phe Asn Ile Ala Arg

1295 1300 1305

Lys Gly Gln Leu Ile Leu Glu Arg Ile Lys Lys Cys Ser Asp Ile

1310 1315 1320

Pro Lys Phe Gly Asn Asp Asn Asn Gly Lys Asn Pro Glu Asn Asn

1325 1330 1335

Tyr Phe Ile Ser Asp Ala Asp Trp Asp Lys Phe Ala Gln Lys

1340 1345 1350

<210> 131

<211> 1108

<212> PRT

<213> Unknown

<220><223

> Description of Unknown:

Cas12 sequence

<400> 131

Met Ala Ile Arg Ser Ile Lys Leu Lys Leu Lys Thr His Thr Gly Pro
1 5 10 15

Glu Ala Gln Asn Leu Arg Lys Gly Ile Trp Arg Thr His Arg Leu Leu
20 25 30

Asn Glu Gly Val Ala Tyr Tyr Met Lys Met Leu Leu Leu Phe Arg Gln
35 40 45

Glu Ser Thr Gly Glu Arg Pro Lys Glu Glu Leu Gln Glu Glu Leu Ile

50 55 60

Cys His Ile Arg Glu Gln Gln Gln Arg Asn Gln Ala Asp Lys Asn Thr
65 70 75 80

Gln Ala Leu Pro Leu Asp Lys Ala Leu Glu Ala Leu Arg Gln Leu Tyr
85 90 95

Glu Leu Leu Val Pro Ser Ser Val Gly Gln Ser Gly Asp Ala Gln Ile
100 105 110

Ile Ser Arg Lys Phe Leu Ser Pro Leu Val Asp Pro Asn Ser Glu Gly

115 120 125

Gly Lys Gly Thr Ser Lys Ala Gly Ala Lys Pro Thr Trp Gln Lys Lys
130 135 140

Lys Glu Ala Asn Asp Pro Thr Trp Glu Gln Asp Tyr Glu Lys Trp Lys
145 150 155 160

Lys Arg Arg Glu Glu Asp Pro Thr Ala Ser Val Ile Thr Thr Leu Glu
165 170 175

Glu Tyr Gly Ile Arg Pro Ile Phe Pro Leu Tyr Thr Asn Thr Val Thr

180 185 190

Asp Ile Ala Trp Leu Pro Leu Gln Ser Asn Gln Phe Val Arg Thr Trp

195 200 205

Asp Arg Asp Met Leu Gln Gln Ala Ile Glu Arg Leu Leu Ser Trp Glu

210 215 220

Ser Trp Asn Lys Arg Val Gln Glu Glu Tyr Ala Lys Leu Lys Glu Lys

225 230 235 240

Met Ala Gln Leu Asn Glu Gln Leu Glu Gly Gly Gln Glu Trp Ile Ser

245 250 255

Leu Leu Glu Gln Tyr Glu Glu Asn Arg Glu Arg Glu Leu Arg Glu Asn

260 265 270

Met Thr Ala Ala Asn Asp Lys Tyr Arg Ile Thr Lys Arg Gln Met Lys

275 280 285

Gly Trp Asn Glu Leu Tyr Glu Leu Trp Ser Thr Phe Pro Ala Ser Ala

290 295 300

Ser His Glu Gln Tyr Lys Glu Ala Leu Lys Arg Val Gln Gln Arg Leu

305 310 315 320

Arg Gly Arg Phe Gly Asp Ala His Phe Phe Gln Tyr Leu Met Glu Glu

325 330 335

Lys Asn Arg Leu Ile Trp Lys Gly Asn Pro Gln Arg Ile His Tyr Phe

340 345 350

Val Ala Arg Asn Glu Leu Thr Lys Arg Leu Glu Glu Ala Lys Gln Ser

355 360 365

Ala Thr Met Thr Leu Pro Asn Ala Arg Lys His Pro Leu Trp Val Arg

370 375 380

Phe Asp Ala Arg Gly Gly Asn Leu Gln Asp Tyr Tyr Leu Thr Ala Glu

385 390 395 400

Ala Asp Lys Pro Arg Ser Arg Arg Phe Val Thr Phe Ser Gln Leu Ile

405 410 415

Trp Pro Ser Glu Ser Gly Trp Met Glu Lys Lys Asp Val Glu Val Glu

420 425 430

Leu Ala Leu Ser Arg Gln Phe Tyr Gln Gln Val Lys Leu Leu Lys Asn

435 440 445

Asp Lys Gly Lys Gln Lys Ile Glu Phe Lys Asp Lys Gly Ser Gly Ser

450 455 460

Thr Phe Asn Gly His Leu Gly Gly Ala Lys Leu Gln Leu Glu Arg Gly

465 470 475 480

Asp Leu Glu Lys Glu Glu Lys Asn Phe Glu Asp Gly Glu Ile Gly Ser

485 490 495

Val Tyr Leu Asn Val Val Ile Asp Phe Glu Pro Leu Gln Glu Val Lys

500 505 510

Asn Gly Arg Val Gln Ala Pro Tyr Gly Gln Val Leu Gln Leu Ile Arg

515 520 525

Arg Pro Asn Glu Phe Pro Lys Val Thr Thr Tyr Lys Ser Glu Gln Leu

530 535 540

Val Glu Trp Ile Lys Ala Ser Pro Gln His Ser Ala Gly Val Glu Ser

545 550 555 560

Leu Ala Ser Gly Phe Arg Val Met Ser Ile Asp Leu Gly Leu Arg Ala

565 570 575

Ala Ala Ala Thr Ser Ile Phe Ser Val Glu Glu Ser Ser Asp Lys Asn

580 585 590

Ala Ala Asp Phe Ser Tyr Trp Ile Glu Gly Thr Pro Leu Val Ala Val

595 600 605

His Gln Arg Ser Tyr Met Leu Arg Leu Pro Gly Glu Gln Val Glu Lys

610 615 620

Gln Val Met Glu Lys Arg Asp Glu Arg Phe Gln Leu His Gln Arg Val

625 630 635 640

Lys Phe Gln Ile Arg Val Leu Ala Gln Ile Met Arg Met Ala Asn Lys

645 650 655

Gln Tyr Gly Asp Arg Trp Asp Glu Leu Asp Ser Leu Lys Gln Ala Val

660 665 670

Glu Gln Lys Lys Ser Pro Leu Asp Gln Thr Asp Arg Thr Phe Trp Glu

675 680 685

Gly Ile Val Cys Asp Leu Thr Lys Val Leu Pro Arg Asn Glu Ala Asp

690 695 700

Trp Glu Gln Ala Val Val Gln Ile His Arg Lys Ala Glu Glu Tyr Val

705 710 715 720

Gly Lys Ala Val Gln Ala Trp Arg Lys Arg Phe Ala Ala Asp Glu Arg

725 730 735

Lys Gly Ile Ala Gly Leu Ser Met Trp Asn Ile Glu Glu Leu Glu Gly

740 745 750

Leu Arg Lys Leu Leu Ile Ser Trp Ser Arg Arg Thr Arg Asn Pro Gln

755 760 765

Glu Val Asn Arg Phe Glu Arg Gly His Thr Ser His Gln Arg Leu Leu

770 775 780

Thr His Ile Gln Asn Val Lys Glu Asp Arg Leu Lys Gln Leu Ser His

785 790 795 800

Ala Ile Val Met Thr Ala Leu Gly Tyr Val Tyr Asp Glu Arg Lys Gln

805 810 815

Glu Trp Cys Ala Glu Tyr Pro Ala Cys Gln Val Ile Leu Phe Glu Asn

820 825 830

Leu Ser Gln Tyr Arg Ser Asn Leu Asp Arg Ser Thr Lys Glu Asn Ser

835 840 845

Thr Leu Met Lys Trp Ala His Arg Ser Ile Pro Lys Tyr Val His Met

850 855 860

Gln Ala Glu Pro Tyr Gly Ile Gln Ile Gly Asp Val Arg Ala Glu Tyr

865 870 875 880

Ser Ser Arg Phe Tyr Ala Lys Thr Gly Thr Pro Gly Ile Arg Cys Lys

885 890 895

Lys Val Arg Gly Gln Asp Leu Gln Gly Arg Arg Phe Glu Asn Leu Gln

900 905 910

Lys Arg Leu Val Asn Glu Gln Phe Leu Thr Glu Glu Gln Val Lys Gln

915 920 925

Leu Arg Pro Gly Asp Ile Val Pro Asp Asp Ser Gly Glu Leu Phe Met

930 935 940

Thr Leu Thr Asp Gly Ser Gly Ser Lys Glu Val Val Phe Leu Gln Ala

945 950 955 960

Asp Ile Asn Ala Ala His Asn Leu Gln Lys Arg Phe Trp Gln Arg Tyr

965 970 975

Asn Glu Leu Phe Lys Val Ser Cys Arg Val Ile Val Arg Asp Glu Glu

980 985 990

Glu Tyr Leu Val Pro Lys Thr Lys Ser Val Gln Ala Lys Leu Gly Lys

995 1000 1005

Gly Leu Phe Val Lys Lys Ser Asp Thr Ala Trp Lys Asp Val Tyr

1010 1015 1020

Val Trp Asp Ser Gln Ala Lys Leu Lys Gly Lys Thr Thr Phe Thr

1025 1030 1035

Glu Glu Ser Glu Ser Pro Glu Gln Leu Glu Asp Phe Gln Glu Ile

1040 1045 1050

Ile Glu Glu Ala Glu Glu Ala Lys Gly Thr Tyr Arg Thr Leu Phe

1055 1060 1065

Arg Asp Pro Ser Gly Val Phe Phe Pro Glu Ser Val Trp Tyr Pro

1070 1075 1080

Gln Lys Asp Phe Trp Gly Glu Val Lys Arg Lys Leu Tyr Gly Lys

1085 1090 1095

Leu Arg Glu Arg Phe Leu Thr Lys Ala Arg

1100 1105

<210> 132

<211> 1125

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 132

Met Arg Lys Lys Leu Phe Lys Gly Tyr Ile Leu His Asn Lys Arg Leu

1 5 10 15

Val Tyr Thr Gly Lys Ala Ala Ile Arg Ser Ile Lys Tyr Pro Leu Val
20 25 30
Ala Pro Asn Lys Thr Ala Leu Asn Asn Leu Ser Glu Lys Ile Ile Tyr
35 40 45
Asp Tyr Glu His Leu Phe Gly Pro Leu Asn Val Ala Ser Tyr Ala Arg
50 55 60
Asn Ser Asn Arg Tyr Ser Leu Val Asp Phe Trp Ile Asp Ser Leu Arg
65 70 75 80

Ala Gly Val Ile Trp Gln Ser Lys Ser Thr Ser Leu Ile Asp Leu Ile
85 90 95
Ser Lys Leu Glu Gly Ser Lys Ser Pro Ser Glu Lys Ile Phe Glu Gln
100 105 110
Ile Asp Phe Glu Leu Lys Asn Lys Leu Asp Lys Glu Gln Phe Lys Asp
115 120 125
Ile Ile Leu Leu Asn Thr Gly Ile Arg Ser Ser Ser Asn Val Arg Ser
130 135 140

Leu Arg Gly Arg Phe Leu Lys Cys Phe Lys Glu Glu Phe Arg Asp Thr
145 150 155 160
Glu Glu Val Ile Ala Cys Val Asp Lys Trp Ser Lys Asp Leu Ile Val
165 170 175
Glu Gly Lys Ser Ile Leu Val Ser Lys Gln Phe Leu Tyr Trp Glu Glu
180 185 190
Glu Phe Gly Ile Lys Ile Phe Pro His Phe Lys Asp Asn His Asp Leu
195 200 205

Pro Lys Leu Thr Phe Phe Val Glu Pro Ser Leu Glu Phe Ser Pro His
210 215 220
Leu Pro Leu Ala Asn Cys Leu Glu Arg Leu Lys Lys Phe Asp Ile Ser
225 230 235 240
Arg Glu Ser Leu Leu Gly Leu Asp Asn Asn Phe Ser Ala Phe Ser Asn
245 250 255

Tyr Phe Asn Glu Leu Phe Asn Leu Leu Ser Arg Gly Glu Ile Lys Lys
260 265 270

Ile Val Thr Ala Val Leu Ala Val Ser Lys Ser Trp Glu Asn Glu Pro
275 280 285
Glu Leu Glu Lys Arg Leu His Phe Leu Ser Glu Lys Ala Lys Leu Leu
290 295 300
Gly Tyr Pro Lys Leu Thr Ser Ser Trp Ala Asp Tyr Arg Met Ile Ile
305 310 315 320
Gly Gly Lys Ile Lys Ser Trp His Ser Asn Tyr Thr Glu Gln Leu Ile
325 330 335

Lys Val Arg Glu Asp Leu Lys Lys His Gln Ile Ala Leu Asp Lys Leu
340 345 350
Gln Glu Asp Leu Lys Lys Val Val Asp Ser Ser Leu Arg Glu Gln Ile
355 360 365
Glu Ala Gln Arg Glu Ala Leu Leu Pro Leu Leu Asp Thr Met Leu Lys
370 375 380
Glu Lys Asp Phe Ser Asp Asp Leu Glu Leu Tyr Arg Phe Ile Leu Ser
385 390 395 400

Asp Phe Lys Ser Leu Leu Asn Gly Ser Tyr Gln Arg Tyr Ile Gln Thr
405 410 415
Glu Glu Glu Arg Lys Glu Asp Arg Asp Val Thr Lys Lys Tyr Lys Asp
420 425 430
Leu Tyr Ser Asn Leu Arg Asn Ile Pro Arg Phe Phe Gly Glu Ser Lys
435 440 445
Lys Glu Gln Phe Asn Lys Phe Ile Asn Lys Ser Leu Pro Thr Ile Asp
450 455 460

Val Gly Leu Lys Ile Leu Glu Asp Ile Arg Asn Ala Leu Glu Thr Val
465 470 475 480
Ser Val Arg Lys Pro Pro Ser Ile Thr Glu Glu Tyr Val Thr Lys Gln
485 490 495
Leu Glu Lys Leu Ser Arg Lys Tyr Lys Ile Asn Ala Phe Asn Ser Asn

500 505 510

Arg Phe Lys Gln Ile Thr Glu Gln Val Leu Arg Lys Tyr Asn Asn Gly

515 520 525

Glu Leu Pro Lys Ile Ser Glu Val Phe Tyr Arg Tyr Pro Arg Glu Ser

530 535 540

His Val Ala Ile Arg Ile Leu Pro Val Lys Ile Ser Asn Pro Arg Lys

545 550 555 560

Asp Ile Ser Tyr Leu Leu Asp Lys Tyr Gln Ile Ser Pro Asp Trp Lys

565 570 575

Asn Ser Asn Pro Gly Glu Val Val Asp Leu Ile Glu Ile Tyr Lys Leu

580 585 590

Thr Leu Gly Trp Leu Leu Ser Cys Asn Lys Asp Phe Ser Met Asp Phe

595 600 605

Ser Ser Tyr Asp Leu Lys Leu Phe Pro Glu Ala Ala Ser Leu Ile Lys

610 615 620

Asn Phe Gly Ser Cys Leu Ser Gly Tyr Tyr Leu Ser Lys Met Ile Phe

625 630 635 640

Asn Cys Ile Thr Ser Glu Ile Lys Gly Met Ile Thr Leu Tyr Thr Arg

645 650 655

Asp Lys Phe Val Val Arg Tyr Val Thr Gln Met Ile Gly Ser Asn Gln

660 665 670

Lys Phe Pro Leu Leu Cys Leu Val Gly Glu Lys Gln Thr Lys Asn Phe

675 680 685

Ser Arg Asn Trp Gly Val Leu Ile Glu Glu Lys Gly Asp Leu Gly Glu

690 695 700

Glu Lys Asn Gln Glu Lys Cys Leu Ile Phe Lys Asp Lys Thr Asp Phe

705 710 715 720

Ala Lys Ala Lys Glu Val Glu Ile Phe Lys Asn Asn Ile Trp Arg Ile

725 730 735

Arg Thr Ser Lys Tyr Gln Ile Gln Phe Leu Asn Arg Leu Phe Lys Lys

740 745 750

Thr Lys Glu Trp Asp Leu Met Asn Leu Val Leu Ser Glu Pro Ser Leu
755 760 765
Val Leu Glu Glu Glu Trp Gly Val Ser Trp Asp Lys Asp Lys Leu Leu
770 775 780

Pro Leu Leu Lys Lys Glu Lys Ser Cys Glu Glu Arg Leu Tyr Tyr Ser
785 790 795 800
Leu Pro Leu Asn Leu Val Pro Ala Thr Asp Tyr Lys Glu Gln Ser Ala
805 810 815
Glu Ile Glu Gln Arg Asn Thr Tyr Leu Gly Leu Asp Val Gly Glu Phe
820 825 830
Gly Val Ala Tyr Ala Val Val Arg Ile Val Arg Asp Arg Ile Glu Leu
835 840 845

Leu Ser Trp Gly Phe Leu Lys Asp Pro Ala Leu Arg Lys Ile Arg Glu
850 855 860
Arg Val Gln Asp Met Lys Lys Lys Gln Val Met Ala Val Phe Ser Ser
865 870 875 880
Ser Ser Thr Ala Val Ala Arg Val Arg Glu Met Ala Ile His Ser Leu
885 890 895
Arg Asn Gln Ile His Ser Ile Ala Leu Ala Tyr Lys Ala Lys Ile Ile
900 905 910

Tyr Glu Ile Ser Ile Ser Asn Phe Glu Thr Gly Gly Asn Arg Met Ala
915 920 925
Lys Ile Tyr Arg Ser Ile Lys Val Ser Asp Val Tyr Arg Glu Ser Gly
930 935 940
Ala Asp Thr Leu Val Ser Glu Met Ile Trp Gly Lys Lys Asn Lys Gln
945 950 955 960
Met Gly Asn His Ile Ser Ser Tyr Ala Thr Ser Tyr Thr Cys Cys Asn
965 970 975

Cys Ala Arg Thr Pro Phe Glu Leu Val Ile Asp Asn Asp Lys Glu Tyr
980 985 990
Glu Lys Gly Gly Asp Glu Phe Ile Phe Asn Val Gly Asp Glu Lys Lys

995 1000 1005

Val Arg Gly Phe Leu Gln Lys Ser Leu Leu Gly Lys Thr Ile Lys

1010 1015 1020

Gly Lys Glu Val Leu Lys Ser Ile Lys Glu Tyr Ala Arg Pro Pro

1025 1030 1035

Ile Arg Glu Val Leu Leu Glu Gly Glu Asp Val Glu Gln Leu Leu

1040 1045 1050

Lys Arg Arg Gly Asn Ser Tyr Ile Tyr Arg Cys Pro Phe Cys Gly

1055 1060 1065

Tyr Lys Thr Asp Ala Asp Ile Gln Ala Ala Leu Asn Ile Ala Cys

1070 1075 1080

Arg Gly Tyr Ile Ser Asp Asn Ala Lys Asp Ala Val Lys Glu Gly

1085 1090 1095

Glu Arg Lys Leu Asp Tyr Ile Leu Glu Val Arg Lys Leu Trp Glu

1100 1105 1110

Lys Asn Gly Ala Val Leu Arg Ser Ala Lys Phe Leu

1115 1120 1125

<210> 133

<211> 1352

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 133

Met Ser Thr Gln Lys Asn Pro Phe Asn Gln Phe Thr Asn Leu Tyr Glu

1 5 10 15

Leu Gln Lys Thr Leu Arg Phe Glu Leu Arg Pro Val Pro Glu Thr Lys

20 25 30

Lys Leu Leu Glu Lys Gly Glu Gly Lys Asn Leu Ile Gln Met Asp Leu

35 40 45

Glu Ile Asp Arg Leu Tyr Glu Lys Glu Met Lys Pro Met Phe Asn Ile

50 55 60

Leu His Glu Lys Phe Ile Asn Glu Ser Leu Gly Leu Val Lys Leu Asp
65 70 75 80
Cys Lys Lys Leu Lys Lys Leu Glu Asn Leu Leu Ala Glu Ala Asp Lys

85 90 95
Leu Arg Lys Gln Ile Lys Glu Gly Arg Lys Asn Lys Asn Asn Ile Ser
100 105 110
Glu Val Glu Lys Arg Leu Lys Ile Ile Ile Gly Asp Asn Ser Gln Gly
115 120 125
Lys Asn Lys Asn Gly Glu Ile Ala Val Leu Gln Asp Glu Leu Arg Val
130 135 140
Leu Ile Val Lys Ala Phe Asn Leu Thr Ala Asp Lys Trp Lys Lys Glu

145 150 155 160
Leu Asn Asn Lys Glu Thr Leu Leu Pro Glu Lys Lys Gly Lys Arg Lys
165 170 175
Ile Lys Ile Lys Lys Ser Gly Pro Lys Ile Leu Gln Glu Glu Asn Val
180 185 190
Leu Ala Ile Leu Ala Tyr Phe Asn Pro Asp Lys Ala Asp Ile Ile Lys
195 200 205
Lys Phe Ala Gly Phe Phe Thr Tyr Phe Ser Gly Phe Asn Gln Asn Arg

210 215 220
Ala Asn Tyr Tyr Thr Val Lys Ala Leu Ala Thr Gly Val Ala Asn Arg
225 230 235 240
Ala Ile Asn Arg Asn Phe Leu Ile Phe Leu Ala Asn Arg Lys Asp Phe
245 250 255
Ala Arg Phe Lys Glu Arg Leu Pro Arg Leu Ala Glu Phe Asp Asn Tyr
260 265 270
Phe Glu Leu Glu Asn Tyr Glu Lys Tyr Leu Ser Gln Thr Gly Ile Glu

275 280 285
Glu Tyr Asn Asp Gln Ile Gly Lys Ile Lys Gln Ile Val Asn Leu Glu
290 295 300
His Asn Gln Gln Gln Lys Asp Asn Lys Phe Gln Leu Lys Gly Leu Ala

305 310 315 320

Thr Leu Glu Lys Gln Ile Gly Cys Arg Thr Lys Lys Gln Arg Glu Glu

325 330 335

Gly Gly Asp Lys Ser Ala Pro Lys Phe Leu Glu Lys Val Gly Leu Gly

340 345 350

Phe Gln Val Ser Gln Asp Asp Asp Gly Glu Tyr Leu Ile Trp Glu Cys

355 360 365

Leu Asn Tyr Ile Asn Lys Glu Leu Ala Gly Lys Leu Lys Ser Ile Lys

370 375 380

Asp Asn Tyr Gln Lys Phe Phe Ala Asp Trp Arg Thr Gly Ala Tyr Asp

385 390 395 400

Leu Glu Lys Ile Trp Phe Arg Lys Glu Ala Leu Asn Thr Ile Ser Gly

405 410 415

Arg Trp Phe Gly Gly Asn Asn Trp Phe Ile Ile Gly Lys Ala Leu Ala

420 425 430

Leu Thr Gly Val Gly Lys Phe Asp Lys Arg Glu Asn Thr Tyr Lys Ile

435 440 445

Pro Glu Phe Val Ser Leu Ala Glu Ile Lys Thr Ala Phe Glu Met Leu

450 455 460

Glu Asn Gly Val Asn Tyr Asp Phe Lys Lys Ser Lys Lys Lys Lys Glu

465 470 475 480

Gly Asp Asp Thr Asp Val Val Lys Tyr Ser Ala Asp Asn Leu Phe Lys

485 490 495

Glu Glu Tyr Lys Lys Lys Gly Leu Ile Lys Asn Ser Leu Phe Glu Thr

500 505 510

Met Leu Ala Val Trp Gln Ser Glu Ile Lys Arg Lys Phe Glu Gln Ile

515 520 525

Phe Asp Gly Tyr Lys Leu Glu Lys Asp Asp Val Phe Gly Arg Lys Lys

530 535 540

Gly Glu Trp Val Glu Pro Phe Ile Glu Asn Phe Gln Lys Val Ser Gln

545 550 555 560

Glu Lys Phe Asp Arg Gly Val Lys Asp Glu Asn Gly Arg Ser Ile His
565 570 575
Thr Glu Val Val Lys Asn Leu Ile Glu Glu Gly Tyr Leu Arg Leu Phe
580 585 590
Gln Leu Thr Lys Tyr His Asn Leu Asp Lys Lys Gly Glu Arg Asp Pro

595 600 605
Arg Pro Phe Asp Gly Asn Phe Tyr Ala Thr Leu Asp Glu Phe Trp Lys
610 615 620
Asp Asn Ile Val Val Val Tyr His Lys Ala Leu Gln Ser Thr Leu Thr
625 630 635 640
Lys Lys Pro Tyr Ser Glu Asp Lys Ile Lys Leu Asn Phe Glu Asn Gly
645 650 655
Ser Leu Leu Gly Gly Phe Ser Asp Gly Gln Glu Arg Ser Lys Ala Gly

660 665 670
Val Val Leu Lys Asn Lys Asn Lys Phe Tyr Leu Gly Ile Leu Ile Asp
675 680 685
Arg Gly Phe Phe Arg Thr Asp Lys Ala Asn Pro Val Tyr Asp Asn Ala
690 695 700
Gln Asn Asn Glu Trp Glu Arg Leu Ile Leu Thr Asn Leu Lys Phe Gln
705 710 715 720
Thr Leu Ala Gly Lys Gly Phe Leu Gly Lys His Gly Val Ser Tyr Gly

725 730 735
Glu Met Gly Lys Asp Asn Pro Met Met Ala Val Glu Tyr Leu Gln Lys
740 745 750
Phe Ile Lys Leu Lys Tyr Leu Asp Lys Tyr Pro Ala Leu Asn Glu Val
755 760 765
Ala His Lys Lys Tyr Thr Ile Lys Lys Glu Phe Asp Ala Asp Val Lys
770 775 780
Asn Ala Leu Lys Asp Cys Phe Thr Met Asn Phe Lys Pro Val Asp Phe

785 790 795 800
Gly Met Ile Arg Gln Gly Leu Thr Glu Ser Leu Phe Tyr Leu Phe Glu

805 810 815

Ile Val Asn Lys Asp Ile Ser Ser Gln Ala Lys Asn Gly Lys Asn Val

820 825 830

His Thr Leu Tyr Trp Glu Ala Leu Phe Gly Asp Gln Asn Leu Lys Lys

835 840 845

Pro Ile Leu Ala Leu Asn Gly Gly Ala Glu Ile Phe Tyr Arg Glu Ser

850 855 860

Gln Arg Glu Lys Leu Glu Lys Lys Leu Asp Lys Ser Gly Lys Glu Val

865 870 875 880

Leu Asp His Lys Arg Tyr Gly Gln Asp Lys Tyr Phe Leu His Ala Ser

885 890 895

Ile Thr Ile Asn Tyr Gly Gln Pro Lys Asn Ile Lys Phe Lys Glu Val

900 905 910

Ile Asn Glu Lys Ile Ser Gln Asn Ala Asp Arg Val Asn Ile Ile Gly

915 920 925

Ile Asp Arg Gly Glu Lys His Leu Leu Tyr Tyr Ser Val Val Ser Pro

930 935 940

Glu Gly Val Leu Leu Glu Gln Gly Ser Phe Asn Gln Ile Glu Thr Lys

945 950 955 960

Asn Lys Val Asp Ile Lys Ala Val Lys Ala Glu Tyr Gly Glu Arg Gly

965 970 975

Glu Leu Lys Lys Val Glu Leu Val Pro Thr Gly Lys Lys Val Lys Tyr

980 985 990

Val Asp Tyr Gln Ile Leu Leu Asp Tyr Tyr Glu Lys Lys Arg Asn Leu

995 1000 1005

Ala Arg Arg Asp Trp Gln Thr Ile Gly Lys Ile Lys Asp Leu Lys

1010 1015 1020

Asp Gly Tyr Leu Ser Gln Thr Val His Arg Ile Tyr Gln Leu Ile

1025 1030 1035

Leu Lys Tyr Asn Ala Val Val Ala Met Glu Asp Leu Asn Val Glu

1040 1045 1050

Phe Lys Ala Lys Arg Ala Ala Lys Val Glu Lys Ser Val Tyr Lys
1055 1060 1065
Asn Phe Glu Met Ala Leu Ala Lys Lys Leu Asn His Leu Ile Leu
1070 1075 1080
Lys Asp Arg Arg Ala Asp Glu Ile Gly Gly Ala Leu Arg Ala Tyr
1085 1090 1095
Gln Leu Thr Pro Ala Ile Pro Ala Asn Asp Val Gly Lys Phe Asp

1100 1105 1110
Lys Ala Lys Gln Trp Gly Ile Met Phe Tyr Val Arg Ala Asn Tyr
1115 1120 1125
Thr Ser Thr Thr Asp Pro Leu Thr Gly Trp Arg Lys His Lys Tyr
1130 1135 1140
Ile Ser Asn Ser Glu Lys Ile Asp Asn Ile Gln Lys Phe Phe Ser
1145 1150 1155
Pro Gly Asp Gly Ile Gln Ile Asp Tyr Asp Thr Glu Lys Gln Cys

1160 1165 1170
Phe Lys Phe Ser Tyr Asp His Glu Leu Glu Gly Gly Ala Lys Lys
1175 1180 1185
His Trp Glu Leu Phe Ala Cys Asp Gly Leu Glu Arg Phe Tyr Trp
1190 1195 1200
Asp Asn Arg Glu Arg Gln Ile Lys Lys Tyr Asn Leu Tyr Glu Glu
1205 1210 1215
Phe Glu Lys Leu Leu Gly Gly Leu Arg Lys Glu Glu Asn Ile Asn

1220 1225 1230
Ile Gln Ile Asp Gly Val Ser Glu Phe Arg Trp Lys Asp Leu Val
1235 1240 1245
Phe Phe Trp Asn Leu Leu Asn Gln Ile Arg Asn Thr Asp Arg Ser
1250 1255 1260
Ala Gln Gly Asp Glu Asn Asp Phe Leu Gln Ser Pro Val Trp Ser
1265 1270 1275
Glu Lys Tyr Asn Cys Phe Tyr Asp Ser Arg Lys Ala Pro Asn Asn

1280 1285 1290

Met Pro Asn Asn Gly Asp Ala Asn Gly Ala Phe Asn Ile Ala Arg

1295 1300 1305

Lys Gly Gln Leu Ile Leu Glu Arg Ile Lys Lys Cys Ser Asp Ile

1310 1315 1320

Pro Lys Phe Gly Asn Asp Asn Asn Gly Lys Asn Pro Glu Asn Asn

1325 1330 1335

Tyr Phe Ile Ser Asp Ala Asp Trp Asp Lys Phe Ala Gln Lys

1340 1345 1350

<210> 134

<211> 767

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 134

Met Ala Gln Ala Ser Ser Thr Pro Ala Val Ser Pro Arg Pro Arg Pro

1 5 10 15

Arg Tyr Arg Glu Glu Arg Thr Leu Val Arg Lys Leu Leu Pro Arg Pro

20 25 30

Gly Gln Ser Lys Gln Glu Phe Arg Glu Asn Val Lys Lys Leu Arg Lys

35 40 45

Ala Phe Leu Gln Phe Asn Ala Asp Val Ser Gly Val Cys Gln Trp Ala

50 55 60

Ile Gln Phe Arg Pro Arg Tyr Gly Lys Pro Ala Glu Pro Thr Glu Thr

65 70 75 80

Phe Trp Lys Phe Phe Leu Glu Pro Glu Thr Ser Leu Pro Pro Asn Asp

85 90 95

Ser Arg Ser Pro Glu Phe Arg Arg Leu Gln Ala Phe Glu Ala Ala Ala

100 105 110

Gly Ile Asn Gly Ala Ala Ala Leu Asp Asp Pro Ala Phe Thr Asn Glu

115 120 125

Leu Arg Asp Ser Ile Leu Ala Val Ala Ser Arg Pro Lys Thr Lys Glu
130 135 140
Ala Gln Arg Leu Phe Ser Arg Leu Lys Asp Tyr Gln Pro Ala His Arg
145 150 155 160
Met Ile Leu Ala Lys Val Ala Ala Glu Trp Ile Glu Ser Arg Tyr Arg

165 170 175
Arg Ala His Gln Asn Trp Glu Arg Asn Tyr Glu Glu Trp Lys Lys Glu
180 185 190
Lys Gln Glu Trp Glu Gln Asn His Pro Glu Leu Thr Pro Glu Ile Arg
195 200 205
Glu Ala Phe Asn Gln Ile Phe Gln Gln Leu Glu Val Lys Glu Lys Arg
210 215 220
Val Arg Ile Cys Pro Ala Ala Arg Leu Leu Gln Asn Lys Asp Asn Cys

225 230 235 240
Gln Tyr Ala Gly Lys Asn Lys His Ser Val Leu Cys Asn Gln Phe Asn
245 250 255
Glu Phe Lys Lys Asn His Leu Gln Gly Lys Ala Ile Lys Phe Phe Tyr
260 265 270
Lys Asp Ala Glu Lys Tyr Leu Arg Cys Gly Leu Gln Ser Leu Lys Pro
275 280 285
Asn Val Gln Gly Pro Phe Arg Glu Asp Trp Asn Lys Tyr Leu Arg Tyr

290 295 300
Met Asn Leu Lys Glu Glu Thr Leu Arg Gly Lys Asn Gly Gly Arg Leu
305 310 315 320
Pro His Cys Lys Asn Leu Gly Gln Glu Cys Glu Phe Asn Pro His Thr
325 330 335
Ala Leu Cys Lys Gln Tyr Gln Gln Gln Leu Ser Ser Arg Pro Asp Leu
340 345 350
Val Gln His Asp Glu Leu Tyr Arg Lys Trp Arg Arg Glu Tyr Trp Arg

355 360 365
Glu Pro Arg Lys Pro Val Phe Arg Tyr Pro Ser Val Lys Arg His Ser

370 375 380

Ile Ala Lys Ile Phe Gly Glu Asn Tyr Phe Gln Ala Asp Phe Lys Asn

385 390 395 400

Ser Val Val Gly Leu Arg Leu Asp Ser Met Pro Ala Gly Gln Tyr Leu

405 410 415

Glu Phe Ala Phe Ala Pro Trp Pro Arg Asn Tyr Arg Pro Gln Pro Gly

420 425 430

Glu Thr Glu Ile Ser Ser Val His Leu His Phe Val Gly Thr Arg Pro

435 440 445

Arg Ile Gly Phe Arg Phe Arg Val Pro His Lys Arg Ser Arg Phe Asp

450 455 460

Cys Thr Gln Glu Glu Leu Asp Glu Leu Arg Ser Arg Thr Phe Pro Arg

465 470 475 480

Lys Ala Gln Asp Gln Lys Phe Leu Glu Ala Ala Arg Lys Arg Leu Leu

485 490 495

Glu Thr Phe Pro Gly Asn Ala Glu Gln Glu Leu Arg Leu Leu Ala Val

500 505 510

Asp Leu Gly Thr Asp Ser Ala Arg Ala Ala Phe Phe Ile Gly Lys Thr

515 520 525

Phe Gln Gln Ala Phe Pro Leu Lys Ile Val Lys Ile Glu Lys Leu Tyr

530 535 540

Glu Gln Trp Pro Asn Gln Lys Gln Ala Gly Asp Arg Arg Asp Ala Ser

545 550 555 560

Ser Lys Gln Pro Arg Pro Gly Leu Ser Arg Asp His Val Gly Arg His

565 570 575

Leu Gln Lys Met Arg Ala Gln Ala Ser Glu Ile Ala Gln Lys Arg Gln

580 585 590

Glu Leu Thr Gly Thr Pro Ala Pro Glu Thr Thr Thr Asp Gln Ala Ala

595 600 605

Lys Lys Ala Thr Leu Gln Pro Phe Asp Leu Arg Gly Leu Thr Val His

610 615 620

Thr Ala Arg Met Ile Arg Asp Trp Ala Arg Leu Asn Ala Arg Gln Ile
625 630 635 640
Ile Gln Leu Ala Glu Glu Asn Gln Val Asp Leu Ile Val Leu Glu Ser
645 650 655
Leu Arg Gly Phe Arg Pro Pro Gly Tyr Glu Asn Leu Asp Gln Glu Lys
660 665 670
Lys Arg Arg Val Ala Phe Phe Ala His Gly Arg Ile Arg Arg Lys Val

675 680 685
Thr Glu Lys Ala Val Glu Arg Gly Met Arg Val Val Thr Val Pro Tyr
690 695 700
Leu Ala Ser Ser Lys Val Cys Ala Glu Cys Arg Lys Lys Gln Lys Asp
705 710 715 720
Asn Lys Gln Trp Glu Lys Asn Lys Lys Arg Gly Leu Phe Lys Cys Glu
725 730 735
Gly Cys Gly Ser Gln Ala Gln Val Asp Glu Asn Ala Ala Arg Val Leu

740 745 750
Gly Arg Val Phe Trp Gly Glu Ile Glu Leu Pro Thr Ala Ile Pro
755 760 765

<210> 135
<211> 1202
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 135
Met Ala Val Arg Ser Val Lys Leu Lys Leu Leu Val Pro Arg Asp Gly
1 5 10 15
Ser Ala Glu Ser Val Arg Lys Arg Lys Ala Leu Trp Ala Thr His Gln

20 25 30
Phe Val Asn Asp Ala Ala Ala Ala Tyr Ala Glu Leu Leu Leu Glu Met
35 40 45
Arg Gln Glu Asp Val Cys Arg Gly Thr Asp Asp His Gly Lys Asp Val

50 55 60

Ile Glu Pro Ala Ala His Trp Gln Ala Lys Leu Arg Ala Arg Leu Ala

65 70 75 80

Ala Lys Gln Leu Pro Pro Val Ala Val Ala Glu Ala Leu Pro Leu Leu

85 90 95

Lys Ala Phe Tyr Gly Ser Arg Leu Ile Lys Ser Phe Val Ala Asn Asp

100 105 110

Lys Gly Val Ala Gly Thr Gly Asn Ala Thr Asp Leu Asn Thr Trp Leu

115 120 125

Ser Gly Leu Val Asp Pro Ala Ser Val Ala Gly Glu Lys Thr Glu Leu

130 135 140

Arg Lys Gln Leu Leu Ala Glu Leu Pro Leu Cys Glu Ala Ala Asp Ala

145 150 155 160

Asp Phe Glu Gly Ala Ala Arg Lys Met Leu Ala Lys Ser Asp Ala Arg

165 170 175

Glu Ala Leu Leu Glu Gly Pro Gly Thr Gly Val Gly Trp Pro Ala Ala

180 185 190

Tyr Asn Ala Asn Pro Thr Asp Ser Val Trp Leu Asp Met Leu His Lys

195 200 205

Ala Ala Ala Lys Ala Arg Leu Glu Leu Ala Asp Thr Thr Val Ser Glu

210 215 220

Leu Lys Lys Leu Gly Val Phe Pro Leu Leu Gln Ala Ala Ser Ser Asn

225 230 235 240

Arg Val Phe Gly Ser Gly Val Leu Asn Pro Phe Glu Arg Met Ala Ala

245 250 255

Ala Gln Ala Ala Ala Ala Leu Leu Pro Trp Glu Thr Lys Arg His Glu

260 265 270

Met Arg Lys Arg Arg Asp Lys Phe Ala Asp Gln Leu Asn Gln Trp Asp

275 280 285

Thr Glu Phe Gly Ala Ser His Ala Thr Ala Leu Ala Ala Ile Arg Ala

290 295 300

Phe Glu Ala Glu Glu Ser Glu Arg Ala Arg Arg Glu Ser Leu Gly Asn
305 310 315 320
Glu Gly Thr Gly Tyr Arg Ile Gly Gly Arg Glu Leu Arg Asp Ala Trp
325 330 335
Thr Leu Leu Arg Asp Trp Leu Lys Gly His Ser Thr Ala Thr Ala Ala

340 345 350
Ala Arg Glu Asp Lys Val Arg Glu Leu Gln Ala Lys Gln Gly Arg Ser
355 360 365
Phe Gly Ser His Arg Leu Leu Ser Trp Leu Ala Lys Pro Ala Gln Gln
370 375 380
Trp Leu Ala Asp His Ser Ala Gly Asp Val Val Thr Arg Ile Ala Val
385 390 395 400
Arg Asn Ala Arg Gln Arg Lys Leu Asp Thr Ala Arg Thr Leu Pro Ile

405 410 415
Trp Thr Gly Ala Asp Ala Val Lys His Pro Arg Phe Ala Asn Phe Asp
420 425 430
Pro Pro Asn Asn Thr Asn Gln Pro Gly Phe Asp Leu Arg Ala Gly Thr
435 440 445
Gln Lys Gly Arg Leu Thr Leu Arg Leu Ser Leu Leu Thr Glu Arg Ala
450 455 460
Asp Gly Leu Leu Leu Ala Gln Asp His Asp Phe Gln Leu Val Pro Ser

465 470 475 480
Arg Gln Met Ala Glu Ile Val Leu His Lys Asp Gly Lys Glu Arg Ala
485 490 495
Leu Ser Trp Gln Ser Gln Asp Gly Ile Gly Arg Gln Val Gly Asp Val
500 505 510
Gly Gly Ser Ala Leu Leu Phe Ser Arg Asp His Ala Glu Cys Leu Leu
515 520 525
Glu Arg Lys Gln Ile Thr Arg Leu Glu Arg Gly Ala Trp Pro Ala Ala

530 535 540
Leu Pro Val Trp Phe Lys Leu Ser Leu Asp Ile Gly Ala Glu His Lys

545 550 555 560

Ala Leu Leu Lys Gln Arg Phe Lys Trp Gly Val Trp Leu Asn Ser Ala

565 570 575

Leu Val Thr Arg Asn Ala Lys Asp Ala Lys Gly Val Pro Pro Pro Val

580 585 590

Gly Thr Arg Val Leu Ala Val Asp Leu Gly Leu Arg Ser Ala Ala Thr

595 600 605

Val Ser Val Trp Gln Val Val Asp Ala Ala Thr Pro Val Val Ala Gly

610 615 620

Lys Trp Arg Val Pro Leu Ser Asp Thr Leu Ser Ala Val His Glu Arg

625 630 635 640

Ser Ala Met Leu Ala Leu Pro Gly Glu His Val Asp Ala Gly Val Leu

645 650 655

Ala Ala Arg Arg Ala Ala Asn Glu Lys Leu Ala Gly Leu Leu Ala Ala

660 665 670

Thr Ser His Leu Ser Thr Val Phe Lys Leu Gly Arg Ala Glu Gln Gly

675 680 685

Asp Arg Arg Arg Glu Leu Leu Glu Arg Leu Gly Glu Gly Asp Asp Arg

690 695 700

Arg Ala Arg Ala Ala Val Ala Thr Thr Ala Ala Glu Arg Asp Gly Leu

705 710 715 720

Arg Ala Val Leu Gly Ala Thr Gln Asp Ala Trp Ala Gly Ala Val Ala

725 730 735

Ala Val Trp Arg Arg Leu Glu Thr Asp Leu Ala Gly Ala Ile Ala Ala

740 745 750

Tyr Arg Lys Gln Gln Arg Glu Asp Val Gln Leu Arg Arg Glu Ala Arg

755 760 765

His Gly Pro Gly Ala Ser Gln Leu Pro Lys Gln Ala Ala Ala Glu Arg

770 775 780

Leu Leu Gly Gly Lys Ser Ala Trp Gln Ile Glu Tyr Lys Glu Arg Val

785 790 795 800

Arg Lys Leu Leu Thr Arg Trp Ile Met Arg Gln Arg Pro Gly Asp Thr
805 810 815
Ala Val Arg Arg Leu Ala Arg Lys Asp Leu Gly Lys Tyr Cys Gly Gly
820 825 830
Leu Leu Asp His Leu Thr Ala Leu Lys Glu Asp Arg Ala Lys Thr Thr
835 840 845
Ala Asp Leu Ile Val Gln Ala Ala Arg Gly Arg Val Arg Ala His Lys

850 855 860
Asp Ala His Gly Arg Gln Gln Asp Arg Glu Leu Trp Leu Ala Lys Tyr
865 870 875 880
Ala Pro Cys Asp Leu Ile Val Met Glu Asp Leu Gly Arg Tyr Arg Phe
885 890 895
Ala Thr Asp Arg Pro Pro Ser Glu Asn Arg Gln Leu Met Gln Trp Thr
900 905 910
His Arg Glu Val Phe Arg Leu Val Gln Met Gln Ala Glu Val Glu Gly

915 920 925
Ile Gln Val Leu Glu Thr Gly Ala Glu Phe Ser Ser Lys Phe Asp Ala
930 935 940
Arg Thr Trp Ala Pro Gly Val Arg Cys Glu Pro Ile Thr Lys Leu Trp
945 950 955 960
Val Glu Arg Tyr Arg Asn Gly Glu Met Pro Trp Leu Ala Asp Lys Ala
965 970 975
Asp Glu Trp Arg Arg Glu Gly Ile Glu Leu Ala Gln Leu Val Pro Gly

980 985 990
Gln Leu Leu Pro Thr Gly Ser Gly Glu Gln Phe Val Ala Val Ser Ala
995 1000 1005
Thr Gly Gly Leu Arg Val Arg His Ala Asp Leu Asn Ala Ala Gln
1010 1015 1020
Cys Ile Ala Leu Arg Ala Leu Thr Gly His Gly Thr Ala Phe Arg
1025 1030 1035
Leu Thr Ala Arg Arg Leu Gly Asp Val Phe Val Ser Ala Lys Gly

1040 1045 1050

Leu Gly Lys Arg Pro Gln Gly Ala Leu Trp Arg Glu Phe Gly Ser

1055 1060 1065

Ala Leu Pro Pro Ala Val Val Val Leu Arg Pro Ala Gly Glu Val

1070 1075 1080

Arg Tyr Ala Leu Arg Pro Phe Ala Ser Ala Arg Asp Ala Ala Ala

1085 1090 1095

Ala Leu Gly Leu Gln Leu Gly Ala Leu Arg Asn Val Asp Ala Thr

1100 1105 1110

Asp Ala Glu Ser Asp Ala Glu Asp Gly Asp Leu Ala Glu Leu Leu

1115 1120 1125

Ala Gly Ala Asp Pro Asp Arg Ala Thr Phe Phe Arg Asp Pro Ser

1130 1135 1140

Gly Asp Val His Gly Gly Ala Trp Val Gln Ala Lys Val Phe Trp

1145 1150 1155

Ala Glu Val Arg Arg His Val Arg Leu Gly Leu Gln Ala Gln Gly

1160 1165 1170

Leu Leu Pro Ala Ala Ala Arg Ser Ser Glu Pro Arg Gln Met Gln

1175 1180 1185

Leu Pro Leu Ala Gly Ala Leu Pro Gly Asp Asp Ile Pro Leu

1190 1195 1200

<210> 136

<211> 1375

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 136

Met Asn Arg Ile Tyr Gln Gly Arg Val Ser Lys Ile Glu Ile Lys Asp

1 5 10 15

Ser Glu Gly Asn Phe Arg Asn Val Pro Val Gly Ser Pro Asp Thr Cys

20 25 30

Pro Leu Trp Arg His His Arg Ile Phe Gln Asp Ala Val Asn Tyr Tyr
35 40 45
Leu Val Ala Leu Gly Ala Leu Ala Gly Thr Gly Ser Glu Asn Ala Phe
50 55 60
Val Gly Leu Gly Ser Lys Asp Arg Val Ile His Asp Leu Tyr Ser Arg
65 70 75 80

Leu Phe Asp Ser Trp Glu Arg Phe Pro Arg Asp Met His Gly Ala Ser
85 90 95
Ser Leu Arg Asp Ser Leu Arg Arg Thr Leu Pro Gly Leu Ser Glu Arg
100 105 110
Ala Ser Leu Gln Asp Ala Phe Asp Ala Ile Leu Ser Gly Asn Glu Ala
115 120 125
Asn Ala Arg Glu Arg Val Leu Ser Leu Leu Ser Leu Ile Gln Asp Leu
130 135 140

Gly Gly Asp Ile Gln Lys Gly Ser Lys Arg Tyr Phe Pro Phe Phe Cys
145 150 155 160
Glu Pro Ala Thr Lys Ala Thr Phe Pro Arg Ala Arg Val Gly Leu Leu
165 170 175
Lys Val Glu Gly Lys Asp Phe Val Pro Arg Leu Leu Trp Ser Ser Asp
180 185 190
Leu Glu Ile Ala Pro Asp Gln Val Val Glu Gln Leu Lys Phe Glu Tyr
195 200 205

Phe Ala Asn Pro Asn Glu Ser Val Gln Pro Ile Glu Gly Asn Glu Ala
210 215 220
Arg Val Arg Leu Ile Glu Ala Leu Asp Asn Pro Gln Leu Gly Ile Glu
225 230 235 240
Leu Pro Ile Glu Ile Leu Ser Asp Leu Arg Lys Arg Val His Leu Ile
245 250 255
Glu Thr Asp Ile Arg Ile Pro Arg Tyr Phe Phe Gly Gly Ala Gly Ala
260 265 270

Glu Leu Arg Lys Phe Arg Leu Asp Leu Phe Leu Ile Ala Ala Tyr Val

275 280 285

Thr Pro Asp Pro Ser Ile Leu Arg Ala Leu Arg Asn Ser Phe Lys Glu

290 295 300

Pro Ser Ala Ser Lys Ser Ser Lys Lys Lys Asp Glu Thr Glu Glu Val

305 310 315 320

Glu Asn Leu Leu Arg Ser Leu Gly Asp Asp Pro Leu Ile Leu Ala Arg

325 330 335

Gly Glu Arg Gly Phe Val Phe Pro Ser Phe Thr Ser Leu Pro Thr Trp

340 345 350

Val Gly Ala Asn Ala Gln Lys Pro Ile Trp Arg Asp Phe Asp Ile Ala

355 360 365

Ala Phe Ala Glu Ala Leu Lys Ser Leu Asn Gln Phe Thr Ala Lys Thr

370 375 380

Glu Glu Arg Glu Glu Lys Leu Lys Lys Ala Glu Glu Thr Leu His Tyr

385 390 395 400

Met Leu Gly Ile Ser Asp Ala Ile Pro Arg Ser Ser Asp Ser Glu Thr

405 410 415

Glu Glu Gln Ala Pro Ser Arg Pro Gly Lys Asp Pro Arg Trp Pro Leu

420 425 430

Val Ala Gln Leu Glu Lys Glu Leu Gly Glu Asn Leu Ser Glu Gly Thr

435 440 445

Trp Gln Leu Ser Arg Ser Ala Met Arg Gly Leu Arg Asp Ile Ile Gly

450 455 460

Leu Trp Arg Lys His Pro Gly Ala Ser Val Val Thr Leu Gln Lys Asp

465 470 475 480

Val Lys Thr Tyr Gln Ala Asp Glu Lys His Lys Arg Glu Ile Gly Ser

485 490 495

Val Gln Leu Phe Leu Leu Leu Cys Glu Glu Arg Tyr His Ala Leu Trp

500 505 510

Gln Thr Glu Thr Asp Asp Glu Arg Gly Asp Glu Ser Glu Glu Asn Asp

515 520 525

Asp Pro Ala Arg Ile Leu Ser Asp Ala Ile Glu Val His Gln Ile Arg
530 535 540
Arg Glu Val Glu Arg Phe Arg Glu Pro Ile Arg Leu Thr Pro Ala Glu
545 550 555 560
Pro Val Phe Ser Arg Arg Leu Phe Met Phe Ser Asp Leu Thr Asp Lys
565 570 575
Leu Ala Lys Val Lys Phe Gly Glu Thr Thr Glu Glu Asn Ser Glu Val
580 585 590

Lys Ser Gln Phe Val Glu Ala Ala Ile Ala Leu Lys Glu Gly Glu Asn
595 600 605
Leu Lys Glu Ala Arg Val Arg Ile Thr Phe Ser Ala Pro Arg Leu His
610 615 620
Arg Asp Glu Leu Leu Gly Gly Ala Glu Ser Arg Trp Leu Gln Pro Ile
625 630 635 640
Thr Ala Ala Leu Gly Phe Ser Asn Pro Ala Pro Ser Val Lys Phe Asp
645 650 655

Ser Ala Val Ala Leu Met Pro Asp His Met Asp Asp Gly Arg Ile Arg
660 665 670
His Leu Leu Asn Phe Pro Val Asn Phe Asp Ser Ala Trp Leu His Gln
675 680 685
Ser Ile Gly Lys Ala Asp Leu Trp Lys Ser Gln Phe Asn Gly Thr Lys
690 695 700
Asp Lys Asn Leu His Leu His Trp Ala Gly Thr Ala Arg Asp Thr Thr
705 710 715 720

Arg Lys Asn Thr Trp Trp Glu Asn Arg Thr Ile Ile Glu Asn Gly Phe
725 730 735
Thr Val Leu Ser Asn Asp Leu Gly Gln Arg Ser Ala Gly Ala Trp Ala
740 745 750
Leu Leu Lys Val Thr Cys Ser Arg Pro Asp Thr Lys His Pro Val Arg
755 760 765
Ser Ile Gly His Asp Gly Thr Arg Glu Trp Phe Ala Thr Val Leu Ala

770 775 780

Thr Gly Ile His Arg Leu Pro Gly Glu Asp Gln Arg Ile Leu Lys Asn
785 790 795 800
Gly Lys Trp Ala Thr Glu Gln Ser Gly Lys Lys Gly Arg Asn Ala Thr
805 810 815
Phe Ser Glu Tyr Glu Ala Ala Cys Val Leu Ala Lys Asn Leu Gly Cys
820 825 830
Glu Ser Val Glu Asn Trp Leu Gly Met Ser Gly Glu Lys Ser Tyr Pro
835 840 845

Ala Leu Asn Asp Gln Leu Val Lys Ile Ala Asn Arg Arg Ile Thr Arg
850 855 860
Leu Gly Thr Tyr His Arg Trp Ser Cys Phe Ser Pro Glu Lys Phe Glu
865 870 875 880
Asp Pro Ala Arg Arg Ala Asn Val Ile Gly Gly Gln Leu Ala Glu Leu
885 890 895
Ser Ala Tyr Gln Asp Glu Asn Val Thr Val Ser Ala Asp Ile Leu Lys
900 905 910

Ser Gly Asp Phe Glu Gly Phe Arg His Arg Ala Gly Ala Ala Phe Glu
915 920 925
Ala Leu Arg Thr Glu Leu Glu Val His Leu Val Asn Leu Ala Asn Leu
930 935 940
Thr Ala Pro Leu Arg Gln Lys Val Trp Ser Trp Gln Lys Arg Pro Asp
945 950 955 960
Ser Ser Gly Tyr Gly Asp Leu Leu Met Val Asp Leu Asp Asp Cys His
965 970 975

Pro Lys Ile Arg Gly Gln Arg Gly Leu Ser Met Ala Arg Leu Glu Gln
980 985 990
Leu Glu Gly Leu Arg Arg Leu Phe Leu Arg Tyr Asn Arg Ser Leu Asp
995 1000 1005
Arg Ser Pro Gly Ile Pro Ala Lys Phe Gly Arg Glu Asp Val Gly
1010 1015 1020

Arg Thr Ser Gly Glu Pro Cys Gln Ala Leu Leu Val Lys Ile Asp
1025 1030 1035

Arg Met Lys Glu Gln Arg Val Asn Gln Thr Ala His Leu Ile Leu
1040 1045 1050
Ala Gln Ala Leu Gly Val Arg Leu Cys Pro His Arg Ile Glu Glu
1055 1060 1065
Asn Glu Arg Lys Ser Arg Asp Leu His Gly Glu Tyr Glu Lys Ile
1070 1075 1080
Pro Gly Arg Glu Pro Val Asp Phe Ile Val Ile Glu Asp Leu Ser
1085 1090 1095

Arg Tyr Leu Ser Ser Gln Gly Arg Ala Pro Ser Glu Asn Ser Arg
1100 1105 1110
Leu Met Lys Trp Ala His Arg Ala Val Arg Asp Lys Leu Lys Met
1115 1120 1125
Leu Ala Glu Glu Pro Phe Gly Ile Pro Val Val Glu Thr Val Pro
1130 1135 1140
Ala Tyr Ser Ser Arg Phe His Ala Leu Asn Gly Gln Ala Gly Ser
1145 1150 1155

Arg Leu His Glu Leu His Glu Leu Glu Ala Tyr Gln Gln Gln Ser
1160 1165 1170
Leu Ile Asn Leu Ala Ala Lys Thr Asp Phe Gln Asn Arg Asp Arg
1175 1180 1185
Ser Lys Ala Ala Gly Glu Leu Phe Glu Gln Phe Gln Ala Leu Ala
1190 1195 1200
Lys Leu Asn Glu Arg Arg Arg Ala Glu Gly Lys Lys Val Pro Arg
1205 1210 1215

Thr Leu Tyr Tyr Pro Lys Ser Gly Gly Pro Leu Phe Leu Ala Ser
1220 1225 1230
Arg Asp Gly Asp Thr Ile His Ala Asp Val Asn Ala Ala Ile Asn
1235 1240 1245
Leu Gly Leu Arg Ala Ile Ala Ala Pro Ala Cys Ile Asp Ile His

1250 1255 1260

Arg Arg Leu Arg Ala Thr Lys Glu Lys Glu Val Tyr Arg Pro Arg

1265 1270 1275

Val Gly Asn Ala Arg Glu Lys Ser Ala Phe Ser Lys Asp Asp Ile

1280 1285 1290

Ile Gln Pro Ser Gly Ala Pro Ser Lys Lys Phe Ala Ser Ser Ser

1295 1300 1305

Ser Pro Asn Phe Phe Tyr Glu Pro Glu Asp Leu Lys Gln Ala Asn

1310 1315 1320

Gly Glu Pro Leu Phe Asp Arg Ala Met Phe Gly Glu Tyr Ser Leu

1325 1330 1335

Val Ser Gly Val Ser Leu Trp Ser Met Val Asn Asn Ala Ile Tyr

1340 1345 1350

Ile Arg Cys Val Glu Leu Asn Arg Thr Arg Leu His Gly Lys Asp

1355 1360 1365

Pro Asp Asp Gln Ile Pro Met

1370 1375

<210> 137

<211> 1496

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 137

Met Ala Asp Asp Leu Ser Thr Gln Arg Ala Tyr Thr Leu Arg Leu Gln

1 5 10 15

Gly Thr Asp Pro Glu Asp Gln Ser Trp Arg Asp Ala Leu Trp Met Thr

20 25 30

His Glu Ala Val Asn Ala Gly Gly Arg Ala Phe Gly Asp Trp Leu Leu

35 40 45

Thr Leu Arg Gly Gly Ile Ala His Glu Leu Ala Asp Thr Pro Val Lys

50 55 60

Gly Lys Lys Asp Ile Thr Asp Glu Leu Arg Lys Lys Arg Arg Ile Leu

65 70 75 80

Leu Ala Leu Ser Trp Leu Ser Val Glu Ser Arg Arg Gly Ala Pro Asp

85 90 95

Lys Phe Ile Val Ala Gly Gly Glu Glu Pro Ala Gly Ser Arg Asn Glu

100 105 110

Lys Val Leu Gln Ala Leu Lys Glu Ile Leu Lys Arg Arg Gly Leu Ser

115 120 125

Ala Glu Glu Ser Glu Ser Trp Met Ser Asp Cys Arg Ala Ser Leu Ser

130 135 140

Ala Ala Ile Arg Asp Asp Ala Val Trp Val Asn Arg Ser Ala Ala Phe

145 150 155 160

Asp Asp Ala Gln Val Arg Ile Gly Ala Ser Leu Thr Arg Glu Asp Ile

165 170 175

Trp Asp Met Leu Asp Pro Phe Phe Gly Ser Arg Glu Ala Tyr Leu Thr

180 185 190

Pro Ala Lys Lys Lys Lys Glu Asp Glu Asp Ser Ser Glu Gly Thr Gly

195 200 205

Glu Glu Lys Ala Lys Asp Leu Val Gln Lys Ala Gly Gln Trp Leu Ser

210 215 220

Ser Arg Phe Gly Thr Gly Lys Gly Ala Asn Phe Asp Ala Met Ala Glu

225 230 235 240

Val Tyr Ser Lys Ile Ser Glu Trp Ala Gly Thr Ala Gln Glu Gly Val

245 250 255

Ser Gly Lys Glu Gly Ile Lys Asn Leu Ala Asp Ala Leu Ala Ala Phe

260 265 270

Ser Pro Val Ser Gln Asn Leu Glu Gly Val Leu Lys Leu Ile Ser Gly

275 280 285

Pro Gly Tyr Lys Ser Ala Thr Arg Asn Leu Leu Gly Glu Leu Asp Ser

290 295 300

Leu Pro Val Val Ser Arg Asp His Leu Ser Ala Leu His Glu Lys Ala

305 310 315 320

Ala Glu Asp Thr Val Lys Cys Lys Glu Ser Thr Gly Thr Lys Gly Arg

325 330 335

Arg Pro Tyr Ala Asp Ala Ile Leu Asn Asp Val Glu Lys Arg Cys Gly

340 345 350

Phe Thr Tyr Leu Thr Asp Ser Asp Asn Arg Ser Val Ser Ile Leu Asp

355 360 365

Thr Ser Glu Phe Pro Ser Asp Tyr Lys Trp Gly Thr Ala Arg His Ser

370 375 380

Glu Phe Ala Val Ile Leu Asp His Ala Ala Arg Arg Ile Ser Val Ala

385 390 395 400

His Ser Trp Ile Lys Leu Ala Glu Ala Glu Arg Asp Arg Cys Glu Glu

405 410 415

Asp Ala Ala Lys Val Tyr Asp Leu Pro Asp Lys Val Lys Glu Trp Leu

420 425 430

Asp Thr Phe Cys Ser Asn Arg Ser Asp Ile Ser Gly Ala Gln Gly Glu

435 440 445

Gly Tyr Arg Ile Arg Arg Lys Ala Ile Glu Gly Trp Lys Glu Val Val

450 455 460

Ala Ser Trp Gly Arg Ser Ser Cys Ile Thr Ala Glu Asp Arg Val Ala

465 470 475 480

Ala Ala Arg Ala Leu Gln Asp Asp Pro Glu Ile Asp Lys Phe Gly Asp

485 490 495

Ile Gln Leu Phe Glu Ile Leu Ala Gln Asp Glu Ala Leu Cys Val Trp

500 505 510

His Lys Asp Gly Asp Val Ala Lys Ser Pro Asp Ala Gln Met Leu Ile

515 520 525

Asp Tyr Val Leu Ala Ser Asp Ala Glu Ser Lys Lys Arg Arg Phe Lys

530 535 540

Val Pro Ala Tyr Arg His Pro Asp Ala Leu Leu His Pro Ile Phe Cys

545 550 555 560

Asp Phe Gly Asn Ser Arg Trp Asp Ile Thr Tyr Asp Ile His Gly Ala
565 570 575
Arg Gly Lys Lys Lys Ala Lys Arg Gly Ser Lys Lys Glu Glu Ala Met

580 585 590
Pro Arg Gly Val Ala Met Lys Leu Trp Thr Gly Ser Asp Val Leu Ser
595 600 605
Val Ser Leu Arg Trp Gln Ser Lys Lys Leu Ala Ala Asp Leu Ala Leu
610 615 620
Asp Gln Glu Ala Glu Glu Val Thr Asp Thr Ala Ala Val Ser Arg Ala
625 630 635 640
Asp Arg Leu Gly Arg Ala Ala Ala Gly Ile Asp Arg Gly Ala Gly Val

645 650 655
Thr Ile Ala Gly Leu Phe Glu Glu Ala His Trp Asn Gly Arg Leu Gln
660 665 670
Ala Pro Arg Gln Gln Leu Glu Ala Ile Ala Ala Val Arg Asp Asn Gln
675 680 685
Lys Leu Ser Ser Glu Glu Arg Glu Arg Arg Ile Ala Phe Met Lys Asp
690 695 700
Arg Ile Arg Trp Leu Val Thr Phe Ser Ala Lys Leu Arg Pro Gln Gly

705 710 715 720
Pro Trp His Ser Tyr Ala Pro Thr Gln Gly Leu Gln Ser Asp Pro Lys
725 730 735
Tyr Trp Pro His Ser Glu Ile Asn Lys Lys Arg Lys Gly Gln Ala Lys
740 745 750
Leu Ile Leu Ser Arg Leu Pro Gly Leu Arg Ile Leu Ser Val Asp Leu
755 760 765
Gly His Arg Phe Ala Ala Ala Cys Ala Val Trp Glu Thr Met Ser Ser

770 775 780
Glu Ala Ile Gln Glu Ala Cys Arg Leu Ala Asn His Gln Leu Pro Ala
785 790 795 800
Pro Ala Asp Leu Tyr Leu His Leu Lys Arg Thr Val Gln Lys Asn Leu

805 810 815

Ile Asp Gly Glu Lys Thr Val Glu Glu Ser Thr Val Tyr Arg Arg Ile

820 825 830

Gly Ala Asp Arg Leu Pro Asp Gly Thr Ala His Pro Ala Pro Trp Ala

835 840 845

Arg Leu Asp Arg Gln Phe Leu Ile Lys Leu Gln Gly Glu Glu Lys Val

850 855 860

Arg Glu Ala Ser Asn Glu Glu Val Trp Gln Val His Leu Met Glu Ser

865 870 875 880

Ala Leu Gly Leu Ser Phe Pro Leu Ile Asp Arg Leu Val Tyr Ala Gly

885 890 895

Trp Gly Gly Thr Glu Lys Gln Ala Ala Arg Leu Glu Ala Leu Arg Glu

900 905 910

Lys Gly Trp Lys Pro Thr Gly Thr Pro Ala Asp Gln Asp Glu Glu Gly

915 920 925

Gly Gly Tyr Lys Pro Ser Leu Ala Val Asp Glu Leu Met Phe Ser Ala

930 935 940

Val Arg Thr Leu Arg Leu Ala Leu Lys Tyr His Gly Asp Arg Ala Arg

945 950 955 960

Ile Ala Phe Ala Leu Thr Ala Asp Tyr Lys Pro Met Pro Gly Asp Thr

965 970 975

Arg Tyr Tyr Phe Ser Glu Ala Lys Asp Arg Ser Ser Gly Ala Asp Ala

980 985 990

Ala Glu Arg Glu Ala Lys His Lys Asp Tyr Leu Leu Asp Met Leu Leu

995 1000 1005

Leu Trp His Asp Leu Ala Phe Ser Arg Lys Trp Arg Asp Glu Glu

1010 1015 1020

Ala Lys Glu Leu Trp Asn Leu His Ile Ala Ala Leu Pro Gly Tyr

1025 1030 1035

Gln Ala Pro Ala Ala Pro Ile Gln Glu Glu Ala Gly Gln Gly Arg

1040 1045 1050

Lys Lys Ala Arg Glu Glu Ala Arg Ala Lys Met Thr Pro Ala Ala
1055 1060 1065
Glu Ala Leu Leu Ala Asp Gly Thr Leu Arg Glu Lys Leu His Gly
1070 1075 1080
Leu Trp Lys Glu Arg Trp Glu Lys Asp Asp Ala Gln Trp Lys Lys

1085 1090 1095
His Leu Arg Trp Met Lys Asp Gly Ile Leu Pro Arg Gly Gly Arg
1100 1105 1110
Ala Ala Thr Pro Ser Ile Arg Tyr Val Gly Gly Leu Ser Leu Thr
1115 1120 1125
Arg Leu Ala Thr Leu Thr Glu Phe Arg Arg Lys Val Gln Val Gly
1130 1135 1140
Phe Tyr Thr Arg Leu Phe Pro Ser Gly Glu Lys Arg Glu Ile Lys

1145 1150 1155
Glu Ala Phe Gly Gln Thr Ala Leu Asp Ala Leu Glu Arg Leu Arg
1160 1165 1170
Glu Gln Arg Val Lys Gln Leu Ala Ser Arg Ile Ala Glu Ala Ala
1175 1180 1185
Leu Gly Ala Gly Arg Val Ser Arg Thr Ala Leu Lys Gln Asp Pro
1190 1195 1200
Lys Arg Pro Glu Ala Arg Val Asp Ala Ala Cys His Ala Val Ile

1205 1210 1215
Ile Glu Asn Leu Glu His Tyr Arg Pro Glu Glu Thr Arg Thr Arg
1220 1225 1230
Arg Glu Asn Arg Gly Leu Met Asn Trp Ala Ser Ser Lys Val Lys
1235 1240 1245
Lys Tyr Leu Ser Glu Ala Cys Gln Leu His Gly Leu Phe Leu Arg
1250 1255 1260
Glu Val Pro Ala Gly Tyr Thr Ser Arg Gln Asp Ser Arg Thr Gly

1265 1270 1275
Ala Pro Gly Met Arg Cys Gln Asp Val Thr Val Lys Thr Phe Leu

1280 1285 1290

Asn Ser Pro Phe Trp Gln Lys Gln Cys Val Gln Ala Gln Lys Asn

1295 1300 1305

Lys Ser Thr Ala Arg Asp Arg Phe Leu Cys Ala Leu Lys Glu Ala

1310 1315 1320

Val Ala Gln Gly Gly Met Glu Glu Glu Lys Lys Met Gly Pro Ile

1325 1330 1335

Arg Val Pro Val Pro Gly Gly Glu Val Phe Val Ser Ala Asp Ala

1340 1345 1350

Ala Ser Pro Ala Ala Lys Gly Leu Gln Ala Asp Leu Asn Ala Ala

1355 1360 1365

Ala Asn Ile Gly Leu Arg Ala Leu Leu Asp Pro Asp Trp Pro Gly

1370 1375 1380

Lys Trp Trp Tyr Val Pro Cys Asp Arg Lys Thr Ala Tyr Pro Ala

1385 1390 1395

Lys Glu Lys Val Glu Gly Ser Ala Ala Val Asp Val Lys Gln Ala

1400 1405 1410

Leu Pro Phe Val Leu Pro Glu Glu Lys Glu Asn Lys Gly Lys Thr

1415 1420 1425

Lys Gly Gly Lys Lys Gly Lys Gly Glu Val Met Asn Leu Trp Arg

1430 1435 1440

Asp Val Ser Ala Glu Pro Leu Met Thr Gly Gln Trp Leu Asp Tyr

1445 1450 1455

Thr Ala Tyr Arg Lys Glu Val Glu Asn Arg Val Ile Gln Val Leu

1460 1465 1470

Thr Ala Gln Leu Lys Ala Arg Asn Pro Leu Arg Phe Gly Asn Leu

1475 1480 1485

Gly Asp Glu Glu Glu Ile Pro Tyr

1490 1495

<210> 138

<211> 1108

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 138

Met Ala Ile Arg Ser Ile Lys Leu Lys Leu Lys Thr His Thr Gly Pro
1 5 10 15

Glu Ala Gln Asn Leu Arg Lys Gly Ile Trp Arg Thr His Arg Leu Leu
20 25 30

Asn Glu Gly Val Ala Tyr Tyr Met Lys Met Leu Leu Leu Phe Arg Gln
35 40 45

Glu Ser Thr Gly Glu Arg Pro Lys Glu Glu Leu Gln Glu Glu Leu Ile
50 55 60

Cys His Ile Arg Glu Gln Gln Gln Arg Asn Gln Ala Asp Lys Asn Thr
65 70 75 80

Gln Ala Leu Pro Leu Asp Lys Ala Leu Glu Ala Leu Arg Gln Leu Tyr
85 90 95

Glu Leu Leu Val Pro Ser Ser Val Gly Gln Ser Gly Asp Ala Gln Ile
100 105 110

Ile Ser Arg Lys Phe Leu Ser Pro Leu Val Asp Pro Asn Ser Glu Gly
115 120 125

Gly Lys Gly Thr Ser Lys Ala Gly Ala Lys Pro Thr Trp Gln Lys Lys
130 135 140

Lys Glu Ala Asn Asp Pro Thr Trp Glu Gln Asp Tyr Glu Lys Trp Lys
145 150 155 160

Lys Arg Arg Glu Glu Asp Pro Thr Ala Ser Val Ile Thr Thr Leu Glu
165 170 175

Glu Tyr Gly Ile Arg Pro Ile Phe Pro Leu Tyr Thr Asn Thr Val Thr
180 185 190

Asp Ile Ala Trp Leu Pro Leu Gln Ser Asn Gln Phe Val Arg Thr Trp
195 200 205

Asp Arg Asp Met Leu Gln Gln Ala Ile Glu Arg Leu Leu Ser Trp Glu

210 215 220

Ser Trp Asn Lys Arg Val Gln Glu Glu Tyr Ala Lys Leu Lys Glu Lys

225 230 235 240

Met Ala Gln Leu Asn Glu Gln Leu Glu Gly Gly Gln Glu Trp Ile Ser

245 250 255

Leu Leu Glu Gln Tyr Glu Glu Asn Arg Glu Arg Glu Leu Arg Glu Asn

260 265 270

Met Thr Ala Ala Asn Asp Lys Tyr Arg Ile Thr Lys Arg Gln Met Lys

275 280 285

Gly Trp Asn Glu Leu Tyr Glu Leu Trp Ser Thr Phe Pro Ala Ser Ala

290 295 300

Ser His Glu Gln Tyr Lys Glu Ala Leu Lys Arg Val Gln Gln Arg Leu

305 310 315 320

Arg Gly Arg Phe Gly Asp Ala His Phe Phe Gln Tyr Leu Met Glu Glu

325 330 335

Lys Asn Arg Leu Ile Trp Lys Gly Asn Pro Gln Arg Ile His Tyr Phe

340 345 350

Val Ala Arg Asn Glu Leu Thr Lys Arg Leu Glu Glu Ala Lys Gln Ser

355 360 365

Ala Thr Met Thr Leu Pro Asn Ala Arg Lys His Pro Leu Trp Val Arg

370 375 380

Phe Asp Ala Arg Gly Gly Asn Leu Gln Asp Tyr Tyr Leu Thr Ala Glu

385 390 395 400

Ala Asp Lys Pro Arg Ser Arg Arg Phe Val Thr Phe Ser Gln Leu Ile

405 410 415

Trp Pro Ser Glu Ser Gly Trp Met Glu Lys Lys Asp Val Glu Val Glu

420 425 430

Leu Ala Leu Ser Arg Gln Phe Tyr Gln Gln Val Lys Leu Leu Lys Asn

435 440 445

Asp Lys Gly Lys Gln Lys Ile Glu Phe Lys Asp Lys Gly Ser Gly Ser

450 455 460

Thr Phe Asn Gly His Leu Gly Gly Ala Lys Leu Gln Leu Glu Arg Gly
465 470 475 480
Asp Leu Glu Lys Glu Glu Lys Asn Phe Glu Asp Gly Glu Ile Gly Ser
485 490 495
Val Tyr Leu Asn Val Val Ile Asp Phe Glu Pro Leu Gln Glu Val Lys
500 505 510

Asn Gly Arg Val Gln Ala Pro Tyr Gly Gln Val Leu Gln Leu Ile Arg
515 520 525
Arg Pro Asn Glu Phe Pro Lys Val Thr Thr Tyr Lys Ser Glu Gln Leu
530 535 540
Val Glu Trp Ile Lys Ala Ser Pro Gln His Ser Ala Gly Val Glu Ser
545 550 555 560
Leu Ala Ser Gly Phe Arg Val Met Ser Ile Asp Leu Gly Leu Arg Ala
565 570 575

Ala Ala Ala Thr Ser Ile Phe Ser Val Glu Glu Ser Ser Asp Lys Asn
580 585 590
Ala Ala Asp Phe Ser Tyr Trp Ile Glu Gly Thr Pro Leu Val Ala Val
595 600 605
His Gln Arg Ser Tyr Met Leu Arg Leu Pro Gly Glu Gln Val Glu Lys
610 615 620
Gln Val Met Glu Lys Arg Asp Glu Arg Phe Gln Leu His Gln Arg Val
625 630 635 640

Lys Phe Gln Ile Arg Val Leu Ala Gln Ile Met Arg Met Ala Asn Lys
645 650 655
Gln Tyr Gly Asp Arg Trp Asp Glu Leu Asp Ser Leu Lys Gln Ala Val
660 665 670
Glu Gln Lys Lys Ser Pro Leu Asp Gln Thr Asp Arg Thr Phe Trp Glu
675 680 685
Gly Ile Val Cys Asp Leu Thr Lys Val Leu Pro Arg Asn Glu Ala Asp
690 695 700

Trp Glu Gln Ala Val Val Gln Ile His Arg Lys Ala Glu Glu Tyr Val

705 710 715 720

Gly Lys Ala Val Gln Ala Trp Arg Lys Arg Phe Ala Ala Asp Glu Arg

725 730 735

Lys Gly Ile Ala Gly Leu Ser Met Trp Asn Ile Glu Glu Leu Glu Gly

740 745 750

Leu Arg Lys Leu Leu Ile Ser Trp Ser Arg Arg Thr Arg Asn Pro Gln

755 760 765

Glu Val Asn Arg Phe Glu Arg Gly His Thr Ser His Gln Arg Leu Leu

770 775 780

Thr His Ile Gln Asn Val Lys Glu Asp Arg Leu Lys Gln Leu Ser His

785 790 795 800

Ala Ile Val Met Thr Ala Leu Gly Tyr Val Tyr Asp Glu Arg Lys Gln

805 810 815

Glu Trp Cys Ala Glu Tyr Pro Ala Cys Gln Val Ile Leu Phe Glu Asn

820 825 830

Leu Ser Gln Tyr Arg Ser Asn Leu Asp Arg Ser Thr Lys Glu Asn Ser

835 840 845

Thr Leu Met Lys Trp Ala His Arg Ser Ile Pro Lys Tyr Val His Met

850 855 860

Gln Ala Glu Pro Tyr Gly Ile Gln Ile Gly Asp Val Arg Ala Glu Tyr

865 870 875 880

Ser Ser Arg Phe Tyr Ala Lys Thr Gly Thr Pro Gly Ile Arg Cys Lys

885 890 895

Lys Val Arg Gly Gln Asp Leu Gln Gly Arg Arg Phe Glu Asn Leu Gln

900 905 910

Lys Arg Leu Val Asn Glu Gln Phe Leu Thr Glu Glu Gln Val Lys Gln

915 920 925

Leu Arg Pro Gly Asp Ile Val Pro Asp Asp Ser Gly Glu Leu Phe Met

930 935 940

Thr Leu Thr Asp Gly Ser Gly Ser Lys Glu Val Val Phe Leu Gln Ala

945 950 955 960

Asp Ile Asn Ala Ala His Asn Leu Gln Lys Arg Phe Trp Gln Arg Tyr
965 970 975
Asn Glu Leu Phe Lys Val Ser Cys Arg Val Ile Val Arg Asp Glu Glu
980 985 990
Glu Tyr Leu Val Pro Lys Thr Lys Ser Val Gln Ala Lys Leu Gly Lys
995 1000 1005
Gly Leu Phe Val Lys Lys Ser Asp Thr Ala Trp Lys Asp Val Tyr
1010 1015 1020

Val Trp Asp Ser Gln Ala Lys Leu Lys Gly Lys Thr Thr Phe Thr
1025 1030 1035
Glu Glu Ser Glu Ser Pro Glu Gln Leu Glu Asp Phe Gln Glu Ile
1040 1045 1050
Ile Glu Glu Ala Glu Glu Ala Lys Gly Thr Tyr Arg Thr Leu Phe
1055 1060 1065
Arg Asp Pro Ser Gly Val Phe Phe Pro Glu Ser Val Trp Tyr Pro
1070 1075 1080

Gln Lys Asp Phe Trp Gly Glu Val Lys Arg Lys Leu Tyr Gly Lys
1085 1090 1095
Leu Arg Glu Arg Phe Leu Thr Lys Ala Arg
1100 1105

<210> 139
<211> 1098
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 139
Met Pro Val Arg Ser Ile Asn Leu Lys Ile Val Ile Ser Arg Asn Thr
1 5 10 15
Gln Gly Glu Lys Ser Arg Gln Ser Ile Trp Thr Thr His Ala Ala Val

20 25 30
Asn Asp Ala Val Arg Tyr Tyr Glu Glu Gln Leu Leu Ile Met Arg Gly

35 40 45

Leu Gly Tyr His Ile Ser Asp Lys Asp Val Val Ser Lys Glu Ser Ile

50 55 60

Gln Gln Glu Arg Leu Ser Arg Ile Arg Arg Ala Gln Leu Glu Asn Gly

65 70 75 80

Leu Pro Glu Pro Leu Gly Thr Asp Ala Glu Leu Asn Ser Leu Val Arg

85 90 95

Lys Phe Tyr Glu Phe Ile Val Pro Ser Ser Val Lys Glu Asp Gly Asn

100 105 110

Ala Gln Gln Ala Asn Gly Phe Leu Ser Pro Leu Thr Asp Pro Ile Ser

115 120 125

Ile Gly Tyr Leu Ser Ile Phe Glu Lys Leu Gly Thr Ile Pro Asp Trp

130 135 140

Val Gly Gln Leu Lys Ala Gly Asp Pro Gln Ala Val Glu Asn Ala Lys

145 150 155 160

Lys Trp Ser Ala Thr Ser Ala Gly Ile Lys Arg Leu Ser Glu Thr Gly

165 170 175

Ala Pro Pro Lys Trp Lys Lys Leu Phe Leu Thr Gly Asp Pro Ser Trp

180 185 190

Pro Gln Ser Phe Ser Glu Asp Ile Asp Lys Lys Ile Lys Glu Ile Glu

195 200 205

Gly Ala Pro Lys Val Ile Cys Gln Leu Met Glu Met Gly Val Leu Pro

210 215 220

Leu Phe Pro Ala Tyr Phe Ala Asp Lys Leu Glu Gly Ser Asp Gly Ser

225 230 235 240

Leu Ser Arg Trp Asp Arg Leu Ala Phe Arg Leu Ala Val Gly His Met

245 250 255

Leu Ser Trp Glu Ser Trp Cys Ile Lys Ser Ala Glu Asp His Phe Glu

260 265 270

Arg Lys Arg Arg Val Glu Ser Phe Ser Glu Lys His Thr Thr Pro Ser

275 280 285

Leu Ile Ile Cys Phe Glu Thr Leu Glu Lys Tyr Gln Lys Glu Arg Gln
290 295 300
Glu Lys Glu Leu Gly Gln Asn Arg Ser Leu Pro Met Gln Arg Pro Phe
305 310 315 320
Arg Ile Thr Arg Arg Gln Ile Arg Gly Trp Glu Asp Leu Arg Asp Lys
325 330 335
Trp Leu Lys Asn Thr Thr Arg Thr Tyr Asp Ser Leu Lys Ser Ile Ala

340 345 350
Ser Lys Glu Gln Thr Lys Lys Gly Gly Arg Phe Gly Asp Pro His Leu
355 360 365
Phe Leu Trp Leu Ala Lys Pro Glu Asn His Ala Val Trp Asp Ala Asp
370 375 380
Glu Asp Ala Leu Ser Ile Phe Ala Lys Met Asn Ala Met Arg Gly Leu
385 390 395 400
Leu Glu Arg Ser Arg Glu Thr Ala Tyr Met Thr Leu Pro Asp Pro Ile

405 410 415
Glu His Pro Arg Ser Ile Gln Trp Glu Ala Glu Gly Gly Ser Asn Phe
420 425 430
Lys Asn Tyr Val Ile Thr His Ser Pro Val Glu Gly Leu His Val Gln
435 440 445
Leu Pro Leu Leu Cys Lys Ser Glu Ser Gly Lys Leu Ile Asp Gln Thr
450 455 460
Phe Glu Phe Pro Leu Ala Pro Ser Asp Gln Phe Lys Val Ala Gln Ile

465 470 475 480
Ser Lys Thr Lys Ser Glu Val Thr Ile Thr His Gln Ser Val Leu Asp
485 490 495
Glu Glu Tyr Arg Ser Lys Val Gly Ala Ala Asp Leu Leu Met Asp Trp
500 505 510
Pro Tyr Leu Lys Asn Arg Arg Phe Glu Ser Val Glu His Gly Asp Ile
515 520 525
Gly Pro Val Phe Leu Lys Leu Ser Leu Asp Ile Glu Arg Ile Leu Pro

530 535 540

Asp Gly Trp Thr Pro Lys Arg Pro Gln Ala Ile Ser His Phe Ser Ser

545 550 555 560

Ala Ser Gly Asn Ser Lys His Lys Leu Ser Val Val Ser Gly Leu Arg

565 570 575

Val Leu Ser Val Asp Leu Gly Ile Arg Ser Phe Gly Ala Cys Ser Val

580 585 590

Phe Glu Leu Ser Glu His Lys Pro Thr Ser Gly Met Ser Phe Glu Ile

595 600 605

Glu Gly Leu Asn Leu Trp Ala Asn His Glu Arg Ser Phe Met Leu Asn

610 615 620

Leu Pro Asp Glu Asp Val Gly Asn Lys Gly Arg Gln Leu Gln Lys Thr

625 630 635 640

Lys Asp Ala Glu Leu Arg Ala Met Arg Arg Val Leu Gly Arg Tyr Arg

645 650 655

Lys Ile Tyr Ala Leu Ala Gly Ile Asp Pro Glu Asp Arg Lys Asp Ile

660 665 670

Leu Glu Leu Leu Cys Gln Asp Gln Asp Ile Phe Glu Phe Glu Arg Thr

675 680 685

Ile Tyr Lys Gly Leu Val Thr Ser Thr Ser Val Ser Gln Pro Leu Trp

690 695 700

Glu Gly Lys Ile Lys Glu Ser Leu Lys Ala Leu Arg Asn Ala Phe Gly

705 710 715 720

Arg Lys Val Arg Glu Trp Arg Arg Ala Asn Arg Leu Asn Ser Asn Leu

725 730 735

Lys Tyr Ala Gly Lys Thr Met Trp Ala Ile Gln His Leu Glu Asp Thr

740 745 750

Arg Arg Phe Leu His Ser Trp Ser His Leu Gly Arg Phe Ser Gly Glu

755 760 765

Ile Arg Arg Ala Asp Arg Val Lys Arg Gly Val Phe Ala Thr Arg Leu

770 775 780

Leu Gln His Leu Asp Ser Val Lys Arg Asp Arg Leu Lys Thr Gly Ala

785 790 795 800

Asp Leu Leu Val Gln Ser Ala Arg Gly Phe Leu Arg Asp Asn Gln Gly

805 810 815

Asn Trp Lys Lys Ser Tyr Ala Pro Cys Gln Val Ile Leu Phe Glu Asp

820 825 830

Leu Ser Arg Tyr Leu Met Gln Thr Asp Arg Pro Arg Arg Glu Asn Ser

835 840 845

Gln Leu Met Lys Trp Ser His Arg Ser Ile Pro Leu Glu Val Ala Met

850 855 860

Gln Gly Glu Leu Tyr Gly Ile His Val Cys Asp Thr Ser Ala Ala Phe

865 870 875 880

Ser Ser Arg Tyr His Ala Arg Leu Ala Thr Pro Gly Ile Arg Cys His

885 890 895

Ala Leu Arg Lys Glu Asp Leu Ser Asn Gln Phe Leu Ile Glu Ser Leu

900 905 910

Gln Lys Glu Asn Pro Asp Ile Asp Phe Gly Ile Cys Lys Ala Gly Asp

915 920 925

Leu Ile Pro Arg Gly Gly Gly Glu Ile Phe Val Ser Cys Asp Gly Asn

930 935 940

Gly Gly Ile Ser Arg Ile His Ala Asp Ile Asn Ala Ala Gln Asn Leu

945 950 955 960

Gln Arg Arg Phe Trp Leu Arg His Gly Glu Ala Ile Arg Ile Pro Ala

965 970 975

Arg Lys Ile Thr Leu Lys Gly Asp Glu Ile Trp Val Pro Arg Ser Ile

980 985 990

Gly Lys Arg Leu Gln Gly Ala Met Ser Gly Cys Gly Tyr Leu Ile Pro

995 1000 1005

Thr Gly His Glu Ser Gly Ser Cys Arg Trp Glu Arg Ile Thr Ala

1010 1015 1020

Ser Lys Trp Glu Ser Ile Ser Arg Ser Ser Val Ala Gln Lys Glu

1025 1030 1035

Glu Val Asn Glu Asp Leu Leu Asp Ile Ala Leu Leu Glu Glu Glu

1040 1045 1050

Ala Leu Glu Leu Ser Asn Glu Tyr Thr Thr Phe Phe Arg Asp Pro

1055 1060 1065

Ser Gly Ile Thr Leu Pro Ser Asp Leu Trp Phe Pro Met Lys Thr

1070 1075 1080

Phe Trp Gly Met Thr Arg Ala Lys Ile Lys Ser Ala Ile Lys Gln

1085 1090 1095

<210> 140

<211> 1130

<212> PRT

<213> Unknown

<

220><223> Description of Unknown:

Cas12 sequence

<400> 140

Met Thr Val Lys Ser Ile Lys Val Lys Leu Arg Leu Asp Asn Met Pro

1 5 10 15

Glu Ile Arg Ala Gly Leu Trp Lys Leu His Thr Glu Val Asn Ala Gly

20 25 30

Val Arg Tyr Tyr Thr Glu Trp Leu Ser Leu Leu Arg Gln Glu Asn Leu

35 40 45

Tyr Arg Arg Ser Pro Asn Gly Asp Gly Glu Gln Glu Cys Tyr Lys Thr

50 55 60

Ala Glu Glu Cys Lys Val Glu Leu Leu Glu Arg Leu Arg Ala Arg Gln

65 70 75 80

Val Glu Asn Gly His Arg Asp Pro Ala Gly Ser Asp Asp Glu Leu Leu

85 90 95

Gln Leu Ala Arg Gln Leu Tyr Glu Leu Leu Val Pro Gln Ala Ile Gly

100 105 110

Ala Lys Gly Asp Ala Gln Gln Ile Ala Arg Lys Phe Leu Ser Pro Leu

115 120 125

Ala Asp Lys Asp Ala Val Gly Gly Leu Gly Ile Ala Lys Ala Gly Asn

130 135 140

Lys Pro Arg Trp Val Arg Met Arg Asp Ala Gly Glu Pro Gly Trp Glu

145 150 155 160

Glu Glu Lys Ala Lys Ala Glu Ala Arg Lys Ser Thr Asp Arg Thr Ala

165 170 175

Asp Val Leu Arg Ala Leu Ala Asp Phe Gly Leu Lys Pro Leu Met Arg

180 185 190

Val Tyr Thr Asp Ser Asp Met Ser Ser Val Gln Trp Lys Pro Leu Arg

195 200 205

Lys Gly Gln Ala Val Arg Thr Trp Asp Arg Asp Met Phe Gln Gln Ala

210 215 220

Ile Glu Arg Met Met Ser Trp Glu Ser Trp Asn Gln Arg Val Gly Glu

225 230 235 240

Ala Tyr Ala Lys Leu Val Glu Gln Lys Ser Arg Phe Glu Gln Lys Asn

245 250 255

Phe Val Gly Gln Glu His Leu Val Gln Leu Val Asn Gln Leu Gln Gln

260 265 270

Asp Met Lys Glu Ala Ser His Gly Leu Glu Ser Lys Glu Gln Thr Ala

275 280 285

His Tyr Leu Thr Gly Arg Ala Leu Arg Gly Ser Asp Lys Val Phe Glu

290 295 300

Lys Trp Glu Lys Leu Asp Pro Asp Ala Pro Phe Asp Leu Tyr Asp Thr

305 310 315 320

Glu Ile Lys Asn Val Gln Arg Arg Asn Thr Arg Arg Phe Gly Ser His

325 330 335

Asp Leu Phe Ala Lys Leu Ala Glu Pro Lys Tyr Gln Ala Leu Trp Arg

340 345 350

Glu Asp Ala Ser Phe Leu Thr Arg Tyr Ala Ala Tyr Asn Ser Ile Leu

355 360 365

Arg Lys Leu Asn His Ala Lys Met Phe Ala Thr Phe Thr Leu Pro Asp

370 375 380

Ala Thr Ala His Pro Ile Trp Thr Arg Phe Asp Lys Leu Gly Gly Asn

385 390 395 400

Leu His Gln Tyr Thr Phe Leu Phe Asn Glu Phe Gly Glu Gly Arg His

405 410 415

Ala Ile Arg Phe Gln Lys Leu Leu Thr Ile Glu His Gly Val Ala Lys

420 425 430

Glu Val Asp Asp Val Thr Val Pro Ile Ser Met Ser Ala Gln Leu Asp

435 440 445

Asp Leu Leu Pro Gly Glu Ser Asn Glu Pro Thr Glu Leu Ser Phe Arg

450 455 460

Asp His Gly Thr Asp Gln His Phe Thr Gly Glu Phe Gly Gly Ala Lys

465 470 475 480

Ile Gln Tyr Arg Arg Asp Gln Leu Asp His Val His Arg Arg Arg Gly

485 490 495

Ala Arg Asp Val Tyr Leu Asn Leu Ser Val Arg Val Gln Ser Gln Ser

500 505 510

Glu Ala Arg Gly Glu Arg Arg Pro Pro Tyr Ala Ala Val Phe Arg Leu

515 520 525

Val Gly Asp Thr His Arg Ala Phe Ala His Phe Asp Lys Leu Ser Asn

530 535 540

Tyr Leu Ala Glu His Pro Asp Asp Gly Lys Leu Gly Ser Glu Gly Leu

545 550 555 560

Leu Ser Gly Leu Arg Val Met Ser Val Asp Leu Gly Leu Arg Thr Ser

565 570 575

Ala Ser Ile Ser Ile Phe Arg Val Ala Arg Lys Asp Glu Leu Lys Pro

580 585 590

Asn Ser Glu Gly Arg Val Pro Phe Phe Phe Pro Ile Lys Gly Asn Asp

595 600 605

Asn Leu Val Ala Val His Glu Arg Ser Gln Leu Leu Lys Leu Pro Gly

610 615 620

Glu Thr Glu Ser Lys Asp Leu Arg Ala Ile Arg Glu Glu Arg Gln Arg

625 630 635 640

Ile Leu Arg Gln Leu Arg Thr Gln Leu Ala Tyr Leu Arg Leu Leu Val

645 650 655

Arg Cys Gly Ser Glu Asp Val Gly Arg Arg Glu Arg Ser Trp Ala Lys

660 665 670

Leu Ile Glu Gln Ser Val Asp Ala Ala Asn His Met Thr Pro Asp Trp

675 680 685

Arg Glu Ala Phe Glu Gly Glu Leu Gln Lys Leu Lys Ser Leu Tyr Gly

690 695 700

Ile Cys Gly Asp Arg Glu Trp Thr Glu Ala Val Tyr Glu Ser Val Arg

705 710 715 720

Arg Val Trp Arg His Met Gly Lys Gln Val Arg Asp Trp Arg Lys Asp

725 730 735

Val Arg Ser Gly Glu Arg Pro Lys Ile Arg Gly Tyr Gln Lys Asp Val

740 745 750

Val Gly Gly Asn Ser Ile Glu Gln Ile Glu Tyr Leu Glu Arg Gln Tyr

755 760 765

Lys Phe Leu Lys Ser Trp Ser Phe Phe Gly Lys Val Ser Gly Gln Val

770 775 780

Ile Arg Ala Glu Lys Gly Ser Arg Phe Ala Thr Thr Leu Arg Glu His

785 790 795 800

Ile Asp His Ala Lys Glu Asp Arg Leu Lys Lys Leu Ala Asp Arg Ile

805 810 815

Ile Met Glu Ala Leu Gly Tyr Val Tyr Ala Leu Asp Ala Glu Arg Gly

820 825 830

Lys Gly Thr Trp Val Ala Lys Tyr Pro Pro Cys Gln Leu Ile Leu Leu

835 840 845

Glu Glu Leu Ser Glu Tyr Arg Phe Asn Asn Asp Arg Pro Pro Ser Glu

850 855 860

Asn Asn Gln Leu Met Gln Trp Ser His Arg Gly Val Phe Gln Glu Leu
865 870 875 880
Leu Asn Gln Ala Gln Val His Asp Leu Leu Val Gly Thr Met Tyr Ala

885 890 895
Ala Phe Ser Ser Arg Phe Asp Ala Arg Thr Gly Ala Pro Gly Ile Arg
900 905 910
Cys Arg Arg Val Pro Ala Arg Cys Ala Arg Glu Gln Asn Pro Glu Pro
915 920 925
Phe Pro Trp Trp Leu Asn Lys Phe Val Ala Glu His Lys Leu Asp Gly
930 935 940
Cys Pro Leu Arg Ala Asp Asp Leu Ile Pro Thr Gly Glu Gly Glu Phe

945 950 955 960
Phe Val Ser Pro Phe Ser Ala Glu Glu Gly Asp Phe His Gln Ile His
965 970 975
Ala Asp Leu Asn Ala Ala Gln Asn Leu Gln Arg Arg Leu Trp Ser Asp
980 985 990
Phe Asp Ile Ser Gln Ile Arg Leu Arg Cys Asp Trp Gly Glu Val Asp
995 1000 1005
Gly Glu Pro Val Leu Ile Pro Arg Leu Thr Gly Lys Arg Thr Ala

1010 1015 1020
Asp Ser Tyr Gly Asn Lys Val Phe Tyr Thr Asn Thr Gly Val Thr
1025 1030 1035
Tyr Tyr Glu Arg Glu Arg Gly Lys Lys Arg Arg Lys Ala Phe Ala
1040 1045 1050
Gln Glu Glu Leu Ser Glu Glu Glu Ala Glu Leu Leu Val Glu Ala
1055 1060 1065
Asp Glu Ala Arg Glu Lys Ser Val Val Leu Met Arg Asp Pro Ser

1070 1075 1080
Gly Ile Ile Asn Arg Gly Asp Trp Thr Arg Gln Lys Glu Phe Trp
1085 1090 1095
Ser Met Val Asn Gln Arg Ile Glu Gly Tyr Leu Val Lys Gln Ile

1100 1105 1110

Arg Ser Arg Val Cys Leu Pro Glu Ser Ala Cys Glu Asn Thr Gly

1115 1120 1125

Asp Ile

1130

<210> 141

<211> 1333

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 141

Met Lys Asn Phe Gln Asp Phe Thr Asn Leu Tyr Glu Leu Ser Lys Thr

1 5 10 15

Leu Arg Phe Glu Leu Lys Pro Ile Gly Gly Thr Lys Lys Leu Ile Glu

20 25 30

Glu Lys Asn Ile Leu Lys Leu Asp Lys Lys Lys Arg Glu Asn Tyr Glu

35 40 45

Lys Val Lys Pro Tyr Phe Asn Lys Ile His Gln Glu Phe Ile Asn Phe

50 55 60

Ala Leu Arg Asn Pro Asn Phe Asp Phe Ser Gln Phe Glu Glu Lys Tyr

65 70 75 80

Leu Asn Trp Leu Lys Asp Lys Lys Asn Lys Asp Leu Leu Lys Glu Lys

85 90 95

Glu Ser Ile Asp Lys Ile Phe Leu Glu Lys Ile Gly Lys Leu Phe Glu

100 105 110

Asn Ser Val Lys Asp Phe Leu Lys Glu Asn Gly Phe Glu Ser Ile Val

115 120 125

Lys Glu Glu Asp Gln Asn Leu Lys Phe Phe Arg Arg Lys Glu Ile Phe

130 135 140

Glu Val Leu Gln Glu Lys Tyr Gly Ser Glu Leu Glu Thr Gln Met Val

145 150 155 160

Asn Lys Asp Gly Glu Ile Lys Ser Ile Phe Asn Gly Trp Glu Lys Trp
165 170 175
Leu Gly Tyr Phe Asp Lys Phe Phe Asn Thr Arg Asp Asn Phe Tyr Lys

180 185 190
Thr Asp Gly Thr Ser Thr Ala Ile Ala Thr Arg Ile Ile Lys Asp Asn
195 200 205
Leu Lys Ile Phe Leu Glu Asn Ile Val Ala Phe Gly Lys Ile Lys Asn
210 215 220
Lys Lys Ile Asp Phe Ser Glu Val Glu Lys Asn Phe Ser Val Ser Ile
225 230 235 240
Asp Thr Phe Phe Glu Ile Asn Asn Phe Asn Asn Cys Phe Leu Gln Asp

245 250 255
Gly Ile Asp Phe Tyr Asn Lys Val Ile Gly Gly Glu Thr Leu Glu Asn
260 265 270
Gly Glu Lys Leu Lys Gly Leu Asn Glu Ile Ile Asn Lys Tyr Arg Gln
275 280 285
Asp Thr Gly Glu Lys Ile Pro Tyr Phe Lys Lys Leu Gln Lys Gln Ile
290 295 300
Leu Ser Glu Lys Asp Gly Val Phe Ile Asp Lys Ile Glu Asp Asp Gly

305 310 315 320
Gly Phe Tyr Glu Val Leu Lys Asn Phe Tyr Lys Asn Ala Ala Glu Lys
325 330 335
Glu Gly Phe Leu Lys Asn Ile Phe Glu Asn Phe Tyr Thr Ile Ser Asp
340 345 350
Lys Asn Leu Glu Lys Ile Tyr Phe Asn Lys Ile Ala Phe Asn Thr Ile
355 360 365
Ser His Lys Phe Gly Ser Ala Leu Glu Phe Glu Arg Ile Leu Tyr Glu

370 375 380
Glu Met Lys Lys Glu Lys Ala Asp Gly Ile Lys Phe Glu Lys Lys Glu
385 390 395 400
Asn Lys Tyr Lys Phe Pro Asp Phe Ile Gln Ile Ile Phe Ile Lys Arg

405 410 415

Ser Leu Glu Asn Tyr Asp Ser Glu Asn Leu Phe Trp Lys Glu Arg Tyr

420 425 430

Tyr Lys Ser Glu Glu Asn Val Asp Gly Phe Leu Glu Lys Asn Asn Asn

435 440 445

Asn Leu Trp Gly Gln Phe Cys Lys Ile Leu Asn Phe Glu Phe Leu Asn

450 455 460

Ile Leu Lys Arg Arg Ile Ile Asp Glu Ala Gly Glu Glu Tyr Glu Val

465 470 475 480

Gly Phe Glu Ile Ser Lys Asn Ile Leu Gly Glu Lys Leu Glu Asn Phe

485 490 495

Glu Leu Asn Gln Glu Asn Lys Gly Ile Ile Lys Asp Phe Ala Asp Tyr

500 505 510

Ser Leu Ala Leu Tyr Ser Phe Gly Lys Tyr Phe Ala Val Glu Lys Gly

515 520 525

Arg Asn Trp Asp Leu Asn Ile Asp Ile Ser Asp Asp Phe Tyr Gly Gly

530 535 540

Glu Asp Gly Tyr Ile Glu Lys Phe Tyr Asn Thr Gly Tyr Asp Glu Ile

545 550 555 560

Val Lys Pro Tyr Asn Leu Met Arg Asn Tyr Ile Ser Lys Lys Pro Trp

565 570 575

Glu Asp Asn Lys Lys Trp Lys Ile Asn Phe Glu Thr Ser Ser Leu Leu

580 585 590

Ser Gly Trp Asp Lys Asn Leu Glu Ser Asn Gly Ser Tyr Ile Phe Gln

595 600 605

Lys Gly Asn Lys Tyr Tyr Leu Gly Ile Ile Asn Gly Ser Lys Pro Ala

610 615 620

Lys Glu Ile Leu Glu Lys Leu Tyr Ser Gly Asp Gly Glu Lys Ile Lys

625 630 635 640

Arg Phe Ile Tyr Asp Phe Gln Lys Pro Asp Asn Lys Asn Thr Pro Arg

645 650 655

Met Phe Ile Arg Ser Lys Lys Asp Ser Phe Ser Pro Ala Val Glu Lys
660 665 670
Tyr Asn Leu Pro Ile Asn Asp Ile Leu Glu Ile Tyr Asp Asn Gly Leu
675 680 685
Phe Lys Thr Glu Asn Lys Gly Asn Pro Asn Tyr Lys Glu Ser Leu Arg

690 695 700
Lys Leu Ile Asp Tyr Phe Lys Leu Gly Phe Ser Arg His Glu Ser Phe
705 710 715 720
Lys His Phe Asn Phe Val Trp Lys Asp Ser Lys Ser Tyr Glu Asn Ile
725 730 735
Ala Asp Phe Tyr Arg Asp Val Glu Lys Ser Cys Tyr Lys Ile Asp Phe
740 745 750
Glu Phe Leu Asn Phe Glu Glu Leu Lys Lys Leu Thr Phe Glu Lys His

755 760 765
Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Glu Leu Asp Glu Ser
770 775 780
Leu Gln Glu Lys Gly Tyr Asn Phe Lys Gly Glu Gly Gln Lys Asn Ile
785 790 795 800
His Thr Lys Tyr Phe Glu Ala Leu Phe Leu Glu Glu Asn Ile Ser Arg
805 810 815
Lys Ser Gly Ala Val Phe Lys Leu Ser Gly Gly Gly Glu Val Phe Phe

820 825 830
Arg Lys Lys Ser Ile Lys Ala Lys Lys Glu Lys Arg Asn Ser Val Glu
835 840 845
Val Ile Lys Asn Lys Arg Tyr Thr Glu Cys Lys Tyr Phe Leu His Phe
850 855 860
Pro Ile Gln Val Asn Phe Lys Glu Glu Ile Ser Gly Asn Phe Asn Gln
865 870 875 880
Glu Ile Asn Lys Phe Leu Ala Asn Asn Pro Asp Ile Asn Val Ile Gly

885 890 895
Ile Asp Arg Gly Glu Lys His Leu Ala Tyr Phe Ser Val Ile Asn Gln

900 905 910

Lys Gly Glu Ile Leu Glu Ser Gly Ser Phe Asn Lys Ile Glu Asn Tyr

915 920 925

Asn Lys Asn Gly Glu Lys Leu Leu Phe Pro Glu Arg Glu Ile Lys Glu

930 935 940

Ile His Lys Asp Gly Ser Leu Ile Asp Leu Glu Leu Val Glu Thr Gly

945 950 955 960

Arg Lys Val Asp Tyr Val Asp Tyr Lys Leu Leu Leu Glu Tyr Lys Glu

965 970 975

Arg Lys Arg Leu Leu Gln Arg Gln Ser Trp Lys Glu Val Glu Gln Ile

980 985 990

Lys Asp Leu Lys Lys Gly Tyr Ile Ser Ala Leu Val Arg Lys Ile Ala

995 1000 1005

Asp Leu Ile Ile Lys His Asn Ala Ile Val Ile Phe Glu Asp Leu

1010 1015 1020

Asn Phe Arg Phe Lys Gln Ile Arg Gly Gly Ile Glu Lys Ser Ile

1025 1030 1035

Tyr Gln Gln Leu Glu Lys Ala Leu Ile Asp Lys Leu Asn Phe Leu

1040 1045 1050

Val Asn Lys Asn Glu Ile Asn Leu Glu Lys Ala Gly Ser Ile Leu

1055 1060 1065

Lys Ala Tyr Gln Leu Thr Val Pro Val Asp Ser Leu Lys Glu Ile

1070 1075 1080

Gly Lys Gln Thr Gly Val Ile Phe Tyr Thr Glu Ala Ala Tyr Thr

1085 1090 1095

Ser Lys Ile Asp Pro Ile Thr Gly Trp Arg Pro Asn Leu Tyr Leu

1100 1105 1110

Lys Lys Asn Asn Ser Lys Ile Asn Lys Glu Asn Ile Leu Lys Phe

1115 1120 1125

Asp Asn Ile Val Phe Asn Ser Lys Glu Asn Arg Phe Glu Phe Thr

1130 1135 1140

Tyr Asp Leu Lys Lys Phe Phe Gly Lys Asp Ser Lys Phe Pro Ala
1145 1150 1155
Lys Thr Val Asn Thr Val Cys Ser Cys Val Glu Arg Phe Lys Trp
1160 1165 1170
Asn Arg Asn Leu Asn Asn Asn Lys Gly Gly Tyr Ile His Tyr Glu
1175 1180 1185
Asn Leu Thr Asp Gly Lys Leu Ala Asn Lys Glu Gln Lys Glu Asp

1190 1195 1200
Glu Phe Ser Asn Phe Lys Glu Leu Phe Glu Lys Tyr Phe Ile Asp
1205 1210 1215
Ile Asn Gly Asn Ile Leu Glu Gln Ile Lys Asn Leu Asp Thr Lys
1220 1225 1230
Asn Asn Glu Lys Phe Phe Ser Ser Phe Ile Asp Leu Phe Thr Leu
1235 1240 1245
Val Cys Gln Ile Arg Asn Thr Asn Gln Asn Ala Lys Gly Asp Glu

1250 1255 1260
Asn Asp Phe Ile Leu Ser Pro Val Glu Pro Phe Phe Asp Ser Arg
1265 1270 1275
Lys Ser Gln Asn Phe Gly Lys Ser Leu Pro Lys Asn Gly Asp Glu
1280 1285 1290
Asn Gly Ala Phe Asn Ile Ala Arg Lys Gly Leu Ile Ile Leu Asn
1295 1300 1305
Arg Ile Ser Glu Asn Pro Glu Lys Pro Asp Leu Leu Ile Phe Asn

1310 1315 1320
Ala Asp Trp Asp Asn Phe Ala Arg Asn Ile
1325 1330
<210> 142
<211> 606
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence

<400> 142

Met Ala Gln Ala Glu Ala Pro Arg Arg Leu Arg Ala Tyr Lys Phe Ala
1 5 10 15
Leu Asp Pro Thr Glu Ala Gln Leu Arg Glu Phe Glu Gln His Ala Gly
20 25 30

Ser Ala Arg Trp Ala Tyr Asn His Ala Asn Ala Ile Leu Ser Arg Tyr
35 40 45
Ser Asp Thr Leu Arg Asn Arg Trp Asn Ala Trp Ile Ala Gln His His
50 55 60
Gly Leu Ser Arg Glu Gln Leu Tyr Ala Leu Pro Asp Arg Glu Arg Thr
65 70 75 80
Ala Ile Gln Ala Ala Ala Arg Ala Ala Val Lys Ala Glu Asn Ala Gln
85 90 95

Leu Ala Ala Glu Leu Arg Ile Ile Asp Asp His Arg Lys Arg Val Thr
100 105 110
His Lys Gly Lys Pro Ser Val Glu Pro Gly Glu Gln Pro Ala Glu Asp
115 120 125
Ala Pro Glu Arg Ala Tyr Gln Leu Trp Arg Glu Arg Val Glu Leu Ala
130 135 140
Arg Leu His Ala Glu Asp Pro Gln Ala Tyr Arg Ala Glu Arg Lys Arg
145 150 155 160

Ile Leu Asp Glu Ile Arg Pro Leu Val Asn Ala Thr Lys Arg Lys Leu
165 170 175
Ile Glu Gln Gly Ala Tyr Arg Pro Thr Ala Met Asp Ile Ser Thr Leu
180 185 190
Trp Arg Glu Ile Arg Asp Leu Pro Pro Asp Glu Gly Gly Ser Pro Trp
195 200 205
Trp Pro Glu Val Ser Ile Tyr Ala Phe Thr Ser Gly Phe Ala His Ala
210 215 220

Glu Thr Ala Trp Lys Asn Tyr Leu Glu Ser Leu Ala Gly Arg Arg Ala
225 230 235 240

Gly Arg Pro Val Gly Lys Pro Arg Phe Lys Lys Lys Arg Arg Ser Arg
245 250 255
Arg Ser Phe Thr Leu Tyr Gly Ser Val Lys Leu Val Thr Tyr Arg Arg
260 265 270
Ile Gln Val Pro Ser Ile Gly Ser Val Arg Leu His Gly Ser Ala Lys
275 280 285

Arg Leu His Arg Ala Leu Glu Arg Arg Gly Gly Ile Ile Lys Ser Ile
290 295 300
Thr Ile Ser Gln Gly Gly His Arg Trp Tyr Ala Ser Val Leu Val Asp
305 310 315 320
Glu Leu Asp Ile Thr Pro Gly Arg Glu Thr Gln Arg Gly Pro Ser Arg
325 330 335
Arg Gln Arg Asp Arg Gly Ala Val Gly Val Asp Leu Gly Val His His
340 345 350

Leu Val Ala Leu Ser Asp Pro Asn Glu Lys Thr Leu Asp Asn Pro Arg
355 360 365
His Leu Arg Lys Ala Arg Lys Arg Leu Leu Lys Ala Gln Arg Ala Met
370 375 380
Ser Arg Arg Arg Gly Pro Asp Lys Arg Thr Gly Gln Glu Pro Ser Arg
385 390 395 400
Arg Trp Val Lys Ala Arg Asn Arg Val Ala Arg Leu His His Glu Leu
405 410 415

Ala Val Arg Arg Ala Gly His Leu His Glu Ile Thr Lys Arg Leu Ala
420 425 430
Thr Ser Tyr Glu Leu Val Ala Ile Glu Asp Leu Asn Val Ala Gly Met
435 440 445
Thr Arg Ser Ala Arg Gly Thr Ile Asp Gln Pro Gly Arg Gly Val Arg
450 455 460
Ala Lys Ala Gly Leu Asn Arg Ser Ile Leu Asp Thr Ser Pro Ala Glu
465 470 475 480

Phe Arg Arg Gln Leu Gln Tyr Lys Ala Ser Trp Tyr Gly Ala Thr Val

485 490 495

Ala Val Ile Asp Arg Trp Ala Pro Thr Ser Arg Thr Cys Ser Ser Cys

500 505 510

Gly Ala Val Lys Ala Lys Leu Ser Leu Ala Glu Arg Thr Phe Phe Cys

515 520 525

Glu His Cys Gly Met Glu Leu Asp Arg Asp Ile Asn Ala Ala Arg Asn

530 535 540

Ile Leu Ala Phe Ala Gln Ser Ala Tyr Pro Gly Glu Gly Lys Ala Leu

545 550 555 560

Asn Ala Cys Gly Gly Ser Val Ser Pro Gly Ser Gln Ser Val Val Gln

565 570 575

Ala Gly Ala Asp Glu Ala Gly Arg Pro Ala Arg Lys Pro Arg Arg Ser

580 585 590

Ser Arg Gly Ser Asp Pro Pro Ala Thr Pro Thr Thr Arg Ala

595 600 605

<210> 143

<211> 1193

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 143

Met Lys Arg Ile Ala Lys Phe Arg His Asp Lys Pro Val Lys Arg Glu

1 5 10 15

Ala Trp Ser Lys Gly Tyr Arg Val His Lys Asn Arg Ile Ile Asn Lys

20 25 30

Val Thr Arg Ser Ile Lys Tyr Pro Leu Val Val Lys Asp Glu Trp Lys

35 40 45

Lys Arg Leu Ile Asp Asp Ala Ala His Asp Tyr Arg Trp Leu Val Gly

50 55 60

Pro Ile Asn Tyr Ser Asp Trp Cys Arg Asp Pro Asn Gln Tyr Ser Ile

65 70 75 80

Leu Glu Phe Trp Ile Asp Phe Leu Cys Val Gly Gly Val Phe Gln Ser
85 90 95
Ser His Ser Asn Ile Cys Arg Leu Ala Ile Gln Leu Ser Gly Gly Ser
100 105 110

Val Phe Glu Gln Glu Trp Lys Asp Leu Ser Pro Phe Val Arg Ala Asn
115 120 125
Leu Ile Gln Gly Ile Lys Pro Ala Glu Phe Ile Gly Phe Leu Thr Ala
130 135 140
Glu Phe Arg Ser Ser Ser Asn Pro Lys Asn Phe Ile Ser Lys Phe Phe
145 150 155 160
Glu Gly Ser Asn Glu Asp Leu Glu Ser Leu Thr Asn Glu Phe Ala Ser
165 170 175

Ile Val Asp Phe Ile Lys Ala Lys Asp Ile Ser Leu Leu Arg Lys Ser
180 185 190
Leu Pro Ser Cys Lys Lys Ile Ala Pro Asn Leu Trp Glu Lys Ala Val
195 200 205
Gly Ser His Ser Thr Asn Glu Leu Leu Lys Leu Leu Thr Lys Tyr Thr
210 215 220
Arg Val Met Leu Val Ala Glu Pro Ser His Ser Asp Arg Val Phe Ser
225 230 235 240

Gln Thr Val Leu Gln Ser Asn Asp Gln Asp Asp Pro Glu Leu Thr Gly
245 250 255
Pro Leu Pro Ser His Lys Val Gly Lys Ala Ser Tyr Leu Phe Ile Pro
260 265 270
Glu Phe Ile Arg Glu Val Asn Leu Asp Lys Ile Ser Lys Leu Asp Leu
275 280 285
Ser Ala Lys Ser Lys Leu Ala Val Glu Gln Val Lys Lys Leu Ser Glu
290 295 300

Leu Thr Ser Asp Phe Lys Gln Ile Glu Asn Gln Ser Glu Ala Tyr Phe
305 310 315 320
Gly Leu Ser Thr Ser Phe Asn Glu Leu Ser Asn Phe Leu Gly Ile Leu

325 330 335

Ile Arg Thr Leu Arg Asn Ala Pro Glu Ala Ile Leu Lys Asp Gln Ile

340 345 350

Ala Leu Cys Ala Pro Leu Asp Lys Asp Ile Leu Lys Ile Thr Leu Asp

355 360 365

Trp Leu Cys Asp Arg Ala Gln Ala Leu Pro Glu Asn Pro Arg Phe Glu

370 375 380

Thr Asn Trp Ala Glu Tyr Arg Ser Tyr Leu Gly Gly Lys Ile Lys Ser

385 390 395 400

Trp Phe Ser Asn Tyr Glu Asn Phe Phe Glu Ile Pro Gln Ala Ala Ser

405 410 415

Ser Gln Gln Asn Asn Asn Arg Glu Lys Lys Leu Gly Asn Arg Ser Ala

420 425 430

Ile Arg Ala Leu Asn Leu Lys Lys Glu Ala Phe Glu Lys Ala Arg Glu

435 440 445

Thr Phe Lys Gly Asp Lys Gly Thr Leu Glu Lys Ile Asp Leu Ala Tyr

450 455 460

Arg Leu Leu Gly Ser Ile Ser Pro Glu Val Leu Gln Cys Asp Glu Gly

465 470 475 480

Leu Lys Leu Tyr Gln Gln Phe Asn Asp Glu Leu Leu Val Leu Asn Glu

485 490 495

Thr Ile Asn Gln Lys Phe Gln Asp Ala Lys Arg Asp Ile Lys Ala Lys

500 505 510

Lys Glu Lys Glu Ser Phe Glu Lys Leu Gln Arg Asn Leu Ser Ser Pro

515 520 525

Leu Pro Arg Ile Pro Glu Phe Phe Gly Glu Arg Ala Lys Lys Gly Tyr

530 535 540

Gln Lys Ala Arg Val Ser Pro Lys Leu Ala Arg His Leu Leu Glu Cys

545 550 555 560

Leu Asn Asp Trp Leu Ala Arg Phe Ala Lys Val Glu Glu Ser Ala Phe

565 570 575

Ser Glu Lys Glu Phe Gln Arg Ile Leu Asp Trp Leu Arg Thr Ser Asp
580 585 590

Phe Leu Pro Val Phe Ile Arg Lys Ser Lys Asp Pro Pro Ser Trp Leu
595 600 605

Arg Tyr Ile Ala Arg Val Ala Thr Gly Lys Tyr Tyr Phe Trp Val Ser
610 615 620

Glu Tyr Ser Arg Lys Arg Val Gln Ile Ile Asp Lys Pro Ile Ala Gln
625 630 635 640

Asn Pro Leu Lys Glu Leu Ile Ser Trp Phe Leu Leu Asn Lys Asp Ala
645 650 655

Phe Ser Arg Asp Asn Glu Leu Phe Lys Gly Leu Ser Ser Lys Met Val
660 665 670

Thr Leu Ala Arg Ile Met Ala Gly Ile Leu Arg Asp Arg Gly Glu Gly
675 680 685

Leu Lys Glu Leu Gln Ala Met Thr Ser Lys Leu Asp Asn Ile Gly Leu
690 695 700

Leu His Pro Ser Phe Ser Val Pro Val Thr Asp Ser Leu Lys Asp Ala
705 710 715 720

Ala Phe Tyr Arg Ala Phe Phe Ser Glu Leu Glu Gly Leu Leu Asn Ile
725 730 735

Gly Arg Ser Arg Leu Ile Ile Glu Arg Ile Thr Leu Gln Ser Gln Gln
740 745 750

Ser Lys Asn Lys Lys Thr Arg Arg Pro Leu Met Pro Glu Pro Phe Ile
755 760 765

Asn Glu Asp Lys Glu Val Phe Leu Ala Phe Pro Lys Phe Glu Thr Lys
770 775 780

Asn Lys Val Lys Gly Thr Arg Val Val Tyr Asn Ser Pro Asp Glu Val
785 790 795 800

Asn Trp Leu Leu Ser Pro Ile Arg Ser Ser Lys Gly Gln Leu Ser Phe
805 810 815

Met Phe Arg Cys Leu Ser Glu Asp Ala Lys Ile Met Thr Thr Ser Gly

820 825 830

Gly Cys Ser Tyr Ile Val Glu Phe Lys Lys Leu Leu Glu Ala Gln Glu

835 840 845

Glu Val Leu Ser Ile His Asp Cys Asp Ile Ile Pro Arg Ala Phe Val

850 855 860

Ser Ile Pro Phe Thr Leu Glu Arg Glu Ser Glu Glu Thr Lys Pro Asp

865 870 875 880

Trp Lys Pro Asn Arg Phe Met Gly Val Asp Ile Gly Glu Tyr Ala Val

885 890 895

Ala Tyr Cys Val Ile Glu Lys Gly Thr Asp Ser Ile Glu Ile Leu Asp

900 905 910

Cys Gly Ile Val Arg Asn Gly Ala His Arg Val Leu Lys Glu Lys Val

915 920 925

Asp Arg Leu Lys Arg Arg Gln Arg Ser Met Thr Phe Gly Ala Met Asp

930 935 940

Thr Ser Ile Ala Ala Ala Arg Glu Ser Leu Val Gly Asn Tyr Arg Asn

945 950 955 960

Arg Leu His Ala Ile Ala Leu Lys His Gly Ala Lys Leu Val Tyr Glu

965 970 975

Tyr Glu Val Ser Ala Phe Glu Ser Gly Gly Asn Arg Ile Lys Lys Val

980 985 990

Tyr Glu Thr Leu Lys Lys Ser Asp Cys Thr Gly Glu Thr Glu Ala Asp

995 1000 1005

Lys Asn Ala Arg Lys His Ile Trp Gly Glu Thr Asn Ala Val Gly

1010 1015 1020

Asp Gln Ile Gly Ala Gly Trp Thr Ser Gln Thr Cys Ala Lys Cys

1025 1030 1035

Gly Arg Ser Phe Gly Ala Asp Leu Lys Ala Gly Asn Phe Gly Val

1040 1045 1050

Ala Val Pro Val Pro Glu Lys Val Glu Asp Ser Lys Gly His Tyr

1055 1060 1065

Ala Tyr His Glu Phe Pro Phe Glu Asp Gly Leu Lys Val Arg Gly
1070 1075 1080
Phe Leu Lys Pro Asn Lys Ile Ile Ser Asp Gln Lys Glu Leu Ala
1085 1090 1095
Lys Ala Val His Ala Tyr Met Arg Pro Pro Leu Val Ala Leu Gly
1100 1105 1110
Lys Arg Lys Leu Pro Lys Asn Ala Arg Tyr Arg Arg Gly Asn Ser
1115 1120 1125

Ser Leu Phe Arg Cys Pro Phe Ser Asp Cys Gly Phe Thr Ala Asp
1130 1135 1140
Ala Asp Ile Gln Ala Ala Tyr Asn Ile Ala Val Lys Gln Leu Tyr
1145 1150 1155
Lys Pro Lys Lys Gly Tyr Pro Lys Glu Arg Lys Trp Gln Asp Phe
1160 1165 1170
Val Ile Leu Lys Pro Lys Glu Pro Ser Lys Leu Phe Asp Lys Gln
1175 1180 1185

Phe Tyr Arg Pro Asn
1190

<210> 144
<211> 606
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 144
Met Ala Gln Ala Glu Ala Pro Arg Arg Leu Arg Ala Tyr Lys Phe Ala
1 5 10 15
Leu Asp Pro Thr Glu Ala Gln Leu Arg Glu Phe Glu Gln His Ala Gly
20 25 30
Ser Ala Arg Trp Ala Tyr Asn His Ala Asn Ala Ile Leu Ser Arg Tyr
35 40 45

Ser Asp Thr Leu Arg Asn Arg Trp Asn Ala Trp Ile Ala Gln His His

50 55 60

Gly Leu Ser Arg Glu Gln Leu Tyr Ala Leu Pro Asp Arg Glu Arg Thr
65 70 75 80

Ala Ile Gln Ala Ala Ala Arg Ala Ala Val Lys Ala Glu Asn Ala Gln
85 90 95

Leu Ala Ala Glu Leu Arg Ile Ile Asp Asp His Arg Lys Arg Val Thr
100 105 110

His Lys Gly Lys Pro Ser Val Glu Pro Gly Glu Gln Pro Ala Glu Asp
115 120 125

Ala Pro Glu Arg Ala Tyr Gln Leu Trp Arg Glu Arg Val Glu Leu Ala
130 135 140

Arg Leu His Ala Glu Asp Pro Gln Ala Tyr Arg Ala Glu Arg Lys Arg
145 150 155 160

Ile Leu Asp Glu Ile Arg Pro Leu Val Asn Ala Thr Lys Arg Lys Leu
165 170 175

Ile Glu Gln Gly Ala Tyr Arg Pro Thr Ala Met Asp Ile Ser Thr Leu
180 185 190

Trp Arg Glu Ile Arg Asp Leu Pro Pro Asp Glu Gly Gly Ser Pro Trp
195 200 205

Trp Pro Glu Val Ser Ile Tyr Ala Phe Thr Ser Gly Phe Ala His Ala
210 215 220

Glu Thr Ala Trp Lys Asn Tyr Leu Glu Ser Leu Ala Gly Arg Arg Ala
225 230 235 240

Gly Arg Pro Val Gly Lys Pro Arg Phe Lys Lys Lys Arg Arg Ser Arg
245 250 255

Arg Ser Phe Thr Leu Tyr Gly Ser Val Lys Leu Val Thr Tyr Arg Arg
260 265 270

Ile Gln Val Pro Ser Ile Gly Ser Val Arg Leu His Gly Ser Ala Lys
275 280 285

Arg Leu His Arg Ala Leu Glu Arg Arg Gly Gly Ile Ile Lys Ser Ile
290 295 300

Thr Ile Ser Gln Gly Gly His Arg Trp Tyr Ala Ser Val Leu Val Asp
305 310 315 320
Glu Leu Asp Ile Thr Pro Gly Arg Glu Thr Gln Arg Gly Pro Ser Arg
325 330 335
Arg Gln Arg Asp Arg Gly Ala Val Gly Val Asp Leu Gly Val His His
340 345 350
Leu Val Ala Leu Ser Asp Pro Asn Glu Lys Thr Leu Asp Asn Pro Arg
355 360 365

His Leu Arg Lys Ala Arg Lys Arg Leu Leu Lys Ala Gln Arg Ala Met
370 375 380
Ser Arg Arg Arg Gly Pro Asp Lys Arg Thr Gly Gln Glu Pro Ser Arg
385 390 395 400
Arg Trp Val Lys Ala Arg Asn Arg Val Ala Arg Leu His His Glu Leu
405 410 415
Ala Val Arg Arg Ala Gly His Leu His Glu Ile Thr Lys Arg Leu Ala
420 425 430

Thr Ser Tyr Glu Leu Val Ala Ile Glu Asp Leu Asn Val Ala Gly Met
435 440 445
Thr Arg Ser Ala Arg Gly Thr Ile Asp Gln Pro Gly Arg Gly Val Arg
450 455 460
Ala Lys Ala Gly Leu Asn Arg Ser Ile Leu Asp Thr Ser Pro Ala Glu
465 470 475 480
Phe Arg Arg Gln Leu Gln Tyr Lys Ala Ser Trp Tyr Gly Ala Thr Val
485 490 495

Ala Val Ile Asp Arg Trp Ala Pro Thr Ser Arg Thr Cys Ser Ser Cys
500 505 510
Gly Ala Val Lys Ala Lys Leu Ser Leu Ala Glu Arg Thr Phe Phe Cys
515 520 525
Glu His Cys Gly Met Glu Leu Asp Arg Asp Ile Asn Ala Ala Arg Asn
530 535 540
Ile Leu Ala Phe Ala Gln Ser Ala Tyr Pro Gly Glu Gly Lys Ala Leu

545 550 555 560

Asn Ala Cys Gly Gly Ser Val Ser Pro Gly Ser Gln Ser Val Val Gln
565 570 575
Ala Gly Ala Asp Glu Ala Gly Arg Pro Ala Arg Lys Pro Arg Arg Ser
580 585 590
Ser Arg Gly Ser Asp Pro Pro Ala Thr Pro Thr Thr Arg Ala
595 600 605

<210> 145
<211> 1108
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 145

Met Ala Ile Arg Ser Ile Lys Leu Lys Leu Lys Thr His Thr Gly Pro
1 5 10 15
Glu Ala Gln Asn Leu Arg Lys Gly Ile Trp Arg Thr His Arg Leu Leu
20 25 30
Asn Glu Gly Val Ala Tyr Tyr Met Lys Met Leu Leu Leu Phe Arg Gln
35 40 45
Glu Ser Thr Gly Glu Arg Pro Lys Glu Glu Leu Gln Glu Glu Leu Ile
50 55 60
Cys His Ile Arg Glu Gln Gln Gln Arg Asn Gln Ala Asp Lys Asn Thr
65 70 75 80
Gln Ala Leu Pro Leu Asp Lys Ala Leu Glu Ala Leu Arg Gln Leu Tyr
85 90 95
Glu Leu Leu Val Pro Ser Ser Val Gly Gln Ser Gly Asp Ala Gln Ile
100 105 110
Ile Ser Arg Lys Phe Leu Ser Pro Leu Val Asp Pro Asn Ser Glu Gly
115 120 125
Gly Lys Gly Thr Ser Lys Ala Gly Ala Lys Pro Thr Trp Gln Lys Lys

130 135 140

Lys Glu Ala Asn Asp Pro Thr Trp Glu Gln Asp Tyr Glu Lys Trp Lys

145 150 155 160

Lys Arg Arg Glu Glu Asp Pro Thr Ala Ser Val Ile Thr Thr Leu Glu

165 170 175

Glu Tyr Gly Ile Arg Pro Ile Phe Pro Leu Tyr Thr Asn Thr Val Thr

180 185 190

Asp Ile Ala Trp Leu Pro Leu Gln Ser Asn Gln Phe Val Arg Thr Trp

195 200 205

Asp Arg Asp Met Leu Gln Gln Ala Ile Glu Arg Leu Leu Ser Trp Glu

210 215 220

Ser Trp Asn Lys Arg Val Gln Glu Glu Tyr Ala Lys Leu Lys Glu Lys

225 230 235 240

Met Ala Gln Leu Asn Glu Gln Leu Glu Gly Gly Gln Glu Trp Ile Ser

245 250 255

Leu Leu Glu Gln Tyr Glu Glu Asn Arg Glu Arg Glu Leu Arg Glu Asn

260 265 270

Met Thr Ala Ala Asn Asp Lys Tyr Arg Ile Thr Lys Arg Gln Met Lys

275 280 285

Gly Trp Asn Glu Leu Tyr Glu Leu Trp Ser Thr Phe Pro Ala Ser Ala

290 295 300

Ser His Glu Gln Tyr Lys Glu Ala Leu Lys Arg Val Gln Gln Arg Leu

305 310 315 320

Arg Gly Arg Phe Gly Asp Ala His Phe Phe Gln Tyr Leu Met Glu Glu

325 330 335

Lys Asn Arg Leu Ile Trp Lys Gly Asn Pro Gln Arg Ile His Tyr Phe

340 345 350

Val Ala Arg Asn Glu Leu Thr Lys Arg Leu Glu Glu Ala Lys Gln Ser

355 360 365

Ala Thr Met Thr Leu Pro Asn Ala Arg Lys His Pro Leu Trp Val Arg

370 375 380

Phe Asp Ala Arg Gly Gly Asn Leu Gln Asp Tyr Tyr Leu Thr Ala Glu

385 390 395 400

Ala Asp Lys Pro Arg Ser Arg Arg Phe Val Thr Phe Ser Gln Leu Ile

405 410 415

Trp Pro Ser Glu Ser Gly Trp Met Glu Lys Lys Asp Val Glu Val Glu

420 425 430

Leu Ala Leu Ser Arg Gln Phe Tyr Gln Gln Val Lys Leu Leu Lys Asn

435 440 445

Asp Lys Gly Lys Gln Lys Ile Glu Phe Lys Asp Lys Gly Ser Gly Ser

450 455 460

Thr Phe Asn Gly His Leu Gly Gly Ala Lys Leu Gln Leu Glu Arg Gly

465 470 475 480

Asp Leu Glu Lys Glu Glu Lys Asn Phe Glu Asp Gly Glu Ile Gly Ser

485 490 495

Val Tyr Leu Asn Val Val Ile Asp Phe Glu Pro Leu Gln Glu Val Lys

500 505 510

Asn Gly Arg Val Gln Ala Pro Tyr Gly Gln Val Leu Gln Leu Ile Arg

515 520 525

Arg Pro Asn Glu Phe Pro Lys Val Thr Thr Tyr Lys Ser Glu Gln Leu

530 535 540

Val Glu Trp Ile Lys Ala Ser Pro Gln His Ser Ala Gly Val Glu Ser

545 550 555 560

Leu Ala Ser Gly Phe Arg Val Met Ser Ile Asp Leu Gly Leu Arg Ala

565 570 575

Ala Ala Ala Thr Ser Ile Phe Ser Val Glu Glu Ser Ser Asp Lys Asn

580 585 590

Ala Ala Asp Phe Ser Tyr Trp Ile Glu Gly Thr Pro Leu Val Ala Val

595 600 605

His Gln Arg Ser Tyr Met Leu Arg Leu Pro Gly Glu Gln Val Glu Lys

610 615 620

Gln Val Met Glu Lys Arg Asp Glu Arg Phe Gln Leu His Gln Arg Val

625 630 635 640

Lys Phe Gln Ile Arg Val Leu Ala Gln Ile Met Arg Met Ala Asn Lys

645 650 655

Gln Tyr Gly Asp Arg Trp Asp Glu Leu Asp Ser Leu Lys Gln Ala Val

660 665 670

Glu Gln Lys Lys Ser Pro Leu Asp Gln Thr Asp Arg Thr Phe Trp Glu

675 680 685

Gly Ile Val Cys Asp Leu Thr Lys Val Leu Pro Arg Asn Glu Ala Asp

690 695 700

Trp Glu Gln Ala Val Val Gln Ile His Arg Lys Ala Glu Glu Tyr Val

705 710 715 720

Gly Lys Ala Val Gln Ala Trp Arg Lys Arg Phe Ala Ala Asp Glu Arg

725 730 735

Lys Gly Ile Ala Gly Leu Ser Met Trp Asn Ile Glu Glu Leu Glu Gly

740 745 750

Leu Arg Lys Leu Leu Ile Ser Trp Ser Arg Arg Thr Arg Asn Pro Gln

755 760 765

Glu Val Asn Arg Phe Glu Arg Gly His Thr Ser His Gln Arg Leu Leu

770 775 780

Thr His Ile Gln Asn Val Lys Glu Asp Arg Leu Lys Gln Leu Ser His

785 790 795 800

Ala Ile Val Met Thr Ala Leu Gly Tyr Val Tyr Asp Glu Arg Lys Gln

805 810 815

Glu Trp Cys Ala Glu Tyr Pro Ala Cys Gln Val Ile Leu Phe Glu Asn

820 825 830

Leu Ser Gln Tyr Arg Ser Asn Leu Asp Arg Ser Thr Lys Glu Asn Ser

835 840 845

Thr Leu Met Lys Trp Ala His Arg Ser Ile Pro Lys Tyr Val His Met

850 855 860

Gln Ala Glu Pro Tyr Gly Ile Gln Ile Gly Asp Val Arg Ala Glu Tyr

865 870 875 880

Ser Ser Arg Phe Tyr Ala Lys Thr Gly Thr Pro Gly Ile Arg Cys Lys

885 890 895

Lys Val Arg Gly Gln Asp Leu Gln Gly Arg Arg Phe Glu Asn Leu Gln

900 905 910

Lys Arg Leu Val Asn Glu Gln Phe Leu Thr Glu Glu Gln Val Lys Gln

915 920 925

Leu Arg Pro Gly Asp Ile Val Pro Asp Asp Ser Gly Glu Leu Phe Met

930 935 940

Thr Leu Thr Asp Gly Ser Gly Ser Lys Glu Val Val Phe Leu Gln Ala

945 950 955 960

Asp Ile Asn Ala Ala His Asn Leu Gln Lys Arg Phe Trp Gln Arg Tyr

965 970 975

Asn Glu Leu Phe Lys Val Ser Cys Arg Val Ile Val Arg Asp Glu Glu

980 985 990

Glu Tyr Leu Val Pro Lys Thr Lys Ser Val Gln Ala Lys Leu Gly Lys

995 1000 1005

Gly Leu Phe Val Lys Lys Ser Asp Thr Ala Trp Lys Asp Val Tyr

1010 1015 1020

Val Trp Asp Ser Gln Ala Lys Leu Lys Gly Lys Thr Thr Phe Thr

1025 1030 1035

Glu Glu Ser Glu Ser Pro Glu Gln Leu Glu Asp Phe Gln Glu Ile

1040 1045 1050

Ile Glu Glu Ala Glu Glu Ala Lys Gly Thr Tyr Arg Thr Leu Phe

1055 1060 1065

Arg Asp Pro Ser Gly Val Phe Phe Pro Glu Ser Val Trp Tyr Pro

1070 1075 1080

Gln Lys Asp Phe Trp Gly Glu Val Lys Arg Lys Leu Tyr Gly Lys

1085 1090 1095

Leu Arg Glu Arg Phe Leu Thr Lys Ala Arg

1100 1105

<210> 146

<211> 1110

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 146

Met Val Val Arg Ser Ile Lys Leu Lys Met Lys Thr Asn Ser Gly Thr
1 5 10 15

Asp Ser Ile Tyr Leu Arg Lys Ala Leu Trp Arg Thr His Arg Leu Ile
20 25 30

Asn Glu Gly Ile Val Tyr Tyr Met Ser Leu Leu Thr Leu Tyr Arg Gln
35 40 45

Asp Thr Leu Gly Asp Arg Thr Lys Glu Glu Ile Gln Ser Glu Leu Ile
50 55 60

Lys Lys Ile Arg Glu Gln Gln Arg Asn Asn Gly Leu Ser Glu Glu Leu
65 70 75 80

Gly Ser Asp Gln Glu Ile Leu Ser Leu Leu Arg His Leu Tyr Glu Leu
85 90 95

Ile Ile Pro Ser Ile Asn Gly Glu Ser Gly Asp Ala Asn Gln Leu Gly
100 105 110

Asn Lys Phe Leu Tyr Pro Leu Val Asp Pro Asn Ser Gln Ser Gly Lys
115 120 125

Gly Thr Ser Asn Ala Gly Arg Lys Ser Lys Trp Lys Arg Met Lys Glu
130 135 140

Glu Gly Asn Pro Asp Trp Glu Val Glu Phe Lys Lys Asp Glu Glu Arg
145 150 155 160

Lys Ala Asn Asp Pro Thr Ile Lys Val Phe Asp His Leu Lys Lys Tyr
165 170 175

Ser Leu Leu Pro Leu Phe Pro Leu Phe Thr Asn Asn Gln Lys Asp Ile
180 185 190

Glu Trp Leu Pro Met Gly Lys Arg Gln Ser Val Arg Lys Trp Asp Lys
195 200 205

Asp Met Phe Ile Gln Ala Ile Glu Arg Leu Leu Ser Trp Glu Ser Trp
210 215 220

Asn Arg Arg Leu Gly Ala Glu Arg Glu Lys Leu Glu Glu Lys Ile Glu
225 230 235 240
Asn Phe Tyr Lys Glu His Leu Ser Gly Gly Gln Ile Trp Ile Glu Lys
245 250 255
Ile Arg Glu Phe Glu Arg Val Arg Asp Arg Glu Leu Gly Glu Thr Ser
260 265 270
Phe Ser Ser Asn Asp Gly Tyr Leu Ile Thr Ser Arg Gln Ile Arg Gly
275 280 285

Trp Asp Arg Val Tyr Glu Lys Trp Ser Lys Ile Ser Glu Ser Ala Ser
290 295 300
Lys Glu Glu Leu Trp Arg Val Val Ala Glu Gln Gln Ser Lys Met Arg
305 310 315 320
Glu Gly Phe Gly Asp Pro Lys Val Phe Ser Phe Leu Ala Glu Leu Glu
325 330 335
Asn Met Asp Ile Trp Arg Lys His Pro Glu Arg Ile Tyr His Ile Ala
340 345 350

Thr Tyr Asn Gly Leu Leu Lys Lys Leu Ser His Thr Lys Ala Gln Ala
355 360 365
Thr Phe Thr Leu Pro Asp Ala Val Lys His Pro Leu Trp Ile Arg Tyr
370 375 380
Glu Ala Gln Gly Gly Thr Asn Leu Asn Leu Phe Lys Leu Glu Glu Thr
385 390 395 400
Thr Lys Lys Asn Cys Lys Val Ile Leu Ser Lys Ile Ile Trp Pro Thr
405 410 415

Glu Asp Gly Trp Phe Glu Lys Glu Asn Val Glu Val Asp Leu Ala Pro
420 425 430
Ser Lys Gln Phe Tyr Arg Gln Ile Lys Leu Gln Asp His Ile Lys Gly
435 440 445
Lys Gln Glu Ile Ser Phe Ser Asp Tyr Ser Ser Gly Ile Ser Leu Lys

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    450                 455                 460
Gly Val Leu Gly Gly Ser Arg Ile Gln Phe Asp Arg Lys Tyr Ile Glu
465                 470                 475                 480

Asn His Gln Glu Leu Leu Pro Ser Gly Asp Ile Gly Pro Val Phe Phe
                485                 490                 495
Asn Leu Val Ile Asp Leu Leu Pro Ile Gln Glu Thr Arg Asn Gly Arg
            500                 505                 510
Leu Lys Ser Pro Ile Gly Lys Thr Leu Lys Val Val Ser Ser Glu Phe
        515                 520                 525
Pro Lys Val Ile Asp Tyr Lys Pro Lys Glu Leu Thr Glu Trp Ile Asn
    530                 535                 540

Val Ser Ser Val Thr Gly Lys Val Gly Val Glu Ser Ile Thr Glu Gly
545                 550                 555                 560
Met Arg Val Met Ser Ile Asp Leu Gly Gln Arg Thr Ser Ala Ser Val
                565                 570                 575
Ser Ile Phe Glu Val Val Lys Glu Leu Pro Lys Asp Lys Glu Lys Met
            580                 585                 590
Leu Tyr Tyr Asn Ile Lys Asp Thr Glu Leu Phe Ala Leu His Lys Arg
        595                 600                 605

Ser Phe Leu Leu Asn Leu Pro Gly Glu Glu Val Thr Lys Arg Asn Arg
    610                 615                 620
Gln Lys Arg Lys Asp Arg Arg Lys Lys Leu Leu Phe Ile Arg Ser Gln
625                 630                 635                 640
Ile Arg Met Leu Ala Ser Val Leu Lys Leu Glu Thr Lys Asn Thr Pro
                645                 650                 655
Asp Glu Arg Lys Lys Ala Ile Asn Lys Leu Val Glu Ile Val Asp Ser
            660                 665                 670

Tyr Glu Trp Thr Glu Ser Glu Lys Glu Ile Trp Asn Ser Glu Phe Glu
        675                 680                 685
Tyr Leu Thr Asn Lys Ala Val Phe Lys Gln Glu Ile Trp Arg Glu Ser
    690                 695                 700
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Leu Ile Lys Ser His His Arg Met Glu Pro His Val Gly Gln Leu Val
705 710 715 720
Ser Glu Trp Arg Lys Ser Leu Asn Glu Gly Arg Arg Asn Leu Ala Gly
725 730 735

Ile Thr Met Trp Asn Ile Glu Glu Leu Glu Asp Thr Arg Arg Leu Leu
740 745 750
Ile Ser Trp Ser Lys Arg Ser Arg Thr Pro Gly Glu Ala Asn Arg Ile
755 760 765
Asn Asn Asp Glu Pro Phe Gly Ala Lys Leu Leu Glu His Ile Gln Asn
770 775 780
Val Lys Asp Asp Arg Leu Lys Gln Leu Ala Asn Leu Ile Val Met Thr
785 790 795 800

Ala Leu Gly Tyr Lys Tyr Asp Lys Glu Glu Lys Ser Arg Asp Lys Arg
805 810 815
Trp Lys Glu Lys Tyr Pro Ala Cys Gln Val Ile Leu Phe Glu Asn Leu
820 825 830
Asn Arg Tyr Leu Phe Ser Leu Asp Arg Ser Lys Arg Glu Asn Ser Lys
835 840 845
Leu Met Lys Trp Ala His Arg Ser Ile Pro Arg Thr Val Trp Met Gln
850 855 860

Gly Glu Met Phe Gly Leu Gln Val Gly Asp Val Arg Ser Glu Tyr Ser
865 870 875 880
Ser Arg Phe His Ala Lys Ser Gly Ala Pro Gly Ile Arg Cys His Ser
885 890 895
Leu Asn Asp Glu Asp Leu Lys Glu Glu Ser Phe Lys Leu Lys His Leu
900 905 910
Ile Glu Thr Gly Phe Ile Ser Glu Glu Glu Ile Ser Ser Leu Lys Lys
915 920 925

Gly Asp Ile Val Pro Trp Pro Gly Gly Glu Leu Phe Val Thr Leu Ser
930 935 940
Lys Pro Tyr Lys Lys Gly Lys Asp Ile Glu Leu Thr Val Ile His Ala

945 950 955 960

Asp Ile Asn Ala Ala Gln Asn Leu Gln Lys Arg Phe Trp Gln Gln Asn

965 970 975

Ser Glu Val Tyr Arg Ile Pro Cys Gln Leu Glu Lys Ala Gly Asp Asp

980 985 990

Glu Phe Phe Ile Pro Lys Ser Gln Thr Glu Ile Val Lys Lys Tyr Phe

995 1000 1005

Gly Lys Gly Arg Phe Val Lys Ile Asn Asp Lys Lys Glu Val Tyr

1010 1015 1020

Asn Trp Glu Glu Ser Glu Lys Met Lys Ile Lys Thr Glu Ser Thr

1025 1030 1035

Ile Thr Leu Gln Asp Leu Glu Gly Phe Glu Asp Ile Phe Gln Thr

1040 1045 1050

Leu Glu Leu Ala Gln Glu Gln Gln Lys Lys Tyr Ser Thr Leu Phe

1055 1060 1065

Arg Asp Pro Ser Gly Tyr Phe Phe Asn Glu Lys Asn Trp Arg Pro

1070 1075 1080

Gln Lys Glu Phe Trp Ser Ile Val Asn Asn Ile Ile Arg Ser Ser

1085 1090 1095

Leu Lys Lys Lys Ile Leu Lys Asn Lys Val Glu Val

1100 1105 1110

<210> 147

<

211> 687

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<220><221> MOD_RES

<222> (156)..(527)

<223> Any amino acid

<400> 147

Met Ser Asn Pro Asn Ile Pro Asn Ile Ser Pro Asn Ile Thr Leu Thr

1 5 10 15

Arg Asp Asp Val Val Asn Leu Leu Met Ser Ser Ile Ala Met Glu Glu

20 25 30

Leu Gly Leu Ala His Ile Ile Asn Ala Glu Gly Glu Lys Ile Gln Phe

35 40 45

Ala Leu Gly Thr Leu Gln Gly Ala Ser Gly Pro Pro Ala Thr Leu Gln

50 55 60

Gln Val Leu Glu Val Asn Gln Ser Thr Gln Ala Met Leu Asp Thr Ile

65 70 75 80

Phe Arg Gln Glu Met Met Leu Asp Ser Lys Leu Lys Thr Ala Thr Asn

85 90 95

Ile Pro Thr Leu Arg Gly Pro Thr Gly Pro Val Gly Pro Thr Gly Ala

100 105 110

Pro Gly Gly Val Ile Ser Ile Asn Gly Gln Thr Gly Val Val Thr Leu

115 120 125

Asp Ala Ser Asn Gly Val Met Pro Phe Met Arg Glu Gln Ser Thr Ser

130 135 140

Ser Leu Asp Asp Tyr Lys Asp Pro Gly Ile Tyr Xaa Xaa Xaa Xaa Xaa

145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

210 215 220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

245 250 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
260 265 270
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
275 280 285
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
290 295 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305 310 315 320
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
325 330 335
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
340 345 350
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
355 360 365

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
370 375 380
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
385 390 395 400
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
405 410 415
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
420 425 430

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
435 440 445
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
450 455 460
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
465 470 475 480
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
485 490 495

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

500 505 510

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly

515 520 525

Ala Thr Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly Pro Gln Glu Pro

530 535 540

Arg Ala Leu Arg Glu Pro Arg Ala Pro Gln Ala Arg Arg Glu Pro Arg

545 550 555 560

Gly Leu Leu Glu Pro Gln Val Leu Arg Gly Pro Gln Glu Pro Arg Ala

565 570 575

Leu Arg Glu Pro Arg Ala Pro Arg Ala Leu Arg Glu Pro Arg Ala Leu

580 585 590

Arg Ala Leu Arg Ala Leu Gln Glu Leu Arg Ala Pro Arg Ala Leu Arg

595 600 605

Gly Leu Gln Glu Pro Arg Val Leu Gln Gly Pro Arg Glu Arg Gln Val

610 615 620

Arg Pro Glu Pro Arg Val Leu Gln Gly Pro Arg Glu Arg Gln Val Arg

625 630 635 640

Gln Gly Leu Gln Gly Leu Leu Glu Pro Arg Ala Lys Arg Glu Arg Gln

645 650 655

Val Arg Pro Glu Pro Arg Glu Pro Gln Glu Arg Gln Ala Pro Leu Val

660 665 670

Gln Gln Ala Leu Leu Glu Pro Gln Ala Leu Leu Gly Gln Ala Leu

675 680 685

<210> 148

<211> 1380

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 148

Met Asn Arg Ile Tyr Gln Gly Arg Val Ser Lys Val Glu Ile Pro Asn

1 5 10 15

Pro Gly Asp Lys Gly Lys Pro Trp Gln Pro Leu Pro Asn Trp Gln Asp
20 25 30
Ile Leu Trp Gln His His Glu Leu Phe Gln Asp Ala Val Asn Tyr Tyr
35 40 45

Leu Leu Ala Leu Leu Ser Leu Ala Arg Asp Ser Ala Asn Pro Ala Thr
50 55 60
Pro Ile Arg Lys Arg Met Asp Asp Pro Ala Ser Glu His Gln Ile Trp
65 70 75 80
Thr Ser Phe Arg Arg Arg Gly Gln Met Arg Ser Gly Met Arg Asp Ser
85 90 95
Val Ala Lys Tyr Leu Cys Pro Val Lys Thr Glu Pro Thr Leu Asp Glu
100 105 110

Cys Phe Ala Ala Val Leu Glu Gly Asn Lys Glu Asn Pro Asp Val Leu
115 120 125
Asp Leu Ala Leu Gln Glu Leu Leu Asp Glu Cys Asp Gly Asp Gly Ala
130 135 140
Ile Gln Gln Glu Gly Arg Ser Met Leu Pro Arg Phe Cys Ser Pro Ser
145 150 155 160
Tyr Lys Gly Asp Phe Pro Gln Ser Ala Ala Ala Lys Asp Lys Lys Ser
165 170 175

Ala Lys Glu Trp Leu Pro Thr Phe Leu His Ser Ala Glu Asn Ala Ser
180 185 190
Asn Leu Lys Leu Val Arg Gln Arg Leu Lys Phe Glu Leu Phe Ala Asn
195 200 205
Arg Asp Leu Thr Gly Arg Ile Leu Asp Ala Val Glu Ser Arg Lys Arg
210 215 220
Leu Thr Glu Met Leu Gly Trp Leu Thr Glu Arg Asn Pro Ser Leu Ala
225 230 235 240

Ala Glu Arg Glu Arg Leu Gln Lys Ile Ile Ala Ala Leu Pro Asp Thr
245 250 255
Phe Asn Leu Pro Ala Trp Arg Gly Gly Ser Val Asn Lys Glu Ala Leu

260 265 270

Lys Gln Arg Phe Tyr Ala Trp Leu Ile Phe Glu His Val Glu Ser Ser

275 280 285

Arg Ile Thr Phe Asp Ile Leu Arg Asp Ser Phe Pro Thr Pro Lys Glu

290 295 300

Lys Arg Lys Ser Val Ser Glu Thr Ile Gln Ser Glu Lys Pro Ser Leu

305 310 315 320

Glu Leu Ser Asp Asp Pro Ile Lys Leu Ala Arg Gly Thr Arg Gly Tyr

325 330 335

Val Phe Arg Ala Phe Thr Ser Leu Pro Cys Trp Gly Ala Asp Asn Ala

340 345 350

Asn Leu Leu Ala Trp Lys Glu Phe Asp Val Ala Ala Phe Lys Glu Ala

355 360 365

Leu Lys Ala Leu His Gln Val Glu Ser Lys Ser Glu Glu Arg Asn Lys

370 375 380

Glu Arg Glu Arg Leu Leu Gln Arg His Ser Val Met Arg Gly Ser Ile

385 390 395 400

Lys Trp Lys Pro Ser Pro Glu Ser Glu Glu Lys Glu Pro Asp Val Leu

405 410 415

Ala Gly Asp Pro Arg Ile Glu Arg Leu Glu Lys Leu Leu Lys Thr Glu

420 425 430

Leu Ala Ser Glu Tyr Glu Met Ser Glu Gly Gln Thr Val Glu Tyr Gly

435 440 445

Leu Gln Pro Arg Thr Ile Arg Gly Phe Arg Asp Leu Arg Lys Glu Trp

450 455 460

Asn Lys Ile Val Lys Pro Gly Glu Pro Phe Thr Glu Gln Lys Lys Gly

465 470 475 480

Asn Leu Val Thr Ala Leu Arg Ser Tyr Gln Ile Glu Asn Pro Asn Val

485 490 495

Ile Gly Ser Val Arg Leu Tyr Glu Ala Leu Leu Glu Lys Gly Asn Trp

500 505 510

Leu Val Trp Gln Glu Ala Asp Ser Ala Thr Val Glu Lys Trp Ala Lys
515 520 525

Gln Lys Phe Ala Ser Asp Pro Leu Glu Ala Leu Thr Glu Glu Arg Gln
530 535 540

Leu Leu Arg Asp Ile Glu Arg Leu Lys Gln Pro Ile Arg Phe Thr Pro
545 550 555 560

Ala Asp Ala Val His Ser Arg Arg Gln Phe Tyr Leu Ala Glu Lys Gly
565 570 575

Asp Leu Ser Val Lys Asn Arg Phe Asp Pro Gln Asn Gln Thr Leu Gln
580 585 590

Val Pro Ile Ala Ile Lys Asn Asp Asp His Trp Lys Gln Gln Phe Val
595 600 605

Lys Ile His Phe Ser Ala Pro Arg Ala Val Arg Asp Gln Leu Ile Asp
610 615 620

Glu Thr Met Glu Glu Ser Lys Glu Ala Arg Trp Gln Gln Pro Met Met
625 630 635 640

Glu Ala Leu Gly Leu Ser Leu Lys Leu Thr Lys Asn Asn Ala Glu Val
645 650 655

Ser Leu Ser Glu Cys Thr Ala Val Ser Leu Met Pro Glu Glu Leu Ala
660 665 670

Ser Gly Asp Arg Arg Ile Leu Leu Asn Phe Pro Ile Thr Leu Glu Thr
675 680 685

Ala Pro Met Val Lys Ala Leu Gly Lys Ala Ser Leu Trp Asp Gly Gln
690 695 700

Phe Ala Ala Tyr Gly Asp Asp Asn Phe Tyr Leu Arg Trp Pro Lys Asp
705 710 715 720

Lys Trp Pro Ala Glu Lys Glu Ser Asn Ala Trp Tyr Arg Arg Leu Thr
725 730 735

Glu Phe Ser Leu Leu Ser Val Asp Leu Gly Gln Arg Asp Ala Gly Ala
740 745 750

Phe Ala Val Ile Gly Ala Thr Thr Gly Lys Pro Thr Arg Pro Ala Ser

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        755                 760                 765
Arg Phe Ile Gly Glu Ala Asn Gly Gln Ser Trp His Ala Ser Val Arg
    770                 775                 780
Ala Thr Gly Val Leu Arg Leu Pro Gly Glu Asp Ala His Val Phe Arg
785                 790                 795                 800
Ser Gly Gln Trp Gln Glu Glu Leu Tyr Gly Glu Arg Gly Arg Ser Ala
                805                 810                 815

Asp Ala Thr Glu Trp Thr Glu Ala Lys Arg Ile Cys Glu Thr Leu Gly
            820                 825                 830
Leu Lys Phe Asp Glu Ile Leu Gly Gly Asp Pro Gln Trp Phe Ser Phe
        835                 840                 845
Pro Glu Leu Asn Asp Arg Leu Leu Phe Ala Val Arg Arg Ala Gln Thr
    850                 855                 860
Arg Leu Ala Arg Leu Gln Ser Trp Ser Trp Met Ile Ala Asp Glu Thr
865                 870                 875                 880

Arg Arg Glu Asn Ile Arg Glu Ala Ile Leu Ala Ala Asp Asp Asp Glu
                885                 890                 895
Leu Ser Leu Lys Ala Ala Ala Glu Lys Ser Leu Trp Pro Val Leu Ala
            900                 905                 910
Glu Lys Leu Ala Ser Glu Val Asn Arg Leu Arg Asn Leu Ile Pro Gln
        915                 920                 925
Gln Leu Val Leu Leu Ala Asn Arg Ile Leu Pro Leu Arg Gly Arg Arg
    930                 935                 940

Trp Glu Trp Ile Lys Arg Asp Asp Thr Ser Gly Cys His Val Leu Arg
945                 950                 955                 960
Glu Thr Asn Pro Gly Thr Asp Thr Thr Ser Lys Lys Val Cys Gly Gln
                965                 970                 975
Arg Gly Leu Ser Met Lys Arg Leu Glu Gln Leu Asp Glu Leu Arg Arg
            980                 985                 990
Arg Phe Gln Ser Leu Asn Arg Ala  Leu Met Gln Thr Pro  Gly Gln Thr
        995                 1000                1005
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Ala Gly Leu Gly Lys Ser Lys Arg Gly Ile Glu Leu Pro Asp Pro
1010 1015 1020
Cys Pro Asp Leu Leu Asp Lys Thr Glu Gln Leu Arg Glu Gln Arg
1025 1030 1035
Val Asn Gln Thr Ala His Leu Ile Leu Ala Gln Ala Leu Gly Val
1040 1045 1050
Arg Leu Arg Thr Pro Gln Lys Gly Asp Ala Leu Arg Glu Gln Asn
1055 1060 1065

Asn Val His Gly Glu Tyr Glu Thr Phe Arg Leu Pro Val Asp Phe
1070 1075 1080
Ile Val Leu Glu Asp Leu Ser Arg Tyr Leu Ser Ser Gln Gly Arg
1085 1090 1095
Gly Arg Asn Glu Asn Ser Arg Leu Met Lys Trp Cys His Arg Ala
1100 1105 1110
Ile Leu Leu Lys Leu Lys Gln Leu Cys Glu Ser Tyr Gly Leu Lys
1115 1120 1125

Ile Leu Glu Thr Asn Ala Ala Tyr Ser Ser Arg Phe Cys Ser Arg
1130 1135 1140
Thr Gly Val Ala Gly Phe Arg Ala Val Glu Leu Thr Pro Asp Ala
1145 1150 1155
Arg Lys Glu Phe Arg Trp Arg Lys His Leu Asn Arg Leu Glu Lys
1160 1165 1170
Ala Ala Ser Gly Glu Ile Lys Leu Asp Arg Glu Ala Arg Ala Glu
1175 1180 1185

Ser Glu His Val Lys Arg Leu Phe Asp Met Leu Asp Gln Leu Asn
1190 1195 1200
Ala Gly Arg Lys Glu Ala Gly Lys Pro Leu Arg Thr Leu Leu Ala
1205 1210 1215
Pro Ile Ala Gly Gly Gln Ile Phe Ile Pro Met Gln Gly His Ala
1220 1225 1230
Thr Gln Ala Asp Ile Asn Ala Ala Ile Asn Leu Gly Leu Arg Ala

1235 1240 1245

Ile Ala Ala Pro Asp Cys His Ala Ile His Val Arg Ile Arg Thr
1250 1255 1260
Glu Arg Lys Asp Lys Thr Leu Arg Val Arg Thr Gly Ser Asn Arg
1265 1270 1275
Glu Lys Val Arg Trp Glu Gly Lys Asn Pro Glu Ile Gln Met Asn
1280 1285 1290
Lys Ala Ala Asp Leu Ala Ser Leu Thr Gly Asp Arg Gln Pro Asn
1295 1300 1305

Phe Phe Pro Asp Pro Ser Ala Ile Ala Cys Tyr Asp Arg Ala Lys
1310 1315 1320
Ile Glu Gly Val Gln Leu Pro Phe Ala Ser Gly Arg Gly Leu Trp
1325 1330 1335
Gly Thr Met Asn Ile Glu Leu Gln Trp Thr Arg Val Asn Gln Leu
1340 1345 1350
Asn Asn Asp Arg Ala Glu Lys Lys Trp Asn Leu Thr Arg Ser Leu
1355 1360 1365

Pro Glu Gln Ser Ser Glu Glu Asp Tyr Ile Pro Met
1370 1375 1380

<210> 149
<211> 1144
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12 sequence
<400> 149
Met Ala Val Lys Ser Ile Lys Val Lys Leu Met Leu Gly His Leu Pro
1 5 10 15
Glu Ile Arg Glu Gly Leu Trp His Leu His Glu Ala Val Asn Leu Gly
20 25 30
Val Arg Tyr Tyr Thr Glu Trp Leu Ala Leu Leu Arg Gln Gly Asn Leu

35 40 45

Tyr Arg Arg Gly Lys Asp Gly Ala Gln Glu Cys Tyr Met Thr Ala Glu

50 55 60

Gln Cys Arg Gln Glu Leu Leu Val Arg Leu Arg Asp Arg Gln Lys Arg

65 70 75 80

Asn Gly His Thr Gly Asp Pro Gly Thr Asp Glu Glu Leu Leu Gly Val

85 90 95

Ala Arg Arg Leu Tyr Glu Leu Leu Val Pro Gln Ser Val Gly Lys Lys

100 105 110

Gly Gln Ala Gln Met Leu Ala Ser Gly Phe Leu Ser Pro Leu Ala Asp

115 120 125

Pro Lys Ser Glu Gly Gly Lys Gly Thr Ser Lys Ser Gly Arg Lys Pro

130 135 140

Ala Trp Met Gly Met Lys Glu Ala Gly Asp Ser Arg Trp Val Glu Ala

145 150 155 160

Lys Ala Arg Tyr Glu Ala Asn Lys Ala Lys Asp Pro Thr Lys Gln Val

165 170 175

Ile Ala Ser Leu Glu Met Tyr Gly Leu Arg Pro Leu Phe Asp Val Phe

180 185 190

Thr Glu Thr Tyr Lys Thr Ile Arg Trp Met Pro Leu Gly Lys His Gln

195 200 205

Gly Val Arg Ala Trp Asp Arg Asp Met Phe Gln Gln Ser Leu Glu Arg

210 215 220

Leu Met Ser Trp Glu Ser Trp Asn Glu Arg Val Gly Ala Glu Phe Ala

225 230 235 240

Arg Leu Val Asp Arg Arg Asp Arg Phe Arg Glu Lys His Phe Thr Gly

245 250 255

Gln Glu His Leu Val Ala Leu Ala Gln Arg Leu Glu Gln Glu Met Lys

260 265 270

Glu Ala Ser Pro Gly Phe Glu Ser Lys Ser Ser Gln Ala His Arg Ile

275 280 285

Thr Lys Arg Ala Leu Arg Gly Ala Asp Gly Ile Ile Asp Asp Trp Leu

290 295 300

Lys Leu Ser Glu Gly Glu Pro Val Asp Arg Phe Asp Glu Ile Leu Arg

305 310 315 320

Lys Arg Gln Ala Gln Asn Pro Arg Arg Phe Gly Ser His Asp Leu Phe

325 330 335

Leu Lys Leu Ala Glu Pro Val Phe Gln Pro Leu Trp Arg Glu Asp Pro

340 345 350

Ser Phe Leu Ser Arg Trp Ala Ser Tyr Asn Glu Val Leu Asn Lys Leu

355 360 365

Glu Asp Ala Lys Gln Phe Ala Thr Phe Thr Leu Pro Ser Pro Cys Ser

370 375 380

Asn Pro Val Trp Ala Arg Phe Glu Asn Ala Glu Gly Thr Asn Ile Phe

385 390 395 400

Lys Tyr Asp Phe Leu Phe Asp His Phe Gly Lys Gly Arg His Gly Val

405 410 415

Arg Phe Gln Arg Met Ile Val Met Arg Asp Gly Val Pro Thr Glu Val

420 425 430

Glu Gly Ile Val Val Pro Ile Ala Pro Ser Arg Gln Leu Asp Ala Leu

435 440 445

Ala Pro Asn Asp Ala Ala Ser Pro Ile Asp Val Phe Val Gly Asp Pro

450 455 460

Ala Ala Pro Gly Ala Phe Arg Gly Gln Phe Gly Gly Ala Lys Ile Gln

465 470 475 480

Tyr Arg Arg Ser Ala Leu Val Arg Lys Gly Arg Arg Glu Glu Lys Ala

485 490 495

Tyr Leu Cys Gly Phe Arg Leu Pro Ser Gln Arg Arg Thr Gly Thr Pro

500 505 510

Ala Asp Asp Ala Gly Glu Val Phe Leu Asn Leu Ser Leu Arg Val Glu

515 520 525

Ser Gln Ser Glu Gln Ala Gly Arg Arg Asn Pro Pro Tyr Ala Ala Val

530 535 540

Phe His Ile Ser Asp Gln Thr Arg Arg Val Ile Val Arg Tyr Gly Glu

545 550 555 560

Ile Glu Arg Tyr Leu Ala Glu His Pro Asp Thr Gly Ile Pro Gly Ser

565 570 575

Arg Gly Leu Thr Ser Gly Leu Arg Val Met Ser Val Asp Leu Gly Leu

580 585 590

Arg Thr Ser Ala Ala Ile Ser Val Phe Arg Val Ala His Arg Asp Glu

595 600 605

Leu Thr Pro Asp Ala His Gly Arg Gln Pro Phe Phe Phe Pro Ile His

610 615 620

Gly Met Asp His Leu Val Ala Leu His Glu Arg Ser His Leu Ile Arg

625 630 635 640

Leu Pro Gly Glu Thr Glu Ser Lys Lys Val Arg Ser Ile Arg Glu Gln

645 650 655

Arg Leu Asp Arg Leu Asn Arg Leu Arg Ser Gln Met Ala Ser Leu Arg

660 665 670

Leu Leu Val Arg Thr Gly Val Leu Asp Glu Gln Lys Arg Asp Arg Asn

675 680 685

Trp Glu Arg Leu Gln Ser Ser Met Glu Arg Gly Gly Glu Arg Met Pro

690 695 700

Ser Asp Trp Trp Asp Leu Phe Gln Ala Gln Val Arg Tyr Leu Ala Gln

705 710 715 720

His Arg Asp Ala Ser Gly Glu Ala Trp Gly Arg Met Val Gln Ala Ala

725 730 735

Val Arg Thr Leu Trp Arg Gln Leu Ala Lys Gln Val Arg Asp Trp Arg

740 745 750

Lys Glu Val Arg Arg Asn Ala Asp Lys Val Lys Ile Arg Gly Ile Ala

755 760 765

Arg Asp Val Pro Gly Gly His Ser Leu Ala Gln Leu Asp Tyr Leu Glu

770 775 780

Arg Gln Tyr Arg Phe Leu Arg Ser Trp Ser Ala Phe Ser Val Gln Ala
785 790 795 800
Gly Gln Val Val Arg Ala Glu Arg Asp Ser Arg Phe Ala Val Ala Leu

805 810 815
Arg Glu His Ile Asp Asn Gly Lys Lys Asp Arg Leu Lys Lys Leu Ala
820 825 830
Asp Arg Ile Leu Met Glu Ala Leu Gly Tyr Val Tyr Val Thr Asp Gly
835 840 845
Arg Arg Ala Gly Gln Trp Gln Ala Val Tyr Pro Pro Cys Gln Leu Val
850 855 860
Leu Leu Glu Glu Leu Ser Glu Tyr Arg Phe Ser Asn Asp Arg Pro Pro

865 870 875 880
Ser Glu Asn Ser Gln Leu Met Val Trp Ser His Arg Gly Val Leu Glu
885 890 895
Glu Leu Ile His Gln Ala Gln Val His Asp Val Leu Val Gly Thr Ile
900 905 910
Pro Ala Ala Phe Ser Ser Arg Phe Asp Ala Arg Thr Gly Ala Pro Gly
915 920 925
Ile Arg Cys Arg Arg Val Pro Ser Ile Pro Leu Lys Asp Ala Pro Ser

930 935 940
Ile Pro Ile Trp Leu Ser His Tyr Leu Lys Gln Thr Glu Arg Asp Ala
945 950 955 960
Ala Ala Leu Arg Pro Gly Glu Leu Ile Pro Thr Gly Asp Gly Glu Phe
965 970 975
Leu Val Thr Pro Ala Gly Arg Gly Ala Ser Gly Val Arg Val Val His
980 985 990
Ala Asp Ile Asn Ala Ala His Asn Leu Gln Arg Arg Leu Trp Glu Asn

995 1000 1005
Phe Asp Leu Ser Asp Ile Arg Val Arg Cys Asp Arg Arg Glu Gly
1010 1015 1020
Lys Asp Gly Thr Val Val Leu Ile Pro Arg Leu Thr Asn Gln Arg

1025 1030 1035

Val Lys Glu Arg Tyr Ser Gly Val Ile Phe Thr Ser Glu Asp Gly

1040 1045 1050

Val Ser Phe Thr Val Gly Asp Ala Lys Thr Arg Arg Arg Ser Ser

1055 1060 1065

Ala Ser Gln Gly Glu Gly Asp Asp Leu Ser Asp Glu Glu Gln Glu

1070 1075 1080

Leu Leu Ala Glu Ala Asp Asp Ala Arg Glu Arg Ser Val Val Leu

1085 1090 1095

Phe Arg Asp Pro Ser Gly Phe Val Asn Gly Gly Arg Trp Thr Ala

1100 1105 1110

Gln Arg Ala Phe Trp Gly Met Val His Asn Arg Ile Glu Thr Leu

1115 1120 1125

Leu Ala Glu Arg Phe Ser Val Ser Gly Ala Ala Glu Lys Val Arg

1130 1135 1140

Gly

<210> 150

<211> 647

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<220><221> MOD_RES

<222> (35)..(498)

<223> Any amino acid

<400> 150

Met Gly Leu Val Asp Thr Ala Gly Gly Phe Leu Ile Pro Ala Ala Leu

1 5 10 15

Asp Pro Ala Ile Leu Leu Ser Gly Asp Gly Ser Thr Asn Pro Ile Arg

20 25 30

Gln Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

210 215 220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

245 250 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

260 265 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

275 280 285

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
290 295 300
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305 310 315 320
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
325 330 335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
340 345 350
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
355 360 365
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
370 375 380
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
385 390 395 400

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
405 410 415
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
420 425 430
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
435 440 445
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
450 455 460

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
465 470 475 480
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
485 490 495
Xaa Xaa Pro Ser Arg Cys Arg Cys Leu Ala Phe Gly Arg Ser Ser Ser
500 505 510
Ala Ile Arg Arg Pro Ala Ala Ser Ser Ser Glu Gly Val Lys Ser Leu
515 520 525

Arg Ser Val Phe Ser Glu Arg Ser Ala Leu Ala Arg Ser Thr Thr Ser

530 535 540

Ala Ile Val Trp His Thr Cys Thr Gly Met Arg Ser His Pro Ser Ser

545 550 555 560

Arg Ala Ala Ser Ser Arg Arg Trp Pro Asn Thr Ser Arg Leu Ser Gly

565 570 575

Val Thr Pro Ile Gly Cys Ser Lys Arg Gln Gly Asp Ser Pro Cys Gly

580 585 590

Cys Cys Cys Gly Ala His Leu Val Val Ala Gln Arg Cys Val Ala Phe

595 600 605

Cys Cys His Asp Arg Gly Val Thr Glu Lys Leu Leu Tyr Ser Ser Gln

610 615 620

Val Val Gly Ala Ala Val Gly Ala Gly Gly Val Ser Val Pro Gln Gly

625 630 635 640

Val His Gly Arg Val Thr Gly

645

<210> 151

<211> 1262

<212> PRT

<213> Unknown

<

220><223> Description of Unknown:

Cas12 sequence

<400> 151

Met Arg Arg Gln His His Gly Gly Gln Asn Ala Arg Asp Trp Arg Arg

1 5 10 15

Lys Val Ala Ala Ala Ala Leu Arg Gln Lys Glu Ser Val Phe Thr Tyr

20 25 30

Lys Phe Gly Leu Ser Val Asn Asp Gly Asp Phe Asp Phe Asp Ala Ala

35 40 45

Ala Arg Thr Tyr Asp Ile Thr Glu Gly Ile Glu Arg Gly Ser Leu Ile

50 55 60

Gly Leu Val Cys Ala Val His Leu Ser Gly Phe Arg Leu Phe Ser Lys

65 70 75 80

Val Ala Glu Thr Arg Gln Phe Leu Asn Arg Ser Arg Tyr Pro Glu Asn
85 90 95
Glu Phe Ala Gln Ala Leu Ala Ala His Thr Glu Ile Glu Asn Pro Ser
100 105 110
Val Thr Val Gln Ser Ile Glu Ser Val Phe Val Thr Pro Pro Arg Lys

115 120 125
Gln Asp Gly Val Ala Arg Leu Trp Ser Ala Asp Glu Leu Ala Lys Arg
130 135 140
Leu Phe Gln Thr Trp Asn Asn Arg Ser Pro Arg Glu Gly Glu Arg Asn
145 150 155 160
His Pro Glu Leu Leu Leu Ala Gln Gly Ile Ala Arg Ala Val Thr Lys
165 170 175
Ala Phe Ser Gly Trp Lys Glu Leu Ala Asp Asn Ala Val His Ala Leu

180 185 190
Thr Cys Ala Asp Asn Tyr Leu Ala Thr Leu Gly Asn Arg Phe Pro Lys
195 200 205
Leu Ser Asp Leu Pro Pro Leu Thr Ala Gly Ser Thr Gln Thr Gly Thr
210 215 220
Leu Ala Phe Asp Pro Glu Ser Pro Phe Leu Asn Met Thr Gly Asn Glu
225 230 235 240
Asp Ile Trp Leu His Gln Val Val Ala Val Cys Ala Gly Arg Leu Lys

245 250 255
Arg Tyr Met Pro Glu Ile Asp Pro Ser Ser Arg Lys Phe Ala Ser Arg
260 265 270
Leu Thr Asp Ser Ile Val Ser Ser Gln Asn Asn Gly Leu Ser Trp Leu
275 280 285
Phe Gly Asn Gly Leu Arg Phe Leu Arg Gln Ser Ser Ile Ala Gln Ile
290 295 300
Ala Glu Thr Leu Ser Val Ser Gln Asn Glu His Arg Arg Val Glu Gln

305 310 315 320
Leu Lys Glu Phe Ala Asp Ala Ile Pro Val Asn Pro Phe Phe Ala Thr

325 330 335

Asp Gly Tyr Ala Glu Phe Arg Gly Ser Val Gly Gly Lys Ile Ser Ser

340 345 350

Trp Val Ser Asn Tyr Trp Lys Arg Ile Cys Glu Leu Thr Val Leu His

355 360 365

Ser Gln Pro Pro Asp Ile Thr Ile Pro Glu Gly Leu Leu Ala Ser Glu

370 375 380

Asn Ala Thr Leu Phe Ser Gly Gln His Thr Ala Ala Ala Gly Leu Val

385 390 395 400

Ala Leu Ser Ala Arg Leu Pro Ser Gln Val Arg Asp Ala Gly Lys Ala

405 410 415

Leu Phe Val Leu Ser Gly Asp Gly Val Pro Arg Ala Asp Asp Ile Ala

420 425 430

Thr Val Glu Asp Val Ala Gly Glu Leu Ala Glu Leu Thr Gly Gln Leu

435 440 445

Ala Met Leu Asp Asn Arg Ile Gln Gln Glu Ile Glu Arg Ala Gln Asp

450 455 460

Ala Asn Asp Glu Gly Arg Val Gly Ser Leu Ala Ser Leu Arg Pro Asn

465 470 475 480

Pro Thr Lys Glu Leu Lys Glu Pro Pro Lys Leu Asn Arg Ile Ser Gly

485 490 495

Gly Thr Ala Asp Ala Ala Gly Glu Leu Ala Arg Leu Glu Thr Ser Leu

500 505 510

Asn Asp Leu Ile Arg Ala Arg Arg Glu His Phe Tyr Arg Leu Ala Glu

515 520 525

Trp Thr Gly Asn Thr Ala Ser Leu Asp Pro Leu Pro Ala Leu Ala Glu

530 535 540

Arg Glu Arg Lys Ala Leu Thr Asp Arg Gly Met Asp Pro Thr Leu Ala

545 550 555 560

Glu Ala Asp Glu Tyr Ala Leu Arg Arg Leu Leu His Arg Ile Ala Gly

565 570 575

Met Ala Arg Arg Leu Ser Pro Asn Glu Ala Lys Arg Val Arg Glu Thr
580 585 590
Met Thr Pro Leu Phe Leu Lys Lys Arg Glu Ala Asn Leu Tyr Phe His
595 600 605
Asn Arg Ala Gly Ala Leu Tyr Arg His Pro Phe Ser Asn Ser Arg His
610 615 620
Gln Pro Tyr Ser Ile Asp Leu Asn Arg Ala Arg Ala Thr Asp Trp Leu

625 630 635 640
Ala Trp Leu Glu Glu Arg Ala Arg Glu Met Leu Gly Leu Leu Gly Ser
645 650 655
Gly Ala Pro Ala Asn His Glu Tyr Leu Arg Asp Leu Leu Ser Ile Glu
660 665 670
Thr Phe Val Phe Thr Thr Arg Leu Ser Gly Leu Pro Ala Gln Val Pro
675 680 685
Gly Tyr Leu Ala Lys Pro Lys Ser Asp Leu Thr Asn Ile Pro Pro Leu

690 695 700
Leu Ala Ala Gln Leu Asp Val Asp Glu Val Ser Arg Asp Val Ala Leu
705 710 715 720
Arg Ala Phe Asn Leu Phe Asn Ser Ala Ile Asn Gly Leu Ser Phe Arg
725 730 735
Ala Phe Arg Asp Ser Phe Ile Val Arg Thr Lys Phe Leu Arg Leu Gly
740 745 750
His Asp Glu Leu Phe Tyr Val Pro Lys Ala Arg Ala Trp Lys Pro Pro

755 760 765
Ala Asp Tyr Arg Ser Ala Lys Gly Lys Ile Ser Lys Gly Leu Ala Leu
770 775 780
Pro Ala Val Lys Arg Asn Glu Ala Gly Ser Ile Leu Pro Arg Glu Thr
785 790 795 800
Thr Gln Gly Leu Ser Arg Ala Lys Phe Pro Glu Gly Ser His Ala Leu
805 810 815
Leu Ser Gln Ala Pro His Asp Trp Phe Val Glu Leu Asp Leu Arg His

820 825 830

Asp Lys Met Pro Gln Leu Ala Gly Leu Pro Val Lys Met Asn Ala Asp

835 840 845

Gly Leu Lys Gly Trp Arg Ala Arg Arg Arg Pro Thr Phe Arg Leu Ala

850 855 860

Gly Pro Pro Ser Phe Lys Thr Trp Leu Asp Arg Ala Leu Thr Ser Thr

865 870 875 880

Ala Val Lys Leu Gly Asp Tyr Thr Leu Ile Leu Asp Gln Ser Phe Lys

885 890 895

Gln Ser Leu Arg Val Glu Asp Gly Glu Val Arg Leu Ser Ala Glu Pro

900 905 910

Ala Gly Ile Lys Ala Glu Ile Ala Val Pro Val Ile Asp Ala Arg Pro

915 920 925

Phe Pro Glu Thr Glu Ala Glu Ala Leu Phe Asp Asn Ile Ile Gly Ile

930 935 940

Asp Leu Gly Glu Arg Arg Ile Gly Tyr Ala Val Phe Ser Leu Pro Ala

945 950 955 960

Leu Leu Lys Ser Gly Asn Pro Thr Arg Val Lys Pro Thr Val Val Gly

965 970 975

Ser Val Ala Ile Pro Ala Phe Arg Arg Leu Met Ala Ala Val Arg Arg

980 985 990

His Arg Gly Ser Arg Gln Pro Asn Gln Lys Val Ser Gln Thr Tyr Ser

995 1000 1005

Thr Ala Leu Gln Gln Phe Arg Glu Asn Val Val Gly Asp Val Cys

1010 1015 1020

Asn Arg Ile Asp Thr Leu Cys Glu Arg Tyr Arg Ala Phe Pro Val

1025 1030 1035

Leu Glu Ser Ser Val Ala Asn Phe Glu Thr Gly Ala Asn Gln Leu

1040 1045 1050

Lys Leu Ile Tyr Gly Thr Val Leu Arg Arg Tyr Thr Phe Ser Asn

1055 1060 1065

Val Asp Ala His Lys Ser Ala Arg Ser Ala Tyr Trp Tyr Ser Ala

1070 1075 1080

Asn Arg Trp Gln His Pro Tyr Leu Phe Val Arg Glu Trp Asn Lys

1085 1090 1095

Ala Gln Arg Thr Phe Thr Gly Ser Ala Lys Pro Leu Ala Ile Tyr

1100 1105 1110

Pro Gly Val Thr Ile His Pro Ala Gly Thr Ser Gln Ile Cys His

1115 1120 1125

Arg Cys Gly Arg Asn Ala Leu Arg Ala Leu Arg Asn Met Pro Asp

1130 1135 1140

Arg Thr Ile Arg Val Gly Lys Asp Gly Leu Ile Val Leu Ala Asp

1145 1150 1155

Ser Thr Ile Arg Leu Leu Glu Arg Ala Asp Tyr Ser Asp Arg Glu

1160 1165 1170

Leu Lys Thr Phe Lys Arg Arg Lys Gln Arg Pro Pro Leu Asn Met

1175 1180 1185

Pro Val Pro Glu Gly Ala Arg Pro Arg Asp Gln Leu Glu Arg Val

1190 1195 1200

Leu Arg Arg Asn Met Arg Gln Gln Pro Gln Ser Glu Met Ser Pro

1205 1210 1215

Asp Thr Thr Gln Ala Arg Phe Thr Cys Val Tyr Thr Asp Cys Gly

1220 1225 1230

Phe Glu Gly His Ala Asp Glu Asn Ala Ala Val Asn Ile Gly Arg

1235 1240 1245

Arg Phe Leu Glu Arg Ile Asp Ile Glu Ala Ser Ser Arg Thr

1250 1255 1260

<210> 152

<211> 978

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 152

Met Gln Glu Ile Lys Arg Ile Asn Lys Ile Arg Arg Arg Leu Val Lys
1 5 10 15

Asp Ser Asn Thr Lys Lys Ala Gly Lys Thr Gly Pro Met Lys Thr Leu
20 25 30

Leu Val Arg Val Met Thr Pro Asp Leu Arg Glu Arg Leu Glu Asn Leu
35 40 45

Arg Lys Lys Pro Glu Asn Ile Pro Gln Pro Ile Ser Asn Thr Ser Arg
50 55 60

Ala Asn Leu Asn Lys Leu Leu Thr Asp Tyr Thr Glu Met Lys Lys Ala
65 70 75 80

Ile Leu His Val Tyr Trp Glu Glu Phe Gln Lys Asp Pro Val Gly Leu
85 90 95

Met Ser Arg Val Ala Gln Pro Ala Pro Lys Asn Ile Asp Gln Arg Lys
100 105 110

Leu Ile Pro Val Lys Asp Gly Asn Glu Arg Leu Thr Ser Ser Gly Phe
115 120 125

Ala Cys Ser Gln Cys Cys Gln Pro Leu Tyr Val Tyr Lys Leu Glu Gln
130 135 140

Val Asn Asp Lys Gly Lys Pro His Thr Asn Tyr Phe Gly Arg Cys Asn
145 150 155 160

Val Ser Glu His Glu Arg Leu Ile Leu Leu Ser Pro His Lys Pro Glu
165 170 175

Ala Asn Asp Glu Leu Val Thr Tyr Ser Leu Gly Lys Phe Gly Gln Arg
180 185 190

Ala Leu Asp Phe Tyr Ser Ile His Val Thr Arg Glu Ser Asn His Pro
195 200 205

Val Lys Pro Leu Glu Gln Ile Gly Gly Asn Ser Cys Ala Ser Gly Pro
210 215 220

Val Gly Lys Ala Leu Ser Asp Ala Cys Met Gly Ala Val Ala Ser Phe

225 230 235 240

Leu Thr Lys Tyr Gln Asp Ile Ile Leu Glu His Gln Lys Val Ile Lys

245 250 255

Lys Asn Glu Lys Arg Leu Ala Asn Leu Lys Asp Ile Ala Ser Ala Asn

260 265 270

Gly Leu Ala Phe Pro Lys Ile Thr Leu Pro Pro Gln Pro His Thr Lys

275 280 285

Glu Gly Ile Glu Ala Tyr Asn Asn Val Val Ala Gln Ile Val Ile Trp

290 295 300

Val Asn Leu Asn Leu Trp Gln Lys Leu Lys Ile Gly Arg Asp Glu Ala

305 310 315 320

Lys Pro Leu Gln Arg Leu Lys Gly Phe Pro Ser Phe Pro Leu Val Glu

325 330 335

Arg Gln Ala Asn Glu Val Asp Trp Trp Asp Met Val Cys Asn Val Lys

340 345 350

Lys Leu Ile Asn Glu Lys Lys Glu Asp Gly Lys Val Phe Trp Gln Asn

355 360 365

Leu Ala Gly Tyr Lys Arg Gln Glu Ala Leu Leu Pro Tyr Leu Ser Ser

370 375 380

Glu Glu Asp Arg Lys Lys Gly Lys Lys Phe Ala Arg Tyr Gln Phe Gly

385 390 395 400

Asp Leu Leu Leu His Leu Glu Lys Lys His Gly Glu Asp Trp Gly Lys

405 410 415

Val Tyr Asp Glu Ala Trp Glu Arg Ile Asp Lys Lys Val Glu Gly Leu

420 425 430

Ser Lys His Ile Lys Leu Glu Glu Glu Arg Arg Ser Glu Asp Ala Gln

435 440 445

Ser Lys Ala Ala Leu Thr Asp Trp Leu Arg Ala Lys Ala Ser Phe Val

450 455 460

Ile Glu Gly Leu Lys Glu Ala Asp Lys Asp Glu Phe Cys Arg Cys Glu

465 470 475 480

Leu Lys Leu Gln Lys Trp Tyr Gly Asp Leu Arg Gly Lys Pro Phe Ala

485 490 495

Ile Glu Ala Glu Asn Ser Ile Leu Asp Ile Ser Gly Phe Ser Lys Gln

500 505 510

Tyr Asn Cys Ala Phe Ile Trp Gln Lys Asp Gly Val Lys Lys Leu Asn

515 520 525

Leu Tyr Leu Ile Ile Asn Tyr Phe Lys Gly Gly Lys Leu Arg Phe Lys

530 535 540

Lys Ile Lys Pro Glu Ala Phe Glu Ala Asn Arg Phe Tyr Thr Val Ile

545 550 555 560

Asn Lys Lys Ser Gly Glu Ile Val Pro Met Glu Val Asn Phe Asn Phe

565 570 575

Asp Asp Pro Asn Leu Ile Ile Leu Pro Leu Ala Phe Gly Lys Arg Gln

580 585 590

Gly Arg Glu Phe Ile Trp Asn Asp Leu Leu Ser Leu Glu Thr Gly Ser

595 600 605

Leu Lys Leu Ala Asn Gly Arg Val Ile Glu Lys Thr Leu Tyr Asn Arg

610 615 620

Arg Thr Arg Gln Asp Glu Pro Ala Leu Phe Val Ala Leu Thr Phe Glu

625 630 635 640

Arg Arg Glu Val Leu Asp Ser Ser Asn Ile Lys Pro Met Asn Leu Ile

645 650 655

Gly Ile Asp Arg Gly Glu Asn Ile Pro Ala Val Ile Ala Leu Thr Asp

660 665 670

Pro Glu Gly Cys Pro Leu Ser Arg Phe Lys Asp Ser Leu Gly Asn Pro

675 680 685

Thr His Ile Leu Arg Ile Gly Glu Ser Tyr Lys Glu Lys Gln Arg Thr

690 695 700

Ile Gln Ala Ala Lys Glu Val Glu Gln Arg Arg Ala Gly Gly Tyr Ser

705 710 715 720

Arg Lys Tyr Ala Ser Lys Ala Lys Asn Leu Ala Asp Asp Met Val Arg

725 730 735

Asn Thr Ala Arg Asp Leu Leu Tyr Tyr Ala Val Thr Gln Asp Ala Met

740 745 750

Leu Ile Phe Glu Asn Leu Ser Arg Gly Phe Gly Arg Gln Gly Lys Arg

755 760 765

Thr Phe Met Ala Glu Arg Gln Tyr Thr Arg Met Glu Asp Trp Leu Thr

770 775 780

Ala Lys Leu Ala Tyr Glu Gly Leu Pro Ser Lys Thr Tyr Leu Ser Lys

785 790 795 800

Thr Leu Ala Gln Tyr Thr Ser Lys Thr Cys Ser Asn Cys Gly Phe Thr

805 810 815

Ile Thr Ser Ala Asp Tyr Asp Arg Val Leu Glu Lys Leu Lys Lys Thr

820 825 830

Ala Thr Gly Trp Met Thr Thr Ile Asn Gly Lys Glu Leu Lys Val Glu

835 840 845

Gly Gln Ile Thr Tyr Tyr Asn Arg Tyr Lys Arg Gln Asn Val Val Lys

850 855 860

Asp Leu Ser Val Glu Leu Asp Arg Leu Ser Glu Glu Ser Val Asn Asn

865 870 875 880

Asp Ile Ser Ser Trp Thr Lys Gly Arg Ser Gly Glu Ala Leu Ser Leu

885 890 895

Leu Lys Lys Arg Phe Ser His Arg Pro Val Gln Glu Lys Phe Val Cys

900 905 910

Leu Asn Cys Gly Phe Glu Thr His Ala Asp Glu Gln Ala Ala Leu Asn

915 920 925

Ile Ala Arg Ser Trp Leu Phe Leu Arg Ser Gln Glu Tyr Lys Lys Tyr

930 935 940

Gln Thr Asn Lys Thr Thr Gly Asn Thr Asp Lys Arg Ala Phe Val Glu

945 950 955 960

Thr Trp Gln Ser Phe Tyr Arg Lys Lys Leu Lys Glu Val Trp Lys Pro

965 970 975

Ala Val

<210> 153

<211> 1488

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 153

Met Gly Lys Gln Ser Thr Asn Ser Ser Gly Leu Lys Ala Thr Ser Gly

1 5 10 15

Ala Pro Ser Ile Glu Lys Pro Val Thr Thr Gln Arg Ala Tyr Thr Leu

20 25 30

Arg Leu Arg Gly Ile Glu Gly Asp Lys Thr Trp Arg Asp Ser Leu Trp

35 40 45

Ala Thr His Glu Ala Ile Asn Leu Gly Ala Lys Ala Phe Gly Asp Trp

50 55 60

Leu Leu Thr Leu Arg Gly Gly Leu Glu His Thr Leu Ala Asp Ala Thr

65 70 75 80

Val Ala Gly Gly Lys Gly Lys Pro Ala Arg Pro Pro Ser Ala Asp Glu

85 90 95

Arg Arg Asp Arg Arg Val Leu Leu Ala Leu Ser Trp Leu Thr Val Glu

100 105 110

Asp Glu Arg Gly Ala Pro Lys Ala Pro Gly Leu Ile Val Ala Tyr Gly

115 120 125

Asp Asp Cys Lys Ser Ala Lys Asp Ser Gln Asp Gly Arg Asp Arg Lys

130 135 140

Val Glu Asp Ala Leu Arg Asp Ile Leu Ile Lys Arg Ser Val Ala Pro

145 150 155 160

Gly Ala Val Glu Ser Trp Val Asn Asp Cys Val Val Ser Leu Lys Ala

165 170 175

Arg Ile Arg Asp Asp Ala Val Trp Val Asn Arg Ser Ala Ala Phe Asp

180 185 190

Ala Leu Arg Ala Ser Trp Arg Gly Leu Thr Cys Pro Asn Ala Arg Thr

195 200 205

Val Leu Glu Gln Phe Phe Gly Pro Val Ala Asp Trp Ile Thr Leu Pro

210 215 220

Ala Arg Ala Ala Asp Asp Gly Glu Gly Asp Thr Gly Gly Pro Thr Ala

225 230 235 240

Ala Gly Ser Ser Asn Asp Thr Glu Phe Lys Leu Val Ala Arg Ser Phe

245 250 255

Leu Ser Glu Asn Phe Gly Thr Gly Leu Lys Ser Ser Lys Ser Asp Ile

260 265 270

Ser Asp Ala Leu Met Gln Ala Thr Arg Ser Leu Ala Ala Leu Arg Gly

275 280 285

Gly Ser Pro Gly Ser Ala Val Trp Ser His Leu Cys Thr Glu Phe Gly

290 295 300

Leu Leu Ala Ala Asp Asp Glu Ala Arg Ala Lys Ala Leu Arg Val Arg

305 310 315 320

Ile Gly Trp Thr Ser Gly Arg Arg Ser Lys Gly Arg Leu Ala Leu Ala

325 330 335

Thr Ala Ala Ser Lys Ala Ser Leu Ala Gln Val Asp Ile Glu Leu Leu

340 345 350

Ile Lys Lys Leu Ser Glu Glu Ala Gln Glu Lys Leu Ala Gly Ser Thr

355 360 365

Lys Leu Pro Leu Pro Trp Val Asn Asp Leu Met Ala Ala Leu Glu Arg

370 375 380

Ser Ile Gly Phe Gly Phe Val Thr Glu Arg Asn Leu Ile Asp Glu Phe

385 390 395 400

Gly Val Met Leu Asp His Ala Ala Arg Arg Val Ser Ile Ala Cys Ser

405 410 415

Trp Ile Lys Leu Ala Glu Leu Glu Arg Arg Gln Phe Glu Glu Asp Ala

420 425 430

Lys Lys Leu Asp Gln Val Arg Thr Gln His Ala Asp Ala Ala Ala Phe
435 440 445
Leu Asp Thr Leu Gly Cys Arg Arg Gly Ser Glu Ser Gly Ser Ala Gly

450 455 460
Gly Ala Ser Val Val Ile Arg Lys Arg Ala Val Leu Gly Trp Asn Glu
465 470 475 480
Val Val Gly Asp Trp Ala Arg Gln Gly Cys Lys Ser Val Gln Glu Arg
485 490 495
Ile Asp Ala Ala Arg Leu Leu Gln Gly Glu Leu Glu Lys Phe Gly Asp
500 505 510
Ile Arg Leu Phe Glu Glu Leu Ala Ala Asn Asp Ala Gln Val Val Trp

515 520 525
Gln Asn Ala Glu Gly Glu Thr Asp Pro Thr Ile Leu Ala Arg Tyr Ser
530 535 540
Ala Gly Ser Val Ala Lys Ala Asn Gln Gln Arg Phe Lys Val Pro Ala
545 550 555 560
Tyr Arg His Pro Asp Pro Leu Arg His Pro Val Phe Gly Asp Phe Gly
565 570 575
Lys Ser Arg Trp Lys Ile Asp Phe Ala Val His Glu Ser Asp Arg Ala

580 585 590
Gln Ser Gly Gly Lys Arg Val Arg Ser Leu Asp Ala Ala Trp Gln Ser
595 600 605
Asp Val Arg Asn Met Arg Met Ala Leu Trp Thr Gly Lys Arg Val Glu
610 615 620
Met Val Pro Leu Arg Trp Ser Ser Lys Arg Leu Ser Lys Asp Leu Gly
625 630 635 640
Ile Ser Asp Leu Ser Leu Lys Asp Pro Thr Val Val Thr Arg Gly Asp

645 650 655
Arg Leu Gly Arg Ala Ala Val Gly Pro Gly Asp Pro Val Arg Val Ala
660 665 670
Ser Val Phe Ala Glu Asp Asn Trp Asn Gly Arg Leu Gln Ala Pro Arg

675 680 685

Val Glu Leu Asn Arg Val Ala Arg Leu Thr Gln Ser Gly Asn Leu Val

690 695 700

Gln Ala Arg Arg Leu Arg Asp Arg Leu Ser Trp Leu Val Ser Phe Ser

705 710 715 720

Pro Lys Leu Ala Pro Ser Gly Pro Phe Ile Asp Tyr Ala Ala Ala His

725 730 735

Gly Ile Glu Pro His Lys Lys Ser Gly Glu Tyr Trp Pro Asn Ser Ala

740 745 750

Met Asn Lys Glu Arg Lys Gly His His Ser Lys Leu Ile Tyr Ser Arg

755 760 765

Leu Pro Ser Leu Arg Val Leu Ser Val Asp Leu Gly His Arg Phe Ala

770 775 780

Ala Ala Cys Ala Val Trp Glu Ser Met Ser Ala Ala Gln Met Arg Leu

785 790 795 800

Ala Ala Ser Lys Gly Lys Val Val Arg Gly Gly Ile Ala Glu Gly Ala

805 810 815

Leu Phe Ile His Ile Glu Ser Thr Val Ala Asp Gly Thr Val Arg Thr

820 825 830

Thr Val Tyr Arg Arg Ile Gly Glu Asp Ala Leu Pro Asp Gly Ser Pro

835 840 845

His Pro Ala Pro Trp Ala Lys Leu Glu Arg Gln Phe Leu Ile Lys Leu

850 855 860

Gln Gly Glu Glu Thr Pro Ser Arg Met Ala Ala Leu Asp Glu Leu Val

865 870 875 880

Met Ile Ala Asp Trp Glu Arg Ala Leu Gly Tyr Gln Pro Val Thr Ala

885 890 895

Ser Ser Thr Lys Gln Ser Asn Gly Val Ala Gly Leu Met Gly Arg Thr

900 905 910

Val Arg Leu Phe Met His Ala Ser Arg Arg His Phe Asp Arg Ala Arg

915 920 925

Ile Ala His Asn Leu Thr Ala Glu His Arg Thr Lys Pro Gly Gly Val

930 935 940

Pro Glu Ser Leu Thr Glu Glu Thr Arg Ile Glu Leu Leu Ile Asp Thr

945 950 955 960

Leu Ala Leu Trp His Gly Leu Phe Ala Gly Asp Arg Trp Arg Asp Pro

965 970 975

Arg Ala Gln Lys Glu Trp Glu Thr Ser Gly Leu Pro Ser Leu Lys Leu

980 985 990

Pro Gly Arg Gly Asp Asp Asp Glu Thr Ala Phe Gly Gly Pro Gly Arg

995 1000 1005

Lys Ala Ala Met Val Val Tyr Arg Asn Glu Leu Lys Pro His Ala

1010 1015 1020

Glu Arg Met Ala His Ser Asp Leu Ser Asn Leu Ser Lys Cys Trp

1025 1030 1035

Thr Asp Arg Trp Ala Gln Asp Asp Arg Glu Trp Thr Ala Lys Ser

1040 1045 1050

Gly Arg Leu Arg Ser Leu Arg Arg Trp Ile Thr Pro Arg Gly Leu

1055 1060 1065

Arg Pro Val Ser Gly Asp Ser Ala Gln Leu Ile Glu Arg Lys Ala

1070 1075 1080

Ala Ala Ala Leu Arg Ala Arg His Val Gly Gly Leu Ser Met Gln

1085 1090 1095

Arg Ile Asn Thr Leu Thr Asp Leu Tyr Arg Leu Leu Lys Ser Phe

1100 1105 1110

Lys Asn Arg Pro Glu Pro Ser Asn Leu Arg Lys Asn Ile Pro Glu

1115 1120 1125

Lys Gly Asp Ala Arg Leu Ile Gly Phe Asn Gln Arg Leu Leu Asp

1130 1135 1140

Val Arg Asp Arg Leu Arg Glu Gln Arg Val Lys Gln Leu Ala Ser

1145 1150 1155

Arg Ile Val Glu Ala Ala Leu Gly Ile Gly Arg Ile Lys Ile Arg

1160 1165 1170

Arg Val Ala Ala Gly Ser Pro Arg Pro Thr Leu Arg Val Asp Ala

1175 1180 1185

Ala Cys His Ala Val Val Thr Glu Asn Leu Ser Asn Tyr Gln Pro

1190 1195 1200

Ala Glu Leu Gln Thr Arg Arg Glu Asn Arg Gln Leu Met Ala Trp

1205 1210 1215

Ala Ser Ser Lys Val His Lys Tyr Leu Ala Glu Ser Cys Gln Leu

1220 1225 1230

His Gly Leu His Leu Arg Glu Val Gln Pro Asn Tyr Thr Ser Arg

1235 1240 1245

Gln Cys Ser Arg Thr Gly Ala Ala Gly Leu Arg Gly Val Ala Val

1250 1255 1260

Ser Ala Thr Asp Leu Leu Thr Asn Pro Trp Trp Met Arg Asp Val

1265 1270 1275

Ala Gln Ala Lys Ala Arg Ile Glu Lys Ala Leu Lys Asn Gly Arg

1280 1285 1290

Asn Gly Ala Val Ala Asp Gln Leu Leu Val Ser Ala Glu Ala Trp

1295 1300 1305

Ala Leu Arg Ile Pro Glu Arg Asp Arg His Asp Arg Lys Ala Asp

1310 1315 1320

Glu Ser Val Lys Ala Phe His Ala Glu Arg Val Ile Leu Pro Arg

1325 1330 1335

Lys Gly Gly Asp Leu Phe Val Ala Glu Ser Ala Arg Cys Asn Gly

1340 1345 1350

Lys Gly His Val Pro Ala Leu Gln Ala Asp Leu Asn Ala Ala Ala

1355 1360 1365

Asn Val Gly Ile Arg Ala Leu Leu Asp Pro Asp Trp Pro Gly Lys

1370 1375 1380

Trp Trp Trp Val Pro Cys Val Gly Gly Thr Tyr Ser Pro Ser Pro

1385 1390 1395

Glu Lys Thr Ser Gly Ala Lys Val Leu Glu His Ile Asp Gln Leu

1400 1405 1410

Pro His Glu Met Val Asp Pro Pro Gln Val Ala Pro Lys Ser Ser

1415 1420 1425

Ala Pro Gln Pro Lys Ser Ser Arg Ala Ala Lys Val Lys Ala Lys

1430 1435 1440

Glu Phe Arg Ala Ile Glu Asn Arg Trp Arg Thr Cys Ser Ser Glu

1445 1450 1455

Leu Leu Ser Gln Gly Lys Trp Ile Pro Ser Gly Glu Tyr Trp Ser

1460 1465 1470

Lys Val Glu Ala Ala Val Cys Leu Val Leu Asn Asp Gln Ile Thr

1475 1480 1485

<210> 154

<211> 1400

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 154

Met Ala Ala Phe Gln Arg Ser Tyr Thr Met Asn Leu Lys Pro Ala Thr

1 5 10 15

Ser Glu Gln Asp Lys Phe Ile Leu Trp Asn Arg Leu Phe Leu Thr His

20 25 30

Trp Ser Val Asn Glu Gly Ala Lys Ile Phe Gly Glu Leu Phe Leu Asn

35 40 45

Leu Arg Gly Gly Leu Ser Pro Glu Leu Asp Ile Phe Asp Leu Asp Lys

50 55 60

Val Lys Asp Asp Lys Lys Lys Lys Ala Phe Val Met Gly Arg Arg Arg

65 70 75 80

Leu Leu Ala Leu Gly Trp Leu Ser Val Glu Asp Asn Leu Ser Ala Gly

85 90 95

Glu His Pro Phe Arg Ile Arg Glu Ile Pro Val Gly Arg Asn Met Gly

100 105 110

Lys Ser Gln Ala Ser Thr Leu Leu Thr Glu Ile Leu Lys Asn Lys Gly

115 120 125

Ile Lys Asp Glu Ala Val Ile Lys Glu Trp Ile Asp Asp Cys Thr Pro

130 135 140

Ser Leu Ile Ala Asn Ile Arg Glu Asp Ala Val Trp Ile Asn Arg Ala

145 150 155 160

Ser Ser Phe Asn Ser Ile Thr Pro Cys Pro Thr Lys Asp Glu Val Trp

165 170 175

Ile Val Leu Ser Gly Leu Leu Gly Leu Arg Phe Leu Asp Leu Ser Leu

180 185 190

Glu Glu Val Lys Gly Lys Glu Thr Glu Tyr Leu Tyr Asp Leu Gly Glu

195 200 205

Lys Glu Thr Gln Ser Lys Ser Asp Pro Ser Lys Lys Ala Arg Glu Leu

210 215 220

Phe Gly Asn Leu Phe Thr Gln Asn Pro Val Leu Met Lys Asn Ser Arg

225 230 235 240

Asp Lys Lys Asp Thr Phe Ala Lys Glu Phe Tyr Leu Ala Phe Lys Glu

245 250 255

Phe Lys Asp Tyr Glu Lys Leu Lys Glu Lys Ile Glu Ser Trp Arg Lys

260 265 270

Glu Lys Glu Phe Pro Leu Ile Glu Asn Pro Val Ala Glu Lys Tyr Pro

275 280 285

Pro Glu Val Thr Phe Thr Gly Ser Pro Cys Thr Val Ser Lys Arg Tyr

290 295 300

Arg Lys Leu Leu Val Ser Leu Glu Leu Trp Pro Ser Ser Gln Asp Glu

305 310 315 320

Asn Gly Asn Ile Pro Lys Thr Glu Lys Thr Glu Asp Lys Thr His Asn

325 330 335

Gln Val Leu Leu Asp Tyr Leu Leu Lys Ala Cys Asn Glu Gly Asn Lys

340 345 350

Gly Thr Gln Lys Ile Ile Thr Pro Val Trp Ala Asn Asn Leu Lys Ala
355 360 365
Glu Leu Glu Leu Lys Met Asn Glu Ile Ile Arg Ile Gly Glu Ser Ser
370 375 380
Ser Thr Glu Leu Gln Arg Leu Met Ile Lys Met Ala Ala Arg Arg Ile

385 390 395 400
Ser Gln Thr Leu Ser Trp Ile Lys Ile Asn Glu Gln Thr Lys His Asp
405 410 415
Ala Tyr Gln Lys Lys Asn Lys Ala Phe Lys Leu Leu Ser Glu Ile Asp
420 425 430
Lys Asn Gly Glu Ala Cys Lys Trp Leu Glu Asn Tyr Glu Leu Phe Arg
435 440 445
Thr Asp Asp Ser Gly Gly Glu Glu Tyr His Ile Ser Leu Arg Ala Ile

450 455 460
Ser Cys Trp Lys Gln Ile Leu Glu Glu Trp Gln Lys Asn Asp Ser Pro
465 470 475 480
Lys Ala Leu Arg Glu Lys Val Lys Glu Val Gln Ala Glu Glu Glu Lys
485 490 495
Phe Gly Asp Ala Arg Leu Phe Glu Asp Leu Ala Asp Asp Asn Ala Arg
500 505 510
Ser Val Trp Leu Leu Pro Asp Gly Asn Lys Thr Pro Asp Ile Leu Asn

515 520 525
Trp Trp Cys Glu Tyr Arg Thr Ala Glu Ile Asp Glu Ser Arg Phe Lys
530 535 540
Ile Pro Cys Tyr Cys His Pro His Pro Phe Lys His Pro Val Tyr Val
545 550 555 560
Glu Tyr Gly Lys Ser Asn Pro Lys Val Ile Phe Ala Met Lys Asn Asn
565 570 575
Lys Val Lys Lys Gly His Ile Glu His Gly Trp Asn Pro Gln Asn Pro

580 585 590
Arg Ser Ile Ala Leu Ser Leu Phe Asn Asn Gly Asn Arg Glu Ser Ser

595 600 605

Leu Val Pro Phe Ile Trp Glu Ser Lys Arg Leu Trp Lys Asp Leu Gly

610 615 620

Gly Glu Ala Thr Gln Ile Gly Asp Ile Pro Arg Ser Asp Arg Met Gly

625 630 635 640

Leu Ser Gly Lys Arg Glu Ser Val Lys Pro Lys Ala Pro Phe Gln Lys

645 650 655

Glu Val Trp Asn Ala Arg Leu Gln Ser Asp Arg Arg Thr Leu Glu Lys

660 665 670

Leu Glu Lys Tyr Trp Asn Pro Glu Ser Met Lys Trp Ile Asp Asp Gly

675 680 685

Lys Phe Leu Ile Gln Ser Lys Trp Phe Ile Thr Phe Gly Pro Asp Met

690 695 700

Glu Thr Ala Glu Gly Pro Trp Lys Leu Tyr Leu Lys Glu Lys Tyr Val

705 710 715 720

Asp Asn Lys Ile Leu Gly Asn Arg Ser Lys Glu Asn Gln Lys Arg Gly

725 730 735

Tyr Arg Ala Lys Lys Leu Leu Ser Gly Tyr Pro Ala Gly Met Arg Ile

740 745 750

Leu Ser Val Asp Leu Gly His Arg Tyr Ala Ala Ser Cys Ala Val Trp

755 760 765

Glu Thr Ile Thr Lys Lys Gln Ile Thr Glu Glu Leu Ala Tyr Gln Pro

770 775 780

Asp Asn Asn Ser Leu Phe Glu His Ser Cys Lys Thr Ile Asp Lys Lys

785 790 795 800

Ile Lys Asn Thr Val Tyr Arg Arg Ile Gly Glu Asp Ser Ile Asp Ala

805 810 815

Pro Trp Ala Lys Leu Glu Lys Gln Phe Thr Ile Lys Leu Gln Gly Glu

820 825 830

Asp Lys Ser Cys Tyr Leu Leu Arg Ser Asp Glu Lys Glu Leu Phe Arg

835 840 845

Ser Ile Leu Ser Lys Leu Ser Cys Leu Asn Asn Asp Thr Gly His Asn
850 855 860
Ile Leu Glu Met Ile Glu Asn Leu Leu Arg Ile Val Lys Ala Lys Ile
865 870 875 880
Tyr Arg Gln Gly Ile Leu Ala Arg Ile Ser Tyr Ser Met Thr Ala Gln
885 890 895
Tyr Lys Pro Gly Lys Gly Gly Gln Lys Ser Pro Leu Ser Asp Glu Asp

900 905 910
Lys Ile His Tyr Leu Ser Glu Asn Leu Ala Ala Trp Ser Ala Ile Met
915 920 925
Gly Asn Gln Glu Trp Asn Glu Asp Val Ile Ser Asp Trp Tyr Lys Thr
930 935 940
Tyr Ile Ser His Leu Val Ser Gly Pro Lys Pro Lys Glu Gly Asn Arg
945 950 955 960
Lys Ser Asp Arg Asp Lys Ile Ile Glu Tyr Phe Leu Pro Ala Ala Arg

965 970 975
Lys Leu Tyr Asp Asp Asn Glu Thr Arg Ile Lys Ile His Asp Leu Phe
980 985 990
Lys Glu Leu Trp Asp Glu Asn Asn Lys Gln Leu Ser Ala Val Leu Lys
995 1000 1005
Glu Ile Lys Lys Ile Ile Leu Pro Lys Gly Ile Arg Tyr Phe Asp
1010 1015 1020
Lys Asn Thr Asp Asn Pro Ser Lys Trp Lys Asn Asn Gln Ser Lys

1025 1030 1035
Leu Lys Gln Ile Thr His Arg Gly Gly Leu Ser Met Gln Arg Ile
1040 1045 1050
Val Ala Ile Glu Glu Tyr Tyr Lys Leu Ala Lys Ala Tyr Lys Asn
1055 1060 1065
His Pro Glu Pro Asp Asp Leu Thr Lys Asn Ile Pro Leu Pro Gly
1070 1075 1080
Asp Asn Ser Ser Ala Gly Phe Asn Gln Arg Ile Arg Asp Thr Leu

1085 1090 1095

Glu Arg Met Lys Glu Gln Arg Val Lys Gln Ile Ala Ser Arg Ile

1100 1105 1110

Val Glu Ser Ala Leu Gly Leu Gly Ile Glu Gly Tyr Lys Lys Arg

1115 1120 1125

Pro Leu Thr Pro Glu Asn Lys Pro Cys Gln Ala Ile Val Ile Glu

1130 1135 1140

Asp Leu Ser His Tyr Arg Pro Asp Glu Leu Gln Thr Arg Arg Glu

1145 1150 1155

Asn Arg Arg Leu Met Gln Trp Ser Ser Ser Lys Val Lys Lys Tyr

1160 1165 1170

Leu Lys Glu Ala Cys Glu Met His Asp Val Arg Leu Val Glu Ile

1175 1180 1185

Ser Pro Glu Tyr Thr Ser Arg Gln Asp Ser Arg Thr Gly Ala Ala

1190 1195 1200

Gly Leu Arg Cys Ile Asp Ile Asn Ile Arg Glu Phe Leu Lys Asp

1205 1210 1215

Ser Ser Arg Trp Gln Asn Lys Ile Asn Thr Ile Gln Lys Lys Pro

1220 1225 1230

Ala Asn Lys Lys Ser Asn Leu Asp Gln Tyr Leu Ile Glu Leu Asn

1235 1240 1245

Glu Ser Leu Gly Asn Lys Tyr Lys Asp Lys Val Ile Pro Ser Asp

1250 1255 1260

Asn Phe Val Arg Ile Pro Arg Lys Gly Gly Asp Val Phe Val Ser

1265 1270 1275

Ser Ser Lys Glu Ser Pro Val Ser Lys Gly Ile Gln Ala Asp Leu

1280 1285 1290

Asn Ala Ala Ala Asn Ile Gly Leu Lys Ala Leu Leu Asp Pro Asp

1295 1300 1305

Trp Ala Gly Ala Trp Trp Tyr Ile Leu Ile Glu Val Lys Ser Asn

1310 1315 1320

His Val Ile Pro Tyr Gly Glu Lys Tyr Lys Gly Ser Glu Cys Leu

1325 1330 1335

Arg Ala Trp Lys Phe Ser Gly Leu Glu Asn Gln Val Met Lys Asn

1340 1345 1350

Asn Met Asn Leu Trp Arg Asp Leu Gln Ser Gln Phe Ser Gly Glu

1355 1360 1365

Asp Lys Trp Met Ser Tyr Lys Glu Tyr Asn Glu Leu Thr Glu Lys

1370 1375 1380

Arg Val Ile Asn Ile Leu Arg Glu Arg Ala Gly Leu Glu Leu Ile

1385 1390 1395

Lys Glu

1400

<210> 155

<211> 1263

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 155

Met Glu Asp Tyr Ser Gly Phe Val Asn Ile Tyr Ser Ile Gln Lys Thr

1 5 10 15

Leu Arg Phe Glu Leu Lys Pro Val Gly Lys Thr Leu Glu His Ile Glu

20 25 30

Lys Lys Gly Phe Leu Lys Lys Asp Lys Ile Arg Ala Glu Asp Tyr Lys

35 40 45

Ala Val Lys Lys Ile Ile Asp Lys Tyr His Arg Ala Tyr Ile Glu Glu

50 55 60

Val Phe Asp Ser Val Leu His Gln Lys Lys Lys Lys Asp Lys Thr Arg

65 70 75 80

Phe Ser Thr Gln Phe Ile Lys Glu Ile Lys Glu Phe Ser Glu Leu Tyr

85 90 95

Tyr Lys Thr Glu Lys Asn Ile Pro Asp Lys Glu Arg Leu Glu Ala Leu

100 105 110

Ser Glu Lys Leu Arg Lys Met Leu Val Gly Ala Phe Lys Gly Glu Phe

115 120 125

Ser Glu Glu Val Ala Glu Lys Tyr Lys Asn Leu Phe Ser Lys Glu Leu

130 135 140

Ile Arg Asn Glu Ile Glu Lys Phe Cys Glu Thr Asp Glu Glu Arg Lys

145 150 155 160

Gln Val Ser Asn Phe Lys Ser Phe Thr Thr Tyr Phe Thr Gly Phe His

165 170 175

Ser Asn Arg Gln Asn Ile Tyr Ser Asp Glu Lys Lys Ser Thr Ala Ile

180 185 190

Gly Tyr Arg Ile Ile His Gln Asn Leu Pro Lys Phe Leu Asp Asn Leu

195 200 205

Lys Ile Ile Glu Ser Ile Gln Arg Arg Phe Lys Asp Phe Pro Trp Ser

210 215 220

Asp Leu Lys Lys Asn Leu Lys Lys Ile Asp Lys Asn Ile Lys Leu Thr

225 230 235 240

Glu Tyr Phe Ser Ile Asp Gly Phe Val Asn Val Leu Asn Gln Lys Gly

245 250 255

Ile Asp Ala Tyr Asn Thr Ile Leu Gly Gly Lys Ser Glu Glu Ser Gly

260 265 270

Glu Lys Ile Gln Gly Leu Asn Glu Tyr Ile Asn Leu Tyr Arg Gln Lys

275 280 285

Asn Asn Ile Asp Arg Lys Asn Leu Pro Asn Val Lys Ile Leu Phe Lys

290 295 300

Gln Ile Leu Gly Asp Arg Glu Thr Lys Ser Phe Ile Pro Glu Ala Phe

305 310 315 320

Pro Asp Asp Gln Ser Val Leu Asn Ser Ile Thr Glu Phe Ala Lys Tyr

325 330 335

Leu Lys Leu Asp Lys Lys Lys Lys Ser Ile Ile Ala Glu Leu Lys Lys

340 345 350

Phe Leu Ser Ser Phe Asn Arg Tyr Glu Leu Asp Gly Ile Tyr Leu Ala

355 360 365

Asn Asp Asn Ser Leu Ala Ser Ile Ser Thr Phe Leu Phe Asp Asp Trp

370 375 380

Ser Phe Ile Lys Lys Ser Val Ser Phe Lys Tyr Asp Glu Ser Val Gly

385 390 395 400

Asp Pro Lys Lys Lys Ile Lys Ser Pro Leu Lys Tyr Glu Lys Glu Lys

405 410 415

Glu Lys Trp Leu Lys Gln Lys Tyr Tyr Thr Ile Ser Phe Leu Asn Asp

420 425 430

Ala Ile Glu Ser Tyr Ser Lys Ser Gln Asp Glu Lys Arg Val Lys Ile

435 440 445

Arg Leu Glu Ala Tyr Phe Ala Glu Phe Lys Ser Lys Asp Asp Ala Lys

450 455 460

Lys Gln Phe Asp Leu Leu Glu Arg Ile Glu Glu Ala Tyr Ala Ile Val

465 470 475 480

Glu Pro Leu Leu Gly Ala Glu Tyr Pro Arg Asp Arg Asn Leu Lys Ala

485 490 495

Asp Lys Lys Glu Val Gly Lys Ile Lys Asp Phe Leu Asp Ser Ile Lys

500 505 510

Ser Leu Gln Phe Phe Leu Lys Pro Leu Leu Ser Ala Glu Ile Phe Asp

515 520 525

Glu Lys Asp Leu Gly Phe Tyr Asn Gln Leu Glu Gly Tyr Tyr Glu Glu

530 535 540

Ile Asp Ser Ile Gly His Leu Tyr Asn Lys Val Arg Asn Tyr Leu Thr

545 550 555 560

Gly Lys Ile Tyr Ser Lys Glu Lys Phe Lys Leu Asn Phe Glu Asn Ser

565 570 575

Thr Leu Leu Lys Gly Trp Asp Glu Asn Arg Glu Val Ala Asn Leu Cys

580 585 590

Val Ile Phe Arg Glu Asp Gln Lys Tyr Tyr Leu Gly Val Met Asp Lys
595 600 605

Glu Asn Asn Thr Ile Leu Ser Asp Ile Pro Lys Val Lys Pro Asn Glu

610 615 620

Leu Phe Tyr Glu Lys Met Val Tyr Lys Leu Ile Pro Thr Pro His Met
625 630 635 640

Gln Leu Pro Arg Ile Ile Phe Ser Ser Asp Asn Leu Ser Ile Tyr Asn
645 650 655

Pro Ser Lys Ser Ile Leu Lys Ile Arg Glu Ala Lys Ser Phe Lys Glu
660 665 670

Gly Lys Asn Phe Lys Leu Lys Asp Cys His Lys Phe Ile Asp Phe Tyr

675 680 685

Lys Glu Ser Ile Ser Lys Asn Glu Asp Trp Ser Arg Phe Asp Phe Lys
690 695 700

Phe Ser Lys Thr Ser Ser Tyr Glu Asn Ile Ser Glu Phe Tyr Arg Glu
705 710 715 720

Val Glu Arg Gln Gly Tyr Asn Leu Asp Phe Lys Lys Val Ser Lys Phe
725 730 735

Tyr Ile Asp Ser Leu Val Glu Asp Gly Lys Leu Tyr Leu Phe Gln Ile

740 745 750

Tyr Asn Lys Asp Phe Ser Ile Phe Ser Lys Gly Lys Pro Asn Leu His
755 760 765

Thr Ile Tyr Phe Arg Ser Leu Phe Ser Lys Glu Asn Leu Lys Asp Val
770 775 780

Cys Leu Lys Leu Asn Gly Glu Ala Glu Met Phe Phe Arg Lys Lys Ser
785 790 795 800

Ile Asn Tyr Asp Glu Lys Lys Lys Arg Glu Gly His His Pro Glu Leu

805 810 815

Phe Glu Lys Leu Lys Tyr Pro Ile Leu Lys Asp Lys Arg Tyr Ser Glu
820 825 830

Asp Lys Phe Gln Phe His Leu Pro Ile Ser Leu Asn Phe Lys Ser Lys

835 840 845

Glu Arg Leu Asn Phe Asn Leu Lys Val Asn Glu Phe Leu Lys Arg Asn

850 855 860

Lys Asp Ile Asn Ile Ile Gly Ile Asp Arg Gly Glu Arg Asn Leu Leu

865 870 875 880

Tyr Leu Val Met Ile Asn Gln Lys Gly Glu Ile Leu Lys Gln Thr Leu

885 890 895

Leu Asp Ser Met Gln Ser Gly Lys Gly Arg Pro Glu Ile Asn Tyr Lys

900 905 910

Glu Lys Leu Gln Glu Lys Glu Ile Glu Arg Asp Lys Ala Arg Lys Ser

915 920 925

Trp Gly Thr Val Glu Asn Ile Lys Glu Leu Lys Glu Gly Tyr Leu Ser

930 935 940

Ile Val Ile His Gln Ile Ser Lys Leu Met Val Glu Asn Asn Ala Ile

945 950 955 960

Val Val Leu Glu Asp Leu Asn Ile Gly Phe Lys Arg Gly Arg Gln Lys

965 970 975

Val Glu Arg Gln Val Tyr Gln Lys Phe Glu Lys Met Leu Ile Asp Lys

980 985 990

Leu Asn Phe Leu Val Phe Lys Glu Asn Lys Pro Thr Glu Pro Gly Gly

995 1000 1005

Val Leu Lys Ala Tyr Gln Leu Thr Asp Glu Phe Gln Ser Phe Glu

1010 1015 1020

Lys Leu Ser Lys Gln Thr Gly Phe Leu Phe Tyr Val Pro Ser Trp

1025 1030 1035

Asn Thr Ser Lys Ile Asp Pro Arg Thr Gly Phe Ile Asp Phe Leu

1040 1045 1050

His Pro Ala Tyr Glu Asn Ile Glu Lys Ala Lys Gln Trp Ile Asn

1055 1060 1065

Lys Phe Asp Ser Ile Arg Phe Asn Ser Lys Met Asp Trp Phe Glu

1070 1075 1080

Phe Thr Ala Asp Thr Arg Lys Phe Ser Glu Asn Leu Met Leu Gly

1085 1090 1095

Lys Asn Arg Val Trp Val Ile Cys Thr Thr Asn Val Glu Arg Tyr

1100 1105 1110

Phe Thr Ser Lys Thr Ala Asn Ser Ser Ile Gln Tyr Asn Ser Ile

1115 1120 1125

Gln Ile Thr Glu Lys Leu Lys Glu Leu Phe Val Asp Ile Pro Phe

1130 1135 1140

Ser Asn Gly Gln Asp Leu Lys Pro Glu Ile Leu Arg Lys Asn Asp

1145 1150 1155

Ala Val Phe Phe Lys Ser Leu Leu Phe Tyr Ile Lys Thr Thr Leu

1160 1165 1170

Ser Leu Arg Gln Asn Asn Gly Lys Lys Gly Glu Glu Glu Lys Asp

1175 1180 1185

Phe Ile Leu Ser Pro Val Val Asp Ser Lys Gly Arg Phe Phe Asn

1190 1195 1200

Ser Leu Glu Ala Ser Asp Asp Glu Pro Lys Asp Ala Asp Ala Asn

1205 1210 1215

Gly Ala Tyr His Ile Ala Leu Lys Gly Leu Met Asn Leu Leu Val

1220 1225 1230

Leu Asn Glu Thr Lys Glu Glu Asn Leu Ser Arg Pro Lys Trp Lys

1235 1240 1245

Ile Lys Asn Lys Asp Trp Leu Glu Phe Val Trp Glu Arg Asn Arg

1250 1255 1260

<210> 156

<211> 1193

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 156

Met Lys Arg Ile Ala Lys Phe Arg His Asp Lys Pro Val Lys Arg Glu

1 5 10 15

Ala Trp Ser Lys Gly Tyr Arg Val His Lys Asn Arg Ile Ile Asn Lys

20 25 30

Val Thr Arg Ser Ile Lys Tyr Pro Leu Val Val Lys Asp Glu Trp Lys

35 40 45

Lys Arg Leu Ile Asp Asp Ala Ala His Asp Tyr Arg Trp Leu Val Gly

50 55 60

Pro Ile Asn Tyr Ser Asp Trp Cys Arg Asp Pro Asn Gln Tyr Ser Ile

65 70 75 80

Leu Glu Phe Trp Ile Asp Phe Leu Cys Val Gly Gly Val Phe Gln Ser

85 90 95

Ser His Ser Asn Ile Cys Arg Leu Ala Ile Gln Leu Ser Gly Gly Ser

100 105 110

Val Phe Glu Gln Glu Trp Lys Asp Leu Ser Pro Phe Val Arg Ala Asn

115 120 125

Leu Ile Gln Gly Ile Lys Pro Ala Glu Phe Ile Gly Phe Leu Thr Ala

130 135 140

Glu Phe Arg Ser Ser Ser Asn Pro Lys Asn Phe Ile Ser Lys Phe Phe

145 150 155 160

Glu Gly Ser Asn Glu Asp Leu Glu Ser Leu Thr Asn Glu Phe Ala Ser

165 170 175

Ile Val Asp Phe Ile Lys Ala Lys Asp Ile Ser Leu Leu Arg Lys Ser

180 185 190

Leu Pro Ser Cys Lys Lys Ile Ala Pro Asn Leu Trp Glu Lys Ala Val

195 200 205

Gly Ser His Ser Thr Asn Glu Leu Leu Lys Leu Leu Thr Lys Tyr Thr

210 215 220

Arg Val Met Leu Val Ala Glu Pro Ser His Ser Asp Arg Val Phe Ser

225 230 235 240

Gln Thr Val Leu Gln Ser Asn Asp Gln Asp Asp Pro Glu Leu Thr Gly

245 250 255

Pro Leu Pro Ser His Lys Val Gly Lys Ala Ser Tyr Leu Phe Ile Pro
260 265 270
Glu Phe Ile Arg Glu Val Asn Leu Asp Lys Ile Ser Lys Leu Asp Leu

275 280 285
Ser Ala Lys Ser Lys Leu Ala Val Glu Gln Val Lys Lys Leu Ser Glu
290 295 300
Leu Thr Ser Asp Phe Lys Gln Ile Glu Asn Gln Ser Glu Ala Tyr Phe
305 310 315 320
Gly Leu Ser Thr Ser Phe Asn Glu Leu Ser Asn Phe Leu Gly Ile Leu
325 330 335
Ile Arg Thr Leu Arg Asn Ala Pro Glu Ala Ile Leu Lys Asp Gln Ile

340 345 350
Ala Leu Cys Ala Pro Leu Asp Lys Asp Ile Leu Lys Ile Thr Leu Asp
355 360 365
Trp Leu Cys Asp Arg Ala Gln Ala Leu Pro Glu Asn Pro Arg Phe Glu
370 375 380
Thr Asn Trp Ala Glu Tyr Arg Ser Tyr Leu Gly Gly Lys Ile Lys Ser
385 390 395 400
Trp Phe Ser Asn Tyr Glu Asn Phe Phe Glu Ile Pro Gln Ala Ala Ser

405 410 415
Ser Gln Gln Asn Asn Asn Arg Glu Lys Lys Leu Gly Asn Arg Ser Ala
420 425 430
Ile Arg Ala Leu Asn Leu Lys Lys Glu Ala Phe Glu Lys Ala Arg Glu
435 440 445
Thr Phe Lys Gly Asp Lys Gly Thr Leu Glu Lys Ile Asp Leu Ala Tyr
450 455 460
Arg Leu Leu Gly Ser Ile Ser Pro Glu Val Leu Gln Cys Asp Glu Gly

465 470 475 480
Leu Lys Leu Tyr Gln Gln Phe Asn Asp Glu Leu Leu Val Leu Asn Glu
485 490 495
Thr Ile Asn Gln Lys Phe Gln Asp Ala Lys Arg Asp Ile Lys Ala Lys

500 505 510

Lys Glu Lys Glu Ser Phe Glu Lys Leu Gln Arg Asn Leu Ser Ser Pro

515 520 525

Leu Pro Arg Ile Pro Glu Phe Phe Gly Glu Arg Ala Lys Lys Gly Tyr

530 535 540

Gln Lys Ala Arg Val Ser Pro Lys Leu Ala Arg His Leu Leu Glu Cys

545 550 555 560

Leu Asn Asp Trp Leu Ala Arg Phe Ala Lys Val Glu Glu Ser Ala Phe

565 570 575

Ser Glu Lys Glu Phe Gln Arg Ile Leu Asp Trp Leu Arg Thr Ser Asp

580 585 590

Phe Leu Pro Val Phe Ile Arg Lys Ser Lys Asp Pro Pro Ser Trp Leu

595 600 605

Arg Tyr Ile Ala Arg Val Ala Thr Gly Lys Tyr Tyr Phe Trp Val Ser

610 615 620

Glu Tyr Ser Arg Lys Arg Val Gln Ile Ile Asp Lys Pro Ile Ala Gln

625 630 635 640

Asn Pro Leu Lys Glu Leu Ile Ser Trp Phe Leu Leu Asn Lys Asp Ala

645 650 655

Phe Ser Arg Asp Asn Glu Leu Phe Lys Gly Leu Ser Ser Lys Met Val

660 665 670

Thr Leu Ala Arg Ile Met Ala Gly Ile Leu Arg Asp Arg Gly Glu Gly

675 680 685

Leu Lys Glu Leu Gln Ala Met Thr Ser Lys Leu Asp Asn Ile Gly Leu

690 695 700

Leu His Pro Ser Phe Ser Val Pro Val Thr Asp Ser Leu Lys Asp Ala

705 710 715 720

Ala Phe Tyr Arg Ala Phe Phe Ser Glu Leu Glu Gly Leu Leu Asn Ile

725 730 735

Gly Arg Ser Arg Leu Ile Ile Glu Arg Ile Thr Leu Gln Ser Gln Gln

740 745 750

Ser Lys Asn Lys Lys Thr Arg Arg Pro Leu Met Pro Glu Pro Phe Ile
755 760 765
Asn Glu Asp Lys Glu Val Phe Leu Ala Phe Pro Lys Phe Glu Thr Lys
770 775 780
Asn Lys Val Lys Gly Thr Arg Val Val Tyr Asn Ser Pro Asp Glu Val

785 790 795 800
Asn Trp Leu Leu Ser Pro Ile Arg Ser Ser Lys Gly Gln Leu Ser Phe
805 810 815
Met Phe Arg Cys Leu Ser Glu Asp Ala Lys Ile Met Thr Thr Ser Gly
820 825 830
Gly Cys Ser Tyr Ile Val Glu Phe Lys Lys Leu Leu Glu Ala Gln Glu
835 840 845
Glu Val Leu Ser Ile His Asp Cys Asp Ile Ile Pro Arg Ala Phe Val

850 855 860
Ser Ile Pro Phe Thr Leu Glu Arg Glu Ser Glu Glu Thr Lys Pro Asp
865 870 875 880
Trp Lys Pro Asn Arg Phe Met Gly Val Asp Ile Gly Glu Tyr Ala Val
885 890 895
Ala Tyr Cys Val Ile Glu Lys Gly Thr Asp Ser Ile Glu Ile Leu Asp
900 905 910
Cys Gly Ile Val Arg Asn Gly Ala His Arg Val Leu Lys Glu Lys Val

915 920 925
Asp Arg Leu Lys Arg Arg Gln Arg Ser Met Thr Phe Gly Ala Met Asp
930 935 940
Thr Ser Ile Ala Ala Ala Arg Glu Ser Leu Val Gly Asn Tyr Arg Asn
945 950 955 960
Arg Leu His Ala Ile Ala Leu Lys His Gly Ala Lys Leu Val Tyr Glu
965 970 975
Tyr Glu Val Ser Ala Phe Glu Ser Gly Gly Asn Arg Ile Lys Lys Val

980 985 990
Tyr Glu Thr Leu Lys Lys Ser Asp Cys Thr Gly Glu Thr Glu Ala Asp

995 1000 1005

Lys Asn Ala Arg Lys His Ile Trp Gly Glu Thr Asn Ala Val Gly

1010 1015 1020

Asp Gln Ile Gly Ala Gly Trp Thr Ser Gln Thr Cys Ala Lys Cys

1025 1030 1035

Gly Arg Ser Phe Gly Ala Asp Leu Lys Ala Gly Asn Phe Gly Val

1040 1045 1050

Ala Val Pro Val Pro Glu Lys Val Glu Asp Ser Lys Gly His Tyr

1055 1060 1065

Ala Tyr His Glu Phe Pro Phe Glu Asp Gly Leu Lys Val Arg Gly

1070 1075 1080

Phe Leu Lys Pro Asn Lys Ile Ile Ser Asp Gln Lys Glu Leu Ala

1085 1090 1095

Lys Ala Val His Ala Tyr Met Arg Pro Pro Leu Val Ala Leu Gly

1100 1105 1110

Lys Arg Lys Leu Pro Lys Asn Ala Arg Tyr Arg Arg Gly Asn Ser

1115 1120 1125

Ser Leu Phe Arg Cys Pro Phe Ser Asp Cys Gly Phe Thr Ala Asp

1130 1135 1140

Ala Asp Ile Gln Ala Ala Tyr Asn Ile Ala Val Lys Gln Leu Tyr

1145 1150 1155

Lys Pro Lys Lys Gly Tyr Pro Lys Glu Arg Lys Trp Gln Asp Phe

1160 1165 1170

Val Ile Leu Lys Pro Lys Glu Pro Ser Lys Leu Phe Asp Lys Gln

1175 1180 1185

Phe Tyr Arg Pro Asn

1190

<210> 157

<211> 1108

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 157

```
Met Ala Ile Arg Ser Ile Lys Leu Lys Leu Lys Thr His Thr Gly Pro
1               5                  10                  15

Glu Ala Gln Asn Leu Arg Lys Gly Ile Trp Arg Thr His Arg Leu Leu

            20                  25                  30

Asn Glu Gly Val Ala Tyr Tyr Met Lys Met Leu Leu Leu Phe Arg Gln
        35                  40                  45

Glu Ser Thr Gly Glu Arg Pro Lys Glu Glu Leu Gln Glu Glu Leu Ile
    50                  55                  60

Cys His Ile Arg Glu Gln Gln Gln Arg Asn Gln Ala Asp Lys Asn Thr
65                  70                  75                  80

Gln Ala Leu Pro Leu Asp Lys Ala Leu Glu Ala Leu Arg Gln Leu Tyr

                85                  90                  95

Glu Leu Leu Val Pro Ser Ser Val Gly Gln Ser Gly Asp Ala Gln Ile
            100                 105                 110

Ile Ser Arg Lys Phe Leu Ser Pro Leu Val Asp Pro Asn Ser Glu Gly
        115                 120                 125

Gly Lys Gly Thr Ser Lys Ala Gly Ala Lys Pro Thr Trp Gln Lys Lys
    130                 135                 140

Lys Glu Ala Asn Asp Pro Thr Trp Glu Gln Asp Tyr Glu Lys Trp Lys

145                 150                 155                 160

Lys Arg Arg Glu Glu Asp Pro Thr Ala Ser Val Ile Thr Thr Leu Glu
                165                 170                 175

Glu Tyr Gly Ile Arg Pro Ile Phe Pro Leu Tyr Thr Asn Thr Val Thr
            180                 185                 190

Asp Ile Ala Trp Leu Pro Leu Gln Ser Asn Gln Phe Val Arg Thr Trp
        195                 200                 205

Asp Arg Asp Met Leu Gln Gln Ala Ile Glu Arg Leu Leu Ser Trp Glu

    210                 215                 220

Ser Trp Asn Lys Arg Val Gln Glu Glu Tyr Ala Lys Leu Lys Glu Lys
```

225 230 235 240

Met Ala Gln Leu Asn Glu Gln Leu Glu Gly Gly Gln Glu Trp Ile Ser

245 250 255

Leu Leu Glu Gln Tyr Glu Glu Asn Arg Glu Arg Glu Leu Arg Glu Asn

260 265 270

Met Thr Ala Ala Asn Asp Lys Tyr Arg Ile Thr Lys Arg Gln Met Lys

275 280 285

Gly Trp Asn Glu Leu Tyr Glu Leu Trp Ser Thr Phe Pro Ala Ser Ala

290 295 300

Ser His Glu Gln Tyr Lys Glu Ala Leu Lys Arg Val Gln Gln Arg Leu

305 310 315 320

Arg Gly Arg Phe Gly Asp Ala His Phe Phe Gln Tyr Leu Met Glu Glu

325 330 335

Lys Asn Arg Leu Ile Trp Lys Gly Asn Pro Gln Arg Ile His Tyr Phe

340 345 350

Val Ala Arg Asn Glu Leu Thr Lys Arg Leu Glu Glu Ala Lys Gln Ser

355 360 365

Ala Thr Met Thr Leu Pro Asn Ala Arg Lys His Pro Leu Trp Val Arg

370 375 380

Phe Asp Ala Arg Gly Gly Asn Leu Gln Asp Tyr Tyr Leu Thr Ala Glu

385 390 395 400

Ala Asp Lys Pro Arg Ser Arg Arg Phe Val Thr Phe Ser Gln Leu Ile

405 410 415

Trp Pro Ser Glu Ser Gly Trp Met Glu Lys Lys Asp Val Glu Val Glu

420 425 430

Leu Ala Leu Ser Arg Gln Phe Tyr Gln Gln Val Lys Leu Leu Lys Asn

435 440 445

Asp Lys Gly Lys Gln Lys Ile Glu Phe Lys Asp Lys Gly Ser Gly Ser

450 455 460

Thr Phe Asn Gly His Leu Gly Gly Ala Lys Leu Gln Leu Glu Arg Gly

465 470 475 480

Asp Leu Glu Lys Glu Glu Lys Asn Phe Glu Asp Gly Glu Ile Gly Ser
485 490 495
Val Tyr Leu Asn Val Val Ile Asp Phe Glu Pro Leu Gln Glu Val Lys
500 505 510
Asn Gly Arg Val Gln Ala Pro Tyr Gly Gln Val Leu Gln Leu Ile Arg
515 520 525
Arg Pro Asn Glu Phe Pro Lys Val Thr Thr Tyr Lys Ser Glu Gln Leu

530 535 540
Val Glu Trp Ile Lys Ala Ser Pro Gln His Ser Ala Gly Val Glu Ser
545 550 555 560
Leu Ala Ser Gly Phe Arg Val Met Ser Ile Asp Leu Gly Leu Arg Ala
565 570 575
Ala Ala Ala Thr Ser Ile Phe Ser Val Glu Glu Ser Ser Asp Lys Asn
580 585 590
Ala Ala Asp Phe Ser Tyr Trp Ile Glu Gly Thr Pro Leu Val Ala Val

595 600 605
His Gln Arg Ser Tyr Met Leu Arg Leu Pro Gly Glu Gln Val Glu Lys
610 615 620
Gln Val Met Glu Lys Arg Asp Glu Arg Phe Gln Leu His Gln Arg Val
625 630 635 640
Lys Phe Gln Ile Arg Val Leu Ala Gln Ile Met Arg Met Ala Asn Lys
645 650 655
Gln Tyr Gly Asp Arg Trp Asp Glu Leu Asp Ser Leu Lys Gln Ala Val

660 665 670
Glu Gln Lys Lys Ser Pro Leu Asp Gln Thr Asp Arg Thr Phe Trp Glu
675 680 685
Gly Ile Val Cys Asp Leu Thr Lys Val Leu Pro Arg Asn Glu Ala Asp
690 695 700
Trp Glu Gln Ala Val Val Gln Ile His Arg Lys Ala Glu Glu Tyr Val
705 710 715 720
Gly Lys Ala Val Gln Ala Trp Arg Lys Arg Phe Ala Ala Asp Glu Arg

725 730 735

Lys Gly Ile Ala Gly Leu Ser Met Trp Asn Ile Glu Glu Leu Glu Gly

740 745 750

Leu Arg Lys Leu Leu Ile Ser Trp Ser Arg Arg Thr Arg Asn Pro Gln

755 760 765

Glu Val Asn Arg Phe Glu Arg Gly His Thr Ser His Gln Arg Leu Leu

770 775 780

Thr His Ile Gln Asn Val Lys Glu Asp Arg Leu Lys Gln Leu Ser His

785 790 795 800

Ala Ile Val Met Thr Ala Leu Gly Tyr Val Tyr Asp Glu Arg Lys Gln

805 810 815

Glu Trp Cys Ala Glu Tyr Pro Ala Cys Gln Val Ile Leu Phe Glu Asn

820 825 830

Leu Ser Gln Tyr Arg Ser Asn Leu Asp Arg Ser Thr Lys Glu Asn Ser

835 840 845

Thr Leu Met Lys Trp Ala His Arg Ser Ile Pro Lys Tyr Val His Met

850 855 860

Gln Ala Glu Pro Tyr Gly Ile Gln Ile Gly Asp Val Arg Ala Glu Tyr

865 870 875 880

Ser Ser Arg Phe Tyr Ala Lys Thr Gly Thr Pro Gly Ile Arg Cys Lys

885 890 895

Lys Val Arg Gly Gln Asp Leu Gln Gly Arg Arg Phe Glu Asn Leu Gln

900 905 910

Lys Arg Leu Val Asn Glu Gln Phe Leu Thr Glu Glu Gln Val Lys Gln

915 920 925

Leu Arg Pro Gly Asp Ile Val Pro Asp Asp Ser Gly Glu Leu Phe Met

930 935 940

Thr Leu Thr Asp Gly Ser Gly Ser Lys Glu Val Val Phe Leu Gln Ala

945 950 955 960

Asp Ile Asn Ala Ala His Asn Leu Gln Lys Arg Phe Trp Gln Arg Tyr

965 970 975

Asn Glu Leu Phe Lys Val Ser Cys Arg Val Ile Val Arg Asp Glu Glu

980 985 990

Glu Tyr Leu Val Pro Lys Thr Lys Ser Val Gln Ala Lys Leu Gly Lys

995 1000 1005

Gly Leu Phe Val Lys Lys Ser Asp Thr Ala Trp Lys Asp Val Tyr

1010 1015 1020

Val Trp Asp Ser Gln Ala Lys Leu Lys Gly Lys Thr Thr Phe Thr

1025 1030 1035

Glu Glu Ser Glu Ser Pro Glu Gln Leu Glu Asp Phe Gln Glu Ile

1040 1045 1050

Ile Glu Glu Ala Glu Glu Ala Lys Gly Thr Tyr Arg Thr Leu Phe

1055 1060 1065

Arg Asp Pro Ser Gly Val Phe Phe Pro Glu Ser Val Trp Tyr Pro

1070 1075 1080

Gln Lys Asp Phe Trp Gly Glu Val Lys Arg Lys Leu Tyr Gly Lys

1085 1090 1095

Leu Arg Glu Arg Phe Leu Thr Lys Ala Arg

1100 1105

<210> 158

<211> 1283

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 158

Met Thr His Ala Lys Lys Ile Pro Phe Pro Val Leu Lys Arg Ser Thr

1 5 10 15

Leu Arg Lys Ala Arg Gln Arg Ile Ala Ala Gly Ser Ile Thr Ala Gly

20 25 30

Glu Arg Pro Phe Asn Ser Thr Val Thr Arg Val Val Pro Val Lys Asp

35 40 45

Pro Val Ser Asp Gln Val Trp Ala Val Ala Arg Glu Ala Ala Met Thr
50 55 60
Leu Arg Gly Phe Gly Gln Gly Ser Leu Phe Asp Met Leu Ile His Leu
65 70 75 80
His Ala Asp Gly Phe Arg Leu Phe Pro Ser Gly Arg Glu Arg Glu Ala
85 90 95
Phe Phe Leu Lys Asp Leu Phe Asp Pro Thr Glu Phe Asp Asp Gly Ala
100 105 110

Arg Arg Ala Phe Gly Asp Val Met Pro Gly Phe Thr Ala Asn Ser Leu
115 120 125
Arg Glu Ile Leu Gly Ala Pro Ala Arg Lys Cys Gly Lys Val Thr Ser
130 135 140
Val Glu Ile Leu Leu Pro Arg Leu Ser Lys Gly Leu Gly Val Lys Lys
145 150 155 160
Ser Ala Ala Pro Pro Glu Val Leu Ser Ser Leu Ala Ala Ala Leu Cys
165 170 175

Glu Ala Phe Pro Thr Trp Ser Leu Leu Thr Ala Val Asp Gly Gly Val
180 185 190
Gly Lys Val Ile Asp Asp Val Leu Arg Thr His Gly Ser Arg Leu Pro
195 200 205
Ser Leu Glu Lys Ala Trp Ser Thr Asn Leu Pro Glu Val Pro Lys Gly
210 215 220
Leu Gly Val Pro Thr Leu Ala Phe Asp Asp Gln Ala Pro Ala Gln Ser
225 230 235 240

Glu Gln Thr Pro Thr Gly Arg Phe Ala Gly Val Val Ala Arg Tyr Leu
245 250 255
Ala Glu Thr Phe Ala Ser Asn Pro Glu Ala Thr Ala Gly Asp Ala Ser
260 265 270
Lys Ala Val Gln Ala Lys Val Thr Thr Pro Asn Gly Asn Ala Leu Ser
275 280 285
Trp Leu Phe Ala Val Gly Arg Arg Ala Met Cys Ser Thr Thr Leu Asp

290 295 300

Glu Leu Ala Ile Gly Leu Asn Ile Thr Ser Pro Arg Gly Arg His Ala
305 310 315 320
Leu Ser Ser Leu Lys Glu Arg Met Met Ala Leu Pro Ala Leu Ser Val
325 330 335
Leu Gly Glu Arg Ala Tyr Pro Asp Ser Arg Ala Thr Leu Gln Gly Thr
340 345 350
Val Asp Ser Leu Ile Ala Asn Tyr Val Asn Arg Leu Phe Glu Leu Ser
355 360 365

Ser Ser Ala Thr Ser Ile Ala Gln Thr Lys Leu Ile Leu Pro Ala Ala
370 375 380
Ile Gln Gly Asp Thr Ala Val Phe Asp Gly Met Pro Phe Ser Ala Glu
385 390 395 400
Asp Val Gly Ala Leu Phe Glu Gln Leu Pro Ser Glu Ile Ala Lys Leu
405 410 415
Glu His Ala Val Lys Val Leu Val Gly Lys Glu Arg Thr Ser Thr Leu
420 425 430

Gly Tyr Gln Lys Ala Val Asp Asp Val Asp Glu Phe Gly Val Trp Ala
435 440 445
Ser Ser Val Asp Ala Val Ile Gly Gln Ile Asn Ala Arg Leu Lys Thr
450 455 460
Leu Glu Arg Ala Gln Glu Pro Leu Gly Lys Leu Met Gly Asp Gly Lys
465 470 475 480
Leu Lys Arg Leu Val Asn Ile His Glu Pro Glu Gly Pro Ala Val Glu
485 490 495

Ile Ile Pro Val Leu Asp Gln Glu Leu Gln Asp Val Leu Thr Ser Cys
500 505 510
Arg Thr Ala Phe Ala Asp Leu Glu Ala Arg Tyr Pro Met Thr Val Ala
515 520 525
Lys Ala Gln Arg His Ala Glu Ala Glu Val Arg Asn Ala Leu Glu Leu
530 535 540

Ala Ser Arg Lys Glu Gly Gly Leu Ser Leu Ala Ser Ala Asp Val Pro
545 550 555 560

Ala Leu Ala Lys Arg Lys Ile Leu Glu Pro Ile Ile Ser Ile Ala Arg
565 570 575

Arg Ser Ser Pro Ala Met Ala Thr Ala Val Leu Thr Glu Cys Leu Arg
580 585 590

Gln Lys Leu Ile Val Lys Gly Thr Gly Ser Glu Arg Ser Leu Arg Gly
595 600 605

Tyr Val Leu Ser Gly Glu Gln Val Ile Tyr Ala His Pro Leu Ser Arg
610 615 620

Arg Arg Ser Ile Val Arg Leu Asp Arg Glu Gly Leu Gln Asn Phe Asp
625 630 635 640

Ala Leu Glu Phe Leu Asp Ala Leu Gln Lys Asp Ala Thr Gln Arg Thr
645 650 655

Asn Val Arg Glu Ser Leu Ile Val Glu Met Ala Arg Gln Ser Leu Leu
660 665 670

Leu Ser Ala Leu Pro Asp Arg Ile Glu Ile Gly Ala Ile Ser Trp Gln
675 680 685

Thr Pro Ser Gln Asn Gln His Ala Pro Trp Ala Asn Leu Arg Pro Val
690 695 700

Asn Gly Thr Val Gly Arg Ser Glu Thr Ile Lys Ser Phe Thr Ala Val
705 710 715 720

Phe His Ser Arg Ile Ser Gly Leu Leu Tyr Arg Leu Asn Arg Gln Lys
725 730 735

Phe Met Glu Lys Tyr Asp Leu Arg Cys Phe Ile Gly Ser Thr Leu Leu
740 745 750

Phe Ser Pro Lys Asn Ala Asp Trp Ala Pro Pro Pro Gln Tyr Arg His
755 760 765

Gly Arg Phe Ser Ala Leu Leu Ala Arg Ser Asp Phe Pro Trp Glu Gly
770 775 780

Ala Glu Gly Thr His Ala Asn Ala Val Arg Leu Ala Lys Phe Leu Ile

785 790 795 800

Asp Glu Thr Arg Asn Ala Thr Asp Leu Gln Gln Ala Ile Ala Ala Lys

805 810 815

Ala Leu Leu Ala Gln Leu Pro His Asp Trp Val Val Cys Cys Asp Phe

820 825 830

Asp Gly Ala Pro Ser Tyr Glu Gly Ala Phe Val Ser Ala Gly Glu Val

835 840 845

Ser Ala Trp Ala Lys Arg Ser Gly Tyr Leu Leu Thr Pro Pro Arg His

850 855 860

Phe Ala Gly Ala Phe Leu Glu Gly Phe Lys Ser Thr Lys Ile Ser Pro

865 870 875 880

His Gly Leu Thr Phe Glu Arg Met Leu Glu Arg Asp Gly Asp Ser Val

885 890 895

Ile Glu Thr Gly Arg Arg Val Thr Ala Ala Phe Pro Ile Thr Gln Glu

900 905 910

Val Ala Pro Ala Ala Gln Pro Trp Lys Pro Arg His Leu Ala Gly Leu

915 920 925

Asp Leu Gly Glu Ala Gly Leu Gly Val Cys Leu Lys Asn Leu Asp Asn

930 935 940

Gly His Glu Gln Thr Leu Leu Leu Lys Thr Arg Lys Thr Arg Leu Leu

945 950 955 960

Ala His Ser Ala Glu His Tyr Arg Arg Lys Asp Gln Pro Arg Gln Val

965 970 975

Phe Arg Lys Gln Tyr Asn Gln Ser Ser Glu Asn Ala Ile Lys Ala Ala

980 985 990

Ile Gly Glu Val Cys Gly Leu Ile Asp Asn Leu Ile Ala Arg Tyr Asp

995 1000 1005

Ala Val Pro Val Phe Glu Ser Gln Ala Ala Ala Ala Arg Gly Ser

1010 1015 1020

Asn Arg Met Val Ala Arg Val Tyr Ala Gly Val Leu Gln Arg Tyr

1025 1030 1035

Thr Tyr Val Val Gly Asn Gly Ala Ala Asp Ala Thr Arg Thr Ser
1040 1045 1050
His Trp Leu Gly Ala Asn Arg Trp Ser Tyr Ser Phe Gly Ala Asp
1055 1060 1065

Val Ile Pro Lys Val Arg Asp Leu Ser Pro Glu Val Leu Arg Ser
1070 1075 1080
Ile Lys Lys Pro Glu Asn Val Phe Arg Asp Ala Leu Gly Phe Pro
1085 1090 1095
Gly Val Leu Ala Asn Ala Trp Arg Thr Ser Met Ile Cys Ser Val
1100 1105 1110
Cys Gly Thr Asp Pro Ile Gly Ala Leu Glu Glu Ala Ile Ala Ala
1115 1120 1125

Asn Gln Ile Ser Phe Val Thr Asp Asn Glu Gly Glu Gly Ser Leu
1130 1135 1140
Asp Leu Gly Asp Gly Arg Lys Val Thr Leu Arg Val Glu Val Pro
1145 1150 1155
Thr Ser Ser Ala Leu Thr Lys Arg Glu Ala Ser Arg Arg Lys Arg
1160 1165 1170
Arg Ala Pro Trp Glu Ala Lys Val Gly Thr Val Trp Thr Leu Thr
1175 1180 1185

Arg Lys Ser His Arg Asp Asp Leu Leu Thr Thr Ile Arg Arg Ser
1190 1195 1200
Leu Arg Arg Pro Ser Ser Thr Phe Gln Gly Ser Thr Thr Lys Gln
1205 1210 1215
Trp Glu Phe His Cys Pro Cys Cys Gly Gln Ile Gln Gln Ala Asp
1220 1225 1230
Val Asn Ala Ala Ser Asn Leu Val Arg Arg Tyr Phe Val Arg Ala
1235 1240 1245

Ser Asp Asn Ala Arg Ala Arg Gln His Trp Ala Asp Asp Ser Lys
1250 1255 1260
Arg Leu Ala Phe Ile Ala Ser Met Gly Pro Asp Arg Ser Ala Arg

1265 1270 1275

Glu Glu Lys Val Ser

1280

<210> 159

<211> 1413

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 159

Met Asn Arg Ile Tyr Gln Gly Arg Val Thr Lys Val Glu Lys Leu Lys

1 5 10 15

Asn Gly Lys Ser Pro Asp Asp Arg Glu Glu Leu Lys Asp Trp Gln Thr

20 25 30

Ala Leu Trp Arg His His Glu Leu Phe Gln Asp Ala Val Ser Tyr Tyr

35 40 45

Thr Leu Ala Leu Ala Ala Met Ala Glu Gly Leu Pro Asp Lys His Pro

50 55 60

Ile Asn Val Leu Arg Lys Arg Met Glu Glu Ala Trp Glu Glu Phe Pro

65 70 75 80

Arg Lys Thr Val Thr Pro Ala Lys Asn Leu Arg Asp Ser Val Arg Pro

85 90 95

Trp Leu Gly Leu Ser Glu Ser Ala Ser Phe Gly Asp Ala Leu Lys Lys

100 105 110

Ile Leu Pro Pro Ala Pro Glu Asn Lys Glu Val Arg Ala Leu Ala Val

115 120 125

Ala Leu Leu Ala Glu Lys Ala Arg Thr Leu Lys Pro Gln Lys Thr Ser

130 135 140

Ala Ser Tyr Trp Gly Arg Phe Cys Asp Asp Leu Lys Lys Lys Pro Asn

145 150 155 160

Trp Asp Tyr Ser Glu Glu Glu Leu Ala Arg Lys Thr Gly Ser Gly Asp

165 170 175

Trp Val Ala Gly Leu Trp Ser Glu Asp Ala Leu Asn Lys Ile Asp Glu
180 185 190
Leu Ala Lys Ser Leu Lys Leu Ser Ser Leu Val Lys Cys Val Pro Asp
195 200 205

Gly Gln Ile Asn Pro Glu Gly Ala Arg Asn Leu Val Lys Glu Ala Leu
210 215 220
Asp His Leu Glu Gly Val Ser Asn Gly Thr Lys Lys Glu Lys Asn Asp
225 230 235 240
Pro Gly Pro Ala Lys Lys Thr Asn Asn Trp Leu Arg Gln His Ala Ser
245 250 255
Asp Val Arg Asn Phe Ile His Lys Asn Lys Asn Gln Phe Ser Ser Leu
260 265 270

Pro Asn Gly Arg Leu Ile Thr Glu Arg Ala Arg Gly Gly Gly Ile Asn
275 280 285
Ile Asn Lys Thr Tyr Ala Gly Val Leu Phe Lys Ala Phe Pro Cys Pro
290 295 300
Phe Thr Phe Asp Tyr Val Arg Ala Ala Val Pro Glu Pro Lys Val Lys
305 310 315 320
Lys Val Asp Gln Glu Lys Lys Ser Glu Gln Ser Ala Thr Trp Thr Glu
325 330 335

Leu Glu Lys Arg Ile Leu Arg Ile Gly Asp Asp Pro Ile Glu Leu Ala
340 345 350
Arg Lys Asn Asn Lys Pro Ile Phe Lys Ala Phe Thr Ala Leu Glu Lys
355 360 365
Trp Ser Asp Gln Asn Ser Lys Ser Cys Trp Ser Asp Phe Asp Lys Cys
370 375 380
Ala Phe Glu Glu Ala Leu Lys Thr Leu Asn Gln Phe Asn Gln Lys Thr
385 390 395 400

Glu Glu Arg Glu Lys Arg Arg Ser Glu Ala Glu Ala Glu Leu Lys Tyr
405 410 415
Met Met Asp Glu Asn Pro Glu Trp Lys Pro Lys Lys Glu Thr Glu Gly

420 425 430

Asp Asp Val Arg Glu Val Pro Ile Leu Lys Gly Asp Pro Arg Tyr Glu

435 440 445

Lys Leu Val Lys Leu Phe Gly Asp Leu Asp Glu Glu Gly Ser Glu His

450 455 460

Ala Thr Gly Lys Ile Tyr Gly Pro Ser Arg Ala Ser Leu Arg Gly Phe

465 470 475 480

Gly Lys Leu Arg Asn Glu Trp Val Asp Leu Phe Thr Lys Ala Asn Asp

485 490 495

Asn Pro Arg Glu Gln Asp Leu Gln Lys Ala Val Thr Gly Phe Gln Arg

500 505 510

Glu His Lys Leu Asp Met Gly Tyr Thr Ala Phe Phe Leu Lys Leu Cys

515 520 525

Glu Arg Asp Tyr Trp Asp Ile Trp Arg Asp Asp Thr Glu Val Glu Val

530 535 540

Lys Lys Ile Arg Glu Lys Arg Trp Val Lys Ser Val Val Tyr Ala Ala

545 550 555 560

Ala Asp Thr Arg Glu Leu Ala Glu Glu Leu Glu Arg Leu Gln Glu Pro

565 570 575

Val Arg Tyr Thr Pro Ala Glu Pro Gln Phe Ser Arg Arg Leu Phe Met

580 585 590

Phe Ser Asp Ile Lys Gly Lys Gln Gly Ala Lys His Ile Arg Glu Gly

595 600 605

Leu Val Glu Val Ser Leu Ala Val Lys Asp Gln Ser Gly Lys Tyr Gly

610 615 620

Thr Cys Arg Val Arg Leu His Tyr Ser Ala Pro Arg Leu Ile Arg Asp

625 630 635 640

His Leu Ser Asp Gly Ser Ser Ser Met Trp Leu Gln Pro Met Met Ala

645 650 655

Ala Leu Gly Leu Ser Ser Asp Ala Arg Gly Cys Phe Thr Arg Asp Ser

660 665 670

Lys Gly Asn Val Lys Glu Pro Ala Val Ala Leu Met Ser Asp Phe Val
675 680 685

Gly Arg Lys Arg Glu Leu Arg Met Leu Leu Asn Phe Pro Val Asp Leu
690 695 700

Asp Ile Ser Lys Leu Glu Glu Asn Ile Gly Lys Lys Ala Arg Trp Glu
705 710 715 720

Lys Gln Met Asn Thr Ala Tyr Glu Lys Asn Lys Leu Lys Gln Arg Phe
725 730 735

His Leu Ile Trp Pro Gly Met Glu Leu Lys Glu Thr Gln Glu Pro Gly
740 745 750

Gln Phe Trp Trp Asp Asn Pro Thr Ile Gln Lys Glu Gly Met Tyr Cys
755 760 765

Leu Ala Ile Asp Leu Ser Gln Arg Arg Ala Ala Asp Tyr Ala Leu Leu
770 775 780

His Ala Gly Val Asn Arg Asp Ser Lys Thr Phe Val Glu Leu Gly Gln
785 790 795 800

Ala Gly Gly Gln Ser Trp Phe Thr Lys Leu Cys Ala Ala Gly Ser Leu
805 810 815

Arg Leu Pro Gly Glu Asp Thr Glu Val Ile Arg Glu Gly Lys Arg Gln
820 825 830

Ile Glu Leu Ser Gly Lys Lys Gly Arg Asn Ala Thr Gln Ser Glu Tyr
835 840 845

Asp Gln Ala Ile Ala Leu Ala Lys Gln Leu Leu His Asn Glu Asn Ser
850 855 860

Ala Glu Leu Glu Ser Ala Ala Arg Asp Trp Leu Gly Asp Asn Ala Lys
865 870 875 880

Arg Phe Ser Phe Pro Glu Gln Asn Asp Lys Leu Ile Asp Leu Tyr Tyr
885 890 895

Gly Ala Leu Ser Arg Tyr Lys Thr Trp Leu Arg Trp Ser Trp Arg Leu
900 905 910

Thr Glu Gln His Lys Glu Leu Trp Asp Lys Thr Leu Asp Glu Ile Arg

915 920 925

Lys Val Pro Tyr Phe Ala Ser Trp Gly Glu Leu Ala Gly Asn Gly Thr

930 935 940

Asn Glu Ala Thr Val Gln Gln Leu Gln Lys Leu Ile Ala Asp Ala Ala

945 950 955 960

Val Asp Leu Arg Asn Phe Leu Glu Lys Ala Leu Leu His Ile Ala Tyr

965 970 975

Arg Ala Leu Pro Leu Arg Glu Asn Thr Trp Arg Trp Ile Glu Asn Gly

980 985 990

Lys Asp Gly Lys Gly Lys Pro Leu His Leu Leu Val Ser Asp Gly Gln

995 1000 1005

Ser Pro Ala Glu Ile Pro Trp Leu Arg Gly Gln Arg Gly Leu Ser

1010 1015 1020

Ile Ala Arg Ile Glu Gln Leu Glu Asn Phe Arg Arg Ala Val Leu

1025 1030 1035

Ser Leu Asn Arg Leu Leu Arg His Glu Ile Gly Thr Lys Pro Glu

1040 1045 1050

Phe Gly Ser Ser Thr Cys Gly Glu Ser Leu Pro Asp Pro Cys Pro

1055 1060 1065

Asp Leu Thr Asp Lys Ile Val Arg Leu Lys Glu Glu Arg Val Asn

1070 1075 1080

Gln Thr Ala His Leu Ile Ile Ala Gln Ser Leu Gly Val Arg Leu

1085 1090 1095

Lys Gly His Ser Leu Phe Thr Glu Glu Arg Glu Lys Ala Asp Met

1100 1105 1110

His Gly Glu His Glu Val Ile Pro Gly Arg Ser Pro Val Asp Phe

1115 1120 1125

Val Val Leu Glu Asp Leu Ser Arg Tyr Thr Thr Asp Lys Ser Arg

1130 1135 1140

Ser Arg Ser Glu Asn Ser Arg Leu Met Lys Trp Cys His Arg Lys

1145 1150 1155

Ile Asn Glu Lys Val Lys Leu Leu Ala Glu Pro Phe Gly Ile Pro
1160 1165 1170
Val Ile Glu Val Phe Ala Ser Tyr Ser Ser Lys Phe Asp Ala Arg
1175 1180 1185
Thr Gly Ala Pro Gly Phe Arg Ala Val Glu Val Thr Ser Glu Asp
1190 1195 1200
Arg Pro Phe Trp Arg Lys Thr Ile Glu Lys Gln Ser Val Ala Arg
1205 1210 1215

Glu Val Phe Asp Cys Leu Asp Asn Leu Val Gly Lys Gly Leu Asn
1220 1225 1230
Gly Ile His Leu Val Leu Pro Gln Asn Gly Gly Pro Leu Phe Ile
1235 1240 1245
Ala Ala Val Lys Glu Asp Gln Pro Leu Pro Ala Ile Arg Gln Ala
1250 1255 1260
Asp Ile Asn Ala Ala Val Asn Ile Gly Leu Arg Ala Ile Ala Gly
1265 1270 1275

Pro Ser Cys Tyr His Ala His Pro Lys Val Arg Leu Ile Lys Gly
1280 1285 1290
Glu Ser Gly Thr Asp Lys Gly Lys Trp Leu Pro Arg Lys Gly Lys
1295 1300 1305
Glu Ala Asn Lys Arg Glu Asn Ala Gln Phe Gly Asn Val Asp Leu
1310 1315 1320
Asp Leu Glu Val Lys Phe Asn Arg Leu Asp Ile Asp Ser Asp Val
1325 1330 1335

Leu Lys Gly Asp Asn Thr Asn Leu Phe His Asp Pro Leu Asn Ile
1340 1345 1350
Ala Cys Tyr Gly Phe Ala Thr Ile Gln Asn Leu Gln His Pro Phe
1355 1360 1365
Leu Ala His Ala Ser Ala Val Phe Ser Arg Gln Lys Gly Ala Val
1370 1375 1380
Ala Arg Leu Gln Trp Glu Val Cys Arg Ala Ile Asn Ser Arg Arg

1385 1390 1395

Leu Glu Ala Trp Gln Lys Lys Ala Glu Lys Ala Ala Val Lys Arg
1400 1405 1410

<210> 160

<211> 1408

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas12 sequence

<400> 160

Met Ser His Glu Leu Ala Glu Gln Pro Ser Pro Pro Lys Asn Lys Glu
1 5 10 15

Pro Thr Cys Glu Glu Ser Asp Ala Ile Arg Lys Asn Arg Arg Ile Leu
20 25 30

Leu Ala Leu Ser Trp Leu Ser Val Glu Asp Asp Cys Ser Ala Pro Thr
35 40 45

Gly Thr Phe Arg Val Ala Ser Gly Lys Asp Ser Glu Ala Glu Arg Lys
50 55 60

Asn Lys Val Leu Thr Ala Phe Arg Ser Ile Leu Thr Ala Arg Arg Met
65 70 75 80

Arg Ser Gln Asp Val Glu Ser Trp Ile Ala Asp Cys Ala Ala Ser Leu
85 90 95

Ser Ala Lys Ile Arg Glu Asp Ala Val Trp Ile Asn Arg Ser Ala Cys
100 105 110

Phe Asp Gln Arg Ala Leu Asp Leu Lys Val Leu Ser Arg Glu Tyr Ala
115 120 125

Lys Ala Ala Val Met Ser Phe Phe Gly Pro Leu Asp Glu Tyr Phe Lys
130 135 140

Leu Pro Asp Glu Ala Asp Asp Thr Lys Pro Ala Val Gly Gly Asp Gly
145 150 155 160

Pro Asp Phe Arg Thr Leu Ala Arg Gln Trp Val Ser Thr Asn Phe Gly

165 170 175

Thr Gly Lys Lys Ser Asp Ser Glu Ala Ile Ala Gln Asn Leu Arg Lys

180 185 190

Leu Ala Asp Ala Asn Leu Ala Pro Phe Ser Gly Lys Pro Lys Ala Ala

195 200 205

Leu Ile Ala His Leu Ser Val Glu Leu Asp Gly Ser Thr Ala Asp Ile

210 215 220

Asp Gly Leu Cys Arg Ala Ile Gly Trp Asn Thr Gly Arg Pro Ser Lys

225 230 235 240

Gly Arg Val Ala Ile Glu Arg Leu Pro Asp Pro Pro Thr Glu Thr Ser

245 250 255

Ile Gln Thr Met Gln Gln Lys Phe Arg Glu Glu Ala Glu Ala Lys Ala

260 265 270

Ser Ser Lys Gly Leu Arg Gln Val Pro Glu Trp Met Pro Ala Phe Gln

275 280 285

Lys Ser Ile Glu Arg Asp Cys Gly Met Pro Phe Lys Leu Gly Glu Gly

290 295 300

Arg Asp His Ile Gly Glu Phe Ser Val Met Leu Asp His Ala Ala Arg

305 310 315 320

Arg Val Ser Ile Gly His Ser Trp Ile Lys Arg Ala Glu Ala Glu Arg

325 330 335

Arg Arg Phe Glu Ala Asp Ala Gln Arg Leu Asn His Ile Pro Ala Ala

340 345 350

Ala Lys Asp Trp Leu Asp Gln Phe Val Gln Phe Arg Ser Gly Ser Ser

355 360 365

Gly Ala Ala Ala Ala Gly Gly Glu Tyr Arg Ile Arg Arg Arg Ala Ile

370 375 380

Glu Gly Trp Asp Glu Ile Ile Lys Arg Trp Lys Arg Ala Ala Cys Lys

385 390 395 400

Ser Pro Glu Asp Arg Val Ala Ala Ala Arg Glu Val Gln Ala Asp Pro

405 410 415

Glu Ile Glu Lys Phe Gly Asp Ile Gln Leu Phe Glu Ala Leu Ala Ala
420 425 430

Asp Asp Ala Glu Cys Val Trp Arg Gly Asp Gly Asn Gly Thr Pro Asp
435 440 445

Pro Leu Lys Asp Tyr Val Ala Ala Thr Asp Ala Leu Asp Lys Met Arg
450 455 460

Arg Phe Lys Val Pro Ala Tyr Arg His Pro Asp Pro Leu Ala His Pro
465 470 475 480

Val Phe Gly Asp Phe Gly Asn Ser Arg Gly Asp Ile Arg Phe Ala Val
485 490 495

His Glu Ala Ala Lys Ala Thr Arg Gly Thr Lys Arg Ile Ala Lys Asp
500 505 510

Gln Lys Glu Trp Ile Arg Glu Arg His Gly Leu Arg Met Gly Leu Trp
515 520 525

Asp Gly Gln Ser Val Arg Thr Ala Asp Leu Arg Trp Ser Ser Lys Arg
530 535 540

Leu Val Asp Asp Leu Ala Leu Arg Asn His Val Thr Thr Arg Arg Thr
545 550 555 560

Gly Pro Val Ser Arg Ala Asp Arg Leu Gly Arg Ala Ala Ala Gly Leu
565 570 575

Gly Ala Asp Glu Ala Ala Cys Val Ala Gly Leu Phe Glu Leu Pro Asp
580 585 590

Trp Asn Gly Arg Leu Gln Ala Pro Arg Ala Gln Leu Asp Ala Ile Ala
595 600 605

Ala Cys Val Ala Ala Asn Gly Gly Lys Trp Asp Asp Lys Ala Arg Lys
610 615 620

Leu Arg Asp Arg Ile Glu Trp Leu Val Ser Phe Ser Ala Lys Leu Glu
625 630 635 640

Cys Cys Gly Pro Phe Met Glu Tyr Ala Ser Gln Asn Gly Ile Gln Pro
645 650 655

Asn Gly Lys Gly Glu Tyr Tyr Pro His Ala Glu Arg Asn Lys Gly Arg

660 665 670

Thr Gly His Ala Lys Leu Ile Leu Ser Arg Leu Pro Gly Leu Arg Val
675 680 685
Leu Ala Val Asp Leu Gly His Arg Phe Ala Ala Ala Cys Ala Val Trp
690 695 700
Glu Ala Leu Ser Lys Ile Ala Phe Asp Ala Glu Thr Lys Gly Arg Glu
705 710 715 720
Val Val Ser Gly Gly Arg Ala Ala Asp Asp Leu Tyr Cys His Thr Arg
725 730 735

His Leu Asp Cys Ala Gly Lys Ala Arg Thr Thr Ile Tyr Arg Arg Ile
740 745 750
Gly Pro Asp Lys Leu Pro Asp Gly Ser Asp His Pro Ala Pro Trp Ala
755 760 765
Arg Leu Asp Arg Gln Phe Leu Ile Lys Leu Gln Gly Glu Glu Arg Pro
770 775 780
Ala Arg Ala Ala Gly Pro Ala Glu Thr Ala Ala Val Gln Gln Ile Glu
785 790 795 800

Thr Asp Leu Gly Arg Ala Arg Gly Gln Glu Asp Leu Pro Pro Arg Pro
805 810 815
Val Asp Ser Leu Met Arg Glu Ala Val Arg Thr Ile Arg Ile Ala Leu
820 825 830
Arg Arg His Gly Asp Ala Ala Arg Ile Ala Tyr Ala Phe Lys Pro Gly
835 840 845
Ala Lys Arg Leu Lys Pro Gly Gly Gly Ala Gln Asp His Thr Pro Glu
850 855 860

Thr His Ala Asp Ala Ile Leu Glu Ala Leu Leu Arg Trp His Glu Leu
865 870 875 880
Ala Thr Gly Ala Arg Trp Arg Asp Pro Trp Ala Glu Thr Gln Trp Lys
885 890 895
Asp Trp Val Gln Pro His Ile Ser Ala Thr Leu Pro Glu Leu Ala Asn
900 905 910

Asp Ala Asp Arg Trp Glu Arg Lys Arg His Arg Ala Ala Leu Glu Gln
915 920 925

Val Leu Arg Pro Val Ala Gln Met Leu Ile Gln Arg Pro Thr Asp Ala
930 935 940
Leu His Gln Val Trp Ser Lys His Trp Ala Asp Glu Asp Leu Lys Trp
945 950 955 960
Pro Ser Arg Leu Arg Trp Leu Arg Asn Trp Leu Leu Pro Arg Gly Pro
965 970 975
Arg Ala Arg Ser Gly Ala Ala Arg Asn Val Gly Gly Leu Ser Leu Leu
980 985 990

Arg Ile Ala Thr Leu Arg Glu Leu Tyr Gln Thr Gln Lys Ala Tyr Ala
995 1000 1005
Met Arg Pro Glu Pro Asp Asp Pro Arg Lys Arg Ile Ala Gly Arg
1010 1015 1020
Asn Asp Asp Arg Tyr Asp Glu Leu Gly Arg Ser Val Leu Gln Val
1025 1030 1035
Ile Glu Arg Leu Arg Glu Gln Arg Val Lys Gln Leu Ala Ser Arg
1040 1045 1050

Ile Val Glu Ala Ala Leu Gly Val Gly Arg Ala Lys Pro Thr Arg
1055 1060 1065
Gly Arg Gln Arg Pro Gln Ser Arg Val Asp Val Pro Cys His Ala
1070 1075 1080
Val Ile Ile Glu Ser Leu Arg Asn Tyr Arg Pro Asp Glu Leu Gln
1085 1090 1095
Thr Arg Arg Glu Asn Arg Ala Ile Met Asn Trp Ser Ala Gly Lys
1100 1105 1110

Val Arg Lys Tyr Leu Glu Glu Ala Cys Gln Leu His Gly Leu His
1115 1120 1125
Leu Arg Glu Val Met Pro Asn Tyr Thr Ser Arg Glu Asp Ser Arg
1130 1135 1140
Thr Gly Leu Pro Gly Val Arg Cys Val Asp Val Pro Val Asp Pro

1145 1150 1155

Lys Leu Gly Lys Pro Lys Ala Tyr Trp Trp Asn Ser Val Leu Ser

1160 1165 1170

Thr Ala Arg Lys Lys Ser Ile Gly Asp Ala Ala Ser His Asp Lys

1175 1180 1185

Gln Gly Asp Ala Thr Ser Arg Phe Ile Val Glu Leu Ala Gly Cys

1190 1195 1200

Leu Asp Arg Leu Lys Ala Asp Gly Lys Pro Leu Pro Lys Thr Val

1205 1210 1215

Arg Val Pro Arg Ile Gly Gly Asp Leu Phe Val Ala Ala Pro Pro

1220 1225 1230

Thr Ser Cys Thr Ala Pro Ala His Gln Pro His Pro Ala Cys Asp

1235 1240 1245

Gly Ala Arg Ala Leu Gln Ala Asp Leu Asn Ala Ala Ala Asn Ile

1250 1255 1260

Gly Leu Arg Ala Leu Leu Asp Pro Asp Phe Pro Ala Lys Trp Trp

1265 1270 1275

Tyr Val Pro Cys Ile Asp Asp Gln Arg Gly Leu Ala Leu Pro Arg

1280 1285 1290

Ala Asp Lys Val Leu Gly Ser Ala Cys Phe Pro Gly Asp Pro Ala

1295 1300 1305

Thr Phe Gly Ser Leu Leu Lys Thr Arg Thr Ala Ala Gly Pro Ala

1310 1315 1320

Val Asp Gly Gln Ala Ala Pro Asp Arg Lys Pro Arg Thr Gly Thr

1325 1330 1335

His Arg Pro Gly Ser Ala Lys Ser Arg Ser Leu Gly Asp Gly Lys

1340 1345 1350

Ala Thr Thr Asn Tyr Trp Ser Asp Arg Ser Ala Arg Asp Leu Arg

1355 1360 1365

Pro Ala Asp Glu Gly Gly His Trp Gln Pro Thr Asn Val Tyr Trp

1370 1375 1380

Asn Trp Val Arg Lys Arg Ala Leu Leu Gly Leu Tyr Ser Phe Asn

1385 1390 1395

Gly Leu Ser Pro Pro Ser Asp Asp Arg Pro

1400 1405

<210> 161

<211> 1108

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 161

Met Ala Ile Arg Ser Ile Lys Leu Lys Leu Lys Thr Asn Thr Gly Pro

1 5 10 15

Glu Ala Gln Asn Leu Arg Lys Gly Ile Trp Arg Thr His Arg Leu Leu

20 25 30

Asn Glu Gly Val Ala Tyr Tyr Met Asn Met Leu Leu Leu Phe Arg Gln

35 40 45

Glu Ser Thr Asp Lys Lys Thr Lys Gln Glu Ile His Glu Glu Leu Ile

50 55 60

Arg His Ile Arg Ala Gln Gln Gln Arg Asn His Ala Asp Glu Lys Thr

65 70 75 80

Gln Ala Leu Pro Leu Glu Lys Ala Leu Glu Ala Leu Arg Lys Leu Tyr

85 90 95

Glu Leu Leu Val Pro Ser Ser Val Gly Gln Ser Gly Asp Ser Gln Ile

100 105 110

Ile Ser Arg Lys Phe Leu Ser Pro Leu Val Asp Pro Asn Ser Glu Gly

115 120 125

Gly Lys Gly Thr Ser Lys Ala Gly Ala Lys Pro Ala Trp Gln Lys Lys

130 135 140

Lys Glu Ala Asn Asp Pro Thr Trp Lys Gln Asp Tyr Glu Lys Trp Lys

145 150 155 160

Lys Arg Arg Glu Glu Asp Pro Thr Ala Ser Val Ile Thr Thr Leu Glu

165 170 175

Glu Tyr Gly Ile Arg Pro Leu Phe Pro Leu Tyr Thr Asn Thr Val Ala

180 185 190

Glu Ile Ala Trp Leu Pro Leu Lys Ser Gly Gln Phe Val Arg Thr Trp

195 200 205

Asp Arg Asp Met Phe Gln Gln Ala Ile Glu Gly Met Leu Ser Trp Glu

210 215 220

Ser Trp Asn Arg Arg Val Gln Glu Glu Tyr Ala Lys Leu Glu Gly Lys

225 230 235 240

Met Ala Gln Leu Asn Glu Gln Leu Glu Gly Gly Glu Glu Trp Ile Arg

245 250 255

Leu Leu Glu Gln Tyr Glu Glu Lys Arg Glu Gln Glu Leu Arg Glu Asn

260 265 270

Met Thr Ala Ala Asn Asp Lys Phe Arg Ile Thr Lys Arg Gln Met Lys

275 280 285

Gly Trp Lys Glu Leu Tyr Glu Val Trp Ser Thr Phe Leu Pro Ser Ala

290 295 300

Ser Gln Glu Gln Tyr Lys Glu Ala Ile Lys Arg Val Gln Gln Arg Leu

305 310 315 320

Arg Gly Lys Phe Gly Asp Phe His Phe Phe Gln Tyr Leu Ser Glu Glu

325 330 335

Glu Asn Arg Leu Ile Trp Lys Gly Asn Pro Gln Arg Ile His Tyr Phe

340 345 350

Val Ala Arg Asn Glu Leu Thr Lys Lys Leu Glu Lys Ala Lys Gln Ser

355 360 365

Ala Arg Arg Thr Leu Pro Asp Ala Asn Lys His Pro Leu Trp Val Arg

370 375 380

Tyr Asp Ala Arg Gly Gly Asn Leu Gln Asp Tyr Tyr Leu Thr Ala Glu

385 390 395 400

Ser Asp Lys Pro Arg Ser Arg Arg Phe Val Thr Phe Ser Gln Leu Ile

405 410 415

Trp Pro Ser Glu Ser Gly Trp Leu Glu Lys Lys Asp Val Gln Ala Glu
420 425 430
Leu Ala Leu Ser Arg Gln Phe Tyr Gln Gln Val Thr Phe Leu Lys Asn

435 440 445
Asp Lys Gly Lys Gln Glu Ile Glu Phe Lys Asp Lys Gly Ser Gly Thr
450 455 460
Thr Phe Ser Gly His Leu Gly Gly Ala Lys Leu Gln Leu Glu Arg Ser
465 470 475 480
Val Leu Glu Asn Lys Glu Arg Lys Phe Glu Glu Gly Glu Ile Gly Lys
485 490 495
Ala Tyr Leu Asn Val Ala Ile Asp Phe Lys Pro Leu Gln Glu Val Lys

500 505 510
Asn Gly Arg Val Gln Ala Pro Tyr Gly Gln Val Leu Gln Leu Ile Arg
515 520 525
Leu Pro Asn Ala Phe Pro Lys Val Arg Thr Tyr Lys Ser Glu Glu Leu
530 535 540
Val Glu Trp Ile Lys Ala Ser Pro Gln His Leu Ser Gly Val Glu Ser
545 550 555 560
Leu Ala Ser Gly Phe Arg Val Met Ser Ile Asp Leu Gly Leu Arg Ala

565 570 575
Ala Ala Ala Thr Ser Ile Phe Ser Val Glu Glu Ser Ser Asp Lys Asn
580 585 590
Ala Thr Lys Leu Ala Tyr Trp Ile Glu Gly Thr Pro Leu Val Ala Val
595 600 605
His Gln Arg Ser Tyr Met Leu Arg Leu Pro Gly Glu Gln Val Glu Gln
610 615 620
His Val Trp Glu Lys Arg Asp Glu Arg Gly Asp Gln His Lys Arg Val

625 630 635 640
Arg Phe Gln Ile Arg Arg Leu Ala Glu Ile Ile Arg Leu Ala Asn Lys
645 650 655
Gln Tyr Gly Asp Arg Trp Asp Glu Leu Asn Arg Leu Asp Glu Ala Val

660 665 670

Ser Lys Glu Lys Ser Pro Leu Asp Gln Ala Asp Arg Thr Phe Trp Glu

675 680 685

Gly Ile Val Ser Asp Leu Thr Thr Ala Leu Pro Leu Asn Asp Ala Asp

690 695 700

Trp Thr Glu Ala Val Val Gln Ile His Arg Lys Ala Glu Leu Tyr Val

705 710 715 720

Gly Lys Val Val Gln Ala Trp Arg Lys Arg Phe Asn Ala Asp Glu Arg

725 730 735

Lys Gly Ile Ala Gly Leu Ser Met Trp Ser Ile Glu Glu Leu Asp Gly

740 745 750

Leu Arg Lys Leu Leu Ile Ser Trp Ser Arg Arg Thr Arg Asn Pro Gln

755 760 765

Glu Val Asn Arg Phe Glu Pro Glu His Thr Gly His Lys Arg Leu Leu

770 775 780

Thr His Ile Gln Asn Val Lys Lys Asp Arg Leu Lys Gln Val Ser His

785 790 795 800

Ala Ile Val Met Thr Ala Leu Gly Tyr Ile Tyr Asp Glu Lys Lys Gln

805 810 815

Lys Trp Cys Ala Lys Tyr Pro Ala Cys Gln Val Ile Leu Phe Glu Asn

820 825 830

Leu Ser Gln Tyr Arg Ser Asn Leu Asp Arg Ser Ala Lys Glu Asn Ser

835 840 845

Thr Leu Met Lys Trp Ala His Arg Ser Ile Pro Lys Tyr Val His Met

850 855 860

Gln Ala Glu Pro Tyr Gly Ile Gln Ile Gly Asp Val Arg Ala Glu Tyr

865 870 875 880

Ser Ser Arg Tyr Tyr Ala Lys Thr Gly Thr Pro Gly Ile Arg Cys Lys

885 890 895

Lys Leu Arg Glu His Asp Val Lys Gly Trp Arg Leu Asp His Leu Lys

900 905 910

Lys Arg Leu Val Asn Glu Gln Phe Leu Thr Glu Ala Gln Val Glu Gln

915 920 925

Leu Lys Ala Gly Asp Ile Ile Pro Asp Asp Ser Gly Glu Leu Phe Met

930 935 940

Thr Met Thr Asp Gly Ser Gly Gly Lys Glu Ile Val Phe Leu Gln Ala

945 950 955 960

Asp Ile Asn Ala Ala Gln Asn Leu Gln Lys Arg Phe Trp Gln Arg Asn

965 970 975

Ser Glu Leu Phe Lys Val Ser Cys Arg Val Ile Val Arg Asp Glu Ala

980 985 990

Glu Tyr Leu Val Pro Gln Ala Lys Lys Val Gln Glu Lys Leu Gly Lys

995 1000 1005

Gly Val Phe Val Lys Lys Ser Asp Thr Ala Trp Lys Glu Val Tyr

1010 1015 1020

Val Trp Asp Ser Gln Ala Lys Leu Lys Gly Lys Thr Thr Phe Thr

1025 1030 1035

Glu Glu Ser Glu Ser Pro Glu Gln Leu Glu Asp Leu Gln Glu Met

1040 1045 1050

Ile Glu Glu Ala Glu Glu Ala Lys Gly Thr Tyr Arg Thr Leu Phe

1055 1060 1065

Arg Asp Pro Ser Gly Val Phe Phe Pro Asp Phe Val Trp Asn Thr

1070 1075 1080

Pro Lys Asp Phe Trp Gly Glu Val Lys Arg Lys Leu Tyr Gly Lys

1085 1090 1095

Leu Arg Glu Arg Leu Leu Thr Lys Val Arg

1100 1105

<210> 162

<211> 1364

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 162

Met Asn Arg Ile Tyr Gln Gly Arg Val Thr Lys Val Glu Val Pro Asp
1 5 10 15

Gly Lys Asp Glu Lys Gly Asn Ile Lys Trp Lys Lys Leu Glu Asn Trp
20 25 30

Ser Asp Ile Leu Trp Gln His His Met Leu Phe Gln Asp Ala Val Asn
35 40 45

Tyr Tyr Thr Leu Ala Leu Ala Ala Ile Ser Gly Ser Ala Val Gly Ser
50 55 60

Asp Glu Lys Ser Ile Ile Leu Arg Glu Trp Ala Val Gln Val Gln Asn
65 70 75 80

Ile Trp Glu Lys Ala Lys Lys Lys Ala Thr Val Phe Glu Gly Pro Gln
85 90 95

Lys Arg Leu Thr Ser Ile Leu Gly Leu Glu Gln Asn Ala Ser Phe Asp
100 105 110

Ile Ala Ala Lys His Ile Leu Arg Thr Ser Glu Ala Lys Pro Glu Gln
115 120 125

Arg Ala Ser Ala Leu Ile Arg Leu Leu Glu Glu Ile Asp Lys Lys Asn
130 135 140

His Asn Val Val Cys Gly Glu Arg Leu Pro Phe Phe Cys Pro Arg Asn
145 150 155 160

Ile Gln Ser Lys Arg Ser Pro Thr Ser Lys Ala Val Ser Ser Val Gln
165 170 175

Glu Gln Lys Arg Gln Glu Glu Val Arg Arg Phe His Asn Met Gln Pro
180 185 190

Glu Glu Val Val Lys Asn Ala Val Thr Leu Asp Ile Ser Leu Phe Lys
195 200 205

Ser Ser Pro Lys Ile Val Phe Leu Glu Asp Pro Lys Lys Ala Arg Ala
210 215 220

Glu Leu Leu Lys Gln Phe Asp Asn Ala Cys Lys Lys His Lys Glu Leu
225 230 235 240

Val Gly Ile Lys Lys Ala Phe Thr Glu Ser Ile Asp Lys His Gly Ser
245 250 255
Ser Leu Lys Val Pro Ala Pro Gly Ser Lys Pro Ser Gly Leu Tyr Pro
260 265 270

Ser Ala Ile Val Phe Lys Tyr Phe Pro Val Asp Ile Thr Lys Thr Val
275 280 285
Phe Leu Lys Ala Thr Glu Lys Leu Ala Met Gly Lys Asp Arg Glu Val
290 295 300
Thr Asn Asp Pro Ile Ala Asp Ala Arg Val Asn Asp Lys Pro His Phe
305 310 315 320
Asp Tyr Phe Thr Asn Ile Ala Leu Ile Arg Glu Lys Glu Lys Asn Arg
325 330 335

Ala Ala Trp Phe Glu Phe Asp Leu Ala Ala Phe Ile Glu Ala Ile Met
340 345 350
Ser Pro His Arg Phe Tyr Gln Asp Thr Gln Lys Arg Lys Glu Ala Ala
355 360 365
Arg Lys Leu Glu Glu Lys Ile Lys Ala Ile Glu Gly Lys Gly Gly Gln
370 375 380
Phe Lys Glu Ser Asp Ser Glu Asp Asp Asp Val Asp Ser Leu Pro Gly
385 390 395 400

Phe Glu Gly Asp Thr Arg Ile Asp Leu Leu Arg Lys Leu Val Thr Asp
405 410 415
Thr Leu Gly Trp Leu Gly Glu Ser Glu Thr Pro Asp Asn Asn Glu Gly
420 425 430
Lys Lys Thr Glu Tyr Ser Ile Ser Glu Arg Thr Leu Arg Ile Phe Pro
435 440 445
Asp Ile Gln Lys Gln Trp Ser Glu Leu Ala Glu Lys Gly Glu Thr Thr
450 455 460

Glu Gly Lys Leu Leu Glu Val Leu Lys His Glu Gln Thr Glu His Gln
465 470 475 480
Ser Asp Phe Gly Ser Ala Thr Leu Tyr Gln His Leu Ala Lys Pro Glu

485 490 495

Phe His Pro Ile Trp Leu Lys Ser Gly Thr Glu Glu Trp His Ala Glu

500 505 510

Asn Pro Leu Lys Ala Trp Leu Asn Tyr Lys Glu Leu Gln Tyr Glu Leu

515 520 525

Thr Asp Lys Lys Arg Pro Ile His Phe Thr Pro Ala His Pro Val Tyr

530 535 540

Ser Pro Arg Tyr Phe Asp Phe Pro Lys Lys Ser Glu Thr Glu Glu Lys

545 550 555 560

Glu Val Ser Lys Asn Thr His Ser Leu Thr Thr Ser Leu Ala Ser Glu

565 570 575

His Ile Lys Asn Ser Leu Gln Phe Thr Ala Gly Leu Ile Arg Lys Thr

580 585 590

Asn Val Gly Lys Lys Ala Ile Lys Ala Arg Phe Ser Tyr Ser Ala Pro

595 600 605

Arg Leu Arg Arg Asp Cys Leu Arg Ser Glu Asn Asn Glu Asn Leu Tyr

610 615 620

Lys Ala Pro Trp Leu Gln Pro Met Met Arg Ala Leu Gly Ile Asp Glu

625 630 635 640

Glu Lys Ala Asp Arg Gln Asn Phe Ala Asn Thr Arg Ile Thr Leu Met

645 650 655

Ala Lys Gly Leu Asp Asp Ile Gln Leu Gly Phe Pro Val Glu Ala Asn

660 665 670

Ser Gln Glu Leu Gln Lys Glu Val Ser Asn Gly Ile Ser Trp Lys Gly

675 680 685

Gln Phe Asn Trp Gly Gly Ile Ala Ser Leu Ser Ala Leu Arg Trp Pro

690 695 700

His Glu Lys Lys Pro Lys Asn Pro Pro Glu Gln Pro Trp Trp Gly Ile

705 710 715 720

Asp Ser Phe Ser Cys Leu Ala Val Asp Leu Gly Gln Arg Tyr Ala Gly

725 730 735

Ala Phe Ala Arg Leu Asp Val Ser Thr Ile Glu Lys Lys Gly Lys Ser
740 745 750

Arg Phe Ile Gly Glu Ala Cys Asp Lys Lys Trp Tyr Ala Lys Val Ser
755 760 765

Arg Met Gly Leu Leu Arg Leu Pro Gly Glu Asp Val Lys Val Trp Arg
770 775 780

Asp Ala Ser Lys Ile Asp Lys Glu Asn Gly Phe Ala Phe Arg Lys Glu
785 790 795 800

Leu Phe Gly Glu Lys Gly Arg Ser Ala Thr Pro Leu Glu Ala Glu Glu
805 810 815

Thr Ala Glu Leu Ile Lys Leu Phe Gly Ala Asn Glu Lys Asp Val Met
820 825 830

Pro Asp Asn Trp Ser Lys Glu Leu Ser Phe Pro Glu Gln Asn Asp Lys
835 840 845

Leu Leu Ile Val Ala Arg Arg Ala Gln Ala Ala Val Ser Arg Leu His
850 855 860

Arg Trp Ala Trp Phe Phe Asp Glu Ala Lys Arg Ser Asp Asp Ala Ile
865 870 875 880

Arg Glu Ile Leu Glu Ser Asp Asp Thr Asp Leu Lys Gln Lys Val Asn
885 890 895

Lys Asn Glu Ile Glu Lys Val Lys Glu Thr Ile Ile Ser Leu Leu Lys
900 905 910

Val Lys Gln Glu Leu Leu Pro Thr Leu Leu Thr Arg Leu Ala Asn Arg
915 920 925

Val Leu Pro Leu Arg Gly Arg Ser Trp Glu Trp Lys Lys His His Gln
930 935 940

Lys Asn Asp Gly Phe Ile Leu Asp Gln Thr Gly Lys Ala Met Pro Asn
945 950 955 960

Val Leu Ile Arg Gly Gln Arg Gly Leu Ser Met Asp Arg Ile Glu Gln
965 970 975

Ile Thr Glu Leu Arg Lys Arg Phe Gln Ala Leu Asn Gln Ser Leu Arg

980 985 990

Arg Gln Ile Gly Lys Lys Ala Pro Ala Lys Arg Asp Asp Ser Ile Pro

995 1000 1005

Asp Cys Cys Pro Asp Leu Leu Glu Lys Leu Asp His Met Lys Glu

1010 1015 1020

Gln Arg Val Asn Gln Thr Ala His Met Ile Leu Ala Glu Ala Leu

1025 1030 1035

Gly Leu Lys Leu Ala Glu Pro Pro Lys Asp Lys Lys Glu Leu Asn

1040 1045 1050

Glu Thr Cys Asp Met His Gly Ala Tyr Ala Lys Val Asp Asn Pro

1055 1060 1065

Val Ser Phe Ile Val Ile Glu Asp Leu Ser Arg Tyr Arg Ser Ser

1070 1075 1080

Gln Gly Arg Ser Pro Arg Glu Asn Ser Arg Leu Met Lys Trp Cys

1085 1090 1095

His Arg Ala Val Arg Asp Lys Leu Lys Glu Met Cys Glu Val Phe

1100 1105 1110

Phe Pro Leu Cys Glu Arg Arg Lys Ala Gly Ser Ala Trp Val Ser

1115 1120 1125

Leu Pro Pro Leu Leu Glu Thr Pro Ala Ala Tyr Ser Ser Arg Phe

1130 1135 1140

Cys Ser Arg Ser Gly Val Ala Gly Phe Arg Ala Val Glu Val Ile

1145 1150 1155

Pro Gly Phe Glu Leu Lys Tyr Pro Trp Ser Trp Leu Lys Asp Lys

1160 1165 1170

Lys Asp Lys Ala Gly Asn Leu Ala Lys Glu Ala Leu Asn Ile Arg

1175 1180 1185

Thr Val Ser Glu Gln Leu Lys Ala Phe Asn Gln Asp Lys Pro Glu

1190 1195 1200

Lys Pro Arg Thr Leu Leu Val Pro Ile Ala Gly Gly Pro Ile Phe

1205 1210 1215

Val Pro Ile Ser Glu Val Gly Leu Ser Ser Phe Gly Leu Lys Pro
1220 1225 1230

Gln Val Val Gln Ala Asp Ile Asn Ala Ala Ile Asn Leu Gly Leu
1235 1240 1245

Arg Ala Ile Ser Asp Pro Arg Ile Trp Glu Ile His Pro Arg Leu
1250 1255 1260

Arg Thr Glu Lys Arg Asp Gly Arg Leu Phe Ala Arg Glu Lys Arg
1265 1270 1275

Lys Tyr Gly Glu Glu Lys Val Glu Val Gln Pro Ser Lys Asn Glu
1280 1285 1290

Lys Ala Lys Lys Val Lys Asp Asp Arg Lys Pro Asn Tyr Phe Ala
1295 1300 1305

Asp Phe Ser Gly Lys Val Asp Trp Gly Phe Gly Asn Ile Lys Asn
1310 1315 1320

Glu Ser Gly Leu Thr Leu Val Ser Gly Lys Ala Leu Trp Trp Thr
1325 1330 1335

Ile Asn Gln Leu Gln Trp Glu Arg Cys Phe Asp Ile Asn Lys Arg
1340 1345 1350

His Ile Glu Asp Trp Ser Asn Lys Gln Lys Gln
1355 1360

<210> 163

<211> 1313

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 163

Met Gly Glu Glu Asn Asn Phe Ser Gln Phe Thr Gly Leu Tyr Glu Leu
1 5 10 15

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Val Trp Glu Thr Glu Lys
20 25 30

Leu Leu Ile Glu Asn Gln Val Phe Pro Lys Asp Lys Ile Val Tyr Glu

35 40 45

Ser Tyr Lys Lys Ile Arg Pro Tyr Leu Asp Lys Leu His Leu Gln Phe

50 55 60

Ile Glu Glu Ser Leu Ser Ser Val Lys Leu Asp Phe Asn Glu Ile Glu

65 70 75 80

Lys Lys Phe Leu Glu Trp Asp Lys Glu Lys Asp Lys Thr Thr Lys Asn

85 90 95

Lys Leu Lys Glu Glu Ile Phe Trp Lys Asn Lys Lys Trp Trp Leu Asn

100 105 110

Ser Asn Leu Arg Lys Asp Met Val Ser Tyr Phe Asn Leu Asn Trp Lys

115 120 125

Lys Trp Ile Asn Asn Phe Glu Asn Lys Thr Ile Val Asn Glu Lys Trp

130 135 140

Lys Glu Glu Lys Ile Lys Ile Lys Trp Glu Trp Tyr Lys Ile Leu Leu

145 150 155 160

Ser Asp Ser Asn Leu Asn Ile Leu Ser Asp Phe Phe Thr Gln Glu Lys

165 170 175

Glu Trp Asp Asn Val Leu Ile Glu Lys Tyr Ile Glu Asn Pro Asn Phe

180 185 190

Lys Glu Asn Asp Trp Glu Lys Lys Phe Ile Leu Glu Lys Gln Asn Leu

195 200 205

Phe Lys Ser Phe Lys Trp Phe Thr Thr Tyr Phe Thr Asn Phe Asn His

210 215 220

Ser Arg Glu Asn Phe Tyr Lys Asp Asp Trp Lys Ser Trp Arg Ile Ala

225 230 235 240

Thr Arg Ile Ile Asp Glu Asn Leu Ile Phe Phe Leu Lys Asn Lys Lys

245 250 255

Ala Phe Asp Glu Lys Tyr Lys Asn Asn Ser Glu Ile Thr Val Lys Phe

260 265 270

Asn Glu Lys Leu Leu Asn Phe Trp Glu Lys Leu Glu Asp Phe Phe Ser

275 280 285

Leu Asp Phe Tyr Asn Arg Cys Tyr Thr Trp Lys Gln Ile Glu Tyr Tyr
290 295 300
Asn Gln Leu Ile Trp Glu Leu Asn Ser Val Val Asn His Glu Lys Gln
305 310 315 320
Ala Lys Phe Ser Glu Tyr Thr Gln Asn Lys Lys Val Ser Glu Asn Asn
325 330 335
Lys Phe Asn Lys Tyr Asp Phe Pro Ile Phe Lys Glu Leu Tyr Lys Gln

340 345 350
Ile Leu Ser Glu Lys Ala Thr Glu Gln Lys Phe Ile Glu Ile Asn Asp
355 360 365
Phe Lys Glu Leu Lys Gln Asn Leu Gln Glu Leu Ile Glu Lys Asn Lys
370 375 380
Gln Lys Asn Lys Phe Ala Ile Asn Leu Thr Lys Ser Leu Ile Glu Lys
385 390 395 400
Ile Asp Glu Tyr Asp Phe Glu Lys Ile Tyr Ile Ser Lys Leu Ser Leu

405 410 415
Asn Thr Ile Ser Ser Lys Phe Phe Trp Ser Asn Lys Trp Phe Phe Ile
420 425 430
Gln Glu Asn Leu Glu Lys Asn Ile Trp Lys Lys Asn Lys Asn Trp Lys
435 440 445
Ile Asp Leu Pro Asp Phe Ile Lys Leu Ser Asp Ile Lys Thr Ala Leu
450 455 460
Glu Asn Phe Asn Lys Ile Leu Phe Glu Asp Lys Glu Asn Lys Glu Asn

465 470 475 480
Ile Phe Lys Glu Glu Phe Asp Asn Ile Thr Glu Asn Asn Ile Phe Ile
485 490 495
Lys Phe Met Lys Ile Tyr Glu Asn Glu Phe Ile Asn Leu Ile Glu Trp
500 505 510
Lys Lys Asn Asn Lys Trp Asp Tyr Glu Ile Ile Trp Tyr Asn Lys Ser
515 520 525
Leu Leu Asp Leu Glu Lys Asn Ile Leu Asn Ile Ser Asp Phe Ser Asp

530 535 540

Lys Lys Glu Glu Lys Glu Lys Gln Ile Glu Tyr Ile Lys Lys Tyr Leu

545 550 555 560

Asp Ser Ser Leu Asn Ile Tyr Arg Val Met Lys Tyr Phe Ala Leu Glu

565 570 575

Lys Gly Lys Glu Ser Val Glu Trp Glu Phe Glu Thr Asp Asp Ile Phe

580 585 590

Tyr Asn Glu Phe Lys Lys Phe Tyr Ile Asp Asn Glu Ile Ile Ser Tyr

595 600 605

Tyr Asn Glu Phe Arg Asn Tyr Leu Thr Lys Lys Pro Tyr Ser Ser Asn

610 615 620

Lys Leu Lys Leu Asn Phe Glu Asn Trp Thr Leu Ile Asp Gly Trp Asp

625 630 635 640

Lys Asn Lys Glu Pro Asp Asn Tyr Trp Thr Ile Leu Arg Lys Asn Trp

645 650 655

Lys Tyr Phe Leu Ala Leu Gln Ile Lys Trp Lys Asn Asn Ile Phe Tyr

660 665 670

Lys Lys Lys Trp Ser Trp Val Ile Asp Ile Glu Glu Ala Tyr Lys Ile

675 680 685

Asp Leu Trp Asp Glu Phe Tyr Glu Lys Met Asp Tyr Lys Phe Leu Pro

690 695 700

Asp Pro Lys Lys Met Leu Pro Lys Val Ile Phe Ala Lys Ser Asn Val

705 710 715 720

Lys Leu Phe Asn Pro Ser Lys Glu Ile Leu Gln Ile Lys Glu Asn Glu

725 730 735

Thr Phe Lys Thr Trp Asp Lys Phe Lys Val Asn Asp Phe Tyr Lys Ile

740 745 750

Val Asp Phe Tyr Lys Glu Asn Ile Ile Lys Tyr Pro Asp Trp Lys Ile

755 760 765

Phe Asn Phe Lys Phe Ser Asp Thr Lys Thr Tyr Asn Asn Leu Ser Asp

770 775 780

Phe Tyr Lys Glu Ile Glu Leu Trp Ser Tyr Asp Leu Asn Phe Arg Lys

785 790 795 800

Val Ser Lys Lys Tyr Ile Leu Lys Ser Ile Glu Glu Lys Asn Ile Tyr

805 810 815

Leu Phe Glu Ile Tyr Asn Lys Asp Phe Ala Asp Trp Lys Thr Trp Ser

820 825 830

Glu Asn Leu His Thr Met Tyr Phe Lys Trp Leu Phe Glu Glu Asn Asn

835 840 845

Leu Asn Asn Ile Val Leu Lys Leu Asn Trp Gln Ala Glu Ile Phe Arg

850 855 860

Arg Glu Ala Ser Leu Lys Glu Lys Glu Val Asn Arg Ala Lys Glu Asn

865 870 875 880

Lys Glu Lys Ser His Asn Ile Ile Glu Asn Ala Arg Tyr Thr Lys Asp

885 890 895

Lys Leu Phe Phe His Cys Pro Ile Lys Leu Asn Phe Ala Lys His Asn

900 905 910

Glu Lys Ile Asn Gln Glu Ile Leu Lys Tyr Ile Ser Asp Asn Lys Glu

915 920 925

Ile Asn Ile Ile Trp Ile Asp Arg Trp Glu Lys His Leu Ala Tyr Tyr

930 935 940

Ser Val Ile Asn Arg Asp Trp Asn Ile Ile Lys Asp Lys Asn Trp Asn

945 950 955 960

Leu Val Lys Trp Ser Leu Asn Ile Val Trp Asn Asn Gln Asn Tyr His

965 970 975

Asp Lys Leu Glu Thr Arg Glu Lys Glu Arg Gln Asp Ala Arg Trp Ser

980 985 990

Trp Lys Thr Ile Trp Asn Ile Lys Asp Leu Lys Gln Gly Tyr Ile Ser

995 1000 1005

Gln Val Val His Lys Leu Ala Glu Leu Val Ile Glu His Asn Ala

1010 1015 1020

Ile Ile Val Phe Glu Asp Leu Asn Ser Trp Phe Lys Arg Trp Arg

1025 1030 1035

Gln Lys Ile Glu Arg Gln Val Tyr Gln Lys Leu Glu Lys Ala Leu

1040 1045 1050

Ile Glu Lys Leu Asn Tyr Leu Thr Phe Lys Asp Lys Asn Phe Trp

1055 1060 1065

Glu Asn Trp His Tyr Leu Lys Ala Tyr Gln Leu Thr Ala Pro Phe

1070 1075 1080

Glu Thr Phe Glu Lys Val Trp Lys Gln Thr Trp Val Ile Phe Tyr

1085 1090 1095

Thr Asp Pro Ser Tyr Thr Ser Ser Thr Cys Pro Ala Cys Trp Phe

1100 1105 1110

Arg Lys Asp Leu Tyr Leu Lys Tyr Ser Asn Leu Lys Asn Ala Leu

1115 1120 1125

Trp Asp Ile Glu Lys Ile Asp Ser Ile Ile Phe Asp Trp Lys Arg

1130 1135 1140

Phe Ile Phe Glu Tyr Asn Asn Lys Lys Val Phe Thr Asp Arg Asp

1145 1150 1155

Arg Lys Arg Asn Ile Ser Ser Glu Glu Ser Trp Ile Lys Trp Trp

1160 1165 1170

Lys Thr Ile Asp Asn Asn Ile Thr Glu Phe Leu Glu Ile Leu Phe

1175 1180 1185

Lys Lys Ser Asn Ile Asp Tyr Thr Ser Trp Asn Asn Leu Ile Leu

1190 1195 1200

Asp Ile Gln Glu Ile Asn Glu Lys Glu Leu Tyr Lys Trp Val Phe

1205 1210 1215

Asp Asn Phe Asn Ala Ile Leu Asn Ile Arg Asn Ser Thr Ile Lys

1220 1225 1230

Asp Asn Ser Arg Thr Trp Asp Phe Ile Cys Cys Pro Ala Cys Asp

1235 1240 1245

Phe Asp Ser Arg Lys Glu Asn Lys Ile Trp Ile Glu Asn Trp Asp

1250 1255 1260

Asp Asn Trp Ala Phe Asn Ile Ala Arg Lys Trp Ile Ile Ile Leu

1265 1270 1275

Asn Lys Ile Asp Ser Tyr Leu Asn Glu Lys Trp Ser Leu Asp Lys

1280 1285 1290

Ile Leu Trp Trp Asp Met Ile Val Lys Gln Ile Asp Trp Asp Asp

1295 1300 1305

Phe Thr His Lys Lys

1310

<210> 164

<211> 767

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 164

Met Ala Gln Ala Ser Ser Thr Pro Ala Val Ser Pro Arg Pro Arg Pro

1 5 10 15

Arg Tyr Arg Glu Glu Arg Thr Leu Val Arg Lys Leu Leu Pro Arg Pro

20 25 30

Gly Gln Ser Lys Gln Glu Phe Arg Glu Asn Val Lys Lys Leu Arg Lys

35 40 45

Ala Phe Leu Gln Phe Asn Ala Asp Val Ser Gly Val Cys Gln Trp Ala

50 55 60

Ile Gln Phe Arg Pro Arg Tyr Gly Lys Pro Ala Glu Pro Thr Glu Thr

65 70 75 80

Phe Trp Lys Phe Phe Leu Glu Pro Glu Thr Ser Leu Pro Pro Asn Asp

85 90 95

Ser Arg Ser Pro Glu Phe Arg Arg Leu Gln Ala Phe Glu Ala Ala Ala

100 105 110

Gly Ile Asn Gly Ala Ala Ala Leu Asp Asp Pro Ala Phe Thr Asn Glu

115 120 125

Leu Arg Asp Ser Ile Leu Ala Val Ala Ser Arg Pro Lys Thr Lys Glu

130 135 140

Ala Gln Arg Leu Phe Ser Arg Leu Lys Asp Tyr Gln Pro Ala His Arg

145 150 155 160

Met Ile Leu Ala Lys Val Ala Ala Glu Trp Ile Glu Ser Arg Tyr Arg

165 170 175

Arg Ala His Gln Asn Trp Glu Arg Asn Tyr Glu Glu Trp Lys Lys Glu

180 185 190

Lys Gln Glu Trp Glu Gln Asn His Pro Glu Leu Thr Pro Glu Ile Arg

195 200 205

Glu Ala Phe Asn Gln Ile Phe Gln Gln Leu Glu Val Lys Glu Lys Arg

210 215 220

Val Arg Ile Cys Pro Ala Ala Arg Leu Leu Gln Asn Lys Asp Asn Cys

225 230 235 240

Gln Tyr Ala Gly Lys Asn Lys His Ser Val Leu Cys Asn Gln Phe Asn

245 250 255

Glu Phe Lys Lys Asn His Leu Gln Gly Lys Ala Ile Lys Phe Phe Tyr

260 265 270

Lys Asp Ala Glu Lys Tyr Leu Arg Cys Gly Leu Gln Ser Leu Lys Pro

275 280 285

Asn Val Gln Gly Pro Phe Arg Glu Asp Trp Asn Lys Tyr Leu Arg Tyr

290 295 300

Met Asn Leu Lys Glu Glu Thr Leu Arg Gly Lys Asn Gly Gly Arg Leu

305 310 315 320

Pro His Cys Lys Asn Leu Gly Gln Glu Cys Glu Phe Asn Pro His Thr

325 330 335

Ala Leu Cys Lys Gln Tyr Gln Gln Gln Leu Ser Ser Arg Pro Asp Leu

340 345 350

Val Gln His Asp Glu Leu Tyr Arg Lys Trp Arg Arg Glu Tyr Trp Arg

355 360 365

Glu Pro Arg Lys Pro Val Phe Arg Tyr Pro Ser Val Lys Arg His Ser

370 375 380

Ile Ala Lys Ile Phe Gly Glu Asn Tyr Phe Gln Ala Asp Phe Lys Asn
385 390 395 400
Ser Val Val Gly Leu Arg Leu Asp Ser Met Pro Ala Gly Gln Tyr Leu

405 410 415
Glu Phe Ala Phe Ala Pro Trp Pro Arg Asn Tyr Arg Pro Gln Pro Gly
420 425 430
Glu Thr Glu Ile Ser Ser Val His Leu His Phe Val Gly Thr Arg Pro
435 440 445
Arg Ile Gly Phe Arg Phe Arg Val Pro His Lys Arg Ser Arg Phe Asp
450 455 460
Cys Thr Gln Glu Glu Leu Asp Glu Leu Arg Ser Arg Thr Phe Pro Arg

465 470 475 480
Lys Ala Gln Asp Gln Lys Phe Leu Glu Ala Ala Arg Lys Arg Leu Leu
485 490 495
Glu Thr Phe Pro Gly Asn Ala Glu Gln Glu Leu Arg Leu Leu Ala Val
500 505 510
Asp Leu Gly Thr Asp Ser Ala Arg Ala Ala Phe Phe Ile Gly Lys Thr
515 520 525
Phe Gln Gln Ala Phe Pro Leu Lys Ile Val Lys Ile Glu Lys Leu Tyr

530 535 540
Glu Gln Trp Pro Asn Gln Lys Gln Ala Gly Asp Arg Arg Asp Ala Ser
545 550 555 560
Ser Lys Gln Pro Arg Pro Gly Leu Ser Arg Asp His Val Gly Arg His
565 570 575
Leu Gln Lys Met Arg Ala Gln Ala Ser Glu Ile Ala Gln Lys Arg Gln
580 585 590
Glu Leu Thr Gly Thr Pro Ala Pro Glu Thr Thr Thr Asp Gln Ala Ala

595 600 605
Lys Lys Ala Thr Leu Gln Pro Phe Asp Leu Arg Gly Leu Thr Val His
610 615 620
Thr Ala Arg Met Ile Arg Asp Trp Ala Arg Leu Asn Ala Arg Gln Ile

625 630 635 640

Ile Gln Leu Ala Glu Glu Asn Gln Val Asp Leu Ile Val Leu Glu Ser

645 650 655

Leu Arg Gly Phe Arg Pro Pro Gly Tyr Glu Asn Leu Asp Gln Glu Lys

660 665 670

Lys Arg Arg Val Ala Phe Phe Ala His Gly Arg Ile Arg Arg Lys Val

675 680 685

Thr Glu Lys Ala Val Glu Arg Gly Met Arg Val Val Thr Val Pro Tyr

690 695 700

Leu Ala Ser Ser Lys Val Cys Ala Glu Cys Arg Lys Lys Gln Lys Asp

705 710 715 720

Asn Lys Gln Trp Glu Lys Asn Lys Lys Arg Gly Leu Phe Lys Cys Glu

725 730 735

Gly Cys Gly Ser Gln Ala Gln Val Asp Glu Asn Ala Ala Arg Val Leu

740 745 750

Gly Arg Val Phe Trp Gly Glu Ile Glu Leu Pro Thr Ala Ile Pro

755 760 765

<210> 165

<211> 1313

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 165

Met Gly Glu Glu Asn Asn Phe Ser Gln Phe Thr Gly Leu Tyr Glu Leu

1 5 10 15

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Val Trp Glu Thr Glu Lys

20 25 30

Leu Leu Ile Glu Asn Gln Val Phe Pro Lys Asp Lys Ile Val Tyr Glu

35 40 45

Ser Tyr Lys Lys Ile Arg Pro Tyr Leu Asp Lys Leu His Leu Gln Phe

50 55 60

Ile Glu Glu Ser Leu Ser Ser Val Lys Leu Asp Phe Asn Glu Ile Glu

65 70 75 80

Lys Lys Phe Leu Glu Trp Asp Lys Glu Lys Asp Lys Thr Thr Lys Asn

85 90 95

Lys Leu Lys Glu Glu Ile Phe Trp Lys Asn Lys Lys Trp Trp Leu Asn

100 105 110

Ser Asn Leu Arg Lys Asp Met Val Ser Tyr Phe Asn Leu Asn Trp Lys

115 120 125

Lys Trp Ile Asn Asn Phe Glu Asn Lys Thr Ile Val Asn Glu Lys Trp

130 135 140

Lys Glu Glu Lys Ile Lys Ile Lys Trp Glu Trp Tyr Lys Ile Leu Leu

145 150 155 160

Ser Asp Ser Asn Leu Asn Ile Leu Ser Asp Phe Phe Thr Gln Glu Lys

165 170 175

Glu Trp Asp Asn Val Leu Ile Glu Lys Tyr Ile Glu Asn Pro Asn Phe

180 185 190

Lys Glu Asn Asp Trp Glu Lys Lys Phe Ile Leu Glu Lys Gln Asn Leu

195 200 205

Phe Lys Ser Phe Lys Trp Phe Thr Thr Tyr Phe Thr Asn Phe Asn His

210 215 220

Ser Arg Glu Asn Phe Tyr Lys Asp Asp Trp Lys Ser Trp Arg Ile Ala

225 230 235 240

Thr Arg Ile Ile Asp Glu Asn Leu Ile Phe Phe Leu Lys Asn Lys Lys

245 250 255

Ala Phe Asp Glu Lys Tyr Lys Asn Asn Ser Glu Ile Thr Val Lys Phe

260 265 270

Asn Glu Lys Leu Leu Asn Phe Trp Glu Lys Leu Glu Asp Phe Phe Ser

275 280 285

Leu Asp Phe Tyr Asn Arg Cys Tyr Thr Trp Lys Gln Ile Glu Tyr Tyr

290 295 300

Asn Gln Leu Ile Trp Glu Leu Asn Ser Val Val Asn His Glu Lys Gln

305 310 315 320

Ala Lys Phe Ser Glu Tyr Thr Gln Asn Lys Lys Val Ser Glu Asn Asn

325 330 335

Lys Phe Asn Lys Tyr Asp Phe Pro Ile Phe Lys Glu Leu Tyr Lys Gln

340 345 350

Ile Leu Ser Glu Lys Ala Thr Glu Gln Lys Phe Ile Glu Ile Asn Asp

355 360 365

Phe Lys Glu Leu Lys Gln Asn Leu Gln Glu Leu Ile Glu Lys Asn Lys

370 375 380

Gln Lys Asn Lys Phe Ala Ile Asn Leu Thr Lys Ser Leu Ile Glu Lys

385 390 395 400

Ile Asp Glu Tyr Asp Phe Glu Lys Ile Tyr Ile Ser Lys Leu Ser Leu

405 410 415

Asn Thr Ile Ser Ser Lys Phe Phe Trp Ser Asn Lys Trp Phe Phe Ile

420 425 430

Gln Glu Asn Leu Glu Lys Asn Ile Trp Lys Lys Asn Lys Asn Trp Lys

435 440 445

Ile Asp Leu Pro Asp Phe Ile Lys Leu Ser Asp Ile Lys Thr Ala Leu

450 455 460

Glu Asn Phe Asn Lys Ile Leu Phe Glu Asp Lys Glu Asn Lys Glu Asn

465 470 475 480

Ile Phe Lys Glu Glu Phe Asp Asn Ile Thr Glu Asn Asn Ile Phe Ile

485 490 495

Lys Phe Met Lys Ile Tyr Glu Asn Glu Phe Ile Asn Leu Ile Glu Trp

500 505 510

Lys Lys Asn Asn Lys Trp Asp Tyr Glu Ile Ile Trp Tyr Asn Lys Ser

515 520 525

Leu Leu Asp Leu Glu Lys Asn Ile Leu Asn Ile Ser Asp Phe Ser Asp

530 535 540

Lys Lys Glu Glu Lys Glu Lys Gln Ile Glu Tyr Ile Lys Lys Tyr Leu

545 550 555 560

Asp Ser Ser Leu Asn Ile Tyr Arg Val Met Lys Tyr Phe Ala Leu Glu
565 570 575
Lys Gly Lys Glu Ser Val Glu Trp Glu Phe Glu Thr Asp Asp Ile Phe

580 585 590
Tyr Asn Glu Phe Lys Lys Phe Tyr Ile Asp Asn Glu Ile Ile Ser Tyr
595 600 605
Tyr Asn Glu Phe Arg Asn Tyr Leu Thr Lys Lys Pro Tyr Ser Ser Asn
610 615 620
Lys Leu Lys Leu Asn Phe Glu Asn Trp Thr Leu Ile Asp Gly Trp Asp
625 630 635 640
Lys Asn Lys Glu Pro Asp Asn Tyr Trp Thr Ile Leu Arg Lys Asn Trp

645 650 655
Lys Tyr Phe Leu Ala Leu Gln Ile Lys Trp Lys Asn Asn Ile Phe Tyr
660 665 670
Lys Lys Lys Trp Ser Trp Val Ile Asp Ile Glu Glu Ala Tyr Lys Ile
675 680 685
Asp Leu Trp Asp Glu Phe Tyr Glu Lys Met Asp Tyr Lys Phe Leu Pro
690 695 700
Asp Pro Lys Lys Met Leu Pro Lys Val Ile Phe Ala Lys Ser Asn Val

705 710 715 720
Lys Leu Phe Asn Pro Ser Lys Glu Ile Leu Gln Ile Lys Glu Asn Glu
725 730 735
Thr Phe Lys Thr Trp Asp Lys Phe Lys Val Asn Asp Phe Tyr Lys Ile
740 745 750
Val Asp Phe Tyr Lys Glu Asn Ile Ile Lys Tyr Pro Asp Trp Lys Ile
755 760 765
Phe Asn Phe Lys Phe Ser Asp Thr Lys Thr Tyr Asn Asn Leu Ser Asp

770 775 780
Phe Tyr Lys Glu Ile Glu Leu Trp Ser Tyr Asp Leu Asn Phe Arg Lys
785 790 795 800
Val Ser Lys Lys Tyr Ile Leu Lys Ser Ile Glu Glu Lys Asn Ile Tyr

805 810 815

Leu Phe Glu Ile Tyr Asn Lys Asp Phe Ala Asp Trp Lys Thr Trp Ser

820 825 830

Glu Asn Leu His Thr Met Tyr Phe Lys Trp Leu Phe Glu Glu Asn Asn

835 840 845

Leu Asn Asn Ile Val Leu Lys Leu Asn Trp Gln Ala Glu Ile Phe Arg

850 855 860

Arg Glu Ala Ser Leu Lys Glu Lys Glu Val Asn Arg Ala Lys Glu Asn

865 870 875 880

Lys Glu Lys Ser His Asn Ile Ile Glu Asn Ala Arg Tyr Thr Lys Asp

885 890 895

Lys Leu Phe Phe His Cys Pro Ile Lys Leu Asn Phe Ala Lys His Asn

900 905 910

Glu Lys Ile Asn Gln Glu Ile Leu Lys Tyr Ile Ser Asp Asn Lys Glu

915 920 925

Ile Asn Ile Ile Trp Ile Asp Arg Trp Glu Lys His Leu Ala Tyr Tyr

930 935 940

Ser Val Ile Asn Arg Asp Trp Asn Ile Ile Lys Asp Lys Asn Trp Asn

945 950 955 960

Leu Val Lys Trp Ser Leu Asn Ile Val Trp Asn Asn Gln Asn Tyr His

965 970 975

Asp Lys Leu Glu Thr Arg Glu Lys Glu Arg Gln Asp Ala Arg Trp Ser

980 985 990

Trp Lys Thr Ile Trp Asn Ile Lys Asp Leu Lys Gln Gly Tyr Ile Ser

995 1000 1005

Gln Val Val His Lys Leu Ala Glu Leu Val Ile Glu His Asn Ala

1010 1015 1020

Ile Ile Val Phe Glu Asp Leu Asn Ser Trp Phe Lys Arg Trp Arg

1025 1030 1035

Gln Lys Ile Glu Arg Gln Val Tyr Gln Lys Leu Glu Lys Ala Leu

1040 1045 1050

Ile Glu Lys Leu Asn Tyr Leu Thr Phe Lys Asp Lys Asn Phe Trp

1055 1060 1065

Glu Asn Trp His Tyr Leu Lys Ala Tyr Gln Leu Thr Ala Pro Phe

1070 1075 1080

Glu Thr Phe Glu Lys Val Trp Lys Gln Thr Trp Val Ile Phe Tyr

1085 1090 1095

Thr Asp Pro Ser Tyr Thr Ser Ser Thr Cys Pro Ala Cys Trp Phe

1100 1105 1110

Arg Lys Asp Leu Tyr Leu Lys Tyr Ser Asn Leu Lys Asn Ala Leu

1115 1120 1125

Trp Asp Ile Glu Lys Ile Asp Ser Ile Ile Phe Asp Trp Lys Arg

1130 1135 1140

Phe Ile Phe Glu Tyr Asn Asn Lys Lys Val Phe Thr Asp Arg Asp

1145 1150 1155

Arg Lys Arg Asn Ile Ser Ser Glu Glu Ser Trp Ile Lys Trp Trp

1160 1165 1170

Lys Thr Ile Asp Asn Asn Ile Thr Glu Phe Leu Glu Ile Leu Phe

1175 1180 1185

Lys Lys Ser Asn Ile Asp Tyr Thr Ser Trp Asn Asn Leu Ile Leu

1190 1195 1200

Asp Ile Gln Glu Ile Asn Glu Lys Glu Leu Tyr Lys Trp Val Phe

1205 1210 1215

Asp Asn Phe Asn Ala Ile Leu Asn Ile Arg Asn Ser Thr Ile Lys

1220 1225 1230

Asp Asn Ser Arg Thr Trp Asp Phe Ile Cys Cys Pro Ala Cys Asp

1235 1240 1245

Phe Asp Ser Arg Lys Glu Asn Lys Ile Trp Ile Glu Asn Trp Asp

1250 1255 1260

Asp Asn Trp Ala Phe Asn Ile Ala Arg Lys Trp Ile Ile Ile Leu

1265 1270 1275

Asn Lys Ile Asp Ser Tyr Leu Asn Glu Lys Trp Ser Leu Asp Lys

1280 1285 1290

Ile Leu Trp Trp Asp Met Ile Val Lys Gln Ile Asp Trp Asp Asp

1295 1300 1305

Phe Thr His Lys Lys

1310

<210> 166

<211> 1500

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 166

Met Ala Thr Ala Ile Asn Tyr Pro Thr Thr Gln Arg Ala Tyr Thr Leu

1 5 10 15

Arg Leu Arg Gly Ile Asp Pro Gln Asp Gln Ser Trp Arg Asp Ala Leu

20 25 30

Trp Ala Thr His Glu Ala Val Asn Arg Gly Ala Lys Val Phe Gly Glu

35 40 45

Trp Leu Leu Thr Leu Arg Gly Gly Leu Asp His Gln Leu Ala Asp Ala

50 55 60

Pro Val Lys Val Arg Gly Gly Thr Thr Arg Leu Pro Ser Asp Glu Glu

65 70 75 80

Arg Arg Asp Arg Arg Val Leu Leu Ala Leu Ser Trp Leu Ser Val Glu

85 90 95

Asp Ala His Gly Ala Pro Pro Asp Ala Ser Leu Ile Val Ala Lys Gly

100 105 110

Thr Asp Ser Ala Asp Cys Arg Ala Arg Lys Leu Ala Asp Ala Leu Ile

115 120 125

Ala Ile Leu Gln Ala Arg Ser Val Ala Ala Ser Glu Ile Gly Asp Pro

130 135 140

Ser Lys Pro Pro Glu Asp Gln Pro Gly Thr Trp Leu Gly Asp Cys Met

145 150 155 160

Gly Ser Leu Ser Ala Ala Ile Arg Asp Asp Ala Val Trp Val Asn Arg
165 170 175
Ser Lys Ala Phe Asp Ala Ala Thr Gln Ser Cys Pro Ser Leu Thr Arg
180 185 190
Asp Glu Ile Trp Asp Phe Leu Glu Pro Phe Phe Ala Ser Pro Asp Ala

195 200 205
Tyr Leu Lys Pro Glu Arg Ala Glu Ser Asp Glu Gly Asp Ser Thr Ser
210 215 220
Ala Ala Thr Glu Asp Lys Ala Lys Asp Leu Val Gln Lys Ala Gly Gly
225 230 235 240
Trp Leu Ser Lys Arg Met Gly Ala Gly Gly Gly Ala Asn Phe Gln Asp
245 250 255
Leu Ala Arg Ala Tyr Gln Ala Ile Ala Gln Trp Ala Ser Ser Ala Gln

260 265 270
Pro Gly Gln Ser Ala Gln Gln Ala Val Gly Ser Leu Ala Gly Tyr Leu
275 280 285
Ser Gln His Gly Phe Ser Pro Thr Ala Asn Asp Ala Thr Gly Val Leu
290 295 300
Ala Val Ile Ser Gly Pro Gly Tyr Lys Ser Ala Thr Arg Asn His Ile
305 310 315 320
Thr Ala Ile Ala Thr Ser Pro Glu Ile Thr Pro Gln Asp Leu Ser Lys

325 330 335
Leu Gln Glu Leu Ala Thr Lys Asp Lys Ala Gly Cys Ser Ser Lys Ile
340 345 350
Gly Gly Lys Gly Pro Arg Pro Tyr Ala Thr Met Ile Leu Gln Gln Val
355 360 365
Glu Ala Ala Cys Gly Phe Thr Tyr Leu Gln Ser Asp Gly Pro Ala Arg
370 375 380
His Arg Glu Phe Ser Val Met Leu Asp His Ala Ala Arg Arg Val Asn

385 390 395 400
Val Ala His Ser Trp Ile Lys Asn Ala Glu Ala Glu Arg Arg Gln Phe

405 410 415

Glu Ser Asp Ala Arg Arg Ile Lys Lys Val Pro Gln Asp Ala Leu Asn

420 425 430

Trp Leu Arg Gly Tyr Cys Glu Glu Arg Gly Gly Ala Ser Gly Ser Leu

435 440 445

Glu Gly Tyr Arg Ile Arg Arg Arg Ala Ile Asp Gly Trp Asp Gln Val

450 455 460

Val Ile Arg Trp Ser Arg Ser Asp Cys Gln Ser Ala Asp Asp Arg Ile

465 470 475 480

Ala Ala Ala Arg Gln Leu Gln Asp Asp Pro Glu Ile Asp Lys Phe Gly

485 490 495

Asp Ile Gln Leu Phe Glu Ala Leu Ala Ala Glu Glu Ala Leu Cys Val

500 505 510

Trp Lys Pro Asp Gly Asn Pro Thr Ala Gln Pro Leu Lys Asp Phe Val

515 520 525

Ala Ala Thr Glu Ala Asp Ala Lys Lys Lys Arg Phe Lys Val Pro Ala

530 535 540

Tyr Arg His Pro Asp Pro Leu Arg His Pro Val Phe Thr Asp Phe Gly

545 550 555 560

Asn Ser Arg Trp Gly Ile Glu Tyr Ser Ala His Arg Ala Pro Ala Lys

565 570 575

Cys Asp Glu Leu Gly Gln Gln Val Asp Arg Leu Thr Gln Ala Val Ala

580 585 590

Glu Ala Gln Arg Asn Leu Asp Gly Ala Thr Ala Ala Gln Arg Ala Ser

595 600 605

Arg Glu Ser Lys Leu Ala Glu Ala Gln Ser Lys Leu Val Ala Ala Gln

610 615 620

Thr Glu Phe Ala Ala Ile Asn Asp Pro His Arg Val Glu Leu Lys Leu

625 630 635 640

Trp Asn Gly Gln Ala Val Ala Ala Ile Pro Met Arg Trp Ser Ser Lys

645 650 655

Arg Leu Ile Ala Asp Leu Ser Leu Arg Arg Ala Thr Gln Pro Ser Ser
660 665 670
Asp Gln Arg Ile Gly Val Thr Arg Ala Asp Arg Leu Gly Arg Ala Ala
675 680 685
Gly Asn Ala Asp Asp Gly Arg Pro Val Thr Ile Thr Gly Leu Phe Gln
690 695 700
Gln Asp His Trp Asn Gly Arg Leu Gln Ala Pro Arg Ala Gln Leu Asp

705 710 715 720
Ala Ile Ala Lys His Val Asp Lys His Gly Trp Asp Ala Lys Ala Arg
725 730 735
Arg Gln Ile Ala Arg Ile Arg Trp Val Val Ser Phe Ser Ala Glu Leu
740 745 750
Ser Gln Gln Gly Pro Trp Phe Glu Phe Cys His Arg Phe Gly Glu Asp
755 760 765
Ala Pro Ala Arg Pro Phe Val Ser Arg His Gly Glu Tyr Ala Val Lys

770 775 780
His Arg Asp Asn Asp Gln Arg Lys Gly His Ala Lys Leu Ile Leu Ser
785 790 795 800
Arg Leu Pro Gly Leu Arg Val Leu Ala Val Asp Leu Gly His Arg Tyr
805 810 815
Ala Ala Ala Cys Ala Val Trp Glu Ala Ile Ser Ser Asp Gln Met Arg
820 825 830
Gln Ala Cys Ala Ala Ala Asn Ala Pro Ala Pro His Pro Leu Ala Met

835 840 845
Tyr Ile His Leu Lys Ser Thr Thr Ala Lys Gly Lys Pro Thr Thr Thr
850 855 860
Ile Tyr Arg Arg Ile Gly Pro Asp Lys Leu Pro Asp Gly Thr Pro His
865 870 875 880
Pro Ala Pro Trp Ala Arg Leu Asp Arg Gln Phe Leu Ile Lys Leu Pro
885 890 895
Gly Glu Asp Arg Pro Ala Arg Ala Ala Ser Pro Asp Glu Ile Lys Ala

900 905 910

Val Glu Asp Phe Glu Asp Ser Val Gly Arg Val Arg Thr Ala Val Asp

915 920 925

Pro Pro Arg Lys Arg Gly Val Asp Leu Leu Met His Asp Ala Val Arg

930 935 940

Thr Ala Arg Leu Ala Leu Ala Arg His Gly Arg Arg Ala Arg Ile Ala

945 950 955 960

Phe Gln Leu Ile Ser Gln Val Arg Ile Leu Pro Gly Gly Arg Pro Gln

965 970 975

Thr Leu Asp Asp Ala Gly Arg Arg Asp Leu Leu Asn Asp Thr Leu Ala

980 985 990

Asp Trp Tyr Ala Leu Ala Thr Asp Ser Arg Trp Thr Asp Ala Ala Ala

995 1000 1005

Arg Gln Leu Trp Asn Glu Arg Leu Ala Ala Leu Asn Gly Gly Phe

1010 1015 1020

Thr Ile Asp Pro Pro Ala Asp Ala Ser Gln Pro Glu Ala Glu Arg

1025 1030 1035

Thr Arg Ala Gln Arg Arg Gln Ala Glu Gln Glu Leu Arg His Arg

1040 1045 1050

Leu Ala Ser Leu Val Glu Ala Leu Phe Cys Asn Pro Thr Leu Cys

1055 1060 1065

Gln Gln Leu His Gln Ala Trp Thr Asp Arg Trp Asn Ala Asp Asp

1070 1075 1080

Gln Gln Trp Arg Ser Arg Leu Lys Trp Leu Ser Arg Trp Leu Leu

1085 1090 1095

Pro Arg Gly Gly Ser Arg Arg Asp Gly Ser Arg Arg His Val Gly

1100 1105 1110

Gly Leu Ser Leu Thr Arg Ile Ser Thr Leu Ile Asp Phe Arg Arg

1115 1120 1125

Lys Val Gln Val Gly Tyr Phe Thr Arg Leu Arg Pro Asp Gly Ser

1130 1135 1140

Arg Ala Glu Ile Gly Pro Gln Phe Gly Gln Ser Thr Leu Asp Ala

1145 1150 1155

Ile Gln Arg Leu Lys Asp Gln Arg Ile Lys Gln Leu Thr Ser Arg

1160 1165 1170

Ile Val Glu Ala Ala Leu Gly Ile Gly Val Glu Gln Asp Arg Ile

1175 1180 1185

Trp Asp Ala Ala Lys Arg Lys Trp Arg Thr Val Lys Arg Pro Arg

1190 1195 1200

Glu Pro Arg Tyr His Val Asp Asp Gln Gly Val Gln Gln Arg Asp

1205 1210 1215

Pro Arg Phe Gln Ala Cys His Ala Val Val Ile Glu Asp Leu Ser

1220 1225 1230

His Tyr Arg Pro Glu Glu Thr Arg Thr Arg Arg Glu Asn Arg Ala

1235 1240 1245

Thr Met Asp Trp Lys Ser Ala Glu Thr Arg Lys Arg Leu Ala Asp

1250 1255 1260

His Cys Gln Leu Tyr Gly Leu His Leu Arg Asp Val Asn Pro Gln

1265 1270 1275

Tyr Thr Ser Arg Gln Asp Ser Arg Thr Gly Ala Pro Gly Cys Arg

1280 1285 1290

Cys Val Asp Val Ser Val Ala Asp Phe Leu Thr Lys Pro Ala Trp

1295 1300 1305

Arg Lys Gln Val Ala Gln Ala Arg Gly Lys Val Ala Ser Asn Arg

1310 1315 1320

Gly Asp Ala Arg Asp Arg Leu Leu Val Glu Leu Asp His Gln Leu

1325 1330 1335

Thr Thr Ala Asn Ser Leu Arg Gly Glu Met Asp Ser Leu Arg Ile

1340 1345 1350

Pro Val Asn Gly Gly Glu Val Phe Val Ser Ala Asp Pro Arg Ser

1355 1360 1365

Pro Leu Ala Ala Gly Ile Gln Ala Asp Leu Asn Ala Ala Ala Asn

1370 1375 1380

Ile Gly Leu Arg Ala Leu Met Asp Pro Asp Phe Leu Gly Thr Trp

1385 1390 1395

Trp Tyr Val Pro Cys Asp Pro Ser Thr Lys Lys Pro His Ile Glu

1400 1405 1410

Lys Val Lys Gly Ser Ile Leu Ala Thr Val Gly Ala Leu Gln Ala

1415 1420 1425

Thr Ser Glu Glu Ala Ala Ala Pro Pro Arg Arg Gly Arg Gly Gly

1430 1435 1440

Thr Arg Ser Ala Ala Pro Arg Glu Val Ile Asn Leu Trp Arg Asp

1445 1450 1455

Pro Ser Ala Val Arg Ile Gln Asp Ala Thr Ala Gly Glu Val Trp

1460 1465 1470

Asp Val Thr Pro Val Tyr Trp Ser Ile Val Lys Asp Arg Val Val

1475 1480 1485

Asp Val Leu Arg Gln Arg Asn Thr Lys Ser Gly Asp

1490 1495 1500

<210> 167

<211> 1202

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 167

Met Ala Val Arg Ser Val Lys Leu Lys Leu Leu Val Pro Arg Asp Gly

1 5 10 15

Ser Ala Glu Ser Val Arg Lys Arg Lys Ala Leu Trp Ala Thr His Gln

20 25 30

Phe Val Asn Asp Ala Ala Ala Ala Tyr Ala Glu Leu Leu Leu Glu Met

35 40 45

Arg Gln Glu Asp Val Cys Arg Gly Thr Asp Asp His Gly Lys Asp Val

50 55 60

Ile Glu Pro Ala Ala His Trp Gln Ala Lys Leu Arg Ala Arg Leu Ala
65 70 75 80
Ala Lys Gln Leu Pro Pro Val Ala Val Ala Glu Ala Leu Pro Leu Leu
85 90 95
Lys Ala Phe Tyr Gly Ser Arg Leu Ile Lys Ser Phe Val Ala Asn Asp
100 105 110
Lys Gly Val Ala Gly Thr Gly Asn Ala Thr Asp Leu Asn Thr Trp Leu
115 120 125

Ser Gly Leu Val Asp Pro Ala Ser Val Ala Gly Glu Lys Thr Glu Leu
130 135 140
Arg Lys Gln Leu Leu Ala Glu Leu Pro Leu Cys Glu Ala Ala Asp Ala
145 150 155 160
Asp Phe Glu Gly Ala Ala Arg Lys Met Leu Ala Lys Ser Asp Ala Arg
165 170 175
Glu Ala Leu Leu Glu Gly Pro Gly Thr Gly Val Gly Trp Pro Ala Ala
180 185 190

Tyr Asn Ala Asn Pro Thr Asp Ser Val Trp Leu Asp Met Leu His Lys
195 200 205
Ala Ala Ala Lys Ala Arg Leu Glu Leu Ala Asp Thr Thr Val Ser Glu
210 215 220
Leu Lys Lys Leu Gly Val Phe Pro Leu Leu Gln Ala Ala Ser Ser Asn
225 230 235 240
Arg Val Phe Gly Ser Gly Val Leu Asn Pro Phe Glu Arg Met Ala Ala
245 250 255

Ala Gln Ala Ala Ala Ala Leu Leu Pro Trp Glu Thr Lys Arg His Glu
260 265 270
Met Arg Lys Arg Arg Asp Lys Phe Ala Asp Gln Leu Asn Gln Trp Asp
275 280 285
Thr Glu Phe Gly Ala Ser His Ala Thr Ala Leu Ala Ala Ile Arg Ala
290 295 300

Phe Glu Ala Glu Glu Ser Glu Arg Ala Arg Arg Glu Ser Leu Gly Asn
305 310 315 320

Glu Gly Thr Gly Tyr Arg Ile Gly Gly Arg Glu Leu Arg Asp Ala Trp
325 330 335

Thr Leu Leu Arg Asp Trp Leu Lys Gly His Ser Thr Ala Thr Ala Ala
340 345 350

Ala Arg Glu Asp Lys Val Arg Glu Leu Gln Ala Lys Gln Gly Arg Ser
355 360 365

Phe Gly Ser His Arg Leu Leu Ser Trp Leu Ala Lys Pro Ala Gln Gln
370 375 380

Trp Leu Ala Asp His Ser Ala Gly Asp Val Val Thr Arg Ile Ala Val
385 390 395 400

Arg Asn Ala Arg Gln Arg Lys Leu Asp Thr Ala Arg Thr Leu Pro Ile
405 410 415

Trp Thr Gly Ala Asp Ala Val Lys His Pro Arg Phe Ala Asn Phe Asp
420 425 430

Pro Pro Asn Asn Thr Asn Gln Pro Gly Phe Asp Leu Arg Ala Gly Thr
435 440 445

Gln Lys Gly Arg Leu Thr Leu Arg Leu Ser Leu Leu Thr Glu Arg Ala
450 455 460

Asp Gly Leu Leu Leu Ala Gln Asp His Asp Phe Gln Leu Val Pro Ser
465 470 475 480

Arg Gln Met Ala Glu Ile Val Leu His Lys Asp Gly Lys Glu Arg Ala
485 490 495

Leu Ser Trp Gln Ser Gln Asp Gly Ile Gly Arg Gln Val Gly Asp Val
500 505 510

Gly Gly Ser Ala Leu Leu Phe Ser Arg Asp His Ala Glu Cys Leu Leu
515 520 525

Glu Arg Lys Gln Ile Thr Arg Leu Glu Arg Gly Ala Trp Pro Ala Ala
530 535 540

Leu Pro Val Trp Phe Lys Leu Ser Leu Asp Ile Gly Ala Glu His Lys

545 550 555 560

Ala Leu Leu Lys Gln Arg Phe Lys Trp Gly Val Trp Leu Asn Ser Ala

565 570 575

Leu Val Thr Arg Asn Ala Lys Asp Ala Lys Gly Val Pro Pro Pro Val

580 585 590

Gly Thr Arg Val Leu Ala Val Asp Leu Gly Leu Arg Ser Ala Ala Thr

595 600 605

Val Ser Val Trp Gln Val Val Asp Ala Ala Thr Pro Val Val Ala Gly

610 615 620

Lys Trp Arg Val Pro Leu Ser Asp Thr Leu Ser Ala Val His Glu Arg

625 630 635 640

Ser Ala Met Leu Ala Leu Pro Gly Glu His Val Asp Ala Gly Val Leu

645 650 655

Ala Ala Arg Arg Ala Ala Asn Glu Lys Leu Ala Gly Leu Leu Ala Ala

660 665 670

Thr Ser His Leu Ser Thr Val Phe Lys Leu Gly Arg Ala Glu Gln Gly

675 680 685

Asp Arg Arg Arg Glu Leu Leu Glu Arg Leu Gly Glu Gly Asp Asp Arg

690 695 700

Arg Ala Arg Ala Ala Val Ala Thr Thr Ala Ala Glu Arg Asp Gly Leu

705 710 715 720

Arg Ala Val Leu Gly Ala Thr Gln Asp Ala Trp Ala Gly Ala Val Ala

725 730 735

Ala Val Trp Arg Arg Leu Glu Thr Asp Leu Ala Gly Ala Ile Ala Ala

740 745 750

Tyr Arg Lys Gln Gln Arg Glu Asp Val Gln Leu Arg Arg Glu Ala Arg

755 760 765

His Gly Pro Gly Ala Ser Gln Leu Pro Lys Gln Ala Ala Ala Glu Arg

770 775 780

Leu Leu Gly Gly Lys Ser Ala Trp Gln Ile Glu Tyr Lys Glu Arg Val

785 790 795 800

Arg Lys Leu Leu Thr Arg Trp Ile Met Arg Gln Arg Pro Gly Asp Thr
805 810 815
Ala Val Arg Arg Leu Ala Arg Lys Asp Leu Gly Lys Tyr Cys Gly Gly
820 825 830

Leu Leu Asp His Leu Thr Ala Leu Lys Glu Asp Arg Ala Lys Thr Thr
835 840 845
Ala Asp Leu Ile Val Gln Ala Ala Arg Gly Arg Val Arg Ala His Lys
850 855 860
Asp Ala His Gly Arg Gln Gln Asp Arg Glu Leu Trp Leu Ala Lys Tyr
865 870 875 880
Ala Pro Cys Asp Leu Ile Val Met Glu Asp Leu Gly Arg Tyr Arg Phe
885 890 895

Ala Thr Asp Arg Pro Pro Ser Glu Asn Arg Gln Leu Met Gln Trp Thr
900 905 910
His Arg Glu Val Phe Arg Leu Val Gln Met Gln Ala Glu Val Glu Gly
915 920 925
Ile Gln Val Leu Glu Thr Gly Ala Glu Phe Ser Ser Lys Phe Asp Ala
930 935 940
Arg Thr Trp Ala Pro Gly Val Arg Cys Glu Pro Ile Thr Lys Leu Trp
945 950 955 960

Val Glu Arg Tyr Arg Asn Gly Glu Met Pro Trp Leu Ala Asp Lys Ala
965 970 975
Asp Glu Trp Arg Arg Glu Gly Ile Glu Leu Ala Gln Leu Val Pro Gly
980 985 990
Gln Leu Leu Pro Thr Gly Ser Gly Glu Gln Phe Val Ala Val Ser Ala
995 1000 1005
Thr Gly Gly Leu Arg Val Arg His Ala Asp Leu Asn Ala Ala Gln
1010 1015 1020

Cys Ile Ala Leu Arg Ala Leu Thr Gly His Gly Thr Ala Phe Arg
1025 1030 1035
Leu Thr Ala Arg Arg Leu Gly Asp Val Phe Val Ser Ala Lys Gly

1040 1045 1050

Leu Gly Lys Arg Pro Gln Gly Ala Leu Trp Arg Glu Phe Gly Ser

1055 1060 1065

Ala Leu Pro Pro Ala Val Val Val Leu Arg Pro Ala Gly Glu Val

1070 1075 1080

Arg Tyr Ala Leu Arg Pro Phe Ala Ser Ala Arg Asp Ala Ala Ala

1085 1090 1095

Ala Leu Gly Leu Gln Leu Gly Ala Leu Arg Asn Val Asp Ala Thr

1100 1105 1110

Asp Ala Glu Ser Asp Ala Glu Asp Gly Asp Leu Ala Glu Leu Leu

1115 1120 1125

Ala Gly Ala Asp Pro Asp Arg Ala Thr Phe Phe Arg Asp Pro Ser

1130 1135 1140

Gly Asp Val His Gly Gly Ala Trp Val Gln Ala Lys Val Phe Trp

1145 1150 1155

Ala Glu Val Arg Arg His Val Arg Leu Gly Leu Gln Ala Gln Gly

1160 1165 1170

Leu Leu Pro Ala Ala Ala Arg Ser Ser Glu Pro Arg Gln Met Gln

1175 1180 1185

Leu Pro Leu Ala Gly Ala Leu Pro Gly Asp Asp Ile Pro Leu

1190 1195 1200

<210> 168

<211> 1397

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 168

Met Ala Ala Phe Gln Arg Ser Tyr Thr Met Asn Leu Lys Pro Ala Thr

1 5 10 15

Ser Glu Gln Asp Lys Phe Ile Leu Trp Asn Arg Leu Phe Leu Thr His

20 25 30

Trp Ser Val Asn Glu Gly Ala Lys Ile Phe Gly Glu Leu Phe Leu Asn
35 40 45

Leu Arg Gly Gly Leu Ser Pro Glu Leu Gly Ile Phe Asp Leu Asn Lys
50 55 60
Asp Lys Asp Asp Arg Lys Lys Lys Ala Leu Val Met Gly Arg Arg Arg
65 70 75 80
Leu Leu Ala Leu Gly Trp Leu Ser Val Glu Asp Asn Leu Ser Ala Gly
85 90 95
Asp His Pro Phe Arg Ile Arg Glu Ile Pro Val Gly Arg Asn Met Glu
100 105 110

Ile Lys Gln Ala Thr Thr Leu Leu Thr Glu Ile Leu Lys Asn Lys Gly
115 120 125
Val Lys Asp Glu Ala Val Ile Lys Glu Trp Ile Asp Asp Cys Thr Pro
130 135 140
Ser Leu Ile Ala Asn Ile Arg Glu Asp Ala Val Trp Ile Asn Arg Ala
145 150 155 160
Lys Ser Phe Tyr Ser Met Asn Pro Cys Pro Thr Lys Asp Glu Val Trp
165 170 175

Lys Ile Leu Ser Tyr Val Leu Asn Thr Ser Phe Leu Asp Leu Ser Leu
180 185 190
Asn Asp Ser Ser Glu Arg Asp Asn Thr Lys Asn Lys Lys Gly Thr Lys
195 200 205
Glu Asn Glu Lys Asp Val Ser Asn Lys Ser Lys Glu Leu Tyr Gly Trp
210 215 220
Leu Phe Thr Lys Asn Pro Asn Lys Met Arg Glu Ala Gly Glu Asn Lys
225 230 235 240

Asp Lys Phe Ile Asn Asn Phe Arg Glu Asn Phe Asn Thr Phe Thr Asp
245 250 255
Tyr Ala Asn Leu Lys Val Glu Ile Glu Leu Trp Arg Lys Asn Asn Ile
260 265 270
Ser Asn Thr Leu Leu Ile Thr Gln Lys Ala Lys Tyr Pro Pro Glu Val

275 280 285

Lys Glu Ala Asn His Pro Ser Lys Phe Ser Val Gly Tyr Arg Lys Leu

290 295 300

Leu Val His Leu Glu Leu Trp Pro Ser Ser Lys Asp Glu Asn Gly Asp

305 310 315 320

Ile Pro Lys Gly Ile Glu Gly Lys Asp Lys Ser His Asn Gln Ile Leu

325 330 335

Leu Asp Tyr Leu Leu Glu Val Cys Asn Glu Gly Asn Lys Thr Thr Lys

340 345 350

Lys Val Ile Val Pro Ala Trp Ala Asp Gly Ile Lys Thr Glu Leu Glu

355 360 365

Ser Lys Ala Ser Ile Lys Val Gly Asp Ser Thr Ser Ser Val Leu Gln

370 375 380

Arg Leu Met Ile Lys Met Ala Ala Arg Arg Ile Ser Gln Thr Leu Ser

385 390 395 400

Trp Ile Lys Ile Asn Glu Gln Val Arg His Asp Ala Tyr Gln Lys Lys

405 410 415

Asn Lys Ala Phe Lys Leu Leu Cys Glu Ile Asp Lys Asn Gly Glu Ala

420 425 430

Cys Lys Trp Leu Glu Asn Tyr Glu Leu Phe Arg Arg Asp Asp Ser Gly

435 440 445

Gly Glu Glu Tyr His Ile Ser Ala Arg Ala Ile Ser Cys Trp Lys Gln

450 455 460

Ile Leu Glu Glu Trp Gln Lys Asn Asp Ser Ser Lys Ala Leu Arg Glu

465 470 475 480

Lys Val Lys Val Val Gln Ala Ala Glu Asp Lys Phe Gly Asp Ala Arg

485 490 495

Leu Phe Glu Asp Leu Ala Asp Asp Asn Ala Arg Ser Val Trp Leu Leu

500 505 510

Pro Asp Gly Asn Lys Thr Pro Asp Ile Leu Asn Trp Trp Cys Glu Tyr

515 520 525

Arg Thr Ala Asp Ile Asp Glu Ser Arg Phe Lys Ile Pro Cys Tyr Cys
530 535 540
His Pro His Pro Phe Lys His Pro Val Tyr Val Glu Tyr Gly Lys Ser
545 550 555 560

Asn Pro Gln Val Ile Phe Ser Leu Lys His Asp Lys Ala Arg Lys Asn
565 570 575
Arg Ile Asp Asn Gly Trp Asn Pro Lys Asn Pro Arg Ile Leu Ala Leu
580 585 590
Leu Leu Leu Asp Ile Val Arg Gln Lys Ser Thr Leu Ala Pro Phe Val
595 600 605
Trp Glu Ser Lys Arg Leu Trp Lys Asp Leu Gly Gly Asp Ala Thr Val
610 615 620

Thr Tyr Lys Ile Pro Arg Ser Asp Arg Met Gly Leu Ser Ser Ile Gly
625 630 635 640
Asn Ile Asp Tyr Ala Arg Pro Glu Val Pro Phe Leu Lys Glu Lys Trp
645 650 655
Asn Ala Arg Leu Gln Ser Asp Arg Arg Thr Leu Glu Lys Leu Glu Lys
660 665 670
Tyr Trp Asn Pro Glu Ser Met Lys Trp Ile Asp Asp Gly Lys Phe Leu
675 680 685

Ile Gln Ser Lys Trp Phe Ile Thr Phe Gly Pro Asp Met Glu Thr Ala
690 695 700
Glu Gly Pro Trp Lys Leu Tyr Leu Lys Glu Asn Ile Asn Asp Asn Asn
705 710 715 720
Tyr Leu Gly Asn Arg Ser Lys Glu Asn Gln Lys Arg Gly Tyr Arg Ala
725 730 735
Lys Lys Leu Leu Ser Gly Tyr Pro Ala Gly Met Arg Ile Leu Ser Val
740 745 750

Asp Leu Gly His Arg Tyr Ala Ala Ser Cys Ala Ile Trp Glu Thr Ile
755 760 765
Thr Lys Lys Gln Ile Thr Glu Glu Leu Ala Tyr Gln Pro Asp Lys Asn

770 775 780

Ser Val Phe Glu His Ser Cys Lys Thr Ile Asp Lys Lys Ile Lys Asn

785 790 795 800

Thr Val Tyr Arg Arg Ile Gly Asp Asp Ser Ile Asp Ala Pro Trp Ala

805 810 815

Lys Leu Glu Lys Gln Phe Thr Ile Lys Leu Gln Gly Glu Asp Lys Ser

820 825 830

Cys Tyr Leu Leu Arg Ser Asp Glu Lys Glu Leu Phe Arg Ser Ile Leu

835 840 845

Ser Lys Leu Ser Cys Leu Asn Asn Asp Thr Gly His Asn Ile Leu Glu

850 855 860

Met Ile Glu Asn Leu Leu Arg Ile Val Lys Ala Lys Ile Tyr Arg Gln

865 870 875 880

Gly Ile Leu Ala Arg Ile Ser Tyr Ser Met Thr Ala Gln Tyr Lys Pro

885 890 895

Gly Lys Gly Gly Gln Lys Ser Pro Leu Ser Asp Glu Asp Lys Ile His

900 905 910

Tyr Leu Ser Glu Asn Leu Ala Ala Trp Ser Ala Leu Met Gly Asn Gln

915 920 925

Glu Trp Asn Glu Asp Gly Ile Ser Asp Trp Tyr Lys Lys Tyr Ile Ser

930 935 940

His Leu Val Ser Gly Pro Lys Pro Lys Glu Gly Asn Arg Lys Ser Asp

945 950 955 960

Arg Asp Lys Ile Ile Glu Tyr Phe Leu Pro Ala Ala Arg Lys Leu Tyr

965 970 975

Asp Asp Asn Glu Thr Arg Ile Asn Ile His Asp Leu Phe Lys Glu Leu

980 985 990

Trp Asp Glu Asn Asn Lys Gln Leu Ser Ala Val Leu Lys Glu Ile Lys

995 1000 1005

Lys Ile Ile Leu Pro Lys Gly Ile Arg Tyr Phe Asp Lys Asn Asn

1010 1015 1020

Asp Ser Ser Ser Arg Trp Lys Asn Asn Gln Ser Lys Leu Lys Gln
1025 1030 1035
Ile Thr His Arg Gly Gly Leu Ser Leu Arg Arg Ile Val Ala Ile
1040 1045 1050
Glu Gly Tyr Tyr Lys Leu Ala Lys Ala Tyr Lys Asn His Pro Glu
1055 1060 1065

Pro Asp Asn Leu Thr Lys Asn Ile Pro Leu Pro Gly Asp Asn Ser
1070 1075 1080
Ser Ala Gly Phe Asn Gln Arg Ile Arg Asp Thr Leu Glu Arg Met
1085 1090 1095
Lys Glu Gln Arg Val Lys Gln Ile Ala Ser Arg Ile Val Glu Ser
1100 1105 1110
Ala Leu Gly Leu Gly Ile Glu Gly Tyr Lys Lys Arg Pro Leu Thr
1115 1120 1125

Pro Glu Ser Lys Pro Cys Gln Ala Ile Val Ile Glu Asp Leu Ser
1130 1135 1140
His Tyr Arg Pro Asp Glu Leu Gln Thr Arg Arg Glu Asn Arg Arg
1145 1150 1155
Leu Met Gln Trp Ser Ser Ser Lys Val Lys Lys Tyr Leu Ser Glu
1160 1165 1170
Ala Cys Glu Met His Asp Val Leu Leu Val Glu Ile Ser Pro Glu
1175 1180 1185

Tyr Thr Ser Arg Gln Asp Ser Arg Thr Gly Val Ala Gly Leu Arg
1190 1195 1200
Cys Ile Asp Ile Asn Ile Arg Glu Phe Leu Lys Asp Ser Ser Ser
1205 1210 1215
Trp Gln Asn Lys Ile Lys Thr Ile Gln Met Lys Pro Thr Asn Lys
1220 1225 1230
Lys Ser Asn Leu Asp Gln Tyr Leu Ile Glu Leu Asn Glu Ser Leu
1235 1240 1245

Gly Glu Arg Tyr Lys Asp Lys Val Ile Pro Ser Asp Lys Phe Val

1250 1255 1260

Arg Ile Pro Arg Lys Gly Gly Asp Ile Phe Val Ser Ser Ser Lys

1265 1270 1275

Glu Ser Pro Val Ser Lys Gly Ile Gln Ala Asp Leu Asn Ala Ala

1280 1285 1290

Ala Asn Ile Gly Leu Lys Ala Leu Leu Asp Pro Asp Trp Ala Gly

1295 1300 1305

Ala Trp Trp Tyr Ile Leu Ile Glu Ala Lys Ser Asn His Val Ile

1310 1315 1320

Pro Tyr Gly Lys Lys Tyr Lys Gly Ala Glu Cys Leu Arg Asp Phe

1325 1330 1335

Lys Phe Ser Gly Leu Glu Asn Gln Val Met Lys Asn Asn Met Asn

1340 1345 1350

Leu Trp Arg Asp Leu Gln Ser Gln Phe Ser Ser Glu Asp Lys Trp

1355 1360 1365

Met Ser Tyr Lys Glu Tyr Asn Glu Leu Thr Glu Lys Arg Val Ile

1370 1375 1380

Asn Ile Leu Arg Glu Arg Ala Gly Leu Glu Leu Ile Glu Glu

1385 1390 1395

<210> 169

<211> 1203

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 169

Met Pro Thr Arg Thr Ile Asn Leu Lys Met Val Leu Gly Arg Lys Asp

1 5 10 15

Asp Thr Ala Glu Leu Arg Arg Ala Leu Trp Thr Thr His Glu His Val

20 25 30

Asn Leu Ala Val Ala Glu Val Glu Arg Val Leu Leu Arg Cys Arg Gly

35 40 45

Arg Ser Tyr Trp Thr Leu Asp Arg Arg Gly Asp Pro Val His Val Pro
50 55 60
Glu Ser Gln Val Ala Glu Asp Ala Leu Ala Met Ala Arg Glu Ala Gln
65 70 75 80
Arg Arg Asn Gly Trp Pro Val Val Gly Glu Asp Glu Glu Ile Leu Leu

85 90 95
Ala Leu Arg Tyr Leu Tyr Glu Gln Ile Val Pro Ser Cys Leu Leu Asp
100 105 110
Asp Leu Gly Lys Pro Leu Lys Gly Asp Ala Gln Lys Ile Gly Thr Asn
115 120 125
Tyr Ala Gly Pro Leu Phe Asp Ser Asp Thr Cys Arg Arg Asp Glu Gly
130 135 140
Lys Asp Val Ala Cys Cys Gly Pro Phe His Glu Val Ala Gly Lys Tyr

145 150 155 160
Leu Gly Ala Leu Pro Glu Trp Ala Thr Pro Ile Ser Lys Gln Glu Phe
165 170 175
Asp Gly Lys Asp Ala Ser His Leu Arg Phe Lys Ala Thr Gly Gly Asp
180 185 190
Asp Ala Phe Phe Arg Val Ser Ile Glu Lys Ala Asn Ala Trp Tyr Glu
195 200 205
Asp Pro Ala Asn Gln Asp Ala Leu Lys Asn Lys Ala Tyr Asn Lys Asp

210 215 220
Asp Trp Lys Lys Glu Lys Asp Lys Gly Ile Ser Ser Trp Ala Val Lys
225 230 235 240
Tyr Ile Gln Lys Gln Leu Gln Leu Gly Gln Asp Pro Arg Thr Glu Val
245 250 255
Arg Arg Lys Leu Trp Leu Glu Leu Gly Leu Leu Pro Leu Phe Ile Pro
260 265 270
Val Phe Asp Lys Thr Met Val Gly Asn Leu Trp Asn Arg Leu Ala Val

275 280 285
Arg Leu Ala Leu Ala His Leu Leu Ser Trp Glu Ser Trp Asn His Arg

290 295 300

Ala Val Gln Asp Gln Ala Leu Ala Arg Ala Lys Arg Asp Glu Leu Ala

305 310 315 320

Ala Leu Phe Leu Gly Met Glu Asp Gly Phe Ala Gly Leu Arg Glu Tyr

325 330 335

Glu Leu Arg Arg Asn Glu Ser Ile Lys Gln His Ala Phe Glu Pro Val

340 345 350

Asp Arg Pro Tyr Val Val Ser Gly Arg Ala Leu Arg Ser Trp Thr Arg

355 360 365

Val Arg Glu Glu Trp Leu Arg His Gly Asp Thr Gln Glu Ser Arg Lys

370 375 380

Asn Ile Cys Asn Arg Leu Gln Asp Arg Leu Arg Gly Lys Phe Gly Asp

385 390 395 400

Pro Asp Val Phe His Trp Leu Ala Glu Asp Gly Gln Glu Ala Leu Trp

405 410 415

Lys Glu Arg Asp Cys Val Thr Ser Phe Ser Leu Leu Asn Asp Ala Asp

420 425 430

Gly Leu Leu Glu Lys Arg Lys Gly Tyr Ala Leu Met Thr Phe Ala Asp

435 440 445

Ala Arg Leu His Pro Arg Trp Ala Met Tyr Glu Ala Pro Gly Gly Ser

450 455 460

Asn Leu Arg Thr Tyr Gln Ile Arg Lys Thr Glu Asn Gly Leu Trp Ala

465 470 475 480

Asp Val Val Leu Leu Ser Pro Arg Asn Glu Ser Ala Ala Val Glu Glu

485 490 495

Lys Thr Phe Asn Val Arg Leu Ala Pro Ser Gly Gln Leu Ser Asn Val

500 505 510

Ser Phe Asp Gln Ile Gln Lys Gly Ser Lys Met Val Gly Arg Cys Arg

515 520 525

Tyr Gln Ser Ala Asn Gln Gln Phe Glu Gly Leu Leu Gly Gly Ala Glu

530 535 540

Ile Leu Phe Asp Arg Lys Arg Ile Ala Asn Glu Gln His Gly Ala Thr
545 550 555 560
Asp Leu Ala Ser Lys Pro Gly His Val Trp Phe Lys Leu Thr Leu Asp
565 570 575
Val Arg Pro Gln Ala Pro Gln Gly Trp Leu Asp Gly Lys Gly Arg Pro
580 585 590
Ala Leu Pro Pro Glu Ala Lys His Phe Lys Thr Ala Leu Ser Asn Lys

595 600 605
Ser Lys Phe Ala Asp Gln Val Arg Pro Gly Leu Arg Val Leu Ser Val
610 615 620
Asp Leu Gly Val Arg Ser Phe Ala Ala Cys Ser Val Phe Glu Leu Val
625 630 635 640
Arg Gly Gly Pro Asp Gln Gly Thr Tyr Phe Pro Ala Ala Asp Gly Arg
645 650 655
Thr Val Asp Asp Pro Glu Lys Leu Trp Ala Lys His Glu Arg Ser Phe

660 665 670
Lys Ile Thr Leu Pro Gly Glu Asn Pro Ser Arg Lys Glu Glu Ile Ala
675 680 685
Arg Arg Ala Ala Met Glu Glu Leu Arg Ser Leu Asn Gly Asp Ile Arg
690 695 700
Arg Leu Lys Ala Ile Leu Arg Leu Ser Val Leu Gln Glu Asp Asp Pro
705 710 715 720
Arg Thr Glu His Leu Arg Leu Phe Met Glu Ala Ile Val Asp Asp Pro

725 730 735
Ala Lys Ser Ala Leu Asn Ala Glu Leu Phe Lys Gly Phe Gly Asp Asp
740 745 750
Arg Phe Arg Ser Thr Pro Asp Leu Trp Lys Gln His Cys His Phe Phe
755 760 765
His Asp Lys Ala Glu Lys Val Val Ala Glu Arg Phe Ser Arg Trp Arg
770 775 780
Thr Glu Thr Arg Pro Lys Ser Ser Ser Trp Gln Asp Trp Arg Glu Arg

785 790 795 800

Arg Gly Tyr Ala Gly Gly Lys Ser Tyr Trp Ala Val Thr Tyr Leu Glu

805 810 815

Ala Val Arg Gly Leu Ile Leu Arg Trp Asn Met Arg Gly Arg Thr Tyr

820 825 830

Gly Glu Val Asn Arg Gln Asp Lys Lys Gln Phe Gly Thr Val Ala Ser

835 840 845

Ala Leu Leu His His Ile Asn Gln Leu Lys Glu Asp Arg Ile Lys Thr

850 855 860

Gly Ala Asp Met Ile Ile Gln Ala Ala Arg Gly Phe Val Pro Arg Lys

865 870 875 880

Asn Gly Ala Gly Trp Val Gln Val His Glu Pro Cys Arg Leu Ile Leu

885 890 895

Phe Glu Asp Leu Ala Arg Tyr Arg Phe Arg Thr Asp Arg Ser Arg Arg

900 905 910

Glu Asn Ser Arg Leu Met Arg Trp Ser His Arg Glu Ile Val Asn Glu

915 920 925

Val Gly Met Gln Gly Glu Leu Tyr Gly Leu His Val Asp Thr Thr Glu

930 935 940

Ala Gly Phe Ser Ser Arg Tyr Leu Ala Ser Ser Gly Ala Pro Gly Val

945 950 955 960

Arg Cys Arg His Leu Val Glu Glu Asp Phe His Asp Gly Leu Pro Gly

965 970 975

Met His Leu Val Gly Glu Leu Asp Trp Leu Leu Pro Lys Asp Lys Asp

980 985 990

Arg Thr Ala Asn Glu Ala Arg Arg Leu Leu Gly Gly Met Val Arg Pro

995 1000 1005

Gly Met Leu Val Pro Trp Asp Gly Gly Glu Leu Phe Ala Thr Leu

1010 1015 1020

Asn Ala Ala Ser Gln Leu His Val Ile His Ala Asp Ile Asn Ala

1025 1030 1035

Ala Gln Asn Leu Gln Arg Arg Phe Trp Gly Arg Cys Gly Glu Ala

1040 1045 1050

Ile Arg Ile Val Cys Asn Gln Leu Ser Val Asp Gly Ser Thr Arg

1055 1060 1065

Tyr Glu Met Ala Lys Ala Pro Lys Ala Arg Leu Leu Gly Ala Leu

1070 1075 1080

Gln Gln Leu Lys Asn Gly Asp Ala Pro Phe His Leu Thr Ser Ile

1085 1090 1095

Pro Asn Ser Gln Lys Pro Glu Asn Ser Tyr Val Met Thr Pro Thr

1100 1105 1110

Asn Ala Gly Lys Lys Tyr Arg Ala Gly Pro Gly Glu Lys Ser Ser

1115 1120 1125

Gly Glu Glu Asp Glu Leu Ala Leu Asp Ile Val Glu Gln Ala Glu

1130 1135 1140

Glu Leu Ala Gln Gly Arg Lys Thr Phe Phe Arg Asp Pro Ser Gly

1145 1150 1155

Val Phe Phe Ala Pro Asp Arg Trp Leu Pro Ser Glu Ile Tyr Trp

1160 1165 1170

Ser Arg Ile Arg Arg Arg Ile Trp Gln Val Thr Leu Glu Arg Asn

1175 1180 1185

Ser Ser Gly Arg Gln Glu Arg Ala Glu Met Asp Glu Met Pro Tyr

1190 1195 1200

<210> 170

<211> 1097

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 170

Met Val Thr Arg Ala Leu Asn Leu Lys Leu Val Val Pro Arg Arg Pro

1 5 10 15

Gly Glu Leu Thr Lys Ala Glu Ala Leu Trp Ser Thr His Asp Ile Val
20 25 30
Asn Arg Ala Thr Ser Tyr Tyr Glu Ser Gln Leu Leu Leu Cys Arg Gln
35 40 45
Gln Asp Tyr Gln Thr Arg Glu Leu Thr Val Ser Ala Gly Asp Gln Ala
50 55 60
Pro Asp Leu Asp Ala Leu Ile Ala Asn Ala Arg Asp Arg Asn Arg Tyr

65 70 75 80
Arg Gly Leu Glu Lys Pro Gln Val Val Arg Glu Lys Leu Arg Asn Leu
85 90 95
Tyr Glu Ala Ile Val Pro Pro Ala Ile Gly Lys Thr Gly Thr Ala Gln
100 105 110
Ala Val Gly Ala Phe Val Ser Pro Leu Leu Asp Ala Asp Ser Arg Gly
115 120 125
Phe Thr Glu Ile Phe Asp Lys Ile Glu Ala Leu Pro Asn Trp Val Asp

130 135 140
Gly Val Arg Ala Glu Glu Pro Asp Ala Leu Glu Ala Ala Ala Asp Trp
145 150 155 160
Leu Lys Ser Pro Gln Gly Lys Glu Arg Leu Arg Pro Thr Gly Ala Pro
165 170 175
Pro Thr Trp Ile Lys Leu Ala Lys Lys Lys Asp Ala Gly Trp Ala Ala
180 185 190
Ala Phe Val Ala Asp Ile Asp Lys Lys Leu Lys Glu Val Glu Gly Thr

195 200 205
Pro Thr Leu Met Gln Glu Leu Arg Ala Leu Gly Val Met Pro Leu Phe
210 215 220
Pro Ser Phe Phe Ala Ser Arg Ile Ala Gly His Lys Gly Ala Val Ser
225 230 235 240
Thr Trp Asp Arg Leu Ala Leu Arg Leu Ala Val Ala His Leu Leu Ser
245 250 255
Trp Glu Ser Trp Val Glu Leu Ala Ala Lys Glu His Ala Ala Arg Val

260 265 270

Ala Lys Leu Glu Lys Phe Arg Asp Asp Asn Ile Leu Gly Glu Ile Ala

275 280 285

Asp Ala Val Glu Ala Leu Arg Leu Tyr Glu Lys Glu Arg Thr Glu Glu

290 295 300

Leu Gln Gln Lys Ala Gln Leu Asp Ala Glu Glu Val Arg Thr Thr Ser

305 310 315 320

Arg Thr Ile Arg Gly Trp Val Asp Leu Arg Glu Lys Trp Leu Lys Thr

325 330 335

Asp Ala Ser Pro Asp Ala Leu Ile Ser Leu Val Ala Ala Glu Gln Lys

340 345 350

Arg Lys Ser Gly Lys Phe Gly Asp Pro Gln Leu Phe Arg Trp Leu Ala

355 360 365

Lys Pro Glu Asn His Phe Val Trp Asn Lys Pro Asp Phe Asp Pro Pro

370 375 380

Ser Leu Phe Ala Ser Leu Arg Met Ile Glu Gly Leu Val Glu Arg Ser

385 390 395 400

Lys Glu Thr Ala Trp Met Thr Leu Pro Asp Ala Arg Leu His Pro Arg

405 410 415

Ser Ser Gln Trp Glu Pro His Gly Gly Gly Asn Leu Lys Thr Phe Arg

420 425 430

Leu Glu Gln Gly Glu Gly Gly Ser Leu Ser Val Thr Leu Pro Leu Leu

435 440 445

Arg Lys Ser Gly Asp Asp Ser Tyr Val Glu Glu Glu His Ala Phe Ser

450 455 460

Leu Ala Gly Ser Lys Gln Ile Pro Asn Ala Ser Leu Asp Val Arg Arg

465 470 475 480

Asn Lys Tyr Cys Leu Ser Tyr Arg Thr Pro Thr Gly Glu Glu Ala Glu

485 490 495

Ala Val Val Gly Ser Ala Asp Leu Leu Leu Asp Trp Tyr Phe Leu Gln

500 505 510

Gln Arg Ser Glu His Arg Pro Glu Glu Gly Asp Ile Gly Pro Ala Phe

515 520 525

Leu Lys Leu Ala Leu Asp Ile Thr Pro Ile Asp Pro Val Trp Gly Glu

530 535 540

Arg Glu Lys Thr Pro Ala Ile His His Phe Lys Thr Ala Ser Gly Lys

545 550 555 560

Asn Thr Arg His Ala Asp Gly Val Ala Pro Gly Phe Arg Met Leu Ala

565 570 575

Val Asp Leu Gly Ile Arg Thr Leu Ala Thr Cys Ser Val Phe Glu Leu

580 585 590

Lys Ala Thr Ala Pro Ala Gly Arg Leu Ser Phe Pro Ile Ala His Leu

595 600 605

Asp Leu His Ala Val His Glu Arg Ser Phe Thr Leu Thr Leu Asp Gly

610 615 620

Glu Asp Pro Asp Arg Asp Ala Glu Arg Trp Arg Glu Asn Lys Ser Ala

625 630 635 640

Glu Leu Arg Arg Leu Arg Met Gly Leu Thr Arg Tyr Arg Asn Ile Arg

645 650 655

Asn Met Arg Glu Asp Ala Pro Asp Glu Arg Glu Val Leu Leu Glu Asp

660 665 670

Leu Gln Glu Lys Val Gln Glu His Gly Trp Ala Phe Glu Glu Pro Leu

675 680 685

Leu Arg Glu Leu Ala Lys His Lys Asp Thr Pro Glu Pro Ile Trp Glu

690 695 700

Ala Glu Leu Thr Lys Ala Leu Ala Gln Phe Arg Ser Asp Phe Gly Val

705 710 715 720

Ile Val Gly Glu Trp Arg Arg Ser Asn Arg Ala Arg Ser Thr Asp Ser

725 730 735

His Ala Gly Lys Ser Met Trp Ala Ile Asp His Leu Thr Asn Ser Arg

740 745 750

Arg Phe Leu Met Ser Trp Ser Leu Leu Ser Lys Pro Gly Gln Ile Arg

755 760 765

Arg Leu Asp Arg Asp Lys Gln Gly Val Phe Ala Lys His Leu Leu Asp

770 775 780

His Leu Glu Gly Leu Lys Ala Asp Arg Leu Lys Thr Gly Ser Asp Leu

785 790 795 800

Ile Val Gln Ala Ala Arg Gly Phe Arg Arg Asp Lys Arg Gly Asn Trp

805 810 815

His Lys Ala Tyr Lys Pro Cys His Gly Ile Leu Phe Glu Asp Leu Ser

820 825 830

Arg Tyr Arg Met Arg Thr Asp Arg Pro Arg Arg Glu Asn Ser Gln Leu

835 840 845

Met Lys Trp Ala His Arg Ala Val Pro Lys Glu Val Gly Met Gln Ala

850 855 860

Glu Val Tyr Gly Ile Arg Val Glu Asp Thr Gly Ala Ala Phe Ser Ser

865 870 875 880

Arg Phe His Ala Ala Ser His Thr Pro Gly Ile Arg Met His Pro Ile

885 890 895

Cys Gln Lys Asp Leu Glu Asn Glu Trp Leu Leu Asp Glu Ile Glu Lys

900 905 910

Gln Asn Ser Gly Val Lys Arg Arg Glu Leu Lys Leu Gly Gln Leu Val

915 920 925

Gln Leu Asn Gly Gly Glu Leu Phe Ala Cys Val Thr Ala Ser Gly Val

930 935 940

Lys Thr Leu His Ala Asp Ile Asn Ala Ala Gln Asn Leu Gln Arg Arg

945 950 955 960

Phe Phe Thr Arg His Gly Asp Ala Phe Arg Ile Val Ala Arg Lys Val

965 970 975

Leu Val Asp Glu Glu Glu Val Trp Val Pro Arg Ser Leu Gly Lys Arg

980 985 990

Leu Leu Gly Ala Leu Gly Ser His Gly Lys Leu Val Pro Thr Gly His

995 1000 1005

Glu Ser Gly Ser Cys Arg Phe Glu Glu Ile Thr Thr Arg Ala Trp

1010 1015 1020

Ser Lys Leu Ser Gly Glu Lys Leu Ser Asp Asp Arg Val Gly Asn

1025 1030 1035

Glu Glu Asp Gln Ile Ile Ala Ser Ile Glu Glu Glu Ala Leu Glu

1040 1045 1050

Arg Thr Gly Glu Val Val Val Phe Phe Arg Asp Pro Ser Gly Gln

1055 1060 1065

Val Leu Pro Arg Asp Leu Trp Tyr Pro Ser Lys Thr Phe Trp Ser

1070 1075 1080

Ile Val Lys Ser Thr Thr Leu Ser Lys Leu Lys Ala Ala Pro

1085 1090 1095

<210> 171

<211> 1272

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 171

Met Glu Asp Lys Gln Phe Leu Glu Arg Tyr Lys Glu Phe Ile Gly Leu

1 5 10 15

Asn Ser Leu Ser Lys Thr Leu Arg Asn Ser Leu Ile Pro Val Gly Ser

20 25 30

Thr Leu Lys His Ile Gln Glu Tyr Gly Ile Leu Glu Glu Asp Ser Leu

35 40 45

Arg Ala Gln Lys Arg Glu Glu Leu Lys Gly Ile Met Asp Asp Tyr Tyr

50 55 60

Arg Asn Tyr Ile Glu Met His Leu Arg Asp Val His Asp Ile Asp Trp

65 70 75 80

Asn Glu Leu Phe Glu Ala Leu Thr Glu Val Lys Lys Asn Gln Thr Asp

85 90 95

Asp Ala Lys Lys Cys Leu Glu Lys Ile Gln Glu Lys Lys Arg Lys Glu

100 105 110

Ile Tyr Gln Tyr Leu Ser Asp Asp Ala Val Phe Ser Glu Met Phe Lys

115 120 125

Glu Lys Met Ile Ser Gly Ile Leu Pro Asp Phe Ile Arg Cys Asn Glu

130 135 140

Glu Tyr Ser Glu Glu Glu Lys Glu Glu Lys Leu Lys Thr Val Ala Leu

145 150 155 160

Phe His Arg Phe Thr Ser Ser Phe Asn Asp Phe Phe Leu Asn Arg Lys

165 170 175

Asn Val Phe Thr Lys Glu Ala Ile Ala Thr Ala Ile Gly Tyr Arg Val

180 185 190

Val His Glu Asn Ala Glu Ile Phe Leu Glu Asn Met Val Ala Phe Gln

195 200 205

Asn Ile Gln Lys Ser Ala Glu Ser Gln Ile Ser Ile Ile Glu Arg Lys

210 215 220

Asn Glu His Tyr Phe Met Glu Trp Lys Leu Ser His Ile Phe Thr Ala

225 230 235 240

Asp Tyr Tyr Met Met Leu Met Thr Gln Lys Ala Ile Glu His Tyr Asn

245 250 255

Glu Met Cys Gly Val Val Asn Gln His Met Lys Glu Tyr Cys Gln Lys

260 265 270

Glu Lys Lys Asn Trp Asn Leu Tyr Arg Met Lys Arg Leu His Lys Gln

275 280 285

Ile Leu Ser Asn Ala Ser Thr Ser Phe Lys Ile Pro Glu Lys Tyr Glu

290 295 300

Asn Asp Ala Glu Val Tyr Glu Ser Val Asn Ser Phe Leu Gln Asn Val

305 310 315 320

Met Glu Lys Thr Val Met Glu Arg Ile Ala Val Leu Lys Asn Asn Thr

325 330 335

Asp Asn Phe Asp Leu Ser Lys Ile Tyr Ile Thr Ala Pro Tyr Tyr Glu

340 345 350

Lys Ile Ser Asn Tyr Leu Cys Gly Ser Trp Asn Thr Ile Ala Asp Cys

355 360 365

Leu Thr His Tyr Tyr Glu Gln Gln Ile Ala Gly Lys Gly Ala Arg Lys

370 375 380

Asp Gln Lys Val Lys Ala Ala Val Lys Ala Asp Lys Trp Lys Ser Leu

385 390 395 400

Ser Glu Ile Glu Gln Leu Leu Lys Glu Tyr Ala Arg Ala Glu Glu Val

405 410 415

Lys Arg Lys Pro Glu Glu Tyr Ile Ala Glu Ile Glu Asn Ile Val Ser

420 425 430

Leu Lys Glu Val His Leu Leu Glu Tyr His Pro Glu Val Asn Leu Ile

435 440 445

Glu Asn Glu Lys Tyr Ala Thr Glu Ile Lys Asp Val Leu Asp Asn Tyr

450 455 460

Met Glu Leu Phe His Trp Met Lys Trp Phe Tyr Ile Glu Glu Ala Val

465 470 475 480

Glu Lys Glu Val Asn Phe Tyr Gly Glu Leu Asp Asp Leu Tyr Glu Glu

485 490 495

Ile Arg Asp Ile Val Pro Leu Tyr Asn Lys Val Arg Asn Tyr Val Thr

500 505 510

Gln Lys Pro Tyr Ser Asp Thr Lys Ile Lys Leu Asn Phe Gly Thr Pro

515 520 525

Thr Leu Ala Asn Gly Trp Ser Lys Ser Lys Glu Tyr Asp Tyr Asn Ala

530 535 540

Ile Leu Leu Gln Lys Asp Gly Lys Tyr Tyr Met Gly Ile Phe Asn Pro

545 550 555 560

Val Gln Lys Pro Glu Lys Glu Ile Ile Glu Gly His Ser His Pro Leu

565 570 575

Glu Gly Asn Glu Tyr Lys Lys Met Val Tyr Tyr Tyr Leu Pro Ser Ala

580 585 590

Asn Lys Met Leu Pro Lys Val Leu Leu Ser Lys Lys Gly Met Glu Ile
595 600 605
Tyr Gln Pro Ser Glu Tyr Ile Ile Asn Gly Tyr Lys Glu Arg Arg His

610 615 620
Ile Lys Ser Glu Glu Lys Phe Asp Leu Gln Phe Cys His Asp Leu Ile
625 630 635 640
Asp Tyr Phe Lys Ser Gly Ile Glu Arg Asn Pro Asp Trp Lys Val Phe
645 650 655
Gly Phe His Phe Ser Asp Thr Asp Thr Tyr Gln Asp Ile Ser Gly Phe
660 665 670
Tyr Arg Glu Val Glu Asp Gln Gly Tyr Lys Ile Asp Trp Thr Tyr Ile

675 680 685
Lys Glu Ala Asp Ile Asp Arg Leu Asn Glu Glu Gly Lys Leu Tyr Leu
690 695 700
Phe Gln Ile Tyr Asn Lys Asp Phe Ser Glu Lys Ser Thr Gly Arg Glu
705 710 715 720
Asn Leu His Thr Met Tyr Leu Lys Asn Leu Phe Ser Glu Glu Asn Ile
725 730 735
Arg Glu Gln Val Leu Lys Leu Asn Gly Glu Ala Glu Ile Phe Phe Arg

740 745 750
Lys Ser Ser Val Lys Lys Pro Ile Ile His Lys Lys Gly Thr Met Leu
755 760 765
Val Asn Arg Thr Tyr Met Glu Glu Met His Gly Glu Ser Val Lys Lys
770 775 780
Asn Ile Pro Glu Lys Glu Tyr Gln Glu Ile Tyr Asn Tyr Met Asn His
785 790 795 800
Arg Trp Lys Gly Glu Leu Ser Ala Glu Ala Lys Glu Tyr Leu Lys Lys

805 810 815
Ala Val Cys His Glu Thr Lys Lys Asp Ile Val Lys Asp Tyr Arg Tyr
820 825 830
Ser Val Asp Lys Phe Phe Ile His Leu Pro Ile Thr Ile Asn Tyr Arg

835 840 845

Ala Ser Gly Lys Glu Ala Leu Asn Ser Val Ala Gln Arg Tyr Ile Ala

850 855 860

His Gln Asn Asp Met His Val Ile Gly Ile Asp Arg Gly Glu Arg Asn

865 870 875 880

Leu Ile Tyr Val Ser Val Ile Asn Met Gln Gly Glu Ile Ile Glu Gln

885 890 895

Lys Ser Phe Asn Val Val Asn Lys Tyr Asn Tyr Lys Glu Lys Leu Lys

900 905 910

Glu Arg Glu Gln Asn Arg Asp Glu Ala Arg Lys Asn Trp Lys Glu Ile

915 920 925

Gly Gln Ile Lys Asp Leu Lys Glu Gly Tyr Leu Ser Gly Val Ile His

930 935 940

Glu Ile Ala Lys Met Met Ile Lys Tyr His Ala Ile Val Ala Met Glu

945 950 955 960

Asp Leu Asn Tyr Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Arg Gln

965 970 975

Val Tyr Gln Lys Phe Glu Asn Met Leu Ile Gln Lys Leu Asn Tyr Leu

980 985 990

Val Phe Lys Asp Arg Ser Ala Asp Glu Asp Gly Gly Val Leu Arg Gly

995 1000 1005

Tyr Gln Leu Ala Tyr Ile Pro Asp Ser Val Lys Lys Leu Gly Arg

1010 1015 1020

Gln Cys Gly Met Ile Phe Tyr Val Pro Ala Ala Phe Thr Ser Lys

1025 1030 1035

Ile Asp Pro Ala Thr Gly Phe Val Asp Ile Phe Asn His Lys Ala

1040 1045 1050

Tyr Thr Thr Asp Gln Ala Lys Arg Glu Phe Ile Leu Ser Phe Asp

1055 1060 1065

Glu Ile Cys Tyr Asp Val Glu Arg Gln Leu Phe Arg Phe Thr Phe

1070 1075 1080

Asp Tyr Ala Asn Phe Ala Thr His Asn Val Thr Leu Ala Arg Asn

1085 1090 1095

Asn Trp Thr Ile Tyr Thr Asn Gly Thr Arg Thr Gln Lys Glu Phe

1100 1105 1110

Val Asn Arg Arg Val Arg Asp Lys Lys Glu Val Phe Asp Pro Thr

1115 1120 1125

Glu Lys Met Leu Lys Leu Leu Glu Leu Glu Gly Val Glu Tyr Gln

1130 1135 1140

Ser Gly Ala Asn Leu Leu Pro Lys Leu Glu Lys Ile Ser Asp Pro

1145 1150 1155

His Leu Phe His Glu Leu Gln Arg Ile Val Arg Phe Thr Val Gln

1160 1165 1170

Leu Arg Asn Ser Lys Asn Glu Glu Asn Asp Val Asp Tyr Asp His

1175 1180 1185

Val Ile Ser Pro Val Leu Asn Glu Glu Gly Lys Phe Phe Asp Ser

1190 1195 1200

Ser Lys Tyr Glu Asn Lys Glu Glu Lys Lys Glu Ser Leu Leu Pro

1205 1210 1215

Val Asp Ala Asp Ala Asn Gly Ala Tyr Cys Ile Ala Leu Lys Gly

1220 1225 1230

Leu Tyr Ile Met Gln Ala Ile Gln Lys Asn Trp Ser Glu Glu Lys

1235 1240 1245

Ala Leu Ser Pro Asp Val Leu Arg Leu Asn Asn Asn Asp Trp Phe

1250 1255 1260

Asp Tyr Ile Gln Asn Lys Arg Tyr Arg

1265 1270

<210> 172

<211> 767

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 172

Met Ala Gln Ala Ser Ser Thr Pro Ala Val Ser Pro Arg Pro Arg Pro
1 5 10 15

Arg Tyr Arg Glu Glu Arg Thr Leu Val Arg Lys Leu Leu Pro Arg Pro
20 25 30

Gly Gln Ser Lys Gln Glu Phe Arg Glu Asn Val Lys Lys Leu Arg Lys
35 40 45

Ala Phe Leu Gln Phe Asn Ala Asp Val Ser Gly Val Cys Gln Trp Ala
50 55 60

Ile Gln Phe Arg Pro Arg Tyr Gly Lys Pro Ala Glu Pro Thr Glu Thr
65 70 75 80

Phe Trp Lys Phe Phe Leu Glu Pro Glu Thr Ser Leu Pro Pro Asn Asp
85 90 95

Ser Arg Ser Pro Glu Phe Arg Arg Leu Gln Ala Phe Glu Ala Ala Ala
100 105 110

Gly Ile Asn Gly Ala Ala Ala Leu Asp Asp Pro Ala Phe Thr Asn Glu
115 120 125

Leu Arg Asp Ser Ile Leu Ala Val Ala Ser Arg Pro Lys Thr Lys Glu
130 135 140

Ala Gln Arg Leu Phe Ser Arg Leu Lys Asp Tyr Gln Pro Ala His Arg
145 150 155 160

Met Ile Leu Ala Lys Val Ala Ala Glu Trp Ile Glu Ser Arg Tyr Arg
165 170 175

Arg Ala His Gln Asn Trp Glu Arg Asn Tyr Glu Glu Trp Lys Lys Glu
180 185 190

Lys Gln Glu Trp Glu Gln Asn His Pro Glu Leu Thr Pro Glu Ile Arg
195 200 205

Glu Ala Phe Asn Gln Ile Phe Gln Gln Leu Glu Val Lys Glu Lys Arg
210 215 220

Val Arg Ile Cys Pro Ala Ala Arg Leu Leu Gln Asn Lys Asp Asn Cys
225 230 235 240

Gln Tyr Ala Gly Lys Asn Lys His Ser Val Leu Cys Asn Gln Phe Asn
245 250 255
Glu Phe Lys Lys Asn His Leu Gln Gly Lys Ala Ile Lys Phe Phe Tyr
260 265 270

Lys Asp Ala Glu Lys Tyr Leu Arg Cys Gly Leu Gln Ser Leu Lys Pro
275 280 285
Asn Val Gln Gly Pro Phe Arg Glu Asp Trp Asn Lys Tyr Leu Arg Tyr
290 295 300
Met Asn Leu Lys Glu Glu Thr Leu Arg Gly Lys Asn Gly Gly Arg Leu
305 310 315 320
Pro His Cys Lys Asn Leu Gly Gln Glu Cys Glu Phe Asn Pro His Thr
325 330 335

Ala Leu Cys Lys Gln Tyr Gln Gln Gln Leu Ser Ser Arg Pro Asp Leu
340 345 350
Val Gln His Asp Glu Leu Tyr Arg Lys Trp Arg Arg Glu Tyr Trp Arg
355 360 365
Glu Pro Arg Lys Pro Val Phe Arg Tyr Pro Ser Val Lys Arg His Ser
370 375 380
Ile Ala Lys Ile Phe Gly Glu Asn Tyr Phe Gln Ala Asp Phe Lys Asn
385 390 395 400

Ser Val Val Gly Leu Arg Leu Asp Ser Met Pro Ala Gly Gln Tyr Leu
405 410 415
Glu Phe Ala Phe Ala Pro Trp Pro Arg Asn Tyr Arg Pro Gln Pro Gly
420 425 430
Glu Thr Glu Ile Ser Ser Val His Leu His Phe Val Gly Thr Arg Pro
435 440 445
Arg Ile Gly Phe Arg Phe Arg Val Pro His Lys Arg Ser Arg Phe Asp
450 455 460

Cys Thr Gln Glu Glu Leu Asp Glu Leu Arg Ser Arg Thr Phe Pro Arg
465 470 475 480
Lys Ala Gln Asp Gln Lys Phe Leu Glu Ala Ala Arg Lys Arg Leu Leu

485 490 495

Glu Thr Phe Pro Gly Asn Ala Glu Gln Glu Leu Arg Leu Leu Ala Val

500 505 510

Asp Leu Gly Thr Asp Ser Ala Arg Ala Ala Phe Phe Ile Gly Lys Thr

515 520 525

Phe Gln Gln Ala Phe Pro Leu Lys Ile Val Lys Ile Glu Lys Leu Tyr

530 535 540

Glu Gln Trp Pro Asn Gln Lys Gln Ala Gly Asp Arg Arg Asp Ala Ser

545 550 555 560

Ser Lys Gln Pro Arg Pro Gly Leu Ser Arg Asp His Val Gly Arg His

565 570 575

Leu Gln Lys Met Arg Ala Gln Ala Ser Glu Ile Ala Gln Lys Arg Gln

580 585 590

Glu Leu Thr Gly Thr Pro Ala Pro Glu Thr Thr Thr Asp Gln Ala Ala

595 600 605

Lys Lys Ala Thr Leu Gln Pro Phe Asp Leu Arg Gly Leu Thr Val His

610 615 620

Thr Ala Arg Met Ile Arg Asp Trp Ala Arg Leu Asn Ala Arg Gln Ile

625 630 635 640

Ile Gln Leu Ala Glu Glu Asn Gln Val Asp Leu Ile Val Leu Glu Ser

645 650 655

Leu Arg Gly Phe Arg Pro Pro Gly Tyr Glu Asn Leu Asp Gln Glu Lys

660 665 670

Lys Arg Arg Val Ala Phe Phe Ala His Gly Arg Ile Arg Arg Lys Val

675 680 685

Thr Glu Lys Ala Val Glu Arg Gly Met Arg Val Val Thr Val Pro Tyr

690 695 700

Leu Ala Ser Ser Lys Val Cys Ala Glu Cys Arg Lys Lys Gln Lys Asp

705 710 715 720

Asn Lys Gln Trp Glu Lys Asn Lys Lys Arg Gly Leu Phe Lys Cys Glu

725 730 735

Gly Cys Gly Ser Gln Ala Gln Val Asp Glu Asn Ala Ala Arg Val Leu
740 745 750

Gly Arg Val Phe Trp Gly Glu Ile Glu Leu Pro Thr Ala Ile Pro
755 760 765

<210> 173

<211> 1147

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas12 sequence

<400> 173

Met Ala Val Lys Ser Ile Lys Val Lys Leu Arg Leu Ser Glu Cys Pro
1 5 10 15

Asp Ile Leu Ala Gly Met Trp Gln Leu His Arg Ala Thr Asn Ala Gly
20 25 30

Val Arg Tyr Tyr Thr Glu Trp Val Ser Leu Met Arg Gln Glu Ile Leu
35 40 45

Tyr Ser Arg Gly Pro Asp Gly Gly Gln Gln Cys Tyr Met Thr Ala Glu
50 55 60

Asp Cys Gln Arg Glu Leu Leu Arg Arg Leu Arg Asn Arg Gln Leu His
65 70 75 80

Asn Gly Arg Gln Asp Gln Pro Gly Thr Asp Ala Asp Leu Leu Ala Ile
85 90 95

Ser Arg Arg Leu Tyr Glu Ile Leu Val Leu Gln Ser Ile Gly Lys Arg
100 105 110

Gly Asp Ala Gln Gln Ile Ala Ser Ser Phe Leu Ser Pro Leu Val Asp
115 120 125

Pro Asn Ser Lys Gly Gly Arg Gly Glu Ala Lys Ser Gly Arg Lys Pro
130 135 140

Ala Trp Gln Lys Met Arg Asp Gln Gly Asp Pro Arg Trp Val Ala Ala
145 150 155 160

Arg Glu Lys Tyr Glu Gln Arg Lys Ala Val Asp Pro Ser Lys Glu Ile

165 170 175

Leu Asn Ser Leu Asp Ala Leu Gly Leu Arg Pro Leu Phe Ala Val Phe

180 185 190

Thr Glu Thr Tyr Arg Ser Gly Val Asp Trp Lys Pro Leu Gly Lys Ser

195 200 205

Gln Gly Val Arg Thr Trp Asp Arg Asp Met Phe Gln Gln Ala Leu Glu

210 215 220

Arg Leu Met Ser Trp Glu Ser Trp Asn Arg Arg Val Gly Glu Glu Tyr

225 230 235 240

Ala Arg Leu Phe Gln Gln Lys Met Lys Phe Glu Gln Glu His Phe Ala

245 250 255

Glu Gln Ser His Leu Val Lys Leu Ala Arg Ala Leu Glu Ala Asp Met

260 265 270

Arg Ala Ala Ser Gln Gly Phe Glu Ala Lys Arg Gly Thr Ala His Gln

275 280 285

Ile Thr Arg Arg Ala Leu Arg Gly Ala Asp Arg Val Phe Glu Ile Trp

290 295 300

Lys Ser Ile Pro Glu Glu Ala Leu Phe Ser Gln Tyr Asp Glu Val Ile

305 310 315 320

Arg Gln Val Gln Ala Glu Lys Arg Arg Asp Phe Gly Ser His Asp Leu

325 330 335

Phe Ala Lys Leu Ala Glu Pro Lys Tyr Gln Pro Leu Trp Arg Ala Asp

340 345 350

Glu Thr Phe Leu Thr Arg Tyr Ala Leu Tyr Asn Gly Val Leu Arg Asp

355 360 365

Leu Glu Lys Ala Arg Gln Phe Ala Thr Phe Thr Leu Pro Asp Ala Cys

370 375 380

Val Asn Pro Ile Trp Thr Arg Phe Glu Ser Ser Gln Gly Ser Asn Leu

385 390 395 400

His Lys Tyr Glu Phe Leu Phe Asp His Leu Gly Pro Gly Arg His Ala

405 410 415

Val Arg Phe Gln Arg Leu Leu Val Val Glu Ser Glu Gly Ala Lys Glu
420 425 430
Arg Asp Ser Val Val Val Pro Val Ala Pro Ser Gly Gln Leu Asp Lys
435 440 445

Leu Val Leu Arg Glu Glu Glu Lys Ser Ser Val Ala Leu His Leu His
450 455 460
Asp Thr Ala Arg Pro Asp Gly Phe Met Ala Glu Trp Ala Gly Ala Lys
465 470 475 480
Leu Gln Tyr Glu Arg Ser Thr Leu Ala Arg Lys Ala Arg Arg Asp Lys
485 490 495
Gln Gly Met Arg Ser Trp Arg Arg Gln Pro Ser Met Leu Met Ser Ala
500 505 510

Ala Gln Met Leu Glu Asp Ala Lys Gln Ala Gly Asp Val Tyr Leu Asn
515 520 525
Ile Ser Val Arg Val Lys Ser Pro Ser Glu Val Arg Gly Gln Arg Arg
530 535 540
Pro Pro Tyr Ala Ala Leu Phe Arg Ile Asp Asp Lys Gln Arg Arg Val
545 550 555 560
Thr Val Asn Tyr Asn Lys Leu Ser Ala Tyr Leu Glu Glu His Pro Asp
565 570 575

Lys Gln Ile Pro Gly Ala Pro Gly Leu Leu Ser Gly Leu Arg Val Met
580 585 590
Ser Val Asp Leu Gly Leu Arg Thr Ser Ala Ser Ile Ser Val Phe Arg
595 600 605
Val Ala Lys Lys Glu Glu Val Glu Ala Leu Gly Asp Gly Arg Pro Pro
610 615 620
His Tyr Tyr Pro Ile His Gly Thr Asp Asp Leu Val Ala Val His Glu
625 630 635 640

Arg Ser His Leu Ile Gln Met Pro Gly Glu Thr Glu Thr Lys Gln Leu
645 650 655
Arg Lys Leu Arg Glu Glu Arg Gln Ala Val Leu Arg Pro Leu Phe Ala

660 665 670

Gln Leu Ala Leu Leu Arg Leu Leu Val Arg Cys Gly Ala Ala Asp Glu

675 680 685

Arg Ile Arg Thr Arg Ser Trp Gln Arg Leu Thr Lys Gln Gly Arg Glu

690 695 700

Phe Thr Lys Arg Leu Thr Pro Ser Trp Arg Glu Ala Leu Glu Leu Glu

705 710 715 720

Leu Thr Arg Leu Glu Ala Tyr Cys Gly Arg Val Pro Asp Asp Glu Trp

725 730 735

Ser Arg Ile Val Asp Arg Thr Val Ile Ala Leu Trp Arg Arg Met Gly

740 745 750

Lys Gln Val Arg Asp Trp Arg Lys Gln Val Lys Ser Gly Ala Lys Val

755 760 765

Lys Val Lys Gly Tyr Gln Leu Asp Val Val Gly Gly Asn Ser Leu Ala

770 775 780

Gln Ile Asp Tyr Leu Glu Gln Gln Tyr Lys Phe Leu Arg Arg Trp Ser

785 790 795 800

Phe Phe Ala Arg Ala Ser Gly Leu Val Val Arg Ala Asp Arg Glu Ser

805 810 815

His Phe Ala Val Ala Leu Arg Gln His Ile Glu Asn Ala Lys Arg Asp

820 825 830

Arg Leu Lys Lys Leu Ala Asp Arg Ile Leu Met Glu Ala Leu Gly Tyr

835 840 845

Val Tyr Glu Ala Ser Gly Pro Arg Glu Gly Gln Trp Thr Ala Gln His

850 855 860

Pro Pro Cys Gln Leu Ile Ile Leu Glu Glu Leu Ser Ala Tyr Arg Phe

865 870 875 880

Ser Asp Asp Arg Pro Pro Ser Glu Asn Ser Lys Leu Met Ala Trp Gly

885 890 895

His Arg Gly Ile Leu Glu Glu Leu Val Asn Gln Ala Gln Val His Asp

900 905 910

Val Leu Val Gly Thr Val Tyr Ala Ala Phe Ser Ser Arg Phe Asp Ala
915 920 925
Arg Thr Gly Ala Pro Gly Val Arg Cys Arg Arg Val Pro Ala Arg Phe
930 935 940
Val Gly Ala Thr Val Asp Asp Ser Leu Pro Leu Trp Leu Thr Glu Phe
945 950 955 960

Leu Asp Lys His Arg Leu Asp Lys Asn Leu Leu Arg Pro Asp Asp Val
965 970 975
Ile Pro Thr Gly Glu Gly Glu Phe Leu Val Ser Pro Cys Gly Glu Glu
980 985 990
Ala Ala Arg Val Arg Gln Val His Ala Asp Ile Asn Ala Ala Gln Asn
995 1000 1005
Leu Gln Arg Arg Leu Trp Gln Asn Phe Asp Ile Thr Glu Leu Arg
1010 1015 1020

Leu Arg Cys Asp Val Lys Met Gly Gly Glu Gly Thr Val Leu Val
1025 1030 1035
Pro Arg Val Asn Asn Ala Arg Ala Lys Gln Leu Phe Gly Lys Lys
1040 1045 1050
Val Leu Val Ser Gln Asp Gly Val Thr Phe Phe Glu Arg Ser Gln
1055 1060 1065
Thr Gly Gly Lys Pro His Ser Glu Lys Gln Thr Asp Leu Thr Asp
1070 1075 1080

Lys Glu Leu Glu Leu Ile Ala Glu Ala Asp Glu Ala Arg Ala Lys
1085 1090 1095
Ser Val Val Leu Phe Arg Asp Pro Ser Gly His Ile Gly Lys Gly
1100 1105 1110
His Trp Ile Arg Gln Arg Glu Phe Trp Ser Leu Val Lys Gln Arg
1115 1120 1125
Ile Glu Ser His Thr Ala Glu Arg Ile Arg Val Arg Gly Val Gly
1130 1135 1140

Ser Ser Leu Asp

1145

<210> 174

<211> 687

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<220><221> MOD_RES

<222> (156)..(527)

<223> Any amino acid

<400> 174

Met Ser Asn Pro Asn Ile Pro Asn Ile Ser Pro Asn Ile Thr Leu Thr
1 5 10 15

Arg Asp Asp Val Val Asn Leu Leu Met Ser Ser Ile Ala Met Glu Glu
20 25 30

Leu Gly Leu Ala His Ile Ile Asn Ala Glu Gly Glu Lys Ile Gln Phe
35 40 45

Ala Leu Gly Thr Leu Gln Gly Ala Ser Gly Pro Pro Ala Thr Leu Gln
50 55 60

Gln Val Leu Glu Val Asn Gln Ser Thr Gln Ala Met Leu Asp Thr Ile
65 70 75 80

Phe Arg Gln Glu Met Met Leu Asp Ser Lys Leu Lys Thr Ala Thr Asn
85 90 95

Ile Pro Thr Leu Arg Gly Pro Thr Gly Pro Val Gly Pro Thr Gly Ala
100 105 110

Pro Gly Gly Val Ile Ser Ile Asn Gly Gln Thr Gly Val Val Thr Leu
115 120 125

Asp Ala Ser Asn Gly Val Met Pro Phe Met Arg Glu Gln Ser Thr Ser
130 135 140

Ser Leu Asp Asp Tyr Lys Asp Pro Gly Ile Tyr Xaa Xaa Xaa Xaa Xaa
145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

210 215 220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

245 250 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

260 265 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

275 280 285

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

290 295 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

305 310 315 320

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

325 330 335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

340 345 350

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

355 360 365

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

385 390 395 400

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

405 410 415

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

420 425 430

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

435 440 445

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

450 455 460

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

465 470 475 480

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

485 490 495

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

500 505 510

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly

515 520 525

Ala Thr Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly Pro Gln Glu Pro

530 535 540

Arg Ala Leu Arg Glu Pro Arg Ala Pro Gln Ala Arg Arg Glu Pro Arg

545 550 555 560

Gly Leu Leu Glu Pro Gln Val Leu Arg Gly Pro Gln Glu Pro Arg Ala

565 570 575

Leu Arg Glu Pro Arg Ala Pro Arg Ala Leu Arg Glu Pro Arg Ala Leu

580 585 590

Arg Ala Leu Arg Ala Leu Gln Glu Leu Arg Ala Pro Arg Ala Leu Arg

595 600 605

Gly Leu Gln Glu Pro Arg Val Leu Gln Gly Pro Arg Glu Arg Gln Val

610 615 620

Arg Pro Glu Pro Arg Val Leu Gln Gly Pro Arg Glu Arg Gln Val Arg

625 630 635 640

Gln Gly Leu Gln Gly Leu Leu Glu Pro Arg Ala Lys Arg Glu Arg Gln

645 650 655

Val Arg Pro Glu Pro Arg Glu Pro Gln Glu Arg Gln Ala Pro Leu Val

660 665 670

Gln Gln Ala Leu Leu Glu Pro Gln Ala Leu Leu Gly Gln Ala Leu

675 680 685

<210> 175

<211> 1212

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 175

Met Ile Lys Lys Ser Asn Phe Trp Gln Phe Thr Gly Leu Tyr Glu Leu

1 5 10 15

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Val Trp Glu Thr Leu Asn

20 25 30

Ile Leu Glu Lys Asp Trp Val Ser Gln Lys Asp Lys Glu Val Glu Glu

35 40 45

Asn Tyr Asn Lys Ile Lys Val Phe Phe Asp Ser Leu His Arg Glu Phe

50 55 60

Val Lys Gln Ser Leu Glu Asn Trp Tyr Leu Glu Leu Leu Glu Asn Phe

65 70 75 80

Tyr Asn Ser Tyr Ile Glu Leu Asn Lys Asn Ile Glu Asn Lys Lys Asn

85 90 95

Lys Ser Leu Gln Lys Leu Phe Glu Lys Ser Ser Lys Glu Leu Lys Lys

100 105 110

Glu Leu Val Ser Phe Phe Glu Trp Lys Trp Asn Asp Trp Lys Gln Lys

115 120 125

Tyr Ser Phe Leu Lys Lys Trp Trp Ile Asp Val Leu Asn Glu Lys Glu

130 135 140

Val Leu Asp Leu Met Trp Glu Phe Tyr Pro Lys Glu Lys Glu Leu Phe

145 150 155 160

Lys Lys Phe Asp Lys Phe Phe Thr Tyr Phe Ser Asn Phe Lys Glu Ser

165 170 175

Arg Lys Asn Phe Tyr Ala Asp Asp Trp Arg Ala Trp Ala Ile Ala Thr

180 185 190

Arg Val Ile Asp Glu Asn Leu Ile Thr Phe Ile Lys Asn Ile Glu Asp

195 200 205

Phe Lys Lys Phe Lys Asn Asn Phe Ser Asp Phe Ile Glu Asn Gly Phe

210 215 220

Ser Asp Trp Lys Ile Lys Ile Asn Trp Phe Thr Leu Glu Glu Lys Gln

225 230 235 240

Val Phe Asp Leu Asp Phe Tyr Asn Asn Cys Leu Leu Gln Asp Trp Ile

245 250 255

Asp Asn Tyr Asn Lys Ile Leu Trp Trp Phe Ser Glu Glu Asn Trp Asn

260 265 270

Lys Ile Gln Trp Ile Asn Glu Lys Ile Asn Leu Phe Lys Gln Asn Gln

275 280 285

Asn Lys Thr Asn Ser Lys Asp Val Lys Phe Pro Arg Phe Lys Leu Leu

290 295 300

Tyr Lys Gln Ile Leu Ser Glu Lys Glu Lys Leu Ile Phe Val Asp Glu

305 310 315 320

Ile Glu Asn Asp Glu Lys Leu Ile Asn Phe Ile Lys Glu Ser Lys Asn

325 330 335

Asn Asn Leu Ile Lys Val Glu Lys Ala Ile Glu Ile Thr Glu Asn Phe

340 345 350

Ile Lys Asn Asn Glu Thr Phe Glu Leu Asp Lys Ile Tyr Leu Ser Lys

355 360 365

Ile Ser Ile Asn Thr Ile Ser Asn Lys Phe Phe Ser Ser Trp Asp Tyr

370 375 380

Ile Leu Lys Glu Gly Phe Asp Lys Trp Glu Ile Lys Glu Phe Ile Ser

385 390 395 400

Phe Glu Asp Leu Lys Asn Ala Phe Gly Lys Ile Lys Tyr Glu Asn Leu

405 410 415

Glu Asp Ile Phe Lys Ser Asn Tyr Ile Thr Asp Tyr Ile Ala Ile Asn

420 425 430

Trp Glu Asp Leu Tyr Lys Asn Phe Leu Asn Ile Phe Leu Tyr Glu Phe

435 440 445

Lys Gln Asn Ile Asn Glu Ile Asn Phe Tyr Asn Ser Glu Leu Glu Lys

450 455 460

Leu Phe Leu Glu Lys Phe Glu Lys Thr Glu Thr Gln Val Gln Ile Ile

465 470 475 480

Lys Asn Tyr Phe Asp Ser Val Leu Ser Leu Tyr Lys Met Thr Lys Tyr

485 490 495

Phe Ala Leu Glu Lys Gly Lys Lys Lys Ile Glu Asp Leu Glu Thr Asp

500 505 510

Asn Asn Phe Tyr Asn Asp Phe Phe Val Tyr Tyr Glu Asp Phe Glu Ile

515 520 525

Trp Lys Asp Tyr Asn Leu Val Arg Asn Phe Ile Thr Lys Lys Gln Val

530 535 540

Lys Thr Asp Lys Phe Lys Leu Asn Phe Glu Asn Ser Gln Phe Leu Thr

545 550 555 560

Gly Trp Asp Lys Asp Lys Glu Lys Glu Arg Leu Trp Ile Ile Leu Lys

565 570 575

Lys Asp Glu Lys Tyr Tyr Leu Trp Ile Leu Lys Asn Asn Lys Ile Phe

580 585 590

Asn Ser Tyr Asn Tyr Glu Ser Trp Asp Phe Tyr Glu Lys Met Ser Tyr

595 600 605

Lys Gln Leu Asn Asn Val Tyr Arg Gln Leu Pro Arg Phe Ala Phe Ser

610 615 620

Lys Ala Lys Arg Glu Val Tyr Trp Ile Thr Pro Glu Leu Glu Gln Ile

625 630 635 640

Lys Glu Glu Phe Asp Ile Phe Gln Lys Asn Lys Glu Lys Trp Glu Lys

645 650 655

Phe Asp Ile Glu Lys Leu Lys Lys Leu Ile Asn Cys Tyr Lys Lys Trp

660 665 670

Phe Ile Lys Thr Tyr Glu Asn Glu Phe Asp Leu Glu Lys Ile Lys Asn

675 680 685

Thr Asp Tyr Leu Asp Leu Ala Thr Phe Tyr Asp Glu Ile Glu Gln Lys

690 695 700

Thr Tyr Lys Ile Asp Phe Asn Lys Ile Ser Glu Asn Phe Ile Asn Ala

705 710 715 720

Lys Val Asn Ser Trp Glu Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp

725 730 735

Phe Ser Glu Thr Lys Lys Ala Trp Ser Lys Glu Asn Ile His Thr Lys

740 745 750

Tyr Phe Lys Leu Leu Phe Asp Glu Lys Asn Leu Glu Lys Leu Val Ile

755 760 765

Lys Leu Ser Trp Trp Ala Glu Met Phe Phe Arg Glu Lys Thr Glu Lys

770 775 780

Leu Lys Thr Lys Leu Asp Lys Ser Trp Lys Glu Val Leu Glu His Arg

785 790 795 800

Arg Tyr Ser Lys Asp Lys Ile Met Leu His Leu Ser Ile Thr Leu Asn

805 810 815

Ala Asn Lys Trp Asp Ser Phe Trp Phe Asn Lys Met Val Asn Glu Tyr

820 825 830

Leu Asn Lys Asn Glu Asp Ile Lys Ile Ile Trp Ile Asp Arg Gly Glu

835 840 845

Lys His Leu Ala Tyr Tyr Ser Val Ile Asp Lys Asn Trp Lys Ile Glu

850 855 860

Glu Ile Asp Thr Leu Asn Ile Ile Lys Ser Ser Asp Trp Lys Ile Thr

865 870 875 880

Asn Tyr Leu Glu Lys Leu Glu Lys Ile Glu Ser Ser Arg Lys Asp Ser

885 890 895

Arg Val Ser Trp Trp Glu Ile Glu Asn Ile Lys Glu Leu Lys Asn Gly

900 905 910

Tyr Ile Ser Gln Val Val Asn Lys Leu Ala Glu Leu Ile Ile Lys Tyr
915 920 925
Asn Ala Ile Ile Val Phe Glu Asp Leu Asn Ile Trp Phe Lys Arg Trp

930 935 940
Arg Gln Lys Ile Glu Lys Gln Ile Tyr Gln Lys Leu Glu Leu Ala Leu
945 950 955 960
Ala Lys Lys Leu Asn Tyr Leu Thr Gln Lys Asp Lys Asn Asp Asn Glu
965 970 975
Val Leu Trp Asn Leu Lys Ala Leu Gln Leu Val Pro Lys Val Asn Asp
980 985 990
Tyr Gln Asp Ile Ala Asn Tyr Lys Gln Ser Gly Ile Met Phe Tyr Thr

995 1000 1005
Arg Ala Asn Tyr Thr Ser Thr Thr Cys Pro Cys Cys Trp Phe Arg
1010 1015 1020
Lys Asn Ile Tyr Ile Ser Asn Ser Asp Thr Lys Glu Lys Gln Lys
1025 1030 1035
Lys Asp Phe Glu Lys Ile Asp Ile Lys Phe Asp Gly Glu Lys Phe
1040 1045 1050
Ile Phe Ser Tyr Glu Ile Ile Gln Asp Lys Lys Ala Lys Gln Lys

1055 1060 1065
Ser Asn Lys Thr Asn Phe Ser Val Asn Ser Asn Phe Ser Arg Phe
1070 1075 1080
Lys Tyr Asn Ser Lys Lys Met Leu Val Glu Glu Val Asn Leu Asn
1085 1090 1095
Leu Glu Leu Gln Asn Leu Phe Lys Asp Ile Asp Leu Lys Trp Asp
1100 1105 1110
Ile Asn Lys Gln Ile Leu Glu Lys Asp Ser Tyr Phe Tyr Lys Ser

1115 1120 1125
Leu Thr Tyr Tyr Phe Asn Leu Ile Leu Gln Leu Arg Asn Ser Asp
1130 1135 1140
Ser Lys Asn Asp Ile Asp Tyr Ile Thr Cys Pro Ser Cys Asn Tyr

1145 1150 1155

His Ser Lys Asp Trp Phe Gln Gly Leu Glu Tyr Asn Ala Asp Ala

1160 1165 1170

Asn Trp Ala Tyr Asn Ile Ala Arg Lys Trp Ile Ile Met Leu Asp

1175 1180 1185

Arg Ile Glu Lys Asn Phe Glu Lys Pro Asp Leu Tyr Val Ser Asp

1190 1195 1200

Ile Asp Trp Asp Asn Phe Thr Gln Lys

1205 1210

<210> 176

<211> 1212

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 176

Met Ile Lys Lys Ser Asn Phe Trp Gln Phe Thr Gly Leu Tyr Glu Leu

1 5 10 15

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Val Trp Glu Thr Leu Asn

20 25 30

Ile Leu Glu Lys Asp Trp Val Ser Gln Lys Asp Lys Glu Val Glu Glu

35 40 45

Asn Tyr Asn Lys Ile Lys Val Phe Phe Asp Ser Leu His Arg Glu Phe

50 55 60

Val Lys Gln Ser Leu Glu Asn Trp Tyr Leu Glu Leu Leu Glu Asn Phe

65 70 75 80

Tyr Asn Ser Tyr Ile Glu Leu Asn Lys Asn Ile Glu Asn Lys Lys Asn

85 90 95

Lys Ser Leu Gln Lys Leu Phe Glu Lys Ser Ser Lys Glu Leu Lys Lys

100 105 110

Glu Leu Val Ser Phe Phe Glu Trp Lys Trp Asn Asp Trp Lys Gln Lys

115 120 125

Tyr Ser Phe Leu Lys Lys Trp Trp Ile Asp Val Leu Asn Glu Lys Glu
130 135 140

Val Leu Asp Leu Met Trp Glu Phe Tyr Pro Lys Glu Lys Glu Leu Phe
145 150 155 160
Lys Lys Phe Asp Lys Phe Phe Thr Tyr Phe Ser Asn Phe Lys Glu Ser
165 170 175
Arg Lys Asn Phe Tyr Ala Asp Asp Trp Arg Ala Trp Ala Ile Ala Thr
180 185 190
Arg Val Ile Asp Glu Asn Leu Ile Thr Phe Ile Lys Asn Ile Glu Asp
195 200 205

Phe Lys Lys Phe Lys Asn Asn Phe Ser Asp Phe Ile Glu Asn Gly Phe
210 215 220
Ser Asp Trp Lys Ile Lys Ile Asn Trp Phe Thr Leu Glu Glu Lys Gln
225 230 235 240
Val Phe Asp Leu Asp Phe Tyr Asn Asn Cys Leu Leu Gln Asp Trp Ile
245 250 255
Asp Asn Tyr Asn Lys Ile Leu Trp Trp Phe Ser Glu Glu Asn Trp Asn
260 265 270

Lys Ile Gln Trp Ile Asn Glu Lys Ile Asn Leu Phe Lys Gln Asn Gln
275 280 285
Asn Lys Thr Asn Ser Lys Asp Val Lys Phe Pro Arg Phe Lys Leu Leu
290 295 300
Tyr Lys Gln Ile Leu Ser Glu Lys Glu Lys Leu Ile Phe Val Asp Glu
305 310 315 320
Ile Glu Asn Asp Glu Lys Leu Ile Asn Phe Ile Lys Glu Ser Lys Asn
325 330 335

Asn Asn Leu Ile Lys Val Glu Lys Ala Ile Glu Ile Thr Glu Asn Phe
340 345 350
Ile Lys Asn Asn Glu Thr Phe Glu Leu Asp Lys Ile Tyr Leu Ser Lys
355 360 365
Ile Ser Ile Asn Thr Ile Ser Asn Lys Phe Phe Ser Ser Trp Asp Tyr

370 375 380

Ile Leu Lys Glu Gly Phe Asp Lys Trp Glu Ile Lys Glu Phe Ile Ser

385 390 395 400

Phe Glu Asp Leu Lys Asn Ala Phe Gly Lys Ile Lys Tyr Glu Asn Leu

405 410 415

Glu Asp Ile Phe Lys Ser Asn Tyr Ile Thr Asp Tyr Ile Ala Ile Asn

420 425 430

Trp Glu Asp Leu Tyr Lys Asn Phe Leu Asn Ile Phe Leu Tyr Glu Phe

435 440 445

Lys Gln Asn Ile Asn Glu Ile Asn Phe Tyr Asn Ser Glu Leu Glu Lys

450 455 460

Leu Phe Leu Glu Lys Phe Glu Lys Thr Glu Thr Gln Val Gln Ile Ile

465 470 475 480

Lys Asn Tyr Phe Asp Ser Val Leu Ser Leu Tyr Lys Met Thr Lys Tyr

485 490 495

Phe Ala Leu Glu Lys Gly Lys Lys Lys Ile Glu Asp Leu Glu Thr Asp

500 505 510

Asn Asn Phe Tyr Asn Asp Phe Phe Val Tyr Tyr Glu Asp Phe Glu Ile

515 520 525

Trp Lys Asp Tyr Asn Leu Val Arg Asn Phe Ile Thr Lys Lys Gln Val

530 535 540

Lys Thr Asp Lys Phe Lys Leu Asn Phe Glu Asn Ser Gln Phe Leu Thr

545 550 555 560

Gly Trp Asp Lys Asp Lys Glu Lys Glu Arg Leu Trp Ile Ile Leu Lys

565 570 575

Lys Asp Glu Lys Tyr Tyr Leu Trp Ile Leu Lys Asn Asn Lys Ile Phe

580 585 590

Asn Ser Tyr Asn Tyr Glu Ser Trp Asp Phe Tyr Glu Lys Met Ser Tyr

595 600 605

Lys Gln Leu Asn Asn Val Tyr Arg Gln Leu Pro Arg Phe Ala Phe Ser

610 615 620

Lys Ala Lys Arg Glu Val Tyr Trp Ile Thr Pro Glu Leu Glu Gln Ile
625 630 635 640
Lys Glu Glu Phe Asp Ile Phe Gln Lys Asn Lys Glu Lys Trp Glu Lys
645 650 655

Phe Asp Ile Glu Lys Leu Lys Lys Leu Ile Asn Cys Tyr Lys Lys Trp
660 665 670
Phe Ile Lys Thr Tyr Glu Asn Glu Phe Asp Leu Glu Lys Ile Lys Asn
675 680 685
Thr Asp Tyr Leu Asp Leu Ala Thr Phe Tyr Asp Glu Ile Glu Gln Lys
690 695 700
Thr Tyr Lys Ile Asp Phe Asn Lys Ile Ser Glu Asn Phe Ile Asn Ala
705 710 715 720

Lys Val Asn Ser Trp Glu Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp
725 730 735
Phe Ser Glu Thr Lys Lys Ala Trp Ser Lys Glu Asn Ile His Thr Lys
740 745 750
Tyr Phe Lys Leu Leu Phe Asp Glu Lys Asn Leu Glu Lys Leu Val Ile
755 760 765
Lys Leu Ser Trp Trp Ala Glu Met Phe Phe Arg Glu Lys Thr Glu Lys
770 775 780

Leu Lys Thr Lys Leu Asp Lys Ser Trp Lys Glu Val Leu Glu His Arg
785 790 795 800
Arg Tyr Ser Lys Asp Lys Ile Met Leu His Leu Ser Ile Thr Leu Asn
805 810 815
Ala Asn Lys Trp Asp Ser Phe Trp Phe Asn Lys Met Val Asn Glu Tyr
820 825 830
Leu Asn Lys Asn Glu Asp Ile Lys Ile Ile Trp Ile Asp Arg Gly Glu
835 840 845

Lys His Leu Ala Tyr Tyr Ser Val Ile Asp Lys Asn Trp Lys Ile Glu
850 855 860
Glu Ile Asp Thr Leu Asn Ile Ile Lys Ser Ser Asp Trp Lys Ile Thr

865 870 875 880

Asn Tyr Leu Glu Lys Leu Glu Lys Ile Glu Ser Ser Arg Lys Asp Ser

885 890 895

Arg Val Ser Trp Trp Glu Ile Glu Asn Ile Lys Glu Leu Lys Asn Gly

900 905 910

Tyr Ile Ser Gln Val Val Asn Lys Leu Ala Glu Leu Ile Ile Lys Tyr

915 920 925

Asn Ala Ile Ile Val Phe Glu Asp Leu Asn Ile Trp Phe Lys Arg Trp

930 935 940

Arg Gln Lys Ile Glu Lys Gln Ile Tyr Gln Lys Leu Glu Leu Ala Leu

945 950 955 960

Ala Lys Lys Leu Asn Tyr Leu Thr Gln Lys Asp Lys Asn Asp Asn Glu

965 970 975

Val Leu Trp Asn Leu Lys Ala Leu Gln Leu Val Pro Lys Val Asn Asp

980 985 990

Tyr Gln Asp Ile Ala Asn Tyr Lys Gln Ser Gly Ile Met Phe Tyr Thr

995 1000 1005

Arg Ala Asn Tyr Thr Ser Thr Thr Cys Pro Cys Cys Trp Phe Arg

1010 1015 1020

Lys Asn Ile Tyr Ile Ser Asn Ser Asp Thr Lys Glu Lys Gln Lys

1025 1030 1035

Lys Asp Phe Glu Lys Ile Asp Ile Lys Phe Asp Gly Glu Lys Phe

1040 1045 1050

Ile Phe Ser Tyr Glu Ile Ile Gln Asp Lys Lys Ala Lys Gln Lys

1055 1060 1065

Ser Asn Lys Thr Asn Phe Ser Val Asn Ser Asn Phe Ser Arg Phe

1070 1075 1080

Lys Tyr Asn Ser Lys Lys Met Leu Val Glu Glu Val Asn Leu Asn

1085 1090 1095

Leu Glu Leu Gln Asn Leu Phe Lys Asp Ile Asp Leu Lys Trp Asp

1100 1105 1110

Ile Asn Lys Gln Ile Leu Glu Lys Asp Ser Tyr Phe Tyr Lys Ser
1115 1120 1125
Leu Thr Tyr Tyr Phe Asn Leu Ile Leu Gln Leu Arg Asn Ser Asp
1130 1135 1140
Ser Lys Asn Asp Ile Asp Tyr Ile Thr Cys Pro Ser Cys Asn Tyr
1145 1150 1155

His Ser Lys Asp Trp Phe Gln Gly Leu Glu Tyr Asn Ala Asp Ala
1160 1165 1170
Asn Trp Ala Tyr Asn Ile Ala Arg Lys Trp Ile Ile Met Leu Asp
1175 1180 1185
Arg Ile Glu Lys Asn Phe Glu Lys Pro Asp Leu Tyr Val Ser Asp
1190 1195 1200
Ile Asp Trp Asp Asn Phe Thr Gln Lys
1205 1210

<210> 177

<211> 1108

<212> PRT

<213

> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<400> 177

Met Ala Thr Arg Ser Phe Ile Leu Lys Ile Glu Pro Asn Glu Glu Val
1 5 10 15
Lys Lys Gly Leu Trp Lys Thr His Glu Val Leu Asn His Gly Ile Ala
20 25 30
Tyr Tyr Met Asn Ile Leu Lys Leu Ile Arg Gln Glu Ala Ile Tyr Glu
35 40 45
His His Glu Gln Asp Pro Lys Asn Pro Lys Lys Val Ser Lys Ala Glu

50 55 60
Ile Gln Ala Glu Leu Trp Asp Phe Val Leu Lys Met Gln Lys Cys Asn
65 70 75 80
Ser Phe Thr His Glu Val Asp Lys Asp Val Val Phe Asn Ile Leu Arg

85 90 95

Glu Leu Tyr Glu Glu Leu Val Pro Ser Ser Val Glu Lys Lys Gly Glu

100 105 110

Ala Asn Gln Leu Ser Asn Lys Phe Leu Tyr Pro Leu Val Asp Pro Asn

115 120 125

Ser Gln Ser Gly Lys Gly Thr Ala Ser Ser Gly Arg Lys Pro Arg Trp

130 135 140

Tyr Asn Leu Lys Ile Ala Gly Asp Pro Ser Trp Glu Glu Glu Lys Lys

145 150 155 160

Lys Trp Glu Glu Asp Lys Lys Lys Asp Pro Leu Ala Lys Ile Leu Gly

165 170 175

Lys Leu Ala Glu Tyr Gly Leu Ile Pro Leu Phe Ile Pro Phe Thr Asp

180 185 190

Ser Asn Glu Pro Ile Val Lys Glu Ile Lys Trp Met Glu Lys Ser Arg

195 200 205

Asn Gln Ser Val Arg Arg Leu Asp Lys Asp Met Phe Ile Gln Ala Leu

210 215 220

Glu Arg Phe Leu Ser Trp Glu Ser Trp Asn Leu Lys Val Lys Glu Glu

225 230 235 240

Tyr Glu Lys Val Glu Lys Glu His Lys Thr Leu Glu Glu Arg Ile Lys

245 250 255

Glu Asp Ile Gln Ala Phe Lys Ser Leu Glu Gln Tyr Glu Lys Glu Arg

260 265 270

Gln Glu Gln Leu Leu Arg Asp Thr Leu Asn Thr Asn Glu Tyr Arg Leu

275 280 285

Ser Lys Arg Gly Leu Arg Gly Trp Arg Glu Ile Ile Gln Lys Trp Leu

290 295 300

Lys Met Asp Glu Asn Glu Pro Ser Glu Lys Tyr Leu Glu Val Phe Lys

305 310 315 320

Asp Tyr Gln Arg Lys His Pro Arg Glu Ala Gly Asp Tyr Ser Val Tyr

325 330 335

Glu Phe Leu Ser Lys Lys Glu Asn His Phe Ile Trp Arg Asn His Pro
340 345 350
Glu Tyr Pro Tyr Leu Tyr Ala Thr Phe Cys Glu Ile Asp Lys Lys Lys
355 360 365
Lys Asp Ala Lys Gln Gln Ala Thr Phe Thr Leu Ala Asp Pro Ile Asn

370 375 380
His Pro Leu Trp Val Arg Phe Glu Glu Arg Ser Gly Ser Asn Leu Asn
385 390 395 400
Lys Tyr Arg Ile Leu Thr Glu Gln Leu His Thr Glu Lys Leu Lys Lys
405 410 415
Lys Leu Thr Val Gln Leu Asp Arg Leu Ile Tyr Pro Thr Glu Ser Gly
420 425 430
Gly Trp Glu Glu Lys Gly Lys Val Asp Ile Val Leu Leu Pro Ser Arg

435 440 445
Gln Phe Tyr Asn Gln Ile Phe Leu Asp Ile Glu Glu Lys Gly Lys His
450 455 460
Ala Phe Thr Tyr Lys Asp Glu Ser Ile Lys Phe Pro Leu Lys Gly Thr
465 470 475 480
Leu Gly Gly Ala Arg Val Gln Phe Asp Arg Asp His Leu Arg Arg Tyr
485 490 495
Pro His Lys Val Glu Ser Gly Asn Val Gly Arg Ile Tyr Phe Asn Met

500 505 510
Thr Val Asn Ile Glu Pro Thr Glu Ser Pro Val Ser Lys Ser Leu Lys
515 520 525
Ile His Arg Asp Asp Phe Pro Lys Phe Val Asn Phe Lys Pro Lys Glu
530 535 540
Leu Thr Glu Trp Ile Lys Asp Ser Lys Gly Lys Lys Leu Lys Ser Gly
545 550 555 560
Ile Glu Ser Leu Glu Ile Gly Leu Arg Val Met Ser Ile Asp Leu Gly

565 570 575
Gln Arg Gln Ala Ala Ala Ala Ser Ile Phe Glu Val Val Asp Gln Lys

580 585 590

Pro Asp Ile Glu Gly Lys Leu Phe Phe Pro Ile Lys Gly Thr Glu Leu

595 600 605

Tyr Ala Val His Arg Ala Ser Phe Asn Ile Lys Leu Pro Gly Glu Thr

610 615 620

Leu Val Lys Ser Arg Glu Val Leu Arg Lys Ala Arg Glu Asp Asn Leu

625 630 635 640

Lys Leu Met Asn Gln Lys Leu Asn Phe Leu Arg Asn Val Leu His Phe

645 650 655

Gln Gln Phe Glu Asp Ile Thr Glu Arg Glu Lys Arg Val Thr Lys Trp

660 665 670

Ile Ser Arg Gln Glu Asn Ser Asp Val Pro Leu Val Tyr Gln Asp Glu

675 680 685

Leu Ile Gln Ile Arg Glu Leu Met Tyr Lys Pro Tyr Lys Asp Trp Val

690 695 700

Ala Phe Leu Lys Gln Leu His Lys Arg Leu Glu Val Glu Ile Gly Lys

705 710 715 720

Glu Val Lys His Trp Arg Lys Ser Leu Ser Asp Gly Arg Lys Gly Leu

725 730 735

Tyr Gly Ile Ser Leu Lys Asn Ile Asp Glu Ile Asp Arg Thr Arg Lys

740 745 750

Phe Leu Leu Arg Trp Ser Leu Arg Pro Thr Glu Pro Gly Glu Val Arg

755 760 765

Arg Leu Glu Pro Gly Gln Arg Phe Ala Ile Asp Gln Leu Asn His Leu

770 775 780

Asn Ala Leu Lys Glu Asp Arg Leu Lys Lys Met Ala Asn Thr Ile Ile

785 790 795 800

Met His Ala Leu Gly Tyr Cys Tyr Asp Val Arg Lys Lys Lys Trp Gln

805 810 815

Ala Lys Asn Pro Ala Cys Gln Ile Ile Leu Phe Glu Asp Leu Ser Asn

820 825 830

Tyr Asn Pro Tyr Glu Glu Arg Ser Arg Phe Glu Asn Ser Lys Leu Met
835 840 845
Lys Trp Ser Arg Arg Glu Ile Pro Arg Gln Val Ala Leu Gln Gly Glu
850 855 860
Ile Tyr Gly Leu Gln Val Gly Glu Val Gly Ala Gln Phe Ser Ser Arg
865 870 875 880
Phe His Ala Lys Thr Gly Ser Pro Gly Ile Arg Cys Ser Val Val Thr

885 890 895
Lys Glu Lys Leu Gln Asp Asn Arg Phe Phe Lys Asn Leu Gln Arg Glu
900 905 910
Gly Arg Leu Thr Leu Asp Lys Ile Ala Val Leu Lys Glu Gly Asp Leu
915 920 925
Tyr Pro Asp Lys Gly Gly Glu Lys Phe Ile Ser Leu Ser Lys Asp Arg
930 935 940
Lys Leu Val Thr Thr His Ala Asp Ile Asn Ala Ala Gln Asn Leu Gln

945 950 955 960
Lys Arg Phe Trp Thr Arg Thr His Gly Phe Tyr Lys Val Tyr Cys Lys
965 970 975
Ala Tyr Gln Val Asp Gly Gln Thr Val Tyr Ile Pro Glu Ser Lys Asp
980 985 990
Gln Lys Gln Lys Ile Ile Glu Glu Phe Gly Glu Gly Tyr Phe Ile Leu
995 1000 1005
Lys Asp Gly Val Tyr Glu Trp Gly Asn Ala Gly Lys Leu Lys Ile

1010 1015 1020
Lys Lys Gly Ser Ser Lys Gln Ser Ser Ser Glu Leu Val Asp Ser
1025 1030 1035
Asp Ile Leu Lys Asp Ser Phe Asp Leu Ala Ser Glu Leu Lys Gly
1040 1045 1050
Glu Lys Leu Met Leu Tyr Arg Asp Pro Ser Gly Asn Val Phe Pro
1055 1060 1065
Ser Asp Lys Trp Met Ala Ala Gly Val Phe Phe Gly Lys Leu Glu

1070 1075 1080

Arg Ile Leu Ile Ser Lys Leu Thr Asn Gln Tyr Ser Ile Ser Thr

1085 1090 1095

Ile Glu Asp Asp Ser Ser Lys Gln Ser Met

1100 1105

<210> 178

<211> 688

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12 sequence

<220><221> MOD_RES

<222> (276)..(564)

<223> Any amino acid

<400> 178

Met Ala Glu Ser Met Tyr Asn Gln Gln Asn Ile Asn Gln Lys Ser Thr

1 5 10 15

Glu Thr Pro Thr Glu Glu Asp Ala Leu Gly Ile Lys Asn Pro Leu Leu

20 25 30

Thr Pro Thr Thr Leu Gly Gln Asn Phe Leu Ser Leu Gln Ser Ile Ser

35 40 45

Pro Leu Gly Ser Arg Ser Ile Asn Leu Ile Asn Trp Ser Leu Ile Ser

50 55 60

Pro Asn Gln Thr Leu Leu Gln Asn Phe Gln Asp Asn Glu Asn Trp Gln

65 70 75 80

Asp Ser Ser Ile Ser Glu Phe Arg Pro Phe Ser Lys Asn Ser Leu Thr

85 90 95

Glu Asn Ser Pro Ile Ile Glu Pro Gln Ser Asp Lys Thr Leu Pro Ser

100 105 110

Ser Val Pro Ile Gln Leu Ser Ser Glu Leu Pro Ile Gln Gln Pro Pro

115 120 125

Glu Thr Ser Phe Ile Asp Ser Glu Ser Pro Ile Pro Gln Pro Pro Glu

130 135 140

Thr Pro Ser Ser Asp Ser Glu Ser Pro Ile Gly Gln Thr Glu Asn Ile

145 150 155 160

Phe Pro Phe Gln Ile Asp Gln Lys Thr Arg Arg Asn Ser Val Ile Gln

165 170 175

Asn Ser Lys Ser Ser Ile Ser His Phe Phe Gln Lys Lys Ser Glu Phe

180 185 190

Pro Arg Glu Lys Ile Ser Gln Glu Asn Val Asn Lys Leu Thr Lys Lys

195 200 205

Ser Ala Glu Asn Gln Asp Ile Ser Thr Thr Glu Glu Ser Val Ile Asn

210 215 220

Ser Ile Glu Thr Asn Asp Leu Gln Thr Ile Asn Pro Thr Asp Ile Pro

225 230 235 240

Asn Pro Glu Ile Pro Val Ser Thr Leu Gln Lys Gln Pro Asp Ser Thr

245 250 255

Ile Asp Asn Ile Pro Gln Thr Glu Ser Val Ser Thr Ile Asn Pro Thr

260 265 270

Asp Ile Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

275 280 285

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

290 295 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

305 310 315 320

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

325 330 335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

340 345 350

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

355 360 365

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

385 390 395 400

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

405 410 415

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

420 425 430

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

435 440 445

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

450 455 460

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

465 470 475 480

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

485 490 495

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

500 505 510

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

515 520 525

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

530 535 540

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

545 550 555 560

Xaa Xaa Xaa Xaa Ser Lys Asn Asn Arg Ile Pro Gln Leu Ile Thr Phe

565 570 575

Leu Lys Leu Asn Gln Tyr Gln Gln Leu Ile Leu Gln Ile Phe Leu Thr

580 585 590

Gln Lys Phe Ser Phe Gln Leu Ser Lys Asn Asn Arg Ile Pro Pro Leu

595 600 605

Ile Thr Phe Leu Lys Leu Asn Gln Tyr Gln Gln Leu Ile Pro Arg Val

610 615 620

Leu Leu His Gln Lys Phe Leu Phe Gln Leu Phe Lys Asn Asn Arg Ile

625 630 635 640

Pro Pro Leu Ile Thr Phe Pro Lys Leu Asn Gln Tyr Gln Gln Leu Ile

645 650 655

Pro Arg Ile Phe Leu Thr Gln Lys Phe Pro Phe Gln Ile Ser Arg Asn

660 665 670

Asn Arg Ile Pro Gln Leu Ile Thr Phe Pro Lys Leu Asn Gln Tyr Gln

675 680 685

<210> 179

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 179

Met Gly Ala Ile Lys Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940
Lys Ile Gly Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975
Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990
Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala
995 1000

<210> 180
<211> 986
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 180
Met Ala Arg Asp Asn Phe Leu Asn Thr Ile Lys Leu Leu Ala Asp Lys
1 5 10 15

Met Lys Leu Gly Ala Ile Ser Gly Phe Gly Lys Asp Gly Asn Glu Val
20 25 30
Asn Asp Ile Asn Lys Leu Phe Gly Asp Lys Asn Thr Tyr Ala Asn Ile
35 40 45
Glu Asn Val Val Glu Phe Tyr Phe Pro Trp Ile Lys Ala Leu Glu Gly
50 55 60
Arg Phe Ser Leu Asp Lys Gly Asp Arg Asn Leu Asn Asp Met Lys Met

65 70 75 80

Phe Tyr Lys Ser Val Leu Thr Ala Phe Phe Thr Ala Val Asp Ser Leu
85 90 95
Arg Asn Lys Tyr Thr His Tyr Ser His Lys Asp Leu Asn Ile Arg Glu
100 105 110
Ile Lys Ile Glu Cys Thr Leu Gly Gly Lys Asp Tyr Cys Ile Gly Leu
115 120 125
Leu Asn Ala Leu Asp Cys Ile Tyr Asp Ser Ala Val Asn Leu Leu Lys
130 135 140

Leu Arg Phe Met Val Gly Glu Asp Glu Val Ala His Leu Arg Arg Cys
145 150 155 160
Lys Ala Val Asn Lys Lys Val Val Val Arg Thr Glu Lys Asp Gly Phe
165 170 175
Tyr Tyr Arg Leu Ser Asp Asn Gly Gly Val Thr Glu Lys Gly Val Ile
180 185 190
Phe Ile Ala Ser Met Phe Leu Asn Arg Lys Tyr Gly Phe Leu Phe Leu
195 200 205

Lys Gln Leu Glu Gly Phe Lys Arg Ser Asp Glu Lys Arg Tyr Arg Leu
210 215 220
Thr Leu Glu Ala Phe Leu Ala Phe Ser Asn Ile Lys Pro Val Asp Arg
225 230 235 240
Leu Lys Ser Asp Lys Leu Asp Arg Ala Ser Leu Gly Leu Asp Met Leu
245 250 255
Asn Glu Leu Thr Lys Ile Pro Lys Glu Leu Ser Glu Thr Leu Ser Val
260 265 270

Asp Cys Leu Tyr Lys Tyr Leu Ala Ser Asp Gly Glu Asp Asp Leu Arg
275 280 285
Ser Arg Ile Arg Tyr Gln Asp Arg Phe Val Pro Leu Ala Leu Glu Phe
290 295 300
Ile Ser Gln Ser Asp Glu Phe Lys Asp Phe Arg Phe Tyr Thr Tyr Val
305 310 315 320

Gly Asn Tyr Val Tyr Lys Gly Tyr Ile Lys Arg Leu Ile Asp Gly Thr
325 330 335

Asp Lys Glu Arg Tyr Leu Ser Asp Arg Leu Cys Gly Phe Tyr Lys Ser
340 345 350
Val Asn Asp Ala Ser Ser Asp Ala Ile Ala Gln Lys Tyr Gly Val Glu
355 360 365
Ile Lys Asp Ser Asn Glu Pro Asp Tyr Met Leu Pro Asp Ser Phe Arg
370 375 380
Pro His Val Leu Arg Ala Thr Pro His Phe Val Ile Asn Asn Asn Asn
385 390 395 400

Ile Gly Ile Lys Ile Cys Gly Asn Asp Cys Leu Pro Ile Val Asn Gly
405 410 415
Lys Gly Val Glu Ser Pro Glu Pro Asp Tyr Trp Leu Ser Ile Tyr Glu
420 425 430
Leu Pro Ala Met Leu Phe Tyr Ala Tyr Leu Arg Glu Lys Asn Gly Lys
435 440 445
Arg Phe Lys Asp Tyr Lys Ser Ile Arg Glu Leu Ile Glu Gly Val Glu
450 455 460

Lys Lys Ala Asp Glu Lys Asn Asp Arg Asp Lys Gly Ala Leu Met Ala
465 470 475 480
Arg His Ile Asp Lys Glu Ile Ile Trp Thr Gln Thr Lys Leu Asp Glu
485 490 495
Val Lys Arg Leu Glu Glu Lys Lys Val Ala Ala Tyr Gly Lys Lys Gly
500 505 510
Arg Val Val Leu Lys Ser Gly Arg Met Ala Asp Leu Leu Ala His Asp
515 520 525

Met Val Arg Leu Gln Pro Ala Thr Lys Gly Ser Asp Lys Ile Thr Gly
530 535 540
Val Asn Phe Gln Ala Leu Gln Val Ser Leu Ala Tyr Phe Lys Arg Asp
545 550 555 560
Ile Leu Ala Asp Val Phe Ser Arg Ala Met Leu Thr Thr Gly Asn His

565 570 575

Arg His Pro Phe Leu Tyr Arg Ile Asp Val Ser His Cys Ser Ser Leu

580 585 590

Arg Asp Phe Tyr Val Ala Tyr Leu Gly Glu Arg Arg Lys Tyr Phe Glu

595 600 605

Asp Val Ala Lys Lys Ile Ala Lys Asn Lys Leu Asn Thr Pro Cys His

610 615 620

Ile Leu Arg Arg Leu Gln Arg Glu Gly Ser Gly Glu Glu Ala Gly Lys

625 630 635 640

Asp Val Lys Pro Lys Phe Leu Pro Arg Gly Ile Phe Thr Asp Ser Ile

645 650 655

Lys Asn Cys Leu Glu Gln Ser Lys Leu Asn Ile Tyr Ile Arg Asn Ala

660 665 670

Arg Asn Asp Val Lys Pro Ala Ile Asn Ala Ala Tyr Leu Ile Leu Met

675 680 685

Tyr Tyr Lys Glu Ile Glu Lys Gly Glu Phe Gln Gly Phe Tyr Gly Glu

690 695 700

Lys Arg Arg Tyr Asp Ile Leu Glu Glu Gly Lys Pro Leu Asp Leu Ala

705 710 715 720

Glu Arg Lys Lys Ala Leu Ala Ser Ile Lys Pro Ala Lys Ile Asp Val

725 730 735

Ser Glu Ala Asn Met Pro Met Ser Lys Glu Glu His Leu Met Arg Lys

740 745 750

Arg Tyr His Ala Val Cys Asn Asn Glu Ser Ala Ile Arg Met Tyr Gln

755 760 765

Val Gln Asp Ile Leu Leu Leu Leu Met Ala Lys Asp Ile Phe Lys Lys

770 775 780

Ala Leu Ser Glu Gly Val Met Ser Lys Lys Ile Gly Leu Glu Asn Leu

785 790 795 800

Asn Gly Ile Phe Asp Ala Pro Val Asn Phe Val Lys Asn Phe Asp Asn

805 810 815

Ile Lys Leu Thr Ala Thr Gly Ile Lys Ile Lys Asn Tyr Gly Lys Val
820 825 830
Cys Arg Leu Gly Thr Asp Phe Lys Phe Asn Ser Leu Ile Lys Ala Phe
835 840 845

His Lys Val Tyr Ser Lys Ser Val Glu Met Asp Tyr Ser Asp Tyr Leu
850 855 860
Lys Glu Glu Glu Glu Phe Glu Lys Tyr Arg Leu Asn Met Val Lys Leu
865 870 875 880
Cys Arg Glu Val Glu Arg Gly Ile Thr Glu Asp Leu His Leu Ser Leu
885 890 895
Asp Gly Lys Ser His Leu Ser Phe Asn Asp Asp Val Ile Lys Pro Tyr
900 905 910

Asn Asp Lys Tyr Asn Val Phe Asn Gly Asp Asp Leu Thr Phe Phe Ile
915 920 925
Asn Ala Arg Asn Met Phe Met His Gly Asp Tyr Lys Tyr Glu Cys Val
930 935 940
Lys Tyr Val Val Ser Glu His Phe Lys Gly Ser Leu Asn Asp Val Ser
945 950 955 960
Phe Ala Lys Glu Thr Tyr Gly His Phe Cys Asn Leu Leu Glu Ser Met
965 970 975

Arg Lys Lys Thr Gly Leu Arg Ile Asp Ile
980 985

<210> 181
<211> 1009
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 181
Met Lys Lys Lys Ile Ser Leu Lys Glu Gln Arg Asn Thr Lys Lys Ala
1 5 10 15
Glu Asn Lys Leu Lys Tyr Gln Lys Ala Gln Ala Glu Arg Ala Ala Ala

20 25 30

Ala Gln Gln Thr Ala Ala Gly Ala Glu Ser Glu Glu Asn Pro Cys Phe

35 40 45

Asp Val Val Lys Asp Thr Lys Arg Lys Ala Leu Asn Pro Leu His Val

50 55 60

Glu Ile Glu Ala Pro Ser Ala Lys Lys Ser Ser Val Lys Ala Asn Gly

65 70 75 80

Leu Lys Ser Leu Leu Leu Thr Asp Gly Lys Thr Val Met Thr Ser Phe

85 90 95

Gly Arg Gly Ser Glu Ala Asn Val Glu Lys Arg Phe Asp Glu Thr Gly

100 105 110

Thr Lys Thr Phe Asp Arg Asp Pro Glu Leu Phe Ser Ala Lys Pro Leu

115 120 125

Glu Thr Gly Tyr Arg Ile Gln Arg Phe Asn Ala Ser Pro Lys Asp Ala

130 135 140

Gly Leu Ala Tyr Arg Pro Ala Gly Val Arg Pro Asp Gln Ile Gly Ala

145 150 155 160

Lys Ala Ala Leu Glu Lys Arg Tyr Phe Gly Lys Glu Thr Pro Gly Asp

165 170 175

Asn Ile His Val Gln Ile Ala Tyr Gln Ile Gln Asp Ile Glu Lys Leu

180 185 190

Leu Ala Val Tyr Ile Ser Asn Ile Ile Tyr Ala Val Asn Asn Val Thr

195 200 205

Gly Val Ser Ala Met Lys Asp Ser Lys Gly Arg Pro Val Asp Leu Leu

210 215 220

Gly Asp Tyr Gly Ile Leu Gly Glu Glu Gly Leu Thr Lys Arg Leu Gln

225 230 235 240

Arg Ile Pro Glu Gln Ala Asp Glu Glu Ala Lys Ala Leu Gln Ala Phe

245 250 255

Leu Cys Ser Glu Arg Leu Ser Tyr Phe Gly Lys Glu Phe Cys Leu Val

260 265 270

Arg Asn Ser Pro Lys Gln Pro Asp Lys Glu Glu Lys Arg Gln Tyr Lys
275 280 285
Leu Met Arg Val Leu Cys Leu Leu Gly Glu Leu Arg Gln Phe Leu Val

290 295 300
His Gly Lys Lys Lys Glu Lys Glu Phe Ala Trp Leu Tyr Arg Leu Asp
305 310 315 320
Arg Gln Leu Ser Gln Glu Tyr Arg Lys Leu Leu Gly Glu Phe Tyr Asp
325 330 335
Ala Gln Val Asp Lys Val Asn Lys Ser Phe Leu Thr Asn Ser Thr Val
340 345 350
Asn Leu Glu Val Leu Phe Arg Ala Leu Lys Thr Gly Thr Asp Pro Glu

355 360 365
Arg Lys Thr Val Thr Gln Glu Tyr Tyr Gln Phe Thr Val Arg Lys Glu
370 375 380
Asp Gly Asn Leu Gly Phe Ser Leu Lys Thr Leu Arg Glu Ile Leu Leu
385 390 395 400
Ser Ala Tyr Lys His Glu Val Arg Asp Lys Glu Tyr Asp Ser Ile Arg
405 410 415
His Lys Leu Tyr Gln Leu Phe Ser Phe Ala Leu Tyr His Tyr Tyr Lys

420 425 430
Thr Gly Val Gly Ala Glu Arg Arg Glu Ala Phe Val Ala Lys Leu Arg
435 440 445
Ala Val Met Thr Ala Glu Ala Lys Gln Arg Ala Tyr Ala Asp Glu Ala
450 455 460
Ala Glu Ile Trp Asn Asp Glu Gly Ser Gly Ile Arg Ala Ala Phe Leu
465 470 475 480
Glu Ile Leu Glu Ala Val Asp Phe Gly Ser Ala Val Lys Gly Ile Lys

485 490 495
Ala Arg Ser Ser Val Ala Gly Asp Lys Arg Phe Ala Glu Trp Leu Glu
500 505 510
Glu Val Arg Ile Arg Pro Glu Gly Val Ser Cys Phe Thr Lys Leu Met

515 520 525

Tyr Leu Leu Thr Arg Phe Leu Asp Gly Lys Glu Ile Asn Glu Leu Leu

530 535 540

Thr Gly Leu Ile Asn Lys Leu Glu Asn Ile Gln Ser Phe Leu Asp Val

545 550 555 560

Met Gln Gln Glu His Ala Glu Thr Gly Leu Ser Asp Ala Phe Ser Phe

565 570 575

Phe Glu Tyr Ser Gly Glu Ile Ala Ala Glu Leu Arg Met Thr Arg Ser

580 585 590

Phe Ala Arg Met Ala Ala Ala Asp Pro Glu Ala Lys Arg Phe Met Val

595 600 605

Val Asp Gly Ala Lys Leu Leu Gly Phe Asn Pro Lys Asp Thr Glu Ser

610 615 620

Glu Asp Glu Gly Ile Ile Arg Ala Ile Tyr Gly Asp Ala Cys Ala Glu

625 630 635 640

Tyr Leu Gln Phe Ser Glu Glu Glu Lys Glu Ala Phe Tyr Val Gln Glu

645 650 655

Gly Leu Tyr Gly Lys Glu Arg Glu Lys Phe Ser Pro Tyr Ala Tyr Phe

660 665 670

His Thr Asp Thr Ser Leu Arg Asn Phe Ile Ala Lys Asn Val Val Glu

675 680 685

Ser Ala Arg Phe Arg Tyr Val Ile Arg Tyr Val Ser Pro Glu Ile Ala

690 695 700

Arg Lys Tyr Ala Arg Gln Glu Ala Leu Val Arg Phe Ala Leu His Arg

705 710 715 720

Val Pro Leu Leu Gln Leu Arg Arg Tyr Tyr Gln Ser Cys Cys Gly Pro

725 730 735

Lys Lys Asp Pro Asp Ala Ala Glu Cys Val Asp Phe Leu Ala Gly Val

740 745 750

Val Asn Arg Val Asp Phe Ala Asn Phe Thr Asp Val Arg Thr Gly Asp

755 760 765

Ser Ser Lys Ser Glu Gln Glu Lys Lys Gln Lys Tyr Gln Ala Ile Val
770 775 780
Gly Leu Tyr Leu Thr Val Val Tyr Trp Ile Val Lys Asn Leu Val Asn
785 790 795 800
Val Asn Ser Arg Tyr Val Met Ala Phe His Ile Leu Glu Arg Asp Thr

805 810 815
Val Leu Leu Glu Gly Lys Arg Leu Phe Val Gly Gly Met Lys Ala Glu
820 825 830
Asp Pro Phe Leu Leu Thr Asp Gly Tyr Val Ser Arg Gln Asp Ala Tyr
835 840 845
Val Arg Lys Arg Ile Gly Glu Asn Lys Arg Ala Asn Arg His Gly Leu
850 855 860
Asn Cys Val Leu Glu Asn Arg Asn Ala Leu Gly Ser Asp Pro Ala Ser

865 870 875 880
Thr Asp Ala Ala Ala Ser Leu Ile Trp Ser Tyr Arg Asn Ala Ala Ala
885 890 895
His Leu Thr Ala Val Ala Ala Ala Gln Glu Tyr Val Ser Glu Leu Arg
900 905 910
Glu Ile His Ser Tyr Phe Glu Val Tyr His Tyr Ala Met Gln Arg Tyr
915 920 925
Leu Lys Ser Gly Ala Glu Phe Ala Glu Leu Val Ser Lys Asn Gly Pro

930 935 940
Ala Ser Gly Lys Ile Ala Ala Trp Ala Asn Ala Val Asp Arg Cys His
945 950 955 960
Ser Phe Cys Lys Asp Trp Leu Trp Leu Leu Asn Val Pro Phe Ala Tyr
965 970 975
Asn Pro Ala Arg Tyr Lys Asn Leu Ser Ile Ala Asn Leu Phe Asp Lys
980 985 990
Asn Glu Ala Ala Pro Val Thr Glu Asp Ala Ser Glu Gln Lys Glu Asp

995 1000 1005
Glu

<210> 182

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 182

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15
Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30
Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45
Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60
Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80
Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95
Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350
Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365
Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380
Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400
Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415
Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430
Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala
995 1000

<210> 183

<211> 985

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 183

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Arg Gly
115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Asn Tyr Thr Leu Val Asn Asn Asn Gly Leu Ser Glu Lys Gly Tyr
165 170 175

Ala Phe Phe Ile Ser Lys Phe Leu Glu Arg Lys Tyr Ser Tyr Leu Phe
180 185 190
Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln Tyr Arg
195 200 205
Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro Val Glu
210 215 220
Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu Asp Ile
225 230 235 240

Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr Leu Glu
245 250 255
Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr Asp Ala
260 265 270
Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe Arg Ser
275 280 285
Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala Asp Phe
290 295 300

Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His Asn Gly
305 310 315 320
Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr Ile Asn
325 330 335
Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser Ala Lys
340 345 350
Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser Thr Asp
355 360 365

Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln Ser Thr

370 375 380

Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val Leu Pro

385 390 395 400

Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala Lys Met

405 410 415

Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala Met Leu

420 425 430

Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His Cys Pro

435 440 445

Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser Thr Lys

450 455 460

Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg Val Met

465 470 475 480

Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu Arg Ile

485 490 495

Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile Leu Lys

500 505 510

Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp Leu Gln

515 520 525

Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn Phe Gln

530 535 540

Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn Asp Leu

545 550 555 560

Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn Pro His

565 570 575

Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile Glu Phe

580 585 590

Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg Ile Gln

595 600 605

Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro Leu Arg

610 615 620

Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu Ala Ile
625 630 635 640
Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys Leu Lys
645 650 655
Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu Lys Ser
660 665 670
Pro Ala Leu Asn Val Ser Tyr Leu Ile His Asn Tyr Phe Arg Ala Tyr
675 680 685

Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn Tyr Arg
690 695 700
Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser Tyr Leu
705 710 715 720
Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro Ser Lys
725 730 735
Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp Arg Leu
740 745 750

Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile Ile Arg
755 760 765
Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys Glu Tyr
770 775 780
Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu Glu Asn
785 790 795 800
Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp Leu Asn
805 810 815

Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr Gly Lys
820 825 830
Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn Lys Val
835 840 845
Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val Lys Ile
850 855 860
Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu Glu Ala

865 870 875 880

Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala Met Val
885 890 895
Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr Tyr Asp
900 905 910
Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln Lys Ile
915 920 925
Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His Asp Lys
930 935 940

Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val Tyr Ala
945 950 955 960
Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile Lys Leu
965 970 975
Glu Asp Leu Ser Asn Asp Ser Ser Ala
980 985

<210> 184
<211> 1082
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 184
Cys Ile Leu Asp Phe Phe Thr Gln Asp Lys Ala Ile Ala Glu Tyr Gln

1 5 10 15
Leu Gly Val Glu Phe Leu Gln Lys Asn Leu Pro Val Ile Arg Tyr Leu
20 25 30
Tyr Leu Pro Thr Ser His Lys Arg Phe Glu Asn Val Pro Lys Asn Gln
35 40 45
Leu Ile Ser Glu Gln Arg Asn Tyr Phe Lys Asn Ser Leu Lys Val Leu
50 55 60
Lys Asn Leu Ile Arg Asp Tyr Arg Asn Phe Tyr Thr His His Phe His

65 70 75 80

Lys Pro Ile Pro Val Phe Pro Glu Thr Tyr Lys Leu Leu Asp Asp Leu

85 90 95

Phe Leu Ala Val Ala Asn Asp Val Lys Lys His Arg Met Lys Thr Asp

100 105 110

Ala Ser Lys Gln Leu Leu Lys Lys Gly Leu Ile Glu Glu Leu Ala Gln

115 120 125

Leu Glu Lys Leu Lys Leu Glu Asp Leu Lys Lys Leu Lys Arg Glu Gly

130 135 140

Lys Lys Val Asn Leu Asn Asp Lys Glu Ala Ile Thr Asn Ala Ile Leu

145 150 155 160

Asn Asp Ser Phe Ser His Leu Leu Pro Lys Glu Asn Thr Ile Ser Lys

165 170 175

Tyr Tyr Ser Ala Val Pro Thr Glu Asp Ile Asp Thr Glu Asn Gly Val

180 185 190

Thr Ile Ser Glu Ser Gly Ile Ile Phe Leu Leu Gly Leu Phe Leu Thr

195 200 205

Lys Lys Gln Ser Glu Asp Leu Arg Ser Arg Val Lys Gly Phe Lys Ala

210 215 220

Lys Leu Ile Val Asn Pro Glu Asn Pro Ile Asn Lys Lys Asn Asn Ser

225 230 235 240

Leu Lys Tyr Met Ala Thr His Trp Val Phe Gly Tyr Leu Gly Phe Lys

245 250 255

Gly Leu Lys Asn Arg Phe Thr Thr Thr Phe Thr Lys Asp Thr Leu Leu

260 265 270

Ala Gln Ile Val Asp Glu Leu Ser Lys Val Pro Asp Glu Leu Tyr Gln

275 280 285

Val Leu Pro Glu Glu Leu Lys Asn Glu Phe Leu Glu Asp Met Asn Glu

290 295 300

Tyr Leu Lys Glu Glu Asn Ser Glu Ser Leu Asp Lys Ala Thr Val Ile

305 310 315 320

His Pro Val Ile Arg Lys Arg Tyr Glu Asn Lys Phe Ala Tyr Phe Ala

325 330 335

Leu Arg Phe Leu Asp Glu Phe Val Asp Phe Pro Thr Leu Arg Phe Gln

340 345 350

Leu His Leu Gly Asn Tyr Val His Asp Lys Arg Glu Lys Pro Ile Glu

355 360 365

Gly Thr Lys Tyr Val Thr Glu Arg Ile Val Lys Glu Lys Ile Lys Ala

370 375 380

Phe Ala Lys Leu Ser Glu Ala Ala Gln Leu Lys Gln Lys Tyr Phe Glu

385 390 395 400

Glu Lys Glu Asn His Gln Ser Ile Gly Leu Gln Leu Tyr Pro Asn Pro

405 410 415

Ser Tyr Asn Phe Val Gly Asn Asn Ile Pro Ile His Leu Asn Leu Asn

420 425 430

Glu His Phe Phe Pro Lys Glu Val Lys Ile Val Ala Gly Arg Leu Lys

435 440 445

Lys Arg Asn Ser Ser Tyr Lys Ser Asp His Pro Glu Glu Tyr Lys Val

450 455 460

Arg Thr Asp Asn Lys Ile Lys Pro Asp Ala Ile Leu Gln Asp Leu Gly

465 470 475 480

Lys Pro Glu Lys Leu Ala Pro Val Ala Met Leu Ser Leu Asn Glu Leu

485 490 495

Pro Ala Leu Leu His Leu Val Leu Thr Lys Lys Thr Pro Glu Glu Ile

500 505 510

Glu Ile Ile Ile Ala Gln Lys Ile Ala Glu Arg Tyr Asn Val Leu Thr

515 520 525

Asn Tyr Lys Ala Gly Asp Asp Ile Ser Lys Gly Gln Ile Thr Lys Asn

530 535 540

Leu Leu Lys Ala Lys Gln Lys Lys Glu Val Asn Leu Asp Lys Leu Gln

545 550 555 560

Leu Ala Ile Glu Lys Glu Ile Ala Val Thr Asn Asp Lys Leu Gln Thr

565 570 575

Ile Ala Leu His Ile Lys Glu Arg Asn Asp Pro Lys Gln Lys Arg Lys

580 585 590

Tyr Val Phe Thr Asn Lys Glu Ile Gly Leu Gln Val Thr Trp Leu Ala

595 600 605

Asn Asp Leu Lys Arg Phe Met Pro Lys Gly Ser Arg Gln Asn Trp Arg

610 615 620

Gly Gln His His Ser Gln Leu Gln Lys Ser Leu Ala Phe Tyr Asp Ile

625 630 635 640

Gln Pro Lys Glu Pro Leu Ser Leu Leu Glu Glu Val Trp Asp Phe Lys

645 650 655

Asn Glu Ala Tyr Leu Trp Asn Asn Gly Ile Arg Arg Ser Phe Asp Lys

660 665 670

Arg Asp Phe Ile Ser Phe Tyr Thr Ser Tyr Leu Asn Asn Arg Lys Glu

675 680 685

Thr Phe Gln Arg Phe Lys Asp Gln Leu Asn Gly Ile Arg Ser Asn Lys

690 695 700

Lys Ile Leu Asp Lys Phe Ile Lys Gln Gln His Leu Trp Asn Leu Phe

705 710 715 720

His Lys Arg Leu Tyr Val Ile Asp Thr Ile Glu Glu Gln Val Glu Lys

725 730 735

Leu Leu Val Lys Pro Met Gln Phe Pro Lys Gly Val Phe Asp His Lys

740 745 750

Pro Thr Tyr Ile Lys Gly Lys Ser Ile Gln Glu Asn Pro Glu Cys Phe

755 760 765

Ala Asp Trp Tyr Val Ala Trp Asn Gln His Thr Asp Tyr Gln Lys Phe

770 775 780

Tyr Ser Trp Asp Arg Asp Tyr Lys Ser Ala Tyr Leu Ser Gly Glu Gln

785 790 795 800

Glu Lys Thr Glu Lys Arg Phe Ile Arg Val Gln Gly Ser Lys Ile Asn

805 810 815

Lys Val Lys Gln Gln Asp Val Leu Leu Ala Lys Met Ala Ser Ile Ile
820 825 830
Phe Asn Glu Leu Tyr Leu Pro Glu Asp Ala Glu His Leu Asp Leu Asn

835 840 845
Leu Ser Asp Ile Tyr Lys Thr Gln Thr Glu Arg Lys Ala Glu Ile Glu
850 855 860
Ala Ala Leu Ile Gln Ser His Lys Thr Thr Gly Asp Asn Ser Ala Asn
865 870 875 880
Ile Ile Lys Ser Thr Ser Ala Trp Thr Leu Thr Val Pro Tyr Cys Ser
885 890 895
Lys Asn Ile Tyr Glu Pro Gln Val Lys Leu Lys Glu Leu Gly Lys Phe

900 905 910
Lys Lys Phe Ile Ala Ser Gln Lys Val Gln Thr Leu Phe Glu Tyr Lys
915 920 925
Pro Gln Lys Ile Trp Asn Lys Thr Glu Leu Glu Glu Val Leu Glu Leu
930 935 940
Lys Ala Asn Ser Tyr Glu Val Ile Arg Arg Asp Tyr Leu Leu Lys Ser
945 950 955 960
Ile Gln Glu Phe Glu Lys Tyr Met Ile Lys Lys Leu Pro Thr Leu Ile

965 970 975
Asp Thr Asn Glu His Pro Asn Phe Asn Lys Tyr Leu Thr Thr Phe Leu
980 985 990
Lys Ser Leu Glu Leu Val Ser Glu Glu Asp Ala Lys Trp Leu Ile Ser
995 1000 1005
Lys Lys Asp Phe Asp Thr Thr Pro Ile Asp Glu Leu Lys Lys Gln
1010 1015 1020
Ser Lys Ile Met Glu Lys Ala Phe Leu Leu Val Met Ile Arg Asn

1025 1030 1035
Lys Phe Ser His Asn Gln Leu Pro Arg Lys Ile Tyr Tyr Asp Glu
1040 1045 1050
Ile Tyr Lys Asn Val Pro Asn Ala Val Ser Ile Asn Phe Asn Glu

1055 1060 1065

Leu Phe Leu Glu Tyr Thr Asn Gln Thr Ile Leu Glu Phe Lys

1070 1075 1080

<210> 185

<211> 708

<212> PRT

<213> Unknown

<220><223>

Description of Unknown:

Cas13 sequence

<400> 185

Asn Arg Arg Asp Met Glu Ala Ser Pro Gly Arg Leu Ala Arg Tyr Ile

1 5 10 15

Val Leu Lys Thr Leu Tyr Glu Arg Ala Phe Pro Arg Trp Leu Glu Ala

20 25 30

Arg Glu Ala Glu Thr Leu Asn Gly Trp Ile Gly Arg Ala Ala Asp Arg

35 40 45

Ala Thr Val Ala Ala Arg His Ile Asn Lys Asp Glu Asn Ala Ala Ala

50 55 60

Arg Met Ala Gly Leu Val Arg Leu Ala Asp Gly Lys Gly Ile Ala Asp

65 70 75 80

Phe Thr Asp Arg Leu Ala Ala Glu Thr Ala Ser Glu Tyr Arg Val Gln

85 90 95

Arg Gly Tyr Asp Ser Asp Pro Ala Val Ala Arg Lys Gln Ala Lys His

100 105 110

Ile Glu Asp Leu Arg Cys Asp Val Val Gly Gln Ala Phe Glu Ala Tyr

115 120 125

Leu Ala Asp Val Ala Arg Lys Leu Ala Trp Thr Met Asn Asp Pro Pro

130 135 140

Gly Gly Pro Leu Pro Asp Glu Lys Lys Ala Ser Leu Glu Thr Ala Ala

145 150 155 160

Pro Pro Ala Glu Asp Ala Gly Ala Glu Ala Glu Glu Asp Trp Leu Ala

165 170 175

Arg Leu Tyr Phe Leu Leu His Met Leu Pro Val Glu Glu Val Gly Gly

180 185 190

Leu Arg His Gln Leu Arg Lys Trp Ser Val Leu Glu Arg Glu Pro Asp

195 200 205

Ser Val Leu Glu Arg Glu Pro Asp Ala Asp Val Glu Ala Ile Glu Arg

210 215 220

Ile Leu Gly Leu Tyr Leu Asp Met His Asp Ala Lys Phe Glu Gly Gly

225 230 235 240

Asp Gly Val Ala Gly Ala Glu Ala Leu Thr Asp Leu Phe Thr Ser Pro

245 250 255

Ala Gln Phe Arg Arg Val Cys Pro Glu Asp Gly Ala Gly Asn Gly Gly

260 265 270

His Val Pro Trp Arg Gly Leu Arg Glu Met Leu Arg Phe Gly Gly Gly

275 280 285

Glu Pro Arg Leu Met Trp Ala Phe Arg Lys Trp Pro Ile Gly Asp Gly

290 295 300

Met Val Asp Gly Leu Asn Ala Leu Glu Ala Thr Val Ala Glu Ala His

305 310 315 320

Lys Gln Arg Glu Asp Leu His Ala Lys Trp Ala Gly Lys Lys Gly Phe

325 330 335

Ser Arg Lys Asp Lys Asp Glu Tyr Arg Ala Ala Leu Glu Thr Val Val

340 345 350

Val His Arg His Leu Ala Ala His Val Gln Leu Val Asn His Ala Arg

355 360 365

Leu His Arg Leu Ala Met Ala Val Leu Ala Arg Leu Ala Asp Tyr Ala

370 375 380

Gly Leu Trp Glu Arg Asp Leu Tyr Phe Thr Thr Leu Ala Leu Ile Arg

385 390 395 400

Leu Glu Asn Gly Lys Pro Glu Asp Val Phe Arg Ser Arg Glu Leu Glu

405 410 415

Trp Leu Arg Glu Gly Arg Ile Val Asp Ala Leu Lys Glu Leu Lys Lys

420 425 430

Asn Ala Asp Gly Ser Glu Pro Ala Val Gly Thr Ala Leu Gln Arg Leu

435 440 445

Phe Gly Lys Gly Ile Leu Thr Gly Gly Gly Thr Val Ser Val Arg Arg

450 455 460

Asp Leu Leu His Phe Asn Met Leu Gln Arg Lys Ala Asn Glu Pro Phe

465 470 475 480

Asn Leu Thr Thr Ala Val Asn Asp Thr Arg Lys Leu Met Ala Tyr Asp

485 490 495

Arg Lys Leu Lys Asn Ala Val Ser Arg Ser Ile Ile Glu Leu Leu Ala

500 505 510

Arg Glu Gly Leu Asp Leu Ala Trp Glu Met Lys Asp His Gln Leu Ala

515 520 525

Gly Ala Val Leu Lys Thr Arg Gln Ala Val His Leu Gly Gly Ala Lys

530 535 540

Val Gly Gly Gly Pro Ile Thr Glu Asp Leu His Gly Pro Glu Phe Thr

545 550 555 560

Ala Met Ala Ala Ala Leu Phe Gly Gly Glu Ala Arg Ala Ala Thr Asp

565 570 575

Ala Ala Glu Ala Ala Thr Gly Arg Pro Asp Arg Arg Glu Arg Lys Ser

580 585 590

Gly Gly Ala Ser Pro Arg Pro Ala Arg Pro Ala Lys Thr Leu Pro Ala

595 600 605

Pro Thr Pro Arg Leu Leu Pro Ala Ala Gly Glu Arg Val Glu Gly Val

610 615 620

Leu Val Glu Glu Lys Thr Arg Lys Gly Gly Trp Lys Ala Ala Val Glu

625 630 635 640

Ile Gly Gly Pro Arg Ile Val Gly Asp Ile Phe Asn Ser Gly Glu Val

645 650 655

Pro Ser Asp Ala Glu Pro Gly Leu Glu Ala Glu Phe Val Val Arg Val

660 665 670

Ala Asn Pro Ala Asn Ala Ser Phe Met Trp Leu Ser Pro Asp Val Glu

675 680 685

Glu Arg Leu Lys Lys Ala Ala Ala Pro Arg Arg Gly Gly Arg Pro Ala

690 695 700

Gly Arg Gln Arg

705

<210> 186

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 186

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415
Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430
Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445
Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460
Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480
Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495
Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510
Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525
Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560
Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940
Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975
Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990
Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala
995 1000

<210> 187
<211> 985
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 187
Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15
Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30
Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60
Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80
Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Arg Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Asn Tyr Thr Leu Val Asn Asn Asn Gly Leu Ser Glu Lys Gly Tyr

165 170 175

Ala Phe Phe Ile Ser Lys Phe Leu Glu Arg Lys Tyr Ser Tyr Leu Phe

180 185 190

Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln Tyr Arg

195 200 205

Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro Val Glu

210 215 220

Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu Asp Ile

225 230 235 240

Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr Leu Glu

245 250 255

Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr Asp Ala

260 265 270

Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe Arg Ser

275 280 285

Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala Asp Phe

290 295 300

Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His Asn Gly

305 310 315 320

Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr Ile Asn

325 330 335

Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser Ala Lys
340 345 350
Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser Thr Asp
355 360 365

Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln Ser Thr
370 375 380
Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val Leu Pro
385 390 395 400
Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala Lys Met
405 410 415
Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala Met Leu
420 425 430

Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His Cys Pro
435 440 445
Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser Thr Lys
450 455 460
Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg Val Met
465 470 475 480
Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu Arg Ile
485 490 495

Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile Leu Lys
500 505 510
Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp Leu Gln
515 520 525
Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn Phe Gln
530 535 540
Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn Asp Leu
545 550 555 560

Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn Pro His
565 570 575
Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile Glu Phe

580 585 590

Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg Ile Gln

595 600 605

Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro Leu Arg

610 615 620

Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu Ala Ile

625 630 635 640

Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys Leu Lys

645 650 655

Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu Lys Ser

660 665 670

Pro Ala Leu Asn Val Ser Tyr Leu Ile His Asn Tyr Phe Arg Ala Tyr

675 680 685

Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn Tyr Arg

690 695 700

Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser Tyr Leu

705 710 715 720

Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro Ser Lys

725 730 735

Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp Arg Leu

740 745 750

Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile Ile Arg

755 760 765

Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys Glu Tyr

770 775 780

Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu Glu Asn

785 790 795 800

Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp Leu Asn

805 810 815

Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr Gly Lys

820 825 830

Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn Lys Val
835 840 845

Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val Lys Ile
850 855 860

Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu Glu Ala
865 870 875 880

Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala Met Val
885 890 895

Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr Tyr Asp
900 905 910

Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln Lys Ile
915 920 925

Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His Asp Lys
930 935 940

Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val Tyr Ala
945 950 955 960

Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile Lys Leu
965 970 975

Glu Asp Leu Ser Asn Asp Ser Ser Ala
980 985

<210> 188

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas13 sequence

<400> 188

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350
Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365
Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380
Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400
Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415
Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430
Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445
Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460
Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480
Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495
Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510
Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525
Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940
Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975
Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990
Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala
995 1000

<210> 189
<211> 985
<212> PRT
<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 189

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Arg Gly
115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160

Arg Asn Tyr Thr Leu Val Asn Asn Asn Gly Leu Ser Glu Lys Gly Tyr
165 170 175

Ala Phe Phe Ile Ser Lys Phe Leu Glu Arg Lys Tyr Ser Tyr Leu Phe
180 185 190

Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln Tyr Arg
195 200 205

Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro Val Glu
210 215 220

Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu Asp Ile
225 230 235 240
Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr Leu Glu
245 250 255
Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr Asp Ala
260 265 270

Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe Arg Ser
275 280 285
Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala Asp Phe
290 295 300
Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His Asn Gly
305 310 315 320
Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr Ile Asn
325 330 335

Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser Ala Lys
340 345 350
Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser Thr Asp
355 360 365
Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln Ser Thr
370 375 380
Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val Leu Pro
385 390 395 400

Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala Lys Met
405 410 415
Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala Met Leu
420 425 430
Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His Cys Pro
435 440 445
Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser Thr Lys
450 455 460

Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg Val Met

465 470 475 480

Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu Arg Ile

485 490 495

Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile Leu Lys

500 505 510

Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp Leu Gln

515 520 525

Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn Phe Gln

530 535 540

Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn Asp Leu

545 550 555 560

Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn Pro His

565 570 575

Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile Glu Phe

580 585 590

Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg Ile Gln

595 600 605

Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro Leu Arg

610 615 620

Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu Ala Ile

625 630 635 640

Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys Leu Lys

645 650 655

Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu Lys Ser

660 665 670

Pro Ala Leu Asn Val Ser Tyr Leu Ile His Asn Tyr Phe Arg Ala Tyr

675 680 685

Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn Tyr Arg

690 695 700

Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser Tyr Leu

705 710 715 720

Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro Ser Lys
725 730 735
Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp Arg Leu
740 745 750
Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile Ile Arg
755 760 765
Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys Glu Tyr
770 775 780

Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu Glu Asn
785 790 795 800
Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp Leu Asn
805 810 815
Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr Gly Lys
820 825 830
Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn Lys Val
835 840 845

Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val Lys Ile
850 855 860
Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu Glu Ala
865 870 875 880
Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala Met Val
885 890 895
Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr Tyr Asp
900 905 910

Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln Lys Ile
915 920 925
Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His Asp Lys
930 935 940
Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val Tyr Ala
945 950 955 960
Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile Lys Leu

965 970 975

Glu Asp Leu Ser Asn Asp Ser Ser Ala
980 985

<210> 190

<211> 1000

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas13 sequence

<400> 190

Met Glu Glu Ala Asn Arg Tyr Ile Tyr Gly Ala Tyr Phe Asn Met Ala
1 5 10 15

Arg Asp Asn Phe Leu Asn Thr Ile Lys Leu Leu Ala Asp Lys Met Lys
20 25 30

Leu Gly Ala Thr Ser Gly Phe Gly Lys Asp Gly Asn Glu Val Asn Asp
35 40 45

Ile Asn Glu Leu Phe Gly Asp Lys Asn Thr Tyr Ala Asn Ile Glu Asn
50 55 60

Val Val Glu Phe Tyr Phe Pro Trp Ile Lys Ala Leu Glu Gly Arg Phe
65 70 75 80

Ser Leu Asp Lys Gly Asp Arg Asn Leu Asn Asp Met Lys Met Phe Tyr
85 90 95

Lys Ser Val Leu Thr Ala Phe Phe Thr Ala Val Asp Ser Leu Arg Asn
100 105 110

Lys Tyr Thr His Tyr Ser His Lys Asp Leu Asn Ile Arg Glu Ile Lys
115 120 125

Ile Glu Cys Thr Leu Gly Gly Lys Asp Tyr Cys Ile Gly Leu Leu Asn
130 135 140

Ala Leu Asp Cys Ile Tyr Asp Ser Ala Val Asn Leu Leu Lys Leu Arg
145 150 155 160

Phe Met Ala Gly Glu Tyr Glu Val Ala His Leu Arg Arg Cys Lys Ala

165 170 175

Val Asn Lys Lys Val Val Val Arg Thr Glu Lys Asp Gly Phe Tyr Tyr

180 185 190

Arg Leu Ser Asp Asn Gly Gly Val Thr Glu Lys Gly Val Ile Phe Ile

195 200 205

Ala Ser Met Phe Leu Asn Arg Lys Tyr Gly Phe Leu Phe Leu Lys Gln

210 215 220

Leu Glu Gly Phe Lys Arg Ser Asp Glu Lys Arg Tyr Arg Leu Thr Leu

225 230 235 240

Glu Thr Phe Leu Ala Phe Ser Asn Ile Lys Pro Val Asp Arg Leu Lys

245 250 255

Ser Asp Lys Leu Asp Arg Ala Ser Leu Gly Leu Asp Met Leu Asn Glu

260 265 270

Leu Thr Lys Ile Pro Arg Glu Leu Ser Glu Thr Leu Ser Val Asp Cys

275 280 285

Leu Tyr Lys Tyr Leu Thr Ser Asp Gly Glu Asp Asp Leu Arg Ser Arg

290 295 300

Ile Arg Tyr Gln Asp Arg Phe Val Pro Leu Ala Leu Glu Phe Ile Ser

305 310 315 320

Gln Ser Asp Glu Phe Lys Asp Phe Arg Phe Tyr Thr Tyr Val Gly Asn

325 330 335

Tyr Val Tyr Lys Gly Tyr Ile Lys Arg Leu Ile Asp Gly Thr Asp Lys

340 345 350

Glu Arg Tyr Leu Ser Asp Arg Leu Cys Gly Phe Tyr Lys Ser Val Asn

355 360 365

Asp Ala Ser Ser Asp Ala Ile Ala Gln Lys Tyr Gly Val Glu Ile Lys

370 375 380

Asp Ser Asn Glu Pro Asp Tyr Met Leu Pro Asp Ser Phe Arg Pro His

385 390 395 400

Val Leu Arg Ala Thr Pro His Phe Val Ile Asn Asn Asn Asn Ile Gly

405 410 415

Ile Lys Ile Cys Gly Asn Asp Cys Leu Pro Ile Val Asn Gly Lys Gly

420 425 430

Val Glu Ser Pro Glu Pro Asp Tyr Trp Leu Ser Ile Tyr Glu Leu Pro

435 440 445

Ala Met Leu Phe Tyr Ala Tyr Leu Arg Glu Lys Asn Gly Lys Leu Leu

450 455 460

Lys Asp Tyr Lys Ser Ile Arg Glu Leu Ile Glu Asp Val Glu Lys Lys

465 470 475 480

Ala Asp Glu Lys Asn Asp Arg Asp Lys Gly Ala Leu Met Ala Arg His

485 490 495

Ile Asp Lys Glu Ile Ile Trp Thr Gln Thr Lys Leu Asp Glu Val Lys

500 505 510

Arg Leu Glu Glu Lys Lys Val Ala Ala Tyr Gly Lys Lys Gly Arg Val

515 520 525

Val Leu Lys Ser Gly Arg Met Ala Asp Leu Leu Ala His Asp Met Val

530 535 540

Arg Leu Gln Pro Ala Thr Lys Gly Ser Asp Lys Ile Thr Gly Ala Asn

545 550 555 560

Phe Gln Ala Leu Gln Val Ser Leu Ala Tyr Phe Lys Arg Asp Ile Leu

565 570 575

Ala Asp Val Phe Ser Arg Ala Met Leu Thr Thr Gly Asn His Arg His

580 585 590

Pro Phe Leu Tyr Arg Ile Asp Val Ser His Cys Ser Ser Leu Arg Asp

595 600 605

Phe Tyr Val Ala Tyr Leu Gly Glu Arg Arg Lys Tyr Phe Glu Asp Val

610 615 620

Ala Lys Lys Ile Ala Lys Asn Lys Leu Asn Thr Pro Cys His Ile Leu

625 630 635 640

Arg Arg Leu Gln Arg Glu Gly Ser Gly Glu Glu Ala Gly Lys Asp Val

645 650 655

Lys Pro Lys Phe Leu Pro Arg Gly Ile Phe Thr Gly Ser Ile Lys Ser

660 665 670

Cys Leu Glu Lys Ser Ala Leu Asn Ile Asn Ile Arg Asn Ala Arg Asn

675 680 685

Asp Val Lys Pro Ala Ile Asn Ala Ala Tyr Leu Ile Leu Met Tyr Tyr

690 695 700

Lys Glu Ile Glu Lys Gly Glu Phe Gln Gly Phe Tyr Gly Glu Lys Arg

705 710 715 720

Arg Tyr Asp Ile Leu Glu Glu Gly Lys Pro Leu Asp Leu Asp Glu Arg

725 730 735

Lys Lys Ala Leu Ala Ser Ile Lys Pro Ala Lys Ile Asp Val Ser Glu

740 745 750

Ala Asn Met Pro Met Ser Lys Glu Glu His Leu Met Arg Lys Arg Tyr

755 760 765

His Ala Val Cys Asn Asn Glu Ser Ala Ile Arg Met Tyr Gln Val Gln

770 775 780

Asp Ile Leu Leu Leu Leu Met Ala Lys Asp Ile Phe Lys Lys Ala Leu

785 790 795 800

Ser Glu Gly Val Met Ser Lys Lys Ile Gly Leu Glu Asn Leu Asn Gly

805 810 815

Ile Phe Asp Ala Pro Val Asn Phe Val Lys Asn Phe Asp Asn Ile Lys

820 825 830

Leu Thr Ala Thr Gly Ile Lys Ile Lys Asp Tyr Gly Lys Val Cys Arg

835 840 845

Leu Gly Thr Asp Phe Lys Phe Asn Ser Leu Val Lys Ala Phe His Lys

850 855 860

Val Tyr Ser Lys Ser Val Glu Met Asp Tyr Ser Asp Tyr Leu Lys Glu

865 870 875 880

Glu Glu Glu Phe Glu Lys Tyr Arg Leu Asn Met Val Lys Leu Cys Arg

885 890 895

Glu Val Glu Arg Gly Ile Thr Glu Asp Leu His Leu Ser Leu Asp Gly

900 905 910

Lys Ser His Leu Gly Phe Asn Asp Asp Val Ile Lys Pro Tyr Asn Asp
915 920 925

Lys Tyr Asn Val Phe Asn Gly Gly Asp Leu Thr Phe Phe Ile Asn Ala

930 935 940

Arg Asn Met Phe Met His Gly Asp Tyr Lys Tyr Glu Cys Val Lys Tyr
945 950 955 960

Val Val Ser Glu His Phe Lys Gly Ser Leu Asn Asp Val Ser Phe Ala
965 970 975

Lys Glu Thr Tyr Gly His Phe Cys Asn Leu Leu Glu Ser Met Arg Lys
980 985 990

Lys Thr Gly Leu Arg Ile Asp Ile
995 1000

<210> 191

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas13 sequence

<400> 191

Met Gly Ala Ile Lys Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380
Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400
Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415
Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445
Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460
Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480
Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510
Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525
Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940

Lys Ile Gly Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975
Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990
Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala
995 1000

<210> 192
<211> 1003

<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 192
Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15
Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30
Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940
Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975
Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990
Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala
995 1000

<210> 193
<211> 1003
<212> PRT
<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 193

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15
Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30
Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45
Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80
Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95
Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Ile Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Val Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255

Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350
Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365
Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400
Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415
Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430
Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460
Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940
Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala

995 1000

<210> 194

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 194

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350
Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365
Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380
Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400
Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720
Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 195

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 195

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300
Arg Ser Arg Phe Glu Thr Phe Ala Leu His Phe Leu Asp Lys Gln Pro
305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Met Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Met Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670

Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700

Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940
Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990
Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala
995 1000

<210> 196
<211> 985
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 196
Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15
Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Arg Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Asn Tyr Thr Leu Val Asn Asn Asn Gly Leu Ser Glu Lys Gly Tyr

165 170 175

Ala Phe Phe Ile Ser Lys Phe Leu Glu Arg Lys Tyr Ser Tyr Leu Phe

180 185 190

Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln Tyr Arg

195 200 205

Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro Val Glu

210 215 220

Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu Asp Ile

225 230 235 240

Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr Leu Glu

245 250 255

Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr Asp Ala

260 265 270

Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe Arg Ser

275 280 285

Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala Asp Phe

290 295 300

Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His Asn Gly

305 310 315 320

Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr Ile Asn

325 330 335

Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser Ala Lys

340 345 350

Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser Thr Asp

355 360 365

Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln Ser Thr

370 375 380

Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val Leu Pro

385 390 395 400

Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala Lys Met

405 410 415

Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala Met Leu

420 425 430

Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His Cys Pro

435 440 445

Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser Thr Lys

450 455 460

Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg Val Met

465 470 475 480

Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu Arg Ile

485 490 495

Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile Leu Lys

500 505 510

Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp Leu Gln

515 520 525

Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn Phe Gln

530 535 540

Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn Asp Leu

545 550 555 560

Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn Pro His

565 570 575

Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile Glu Phe

580 585 590

Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg Ile Gln

595 600 605

Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro Leu Arg

610 615 620

Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu Ala Ile

625 630 635 640

Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys Leu Lys

645 650 655

Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu Lys Ser

660 665 670

Pro Ala Leu Asn Val Ser Tyr Leu Ile His Asn Tyr Phe Arg Ala Tyr

675 680 685

Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn Tyr Arg

690 695 700

Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser Tyr Leu

705 710 715 720

Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro Ser Lys

725 730 735

Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp Arg Leu

740 745 750

Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile Ile Arg

755 760 765

Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys Glu Tyr
770 775 780
Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu Glu Asn

785 790 795 800
Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp Leu Asn
805 810 815
Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr Gly Lys
820 825 830
Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn Lys Val
835 840 845
Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val Lys Ile

850 855 860
Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu Glu Ala
865 870 875 880
Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala Met Val
885 890 895
Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr Tyr Asp
900 905 910
Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln Lys Ile

915 920 925
Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His Asp Lys
930 935 940
Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val Tyr Ala
945 950 955 960
Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile Lys Leu
965 970 975
Glu Asp Leu Ser Asn Asp Ser Ser Ala
980 985

<210> 197
<211> 1003
<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 197

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Ile Glu His Leu
145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175

Asp His Phe Tyr Tyr Thr Leu Val Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255

Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala

995 1000

<210> 198

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 198

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255
Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350
Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365
Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380
Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400
Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Leu Asn Tyr Phe Arg

690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Asn Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 199

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 199

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700

Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala

995 1000

<210> 200

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 200

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Lys Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560
Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Leu Asn Tyr Phe Arg
690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Asn Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 201

<211> 1150

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 201

Met Lys His Val Phe Ala Ala Tyr Phe Ser Asp Ala Arg Leu Asn Ile
1 5 10 15

Met Ala Ser Leu Asn Asp Val Arg Glu Lys Ser Gly Leu Lys Arg Tyr
20 25 30

Lys Asn Glu Ala Glu Asn Val Gln Asn Phe Glu Gly Ile Phe Pro Lys
35 40 45

Asn Ile Ala Ser Asp Ile Arg Asp Lys Arg Ile Thr Leu Leu Arg Ile
50 55 60

Arg Phe Pro Phe Ile Glu Thr Ile Val Asp Pro Gly Arg Gly Lys Glu
65 70 75 80

Asn Pro Ala Ser Lys Tyr Gly Glu Leu Ser Trp Leu Phe Gln Leu Val
85 90 95

Asn Asp Met Arg Asn Val Phe Ile His Ser Thr Gly Ser Glu Glu Glu
100 105 110

Ile Asp Tyr Gln His His Lys Lys Ile Phe Asn Ala Leu Arg Lys Val
115 120 125

Tyr Asp Cys Gly Leu Arg Thr Val Lys Ser Arg Phe Gln Leu Glu Asn
130 135 140

Asp Thr Thr Met Pro Leu Leu Arg Cys Asp Asn Arg Gly Arg Pro Lys
145 150 155 160

Pro Phe Asn Lys Phe Ser Leu Ala Leu Cys Thr Ser Pro Glu Arg Asn
165 170 175

Gly Asn Lys Lys Gln Ser Asp Val Leu His Asp Phe Gly Arg Val Leu
180 185 190

Leu Cys Ser Leu Phe Leu Glu Lys Arg Gln Ile Ser Gly Leu Val Ser
195 200 205

His Phe Trp Asp Lys Asn Gly Tyr Gly Thr Asp Trp Asn Asp Ser Glu

210 215 220

Gln Thr Ile Ile Arg Glu Leu Leu Tyr Val Asn Arg Ile Arg Leu Pro
225 230 235 240

Ser Gln Arg Leu Arg Thr Asp Ser Thr Leu Thr Ser Val Thr Leu Asp
245 250 255

Thr Ile Ser Glu Leu Ala Arg Cys Pro Arg Pro Leu Phe Glu Leu Leu
260 265 270

Asp Ala Asp Gly Gln Glu Asn Phe Arg Val Gly Arg Ser Pro Lys Asn
275 280 285

Pro Gln Asn Arg Asn Asp Asp Pro Ser Tyr Leu Leu Leu Arg Gly His
290 295 300

Gln Ser Arg Phe Ile Pro Leu Ala Met Arg His Leu Asp Phe Asp Ser
305 310 315 320

Lys Cys Lys Leu Arg Phe Ala Val Asp Leu Gly Gln Tyr Tyr His Ser
325 330 335

Val Arg Leu Lys Pro Ala Glu Ser Phe Ile Asp Gly Asn Pro Gly Ile
340 345 350

Arg Arg Leu Gly Gln Lys Ile Ile Ala Phe Gly Arg Leu Lys Asp Phe
355 360 365

Glu Asp Ala Glu Lys Pro Glu Ile Trp Lys Lys Leu Glu Glu Asn Gly
370 375 380

Gln Lys Phe Ala Glu Glu Glu Glu Glu Leu Leu Lys Arg Ala Ser Ile
385 390 395 400

Thr Gly Ser Pro Glu Glu Leu Lys Pro Tyr Ile Ile Lys Thr Phe Pro
405 410 415

His Tyr His Leu Tyr Arg Asp Lys Ile Gly Phe Cys Ile Asp Trp Glu
420 425 430

Glu Lys Lys Asp Gln Lys Val Lys Tyr Pro Asn Leu Gly Val Arg Gly
435 440 445

Glu Asp Ser Lys Ser Thr Asp Ser Gly Gly Ile Lys Lys Arg Glu Asn
450 455 460

Arg Gln Leu Ser Arg His Gln Phe Trp Ile Ser Pro Asn Lys Ile Ile
465 470 475 480
Asp Leu Ala Phe Tyr His Tyr Leu Gln Thr Glu Ile Lys Gln Glu Ile
485 490 495
Thr Ala Ser Val Lys Thr Gly Arg Lys Lys Cys Pro Tyr Pro Ser Val
500 505 510
Glu Asn Ile Leu Lys Glu Tyr Tyr Glu Gly Met Val Val Leu Ile Lys
515 520 525

Glu Leu Lys Glu Gln Gly Pro Leu Pro Pro Trp Thr Glu Ile Pro Gln
530 535 540
Ile Ser Glu Arg Arg Ala Glu Cys His Arg Trp Ile Asn Lys Glu Ile
545 550 555 560
Ile Lys Ala Glu Asn Phe Thr Ile Ser Leu Ala Asp Leu Pro Lys Ala
565 570 575
Ile Arg Arg His Leu Lys Val Leu Asp Ser Arg Glu Thr Ser Val Ser
580 585 590

Asp Ile Ile Lys Arg Thr Lys Thr Met Ile Glu Glu Thr Cys Lys Lys
595 600 605
Gln Lys Glu Ile Glu Tyr Leu Leu Lys Tyr Pro Lys Lys Arg Gly Lys
610 615 620
Lys Gly Phe Arg Pro Ile Lys His Gly Asn Ile Ala Asp Phe Leu Thr
625 630 635 640
Glu Asp Leu Leu Arg Phe Gln Pro Lys Asp Ser Ser Lys Lys Asn Gly
645 650 655

Gly Lys Leu Thr Ser Lys Asn Tyr Gln Ile Leu Gln Lys Ala Ile Ala
660 665 670
Tyr Tyr Asp Lys Pro Tyr Cys Ile Val Asp Leu Leu Lys Lys Ser Gly
675 680 685
Leu Leu Glu Gly Glu Phe Lys His Pro Phe Leu Cys Lys Ile Ile Thr
690 695 700
Glu Glu Asn His Glu Gln Tyr Ser Thr Leu Ile Asp Phe Tyr Gln Lys

705 710 715 720

Tyr Leu Glu Glu Arg Lys Ala Phe Leu Glu Gly Phe Ile Asp Thr Phe
725 730 735
Val Ala Gly Ser Ser Ile Pro Gly Trp Leu Arg Leu Arg Lys Pro Ser
740 745 750
Thr Phe Glu Ser Trp Leu Asp Gln Gln Leu Asp Glu Asp Glu Lys Leu
755 760 765
Cys Gln Pro Leu Pro Val Pro Lys Ser Leu Phe Tyr Gln Met Leu Leu
770 775 780

Lys Met Thr Ala Glu Lys Leu Asp Leu Thr Pro Glu Met Leu Cys Lys
785 790 795 800
Lys Gly Thr Gln Arg Phe Ile Arg Asp Ser Gln Glu Val Glu Val Lys
805 810 815
Pro Ser Val Ser Trp Phe Ile Arg Gln Tyr Met Glu His Arg Asp Asp
820 825 830
Thr Ala Gln Glu Met Tyr Met Phe Lys Arg Arg His Glu Leu Phe Asp
835 840 845

Phe Phe His Asp Lys Lys Lys Thr Thr Lys Lys Leu His Glu Glu Lys
850 855 860
Thr Cys Cys Leu Ser Glu Lys Val Arg Gln Glu Glu Leu Glu Ser Val
865 870 875 880
His Lys Gly Ile Glu Lys Leu Lys Lys Leu Leu Arg Thr Tyr Lys Arg
885 890 895
Ser Glu Lys Lys Ile Arg His Phe Ser Thr Met Asp Met Val Leu Tyr
900 905 910

Leu Leu Ala Lys Lys Asn Phe Glu Lys Leu Ile Leu Cys Asp Glu Thr
915 920 925
Ser Gly Pro Asp Trp Ser Leu Lys Thr Leu Glu Thr Lys Ile Leu Ser
930 935 940
Thr Lys Ile Lys Tyr Glu Leu Asn Val Pro Gly Thr Asp Arg Thr Ile
945 950 955 960

Val His Arg Ala Cys Ala Ile Lys Lys Thr Gly Glu Leu Arg Leu Leu
965 970 975

Val Arg Asp Arg Arg Leu Pro Ser Leu Leu Asp Tyr Tyr Pro Lys Thr
980 985 990

Glu Lys Ser Ile Asp Gln Glu Glu Ile Lys Val Glu Leu Ala Asp Tyr
995 1000 1005

Ser Cys Lys Arg Ile Glu Ala Met Lys Leu Ile Ser Asp Leu Glu
1010 1015 1020

Gln Lys Ile Glu Glu Ser Cys Asn Arg Gly Phe Cys Lys Pro Val
1025 1030 1035

Pro Asp Lys Leu Lys Lys Ile Phe Gly Ala Lys Lys His Gly Thr
1040 1045 1050

Leu Leu Tyr Ala Leu Tyr His Arg Phe His Glu Glu Lys Asp Lys
1055 1060 1065

Ser Val Asp Glu Gln Gly Phe Asn Lys Asp Cys Phe Ala His Ala
1070 1075 1080

Arg Gln Ile Arg Asn Ala Phe Ala His Asn Glu Tyr Pro Val Ser
1085 1090 1095

Glu Gln Phe Asn Gln Ile Val Arg Gln Val Asn Glu Thr Ser Gln
1100 1105 1110

Pro His Asn His Asn Ser Pro Val Asn His Pro Lys Ile Ala Asp
1115 1120 1125

Gln Leu Val Lys Glu Leu Asp Lys Leu Tyr Lys Pro Trp Arg Asn
1130 1135 1140

Phe Leu Lys Arg Ile Ala Gly
1145 1150

<210> 202

<211> 985

<212> PRT

<213> Unknown

<220

><223> Description of Unknown:

Cas13 sequence

<400> 202

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Arg Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160

Arg Asn Tyr Thr Leu Val Asn Asn Asn Gly Leu Ser Glu Lys Gly Tyr
165 170 175

Ala Phe Phe Ile Ser Lys Phe Leu Glu Arg Lys Tyr Ser Tyr Leu Phe

180 185 190

Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln Tyr Arg
195 200 205

Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro Val Glu
210 215 220

Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu Asp Ile
225 230 235 240

Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr Leu Glu

245 250 255

Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr Asp Ala

260 265 270

Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe Arg Ser

275 280 285

Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala Asp Phe

290 295 300

Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His Asn Gly

305 310 315 320

Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr Ile Asn

325 330 335

Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser Ala Lys

340 345 350

Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser Thr Asp

355 360 365

Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln Ser Thr

370 375 380

Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val Leu Pro

385 390 395 400

Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala Lys Met

405 410 415

Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala Met Leu

420 425 430

Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His Cys Pro

435 440 445

Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser Thr Lys

450 455 460

Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg Val Met

465 470 475 480

Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu Arg Ile

485 490 495

Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile Leu Lys

500 505 510

Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp Leu Gln

515 520 525

Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn Phe Gln

530 535 540

Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn Asp Leu

545 550 555 560

Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn Pro His

565 570 575

Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile Glu Phe

580 585 590

Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg Ile Gln

595 600 605

Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro Leu Arg

610 615 620

Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu Ala Ile

625 630 635 640

Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys Leu Lys

645 650 655

Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu Lys Ser

660 665 670

Pro Ala Leu Asn Val Ser Tyr Leu Ile His Asn Tyr Phe Arg Ala Tyr

675 680 685

Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn Tyr Arg

690 695 700

Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser Tyr Leu

705 710 715 720

Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro Ser Lys

725 730 735

Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp Arg Leu
740 745 750
Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile Ile Arg

755 760 765
Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys Glu Tyr
770 775 780
Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu Glu Asn
785 790 795 800
Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp Leu Asn
805 810 815
Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr Gly Lys

820 825 830
Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn Lys Val
835 840 845
Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val Lys Ile
850 855 860
Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu Glu Ala
865 870 875 880
Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala Met Val

885 890 895
Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr Tyr Asp
900 905 910
Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln Lys Ile
915 920 925
Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His Asp Lys
930 935 940
Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val Tyr Ala

945 950 955 960
Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile Lys Leu
965 970 975
Glu Asp Leu Ser Asn Asp Ser Ser Ala

980 985

<210> 203

<211> 985

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 203

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Arg Gly
115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160

Arg Asn Tyr Thr Leu Val Asn Asn Asn Gly Leu Ser Glu Lys Gly Tyr
165 170 175

Ala Phe Phe Ile Ser Lys Phe Leu Glu Arg Lys Tyr Ser Tyr Leu Phe
180 185 190

Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln Tyr Arg
195 200 205

Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro Val Glu
210 215 220
Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu Asp Ile
225 230 235 240
Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr Leu Glu
245 250 255
Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr Asp Ala
260 265 270

Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe Arg Ser
275 280 285
Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala Asp Phe
290 295 300
Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His Asn Gly
305 310 315 320
Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr Ile Asn
325 330 335

Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser Ala Lys
340 345 350
Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser Thr Asp
355 360 365
Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln Ser Thr
370 375 380
Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val Leu Pro
385 390 395 400

Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala Lys Met
405 410 415
Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala Met Leu
420 425 430
Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His Cys Pro

435 440 445

Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser Thr Lys

450 455 460

Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg Val Met

465 470 475 480

Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu Arg Ile

485 490 495

Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile Leu Lys

500 505 510

Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp Leu Gln

515 520 525

Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn Phe Gln

530 535 540

Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn Asp Leu

545 550 555 560

Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn Pro His

565 570 575

Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile Glu Phe

580 585 590

Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg Ile Gln

595 600 605

Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro Leu Arg

610 615 620

Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu Ala Ile

625 630 635 640

Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys Leu Lys

645 650 655

Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu Lys Ser

660 665 670

Pro Ala Leu Asn Val Ser Tyr Leu Ile His Asn Tyr Phe Arg Ala Tyr

675 680 685

Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn Tyr Arg
690 695 700
Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser Tyr Leu
705 710 715 720

Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro Ser Lys
725 730 735
Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp Arg Leu
740 745 750
Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile Ile Arg
755 760 765
Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys Glu Tyr
770 775 780

Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu Glu Asn
785 790 795 800
Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp Leu Asn
805 810 815
Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr Gly Lys
820 825 830
Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn Lys Val
835 840 845

Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val Lys Ile
850 855 860
Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu Glu Ala
865 870 875 880
Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala Met Val
885 890 895
Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr Tyr Asp
900 905 910

Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln Lys Ile
915 920 925
Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His Asp Lys

930 935 940

Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val Tyr Ala

945 950 955 960

Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile Lys Leu

965 970 975

Glu Asp Leu Ser Asn Asp Ser Ser Ala

980 985

<210> 204

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 204

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350
Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365
Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380
Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 205

<211> 985

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 205

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95
Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Arg Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Asn Tyr Thr Leu Val Asn Asn Asn Gly Leu Ser Glu Lys Gly Tyr
165 170 175

Ala Phe Phe Ile Ser Lys Phe Leu Glu Arg Lys Tyr Ser Tyr Leu Phe
180 185 190
Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln Tyr Arg
195 200 205
Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro Val Glu
210 215 220
Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu Asp Ile
225 230 235 240

Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr Leu Glu
245 250 255
Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr Asp Ala
260 265 270
Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe Arg Ser
275 280 285
Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala Asp Phe
290 295 300

Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His Asn Gly
305 310 315 320
Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr Ile Asn

325 330 335

Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser Ala Lys

340 345 350

Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser Thr Asp

355 360 365

Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln Ser Thr

370 375 380

Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val Leu Pro

385 390 395 400

Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala Lys Met

405 410 415

Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala Met Leu

420 425 430

Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His Cys Pro

435 440 445

Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser Thr Lys

450 455 460

Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg Val Met

465 470 475 480

Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu Arg Ile

485 490 495

Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile Leu Lys

500 505 510

Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp Leu Gln

515 520 525

Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn Phe Gln

530 535 540

Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn Asp Leu

545 550 555 560

Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn Pro His

565 570 575

Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile Glu Phe
580 585 590

Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg Ile Gln
595 600 605

Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro Leu Arg
610 615 620

Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu Ala Ile
625 630 635 640

Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys Leu Lys
645 650 655

Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu Lys Ser
660 665 670

Pro Ala Leu Asn Val Ser Tyr Leu Ile His Asn Tyr Phe Arg Ala Tyr
675 680 685

Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn Tyr Arg
690 695 700

Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser Tyr Leu
705 710 715 720

Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro Ser Lys
725 730 735

Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp Arg Leu
740 745 750

Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile Ile Arg
755 760 765

Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys Glu Tyr
770 775 780

Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu Glu Asn
785 790 795 800

Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp Leu Asn
805 810 815

Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr Gly Lys

820 825 830

Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn Lys Val

835 840 845

Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val Lys Ile

850 855 860

Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu Glu Ala

865 870 875 880

Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala Met Val

885 890 895

Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr Tyr Asp

900 905 910

Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln Lys Ile

915 920 925

Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His Asp Lys

930 935 940

Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val Tyr Ala

945 950 955 960

Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile Lys Leu

965 970 975

Glu Asp Leu Ser Asn Asp Ser Ser Ala

980 985

<210> 206

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 206

Met Gly Ala Ile Lys Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45
Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60
Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80
Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95
Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560
Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu

645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Gly Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala

995 1000

<210> 207

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 207

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Lys Lys
180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255

Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480
Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495
Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510
Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560
Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Leu Asn Tyr Phe Arg
690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Asn Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940
Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala
995 1000

<210> 208

<211> 985

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas13 sequence

<400> 208

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Lys His Leu

145 150 155 160

Arg Asn Tyr Thr Leu Val Asn Asn Asn Gly Leu Ser Glu Lys Gly Tyr

165 170 175

Ala Phe Phe Ile Ser Lys Phe Leu Glu Arg Lys Tyr Ser Tyr Leu Phe

180 185 190

Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln Tyr Arg

195 200 205

Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro Val Glu

210 215 220

Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu Asp Ile

225 230 235 240

Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr Leu Glu

245 250 255

Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr Asp Ala

260 265 270

Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe Arg Ser

275 280 285

Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala Asp Phe

290 295 300

Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His Asn Gly

305 310 315 320

Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr Ile Asn

325 330 335

Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser Ala Lys

340 345 350

Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser Thr Asp

355 360 365

Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln Ser Thr

370 375 380

Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val Leu Pro

385 390 395 400

Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala Lys Met

405 410 415

Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala Met Leu

420 425 430

Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His Cys Pro

435 440 445

Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser Thr Lys

450 455 460

Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg Val Met

465 470 475 480

Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu Arg Ile

485 490 495

Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile Leu Lys

500 505 510

Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp Leu Gln

515 520 525

Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn Phe Gln

530 535 540

Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn Asp Leu

545 550 555 560

Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn Pro His

565 570 575

Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile Glu Phe

580 585 590

Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg Ile Gln

595 600 605

Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro Leu Arg

610 615 620

Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu Ala Ile

625 630 635 640

Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys Leu Lys
645 650 655
Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu Lys Ser

660 665 670
Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg Thr Tyr
675 680 685
Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn Tyr Arg
690 695 700
Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser Tyr Leu
705 710 715 720
Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro Ser Lys

725 730 735
Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp Arg Leu
740 745 750
Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile Ile Arg
755 760 765
Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys Glu Tyr
770 775 780
Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu Glu Asn

785 790 795 800
Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp Leu Asn
805 810 815
Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr Gly Lys
820 825 830
Leu Phe Tyr Ile His His Asp Thr Arg Ile Asn Ser Leu Asn Lys Val
835 840 845
Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val Lys Ile

850 855 860
Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu Glu Ala
865 870 875 880
Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala Met Val

885 890 895

Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr Tyr Asp

900 905 910

Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln Lys Ile

915 920 925

Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His Asp Lys

930 935 940

Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Leu Val Tyr Ala

945 950 955 960

Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile Lys Leu

965 970 975

Glu Asp Leu Ser Asn Asp Ser Ser Ala

980 985

<210> 209

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 209

Met Gly Ala Ile Lys Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Gly Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala

995 1000

<210> 210

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 210

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45
Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60
Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80
Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95
Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255
Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560
Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Leu Asn Tyr Phe Arg

690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Asn Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 211

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 211

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Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1               5                  10                  15
Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
            20                  25                  30
Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
        35                  40                  45
Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
    50                  55                  60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65                  70                  75                  80
Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
                85                  90                  95
Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
            100                 105                 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
        115                 120                 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
    130                 135                 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145                 150                 155                 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
                165                 170                 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
            180                 185                 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
        195                 200                 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
```

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480
Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495
Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525
Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560
Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700

Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 212

<211> 985

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 212

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Arg Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Asn Tyr Thr Leu Val Asn Asn Asn Gly Leu Ser Glu Lys Gly Tyr

165 170 175

Ala Phe Phe Ile Ser Lys Phe Leu Glu Arg Lys Tyr Ser Tyr Leu Phe

180 185 190

Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln Tyr Arg

195 200 205

Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro Val Glu

210 215 220

Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu Asp Ile

225 230 235 240

Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr Leu Glu

245 250 255

Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr Asp Ala

260 265 270

Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe Arg Ser

275 280 285

Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala Asp Phe

290 295 300

Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His Asn Gly

305 310 315 320

Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr Ile Asn

325 330 335

Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser Ala Lys

340 345 350

Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser Thr Asp

355 360 365

Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln Ser Thr

370 375 380

Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val Leu Pro

385 390 395 400

Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala Lys Met
405 410 415
Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala Met Leu
420 425 430
Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His Cys Pro
435 440 445
Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser Thr Lys

450 455 460
Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg Val Met
465 470 475 480
Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu Arg Ile
485 490 495
Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile Leu Lys
500 505 510
Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp Leu Gln

515 520 525
Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn Phe Gln
530 535 540
Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn Asp Leu
545 550 555 560
Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn Pro His
565 570 575
Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile Glu Phe

580 585 590
Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg Ile Gln
595 600 605
Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro Leu Arg
610 615 620
Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu Ala Ile
625 630 635 640
Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys Leu Lys

645 650 655

Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu Lys Ser

660 665 670

Pro Ala Leu Asn Val Ser Tyr Leu Ile His Asn Tyr Phe Arg Ala Tyr

675 680 685

Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn Tyr Arg

690 695 700

Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser Tyr Leu

705 710 715 720

Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro Ser Lys

725 730 735

Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp Arg Leu

740 745 750

Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile Ile Arg

755 760 765

Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys Glu Tyr

770 775 780

Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu Glu Asn

785 790 795 800

Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp Leu Asn

805 810 815

Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr Gly Lys

820 825 830

Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn Lys Val

835 840 845

Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val Lys Ile

850 855 860

Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu Glu Ala

865 870 875 880

Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala Met Val

885 890 895

Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr Tyr Asp

900 905 910

Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln Lys Ile

915 920 925

Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His Asp Lys

930 935 940

Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val Tyr Ala

945 950 955 960

Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile Lys Leu

965 970 975

Glu Asp Leu Ser Asn Asp Ser Ser Ala

980 985

<210> 213

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 213

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Ala Thr Leu Gln Pro Thr
275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670

Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Leu Asn Tyr Phe Arg
690 695 700

Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Asn Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 214

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 214

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Thr Phe Ala Leu His Phe Leu Asp Lys Gln Pro

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Met Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Met Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560
Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala

995 1000

<210> 215

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 215

Met Gly Ala Ile Lys Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480
Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510
Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525
Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Gly Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975
Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990
Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala
995 1000

<210> 216
<211> 1359

<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 216
Met Gly Lys Leu Tyr Gly Tyr Lys Arg Trp Tyr Glu Ile Glu Gln Asn
1 5 10 15
Asn Gly Glu Lys Gly Ser Phe Lys Arg Lys Ile Arg Val Lys Arg Val
20 25 30
Tyr Asp Glu Glu Ser Lys Ser Tyr Val Val Arg Arg Asp Glu Val Glu
35 40 45
Asp Thr Glu Leu Ile Lys Asn Lys Asn Phe Ile Ile Asn Leu Lys Asp
50 55 60
Tyr Lys Thr Arg Asn Ser Asn Ile Gln Lys Phe Tyr Asp Lys Phe His
65 70 75 80
Val Gly Asn Ile Leu Phe Lys Leu Lys Ala Ser Val Lys Lys Gly Lys
85 90 95
Lys Thr Phe Tyr Lys Asp Leu Glu Lys Ala Glu Thr Val Leu Thr Asn
100 105 110
Val Glu Ile Leu Glu Gln Thr Ile Lys Leu Ala Asn Asn Ser Lys Ile
115 120 125
Asn Arg Lys Lys Leu Glu Lys Glu Leu Thr Gln Leu Asn Ile Asn Glu
130 135 140
Lys Ser Glu Glu Val Thr Ile Asp Asn Ile Lys Ile Tyr Leu Arg Gln

145 150 155 160

Gly Glu Lys Phe Asp Lys Lys Glu Asn Ile Asn Ala Ile Lys Trp Arg

165 170 175

Lys Leu Thr Ser Glu Glu Leu Thr Ile Lys Val Glu Ile Tyr Arg Glu

180 185 190

Cys Gln Ser Ile Asn Ser Asn Leu Tyr Ser Leu Leu Asp Tyr Val Leu

195 200 205

Ser Asn Glu Glu Tyr Asp Asp Arg Tyr Tyr Leu Glu Glu Val Glu Asn

210 215 220

Lys Leu Leu Ile Phe Gly Thr Gly Asn Lys Asn Lys Asn Gly Arg Asn

225 230 235 240

Tyr Tyr Tyr Phe Asp Tyr Val Leu Lys Ser Leu Ser Lys Ile Lys Gly

245 250 255

Leu Ile Lys Lys Asp Asp Arg Asn Leu Asn Tyr Leu Met Phe Leu Phe

260 265 270

Asn Ile Gln Lys Thr Ser Glu Asn Lys Glu His Phe Ile Asn Lys Ile

275 280 285

Phe Asn Tyr Phe Lys Tyr Glu Val Arg Ile Glu Lys Glu Asp Ile Val

290 295 300

Glu Phe Leu Val Gly Glu Leu Glu Tyr Tyr Asp Leu Ile Lys Arg Ile

305 310 315 320

Glu Lys Lys Pro Ser Glu Asn Gln Asn Gln Thr Asn Leu Glu Lys Thr

325 330 335

Tyr Ile Leu Leu Asp Lys His Glu Lys Leu Lys Glu Thr Ile Asp Thr

340 345 350

Lys Asn Glu Ile Val Gln Lys Leu Thr Ile Glu Leu Lys Asn Asn Asn

355 360 365

Leu Arg Asn Arg Ile Glu Ile Ile Leu His Lys Tyr Lys Ile Leu Glu

370 375 380

Leu Val Asp Lys Leu Asn Lys Asn Ile Lys Asn Gly Lys Ile Asn Thr

385 390 395 400

Glu Leu Tyr Gly Ile Tyr Lys Glu His Tyr Gly Gln Cys Ile Glu Tyr
405 410 415
Ile Asn Phe Asn Glu Leu Ala Leu Glu Glu Lys Glu Leu Tyr Lys Ile
420 425 430
Ile Tyr Arg Tyr Leu Lys Gly Arg Ile Glu Lys Leu Leu Gln Asn Arg

435 440 445
Asn Lys Ile Lys Ile Gly Glu Leu Arg Ile Glu Asp Ile Phe Ile Phe
450 455 460
Gln Lys Leu Leu Glu Lys Ile Glu Ile Arg Val Lys Gln Tyr Leu Leu
465 470 475 480
Glu His Ile Leu Tyr Leu Gly Lys Leu Lys His His Asn Ile Asp Glu
485 490 495
Val Asn Thr Ile Arg Phe Val Glu Glu His Ala Asn Glu Glu Leu Ser

500 505 510
Leu Glu Leu Ile Thr Leu Phe Ser Ala Thr Asn Val Glu Leu Asn Arg
515 520 525
Leu Leu Lys Val Lys Gly Glu Asn Gly Ser Tyr Glu Lys Asp Tyr Asp
530 535 540
Phe Phe Ser Ala Lys Pro Asp Lys Gly Lys Ile Lys Ile Lys Asp Thr
545 550 555 560
Asn Ser Val Met Lys Phe Glu Leu Leu Lys Lys Leu Lys Phe Ile Asn

565 570 575
Ser Glu Ala Thr Glu Thr Asn Gln Glu Ala Ile Asp Phe Leu Lys Glu
580 585 590
Ala Tyr Asn Leu Arg Asn Asn Ile Leu His Gly Lys Asn Glu Glu Ile
595 600 605
Ile Glu Asp Asn Lys Lys Asn Leu Ser Lys Ser Tyr Lys Asn Ile Asn
610 615 620
Glu Leu Ile Glu Glu Leu Arg Pro Ser Asp Asn Glu Ile Cys Lys Ser

625 630 635 640
Leu Asn Leu Asp Ile Ile Phe Lys Gly Asn Arg Lys Ile Asn Asp Ile

645 650 655

Asn Ala Lys Leu Phe Gly Asn Asn Arg Glu Lys Ile Tyr Leu Pro Ser

660 665 670

Phe Ser Lys Leu Val Pro Glu Ile Lys Asn Ile Ile Glu Ser Tyr Asp

675 680 685

Lys Asn Gly Thr Phe Asn Asp Glu Arg Ile Lys Lys Ile Val Leu Asn

690 695 700

Gly Ala Ile Tyr Val Asn Lys Ile Leu Tyr Leu Lys Glu Cys Ser Asn

705 710 715 720

Lys Asp Gly Glu Phe Ile Lys Asn Leu Lys Glu Glu Leu Asn Lys Asp

725 730 735

Ser Lys Glu Lys Ser Lys Tyr Val Ser Ile Glu Glu Leu Tyr Lys Lys

740 745 750

Ser Gln Ile Ser Ala Ser Lys Gly Asn Lys Lys Ala Ile Tyr Lys Tyr

755 760 765

Gln Arg Lys Ile Ile Glu Ile Tyr Leu Lys Tyr Leu Lys Glu Asn Tyr

770 775 780

Val Glu Ile Leu Asp Phe Ser Lys Leu Asn Leu Asn Ile Glu Gln Ile

785 790 795 800

Glu Asn Asp Ile Lys Asn Arg Lys Asn Ser Glu Asn Lys Val Leu Ile

805 810 815

Glu Ser Ile Lys Gln Lys Val Phe Pro Glu Asn Asp Phe Glu Tyr Ile

820 825 830

Ile Ser Ile Phe Ala Leu Leu Asn Asp Asn Ile Phe Ile Asn Lys Ile

835 840 845

Arg Asn Arg Phe Phe Ser Thr Asp Thr Trp Leu Lys Asn Asn Arg Tyr

850 855 860

Ser Asn Ile Ile Lys Ile Leu Asp Glu Val Ile Ser Val Asn Leu Leu

865 870 875 880

Arg Thr Glu Leu Leu Asn Thr Ser Ile Asp Ile Glu Glu Ile Lys Asp

885 890 895

Asp Val Leu Thr Glu Asp Ile Glu Asn Ile Ile Pro Glu Ile Arg Glu

900 905 910

Glu Ile Leu Gln Arg Thr Lys Lys Asp Phe Lys Thr Leu Leu Gly Asn

915 920 925

Asn Ala Ile Ser Lys Glu Gly Leu Ser Asn Glu Asp Ile Asp Lys Ile

930 935 940

Arg Asn Ile Glu Asp Ala Lys Ile Asn Leu Asp Phe Val Asn Asn Glu

945 950 955 960

Ile Lys Val Ser Leu Lys Glu Tyr Gly Ser Leu Pro Pro Asn Gly Val

965 970 975

Leu Ser Arg Asn Thr Ser Lys Tyr Tyr Asn Asn Glu Ile Ala Lys Lys

980 985 990

Ile Asp Gln Ile Ser Ile Leu Thr Phe Thr Lys Lys Ser Ile Gly Thr

995 1000 1005

Ile Ser Asp Glu Lys Phe Arg Asn Ile Tyr Trp Gln Glu Arg Lys

1010 1015 1020

Glu Ser Asp Glu Ser Lys Lys Ile Phe Val Tyr Asn Lys Asn Ile

1025 1030 1035

Leu Tyr Leu Val Thr Lys His Ser Phe Glu Lys Leu Tyr Lys Asn

1040 1045 1050

Phe Leu Glu Glu Glu Leu Asn Asn Leu Lys Leu Glu Asp Thr Lys

1055 1060 1065

Tyr Leu Arg Asp Leu Asp Leu Arg Arg Glu Lys Asn Leu Lys Val

1070 1075 1080

Asp Asn Thr Leu Lys Glu Ile Asn Glu Lys Val Arg Gly Tyr Ser

1085 1090 1095

Lys Glu Tyr Lys Lys Lys Phe Ile Glu Asn Leu Lys Asn Asn Asp

1100 1105 1110

Glu Tyr Phe Gly Lys Val Val Ser Gly Arg Phe Lys Asn Tyr Gln

1115 1120 1125

Glu Phe Lys Glu Ile Tyr Asp Glu Val Ser Glu Tyr Lys Lys Ile

1130 1135 1140

Arg Asp Val Val Asn Phe Asn Pro Leu Asn Lys Val Tyr Asn Tyr

1145 1150 1155

Leu Ile Glu Ile Asn Trp Lys Leu Ala Ile Gln Met Ala Arg Ala

1160 1165 1170

Glu Arg Asp Leu His Tyr Ile Val Asn Gly Leu Asn Glu Leu Lys

1175 1180 1185

Leu Ile Glu Leu Asn Gln Gly Gln Asn Asp Gly Ile Ser Arg Ala

1190 1195 1200

Tyr Pro Lys Tyr Lys Leu Asn Lys Glu Lys Asn Lys Lys Glu Leu

1205 1210 1215

Arg Leu Glu Glu Cys His Tyr Asn Phe Asp Ile Asp Asn Tyr Lys

1220 1225 1230

Lys Phe Glu Lys Ile Cys Glu Lys Leu Gly Ile Asp Leu Ser Glu

1235 1240 1245

Asn Gly Glu Leu Gln Gln Glu Asn Glu Thr Asn Ile Arg Asn Tyr

1250 1255 1260

Ile Ser His Phe Tyr Ile Leu Arg Lys Pro Phe Val Asp Ile Ser

1265 1270 1275

Ile Ser Glu Ala Ile Lys Arg Val Ser Lys Leu Leu Ser Tyr Arg

1280 1285 1290

Thr Arg Tyr Asn Asn Ser Thr Tyr Ser Ser Val Phe Glu Val Phe

1295 1300 1305

Lys Lys Asp Val Glu Leu Asn Tyr Asp Phe Leu Lys Lys Lys Ile

1310 1315 1320

Glu Leu Asn Gly Lys Thr Tyr Asp Glu Val Val Gln Arg Lys Lys

1325 1330 1335

Ile Ser Cys Leu Glu Leu Glu Ser Tyr Leu Asp Tyr Lys Pro Ile

1340 1345 1350

Ile Lys Lys Ile Leu Phe

1355

<210> 217

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 217

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975
Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990
Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala
995 1000

<210> 218
<211> 1003
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 218
Met Gly Ala Ile Lys Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30
Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45
Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60
Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95
Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350
Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365
Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940
Lys Ile Gly Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990
Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala
995 1000

<210> 219
<211> 1003
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 219
Met Gly Ala Ile Lys Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15
Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30
Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45
Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60
Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350
Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365
Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380
Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400
Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415
Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430
Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445
Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460
Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480
Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495
Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510
Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525
Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560
Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940
Lys Ile Gly Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975
Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990
Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala
995 1000

<210> 220
<211> 1359
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 220
Met Gly Lys Leu Tyr Gly Tyr Lys Arg Trp Tyr Glu Ile Glu Gln Asn

1 5 10 15

Asn Gly Glu Lys Gly Ser Phe Lys Arg Lys Ile Arg Val Lys Arg Val

20 25 30

Tyr Asp Glu Glu Ser Lys Ser Tyr Val Val Arg Arg Asp Glu Val Glu

35 40 45

Asp Thr Glu Leu Ile Lys Asn Lys Asn Phe Ile Ile Asn Leu Lys Asp

50 55 60

Tyr Lys Thr Arg Asn Ser Asn Ile Gln Lys Phe Tyr Asp Lys Phe His

65 70 75 80

Val Gly Asn Ile Leu Phe Lys Leu Lys Ala Ser Val Lys Lys Gly Lys

85 90 95

Lys Thr Phe Tyr Lys Asp Leu Glu Lys Ala Glu Thr Val Leu Thr Asn

100 105 110

Val Glu Ile Leu Glu Gln Thr Ile Lys Leu Ala Asn Asn Ser Lys Ile

115 120 125

Asn Arg Lys Lys Leu Glu Lys Glu Leu Thr Gln Leu Asn Ile Asn Glu

130 135 140

Lys Ser Glu Glu Val Thr Ile Asp Asn Ile Lys Ile Tyr Leu Arg Gln

145 150 155 160

Gly Glu Lys Phe Asp Lys Lys Glu Asn Ile Asn Ala Ile Lys Trp Arg

165 170 175

Lys Leu Thr Ser Glu Glu Leu Thr Ile Lys Val Glu Ile Tyr Arg Glu

180 185 190

Cys Gln Ser Ile Asn Ser Asn Leu Tyr Ser Leu Leu Asp Tyr Val Leu

195 200 205

Ser Asn Glu Glu Tyr Asp Asp Arg Tyr Tyr Leu Glu Glu Val Glu Asn

210 215 220

Lys Leu Leu Ile Phe Gly Thr Gly Asn Lys Asn Lys Asn Gly Arg Asn

225 230 235 240

Tyr Tyr Tyr Phe Asp Tyr Val Leu Lys Ser Leu Ser Lys Ile Lys Gly

245 250 255

Leu Ile Lys Lys Asp Asp Arg Asn Leu Asn Tyr Leu Met Phe Leu Phe
260 265 270
Asn Ile Gln Lys Thr Ser Glu Asn Lys Glu His Phe Ile Asn Lys Ile
275 280 285

Phe Asn Tyr Phe Lys Tyr Glu Val Arg Ile Glu Lys Glu Asp Ile Val
290 295 300
Glu Phe Leu Val Gly Glu Leu Glu Tyr Tyr Asp Leu Ile Lys Arg Ile
305 310 315 320
Glu Lys Lys Pro Ser Glu Asn Gln Asn Gln Thr Asn Leu Glu Lys Thr
325 330 335
Tyr Ile Leu Leu Asp Lys His Glu Lys Leu Lys Glu Thr Ile Asp Thr
340 345 350

Lys Asn Glu Ile Val Gln Lys Leu Thr Ile Glu Leu Lys Asn Asn Asn
355 360 365
Leu Arg Asn Arg Ile Glu Ile Ile Leu His Lys Tyr Lys Ile Leu Glu
370 375 380
Leu Val Asp Lys Leu Asn Lys Asn Ile Lys Asn Gly Lys Ile Asn Thr
385 390 395 400
Glu Leu Tyr Gly Ile Tyr Lys Glu His Tyr Gly Gln Cys Ile Glu Tyr
405 410 415

Ile Asn Phe Asn Glu Leu Ala Leu Glu Glu Lys Glu Leu Tyr Lys Ile
420 425 430
Ile Tyr Arg Tyr Leu Lys Gly Arg Ile Glu Lys Leu Leu Gln Asn Arg
435 440 445
Asn Lys Ile Lys Ile Gly Glu Leu Arg Ile Glu Asp Ile Phe Ile Phe
450 455 460
Gln Lys Leu Leu Glu Lys Ile Glu Ile Arg Val Lys Gln Tyr Leu Leu
465 470 475 480

Glu His Ile Leu Tyr Leu Gly Lys Leu Lys His His Asn Ile Asp Glu
485 490 495
Val Asn Thr Ile Arg Phe Val Glu Glu His Ala Asn Glu Glu Leu Ser

500 505 510

Leu Glu Leu Ile Thr Leu Phe Ser Ala Thr Asn Val Glu Leu Asn Arg

515 520 525

Leu Leu Lys Val Lys Gly Glu Asn Gly Ser Tyr Glu Lys Asp Tyr Asp

530 535 540

Phe Phe Ser Ala Lys Pro Asp Lys Gly Lys Ile Lys Ile Lys Asp Thr

545 550 555 560

Asn Ser Val Met Lys Phe Glu Leu Leu Lys Lys Leu Lys Phe Ile Asn

565 570 575

Ser Glu Ala Thr Glu Thr Asn Gln Glu Ala Ile Asp Phe Leu Lys Glu

580 585 590

Ala Tyr Asn Leu Arg Asn Asn Ile Leu His Gly Lys Asn Glu Glu Ile

595 600 605

Ile Glu Asp Asn Lys Lys Asn Leu Ser Lys Ser Tyr Lys Asn Ile Asn

610 615 620

Glu Leu Ile Glu Glu Leu Arg Pro Ser Asp Asn Glu Ile Cys Lys Ser

625 630 635 640

Leu Asn Leu Asp Ile Ile Phe Lys Gly Asn Arg Lys Ile Asn Asp Ile

645 650 655

Asn Ala Lys Leu Phe Gly Asn Asn Arg Glu Lys Ile Tyr Leu Pro Ser

660 665 670

Phe Ser Lys Leu Val Pro Glu Ile Lys Asn Ile Ile Glu Ser Tyr Asp

675 680 685

Lys Asn Gly Thr Phe Asn Asp Glu Arg Ile Lys Lys Ile Val Leu Asn

690 695 700

Gly Ala Ile Tyr Val Asn Lys Ile Leu Tyr Leu Lys Glu Cys Ser Asn

705 710 715 720

Lys Asp Gly Glu Phe Ile Lys Asn Leu Lys Glu Glu Leu Asn Lys Asp

725 730 735

Ser Lys Glu Lys Ser Lys Tyr Val Ser Ile Glu Glu Leu Tyr Lys Lys

740 745 750

Ser Gln Ile Ser Ala Ser Lys Gly Asn Lys Lys Ala Ile Tyr Lys Tyr
755 760 765

Gln Arg Lys Ile Ile Glu Ile Tyr Leu Lys Tyr Leu Lys Glu Asn Tyr
770 775 780

Val Glu Ile Leu Asp Phe Ser Lys Leu Asn Leu Asn Ile Glu Gln Ile
785 790 795 800

Glu Asn Asp Ile Lys Asn Arg Lys Asn Ser Glu Asn Lys Val Leu Ile
805 810 815

Glu Ser Ile Lys Gln Lys Val Phe Pro Glu Asn Asp Phe Glu Tyr Ile
820 825 830

Ile Ser Ile Phe Ala Leu Leu Asn Asp Asn Ile Phe Ile Asn Lys Ile
835 840 845

Arg Asn Arg Phe Phe Ser Thr Asp Thr Trp Leu Lys Asn Asn Arg Tyr
850 855 860

Ser Asn Ile Ile Lys Ile Leu Asp Glu Val Ile Ser Val Asn Leu Leu
865 870 875 880

Arg Thr Glu Leu Leu Asn Thr Ser Ile Asp Ile Glu Glu Ile Lys Asp
885 890 895

Asp Val Leu Thr Glu Asp Ile Glu Asn Ile Ile Pro Glu Ile Arg Glu
900 905 910

Glu Ile Leu Gln Arg Thr Lys Lys Asp Phe Lys Thr Leu Leu Gly Asn
915 920 925

Asn Ala Ile Ser Lys Glu Gly Leu Ser Asn Glu Asp Ile Asp Lys Ile
930 935 940

Arg Asn Ile Glu Asp Ala Lys Ile Asn Leu Asp Phe Val Asn Asn Glu
945 950 955 960

Ile Lys Val Ser Leu Lys Glu Tyr Gly Ser Leu Pro Pro Asn Gly Val
965 970 975

Leu Ser Arg Asn Thr Ser Lys Tyr Tyr Asn Asn Glu Ile Ala Lys Lys
980 985 990

Ile Asp Gln Ile Ser Ile Leu Thr Phe Thr Lys Lys Ser Ile Gly Thr

995 1000 1005

Ile Ser Asp Glu Lys Phe Arg Asn Ile Tyr Trp Gln Glu Arg Lys

1010 1015 1020

Glu Ser Asp Glu Ser Lys Lys Ile Phe Val Tyr Asn Lys Asn Ile

1025 1030 1035

Leu Tyr Leu Val Thr Lys His Ser Phe Glu Lys Leu Tyr Lys Asn

1040 1045 1050

Phe Leu Glu Glu Glu Leu Asn Asn Leu Lys Leu Glu Asp Thr Lys

1055 1060 1065

Tyr Leu Arg Asp Leu Asp Leu Arg Arg Glu Lys Asn Leu Lys Val

1070 1075 1080

Asp Asn Thr Leu Lys Glu Ile Asn Glu Lys Val Arg Gly Tyr Ser

1085 1090 1095

Lys Glu Tyr Lys Lys Lys Phe Ile Glu Asn Leu Lys Asn Asn Asp

1100 1105 1110

Glu Tyr Phe Gly Lys Val Val Ser Gly Arg Phe Lys Asn Tyr Gln

1115 1120 1125

Glu Phe Lys Glu Ile Tyr Asp Glu Val Ser Glu Tyr Lys Lys Ile

1130 1135 1140

Arg Asp Val Val Asn Phe Asn Pro Leu Asn Lys Val Tyr Asn Tyr

1145 1150 1155

Leu Ile Glu Ile Asn Trp Lys Leu Ala Ile Gln Met Ala Arg Ala

1160 1165 1170

Glu Arg Asp Leu His Tyr Ile Val Asn Gly Leu Asn Glu Leu Lys

1175 1180 1185

Leu Ile Glu Leu Asn Gln Gly Gln Asn Asp Gly Ile Ser Arg Ala

1190 1195 1200

Tyr Pro Lys Tyr Lys Leu Asn Lys Glu Lys Asn Lys Lys Glu Leu

1205 1210 1215

Arg Leu Glu Glu Cys His Tyr Asn Phe Asp Ile Asp Asn Tyr Lys

1220 1225 1230

Lys Phe Glu Lys Ile Cys Glu Lys Leu Gly Ile Asp Leu Ser Glu
1235 1240 1245
Asn Gly Glu Leu Gln Gln Glu Asn Glu Thr Asn Ile Arg Asn Tyr
1250 1255 1260
Ile Ser His Phe Tyr Ile Leu Arg Lys Pro Phe Val Asp Ile Ser
1265 1270 1275
Ile Ser Glu Ala Ile Lys Arg Val Ser Lys Leu Leu Ser Tyr Arg
1280 1285 1290

Thr Arg Tyr Asn Asn Ser Thr Tyr Ser Ser Val Phe Glu Val Phe
1295 1300 1305
Lys Lys Asp Val Glu Leu Asn Tyr Asp Phe Leu Lys Lys Lys Ile
1310 1315 1320
Glu Leu Asn Gly Lys Thr Tyr Asp Glu Val Val Gln Arg Lys Lys
1325 1330 1335
Ile Ser Cys Leu Glu Leu Glu Ser Tyr Leu Asp Tyr Lys Pro Ile
1340 1345 1350

Ile Lys Lys Ile Leu Phe
1355

<210> 221
<211> 1003
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 221
Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15
Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30
Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Ile Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Val Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350
Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380
Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400
Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415
Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445
Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460
Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480
Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510
Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525
Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940

Lys Ile Asp Ser Ser Phe Arg Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990

Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala
995 1000

<210> 222

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 222

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925
Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940
Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975
Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 223

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 223

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Ile Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255

Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Val Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700

Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880
Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 224

<211> 985

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 224

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Lys His Leu
145 150 155 160
Arg Asn Tyr Thr Leu Val Asn Asn Asn Gly Leu Ser Glu Lys Gly Tyr
165 170 175
Ala Phe Phe Ile Ser Lys Phe Leu Glu Arg Lys Tyr Ser Tyr Leu Phe
180 185 190
Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln Tyr Arg

195 200 205
Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro Val Glu
210 215 220
Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu Asp Ile
225 230 235 240
Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr Leu Glu
245 250 255
Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr Asp Ala

260 265 270
Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe Arg Ser
275 280 285
Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala Asp Phe
290 295 300
Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His Asn Gly
305 310 315 320
Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr Ile Asn

325 330 335
Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser Ala Lys
340 345 350
Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser Thr Asp

355 360 365

Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln Ser Thr

370 375 380

Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val Leu Pro

385 390 395 400

Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala Lys Met

405 410 415

Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala Met Leu

420 425 430

Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His Cys Pro

435 440 445

Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser Thr Lys

450 455 460

Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg Val Met

465 470 475 480

Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu Arg Ile

485 490 495

Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile Leu Lys

500 505 510

Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp Leu Gln

515 520 525

Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn Phe Gln

530 535 540

Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn Asp Leu

545 550 555 560

Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn Pro His

565 570 575

Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile Glu Phe

580 585 590

Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg Ile Gln

595 600 605

Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro Leu Arg
610 615 620
Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu Ala Ile
625 630 635 640
Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys Leu Lys

645 650 655
Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu Lys Ser
660 665 670
Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg Thr Tyr
675 680 685
Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn Tyr Arg
690 695 700
Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser Tyr Leu

705 710 715 720
Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro Ser Lys
725 730 735
Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp Arg Leu
740 745 750
Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile Ile Arg
755 760 765
Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys Glu Tyr

770 775 780
Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu Glu Asn
785 790 795 800
Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp Leu Asn
805 810 815
Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr Gly Lys
820 825 830
Leu Phe Tyr Ile His His Asp Thr Arg Ile Asn Ser Leu Asn Lys Val

835 840 845
Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val Lys Ile

850 855 860

Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu Glu Ala

865 870 875 880

Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala Met Val

885 890 895

Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr Tyr Asp

900 905 910

Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln Lys Ile

915 920 925

Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His Asp Lys

930 935 940

Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Leu Val Tyr Ala

945 950 955 960

Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile Lys Leu

965 970 975

Glu Asp Leu Ser Asn Asp Ser Ser Ala

980 985

<210> 225

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 225

Met Gly Ala Ile Lys Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80
Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670

Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Gly Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala

995 1000

<210> 226

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 226

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15
Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30
Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45
Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60
Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80
Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95
Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn

100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510
Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525
Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540
Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560
Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590
Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Leu Asn Tyr Phe Arg
690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Asn Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 227

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 227

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670

Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp
820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr
835 840 845
Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn
850 855 860
Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val
865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu
885 890 895
Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala
900 905 910
Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr
915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln
930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His
945 950 955 960
Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val
965 970 975
Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile
980 985 990
Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala
995 1000

<210> 228

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas13 sequence

<400> 228

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu
1 5 10 15
Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu
20 25 30
Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr
35 40 45
Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60
Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80
Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95
Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110

Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125

Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn

130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu

145 150 155 160

Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp

165 170 175

Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190

Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr

195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln

210 215 220

Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro

225 230 235 240

Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255

Asp Ile Leu Asn Glu Leu Ser Lys Ile Pro Ile Glu Leu Tyr Gln Thr

260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr

275 280 285

Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His

325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile

595 600 605

Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg

610 615 620

Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640

Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu

645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys

660 665 670

Leu Lys Lys Ser Lys Leu Lys His Leu Ile Glu Ser Pro Thr Arg Glu

675 680 685

Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg

690 695 700

Ala Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn

705 710 715 720

Tyr Arg Leu Phe Asp Asn Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser

725 730 735

Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro

740 745 750

Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765

Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile

770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 229

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 229

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp

35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175
Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His
180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg
195 200 205
Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe
210 215 220
Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys
225 230 235 240
Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr
245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu
260 265 270
Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu
275 280 285
Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu
305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg
325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys
340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr
355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr
370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560
Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605
Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620
Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655
Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn
660 665 670
Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685
Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720
Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg
725 730 735
Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750
Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780
Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr

885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly

900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys

930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp

945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu

965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu

980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn

995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala

1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050
Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065
Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile
1085 1090 1095

<210> 230
<211> 1095
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 230

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp

35 40 45
Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu

100 105 110
Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125
Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400
Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415
Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430
Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445
Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460
Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480
Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510
Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560
Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575
Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605
Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr

610 615 620
Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu

770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895
Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910
Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu
915 920 925
Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys

930 935 940
Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960
Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975
Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990
Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn

995 1000 1005
Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020
Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val
1025 1030 1035
Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050
Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr

1055 1060 1065
Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080
Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile
1085 1090 1095

<210> 231
<211> 1008
<212> PRT
<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 231

Met Asp Thr Pro Asn Phe Ser Glu Arg Ile Pro Val Ser Leu Gln Ser
1 5 10 15

His Pro Tyr Tyr Phe Ala His Tyr Leu Asn Met Ala Arg His Asn Ala
20 25 30

Tyr Val Ile Leu Glu Tyr Val Asn Arg Glu Leu Ile Lys Pro Gly Lys
35 40 45

Asn Leu Asp Glu Asp Asn Leu Ile Gln Ser Thr Val Leu Lys Asp Gly
50 55 60

Tyr Phe Asp Arg Lys Pro Asp Glu Leu Ser His Arg Asn Arg Leu Leu
65 70 75 80

Val Gln His Phe Pro Phe Leu Arg Glu Ala Glu Asn Glu Gly Ala Arg
85 90 95

Thr Cys Asn Pro Val Ser Tyr Lys Leu Lys Thr Ala Leu Ala Ala Leu
100 105 110

Asn Gln Trp Arg Asn Asn Ala Ser His Tyr Pro Leu Asn Gln Asn His
115 120 125

Glu Lys Asp Phe Asp Leu Gln Pro Phe Phe Ser Phe Ala Ile Glu Ala
130 135 140

Cys Lys Lys Arg Met Arg Glu Val Phe Gln Pro Asp Asp Phe Tyr Leu
145 150 155 160

Leu Glu Thr Asn Glu Lys Gln Phe Tyr Thr Leu His Asn Glu Asn Gly
165 170 175

Phe Thr Glu Lys Gly Leu Tyr Cys Phe Ile Cys Phe Phe Leu Glu Lys
180 185 190

Lys Tyr Ala Phe Gln Phe Leu Ala Gly Ile Lys Gly Phe Lys Asn Thr
195 200 205

Thr Asp Asn Lys Phe Arg Ala Thr Leu Glu Thr Phe Thr Glu His Cys
210 215 220

Cys Arg Leu Pro Lys Pro Lys Leu Asp Ser Ser Asp Ile Lys Leu Asp
225 230 235 240
Met Leu Gly Glu Leu Ser Arg Cys Pro Ala Pro Leu Phe Asp Leu Leu
245 250 255
Asp Ile Glu Glu Arg Lys Lys Phe Ile Arg Glu Pro Glu Glu Val Lys
260 265 270

Pro Asp Glu Ser Gly Asp Arg Glu Glu Val Gln Gln Val Leu Met Lys
275 280 285
Arg Tyr Asp Asp Arg Phe Pro Tyr Phe Ala Leu Arg Tyr Phe Glu Glu
290 295 300
Lys Asn Leu Leu Lys Gly Ile Ser Phe His Ile His Ile Gly Arg Trp
305 310 315 320
Ile Lys Ser Glu His Thr Lys Lys Ile Met Gly Ala Glu Arg Asp Arg
325 330 335

Arg Leu Leu Lys Asp Ile Arg Thr Phe Gly Glu Leu Lys Glu Phe Ser
340 345 350
Pro Glu His Ala Pro Asp Tyr Trp Leu Arg Asp Gly Ile Thr Pro Asp
355 360 365
Asp Val Asp Gln Phe Ser Pro Gln Tyr Arg Ile Val Gly Asn Arg Ile
370 375 380
Gly Ile Lys Leu Asn Tyr Asn Gly His Asn Arg Trp Ser Val Pro Asp
385 390 395 400

Lys Glu Ile Asn Val Lys Pro Asp Ala Ile Ile Ser Thr Tyr Glu Phe
405 410 415
Leu Asn Leu Phe Leu Tyr Glu His Leu Tyr Gln Lys Lys Leu Thr Gly
420 425 430
Leu Ser Pro Ala Glu Phe Ile Gln Asp Tyr Leu Asp Arg Phe Asn Asn
435 440 445
Phe Leu Ser Glu Phe Lys Ala Gly His Ile Arg Pro Val Gly Asp Phe
450 455 460

Ser Leu Glu Lys Arg Arg Gly Gln Gly Asp Glu Pro Asp Leu Thr Ala

465 470 475 480

Arg Arg Lys Ser Leu Gln Lys Glu Leu Asp Arg Phe Val Leu Lys Gly

485 490 495

Lys Asp Leu Pro Asp Lys Ile Arg Glu Tyr Leu Leu Gly Tyr Lys Gln

500 505 510

Lys Ser Glu Lys Lys Gln Ala Lys Trp Ile Leu Gly Gly Met Ile Lys

515 520 525

Glu Thr Val Tyr Trp Arg Asn Lys Ala Glu Gln Ser Pro Glu Lys Met

530 535 540

Arg Ser Gly Asp Met Ala Gln Gln Leu Ala Arg Asp Ile Ile Phe Leu

545 550 555 560

Thr Pro Pro His Thr Val Lys Glu His Lys Gln Lys Leu Asn Ser Leu

565 570 575

Glu Tyr Asp Val Leu Gln Tyr Ala Leu Ala Tyr Phe Ser Ser Asn Arg

580 585 590

Glu Lys Leu Tyr Ser Phe Phe Lys Glu His Gln Leu Thr Val Lys Gly

595 600 605

Asp Arg Ala His Pro Phe Leu Tyr Lys Ile Arg Leu Asp Glu Cys Gln

610 615 620

Gly Ile Leu Asp Phe Phe Ile Val Tyr Met Gln Gln Lys Glu Lys Trp

625 630 635 640

Leu Gly Trp Leu Asp Arg Asn Leu Lys Ser Pro Arg Leu Asn Glu Glu

645 650 655

Glu Phe Phe Asn Thr Tyr Ser Tyr Phe Ile Lys Thr Asp Thr Lys Arg

660 665 670

Ala Ile Glu Met Asp Tyr Glu Ser Cys Pro Asn Tyr Leu Pro Arg Gly

675 680 685

Ile Phe Asn Glu Pro Ile Ala Lys Ala Leu Gln Lys Ala Gly Val Lys

690 695 700

Ile Lys Asp Glu Asp Asn Ala Ser Tyr Ala Leu Ser Val Tyr Ser Asn

705 710 715 720

Gly Lys Thr Gln Pro Phe Tyr Asn Lys Glu Arg Tyr Tyr Asn Lys Gly
725 730 735
Ile Phe Arg Met Glu Glu Leu Pro Glu Lys Leu Gln Pro Lys Glu Leu
740 745 750
Leu Gly Lys Ile Gln Trp Thr Ile Lys Ser Ser Gly Lys Asp Thr Glu
755 760 765
Glu Phe Arg Ser Leu Gln Asn Leu Lys Asn Arg Ile Leu Asn Thr Glu
770 775 780

Lys Glu Ile Arg Tyr Val Gln Ser Thr Asp Arg Ala Leu Trp Ile Met
785 790 795 800
Val Ala Asp Leu Phe Pro Glu Thr Phe Glu Leu Arg Pro Asp Asp Leu
805 810 815
Glu Cys Ile Gly His Asp Leu Ser Asp Asp Leu Leu Ser Arg Pro Tyr
820 825 830
Gln Met Lys Glu Lys Val Tyr Asn Tyr Thr Ile Thr Asp Tyr Leu Pro
835 840 845

Ile Lys Arg Tyr Gly Glu Phe Arg Arg Phe Leu Lys Asp Arg Arg Leu
850 855 860
Glu Asn Leu Leu Thr Tyr Phe Glu Glu Gly Val Pro Leu His Arg Glu
865 870 875 880
Ala Leu Val Ala Glu Leu Glu Ala Tyr Asp Leu Gln Arg Lys Asn Leu
885 890 895
Leu Glu Ile Ile Tyr Arg Phe Glu Lys Leu Val Phe Asp Arg His Arg
900 905 910

His Glu Leu Thr Phe Ser Gly Glu Gly Glu Asn Gln Tyr Val Asn His
915 920 925
Trp Asp Tyr Leu Asp Phe Val Ala Arg Lys Tyr Gly Leu Ser Ala Glu
930 935 940
Val Lys Glu Leu Asn Ser Glu Arg Phe Thr Glu Leu Arg Asn Lys Met
945 950 955 960
Leu His Asn Gln Ile Pro Tyr Gln Leu Trp Ile Lys Glu Ala Ile Ala

965 970 975

Ala Arg Glu Glu Asn Thr Val Cys Gly Arg Ile Met Gly Met Ile Gly
980 985 990
Glu Ile Tyr Glu Arg Met Thr Thr Glu Ile Glu Lys Gln Met Gln Val
995 1000 1005

<210> 232

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas13 sequence

<400> 232

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45
Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80

Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125
Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415
Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430
Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445
Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480
Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510
Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560
Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575
Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605
Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620
Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640
Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn
660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg
725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His
785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln
805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr
820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln
835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe
850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala
865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu
915 920 925
Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940
Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960
Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990
Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005
Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020
Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val
1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050
Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065
Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080
Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile
1085 1090 1095

<210> 233

<

211> 1224

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 233

Met Glu Asn Lys Thr Ser Leu Gly Asn Asn Ile Tyr Tyr Asn Pro Phe
1 5 10 15

Lys Pro Gln Asp Lys Ser Tyr Phe Ala Gly Tyr Phe Asn Ala Ala Met
20 25 30

Glu Asn Thr Asp Ser Val Phe Arg Glu Leu Gly Lys Arg Leu Lys Gly
35 40 45

Lys Glu Tyr Thr Ser Glu Asn Phe Phe Asp Ala Ile Phe Lys Glu Asn

50 55 60

Ile Ser Leu Val Glu Tyr Glu Arg Tyr Val Lys Leu Leu Ser Asp Tyr
65 70 75 80

Phe Pro Met Ala Arg Leu Leu Asp Lys Lys Glu Val Pro Ile Lys Glu
85 90 95

Arg Lys Glu Asn Phe Lys Lys Asn Phe Lys Gly Ile Ile Lys Ala Val
100 105 110

Arg Asp Leu Arg Asn Phe Tyr Thr His Lys Glu His Gly Glu Val Glu

115 120 125

Ile Thr Asp Glu Ile Phe Gly Val Leu Asp Glu Met Leu Lys Ser Thr
130 135 140

Val Leu Thr Val Lys Lys Lys Lys Val Lys Thr Asp Lys Thr Lys Glu
145 150 155 160

Ile Leu Lys Lys Ser Ile Glu Lys Gln Leu Asp Ile Leu Cys Gln Lys
165 170 175

Lys Leu Glu Tyr Leu Arg Asp Thr Ala Arg Lys Ile Glu Glu Lys Arg

180 185 190

Arg Asn Gln Arg Glu Arg Gly Glu Lys Glu Leu Val Ala Pro Phe Lys
195 200 205

Tyr Ser Asp Lys Arg Asp Asp Leu Ile Ala Ala Ile Tyr Asn Asp Ala
210 215 220

Phe Asp Val Tyr Ile Asp Lys Lys Lys Asp Ser Leu Lys Glu Ser Ser
225 230 235 240

Lys Ala Lys Tyr Asn Thr Lys Ser Asp Pro Gln Gln Glu Glu Gly Asp

245 250 255

Leu Lys Ile Pro Ile Ser Lys Asn Gly Val Val Phe Leu Leu Ser Leu

260 265 270

Phe Leu Thr Lys Gln Glu Ile His Ala Phe Lys Ser Lys Ile Ala Gly

275 280 285

Phe Lys Ala Thr Val Ile Asp Glu Ala Thr Val Ser Glu Ala Thr Val

290 295 300

Ser His Gly Lys Asn Ser Ile Cys Phe Met Ala Thr His Glu Ile Phe

305 310 315 320

Ser His Leu Ala Tyr Lys Lys Leu Lys Arg Lys Val Arg Thr Ala Glu

325 330 335

Ile Asn Tyr Gly Glu Ala Glu Asn Ala Glu Gln Leu Ser Val Tyr Ala

340 345 350

Lys Glu Thr Leu Met Met Gln Met Leu Asp Glu Leu Ser Lys Val Pro

355 360 365

Asp Val Val Tyr Gln Asn Leu Ser Glu Asp Val Gln Lys Thr Phe Ile

370 375 380

Glu Asp Trp Asn Glu Tyr Leu Lys Glu Asn Asn Gly Asp Val Gly Thr

385 390 395 400

Met Glu Glu Glu Gln Val Ile His Pro Val Ile Arg Lys Arg Tyr Glu

405 410 415

Asp Lys Phe Asn Tyr Phe Ala Ile Arg Phe Leu Asp Glu Phe Ala Gln

420 425 430

Phe Pro Thr Leu Arg Phe Gln Val His Leu Gly Asn Tyr Leu His Asp

435 440 445

Ser Arg Pro Lys Glu Asn Leu Ile Ser Asp Arg Arg Ile Lys Glu Lys

450 455 460

Ile Thr Val Phe Gly Arg Leu Ser Glu Leu Glu His Lys Lys Ala Leu

465 470 475 480

Phe Ile Lys Asn Thr Glu Thr Asn Glu Asp Arg Glu His Tyr Trp Glu

485 490 495

Ile Phe Pro Asn Pro Asn Tyr Asp Phe Pro Lys Glu Asn Ile Ser Val

500 505 510

Asn Asp Lys Asp Phe Pro Ile Ala Gly Ser Ile Leu Asp Arg Glu Lys

515 520 525

Gln Pro Val Ala Gly Lys Ile Gly Ile Lys Val Lys Leu Leu Asn Gln

530 535 540

Gln Tyr Val Ser Glu Val Asp Lys Ala Val Lys Ala His Gln Leu Lys

545 550 555 560

Gln Arg Lys Ala Ser Lys Pro Ser Ile Gln Asn Ile Ile Glu Glu Ile

565 570 575

Val Pro Ile Asn Glu Ser Asn Pro Lys Glu Ala Ile Val Phe Gly Gly

580 585 590

Gln Pro Thr Ala Tyr Leu Ser Met Asn Asp Ile His Ser Ile Leu Tyr

595 600 605

Glu Phe Phe Asp Lys Trp Glu Lys Lys Lys Glu Lys Leu Glu Lys Lys

610 615 620

Gly Glu Lys Glu Leu Arg Lys Glu Ile Gly Lys Glu Leu Glu Lys Lys

625 630 635 640

Ile Val Gly Lys Ile Gln Ala Gln Ile Gln Gln Ile Ile Asp Lys Asp

645 650 655

Thr Asn Ala Lys Ile Leu Lys Pro Tyr Gln Asp Gly Asn Ser Thr Ala

660 665 670

Ile Asp Lys Glu Lys Leu Ile Lys Asp Leu Lys Gln Glu Gln Asn Ile

675 680 685

Leu Gln Lys Leu Lys Asp Glu Gln Thr Val Arg Glu Lys Glu Tyr Asn

690 695 700

Asp Phe Ile Ala Tyr Gln Asp Lys Asn Arg Glu Ile Asn Lys Val Arg

705 710 715 720

Asp Arg Asn His Lys Gln Tyr Leu Lys Asp Asn Leu Lys Arg Lys Tyr

725 730 735

Pro Glu Ala Pro Ala Arg Lys Glu Val Leu Tyr Tyr Arg Glu Lys Gly
740 745 750
Lys Val Ala Val Trp Leu Ala Asn Asp Ile Lys Arg Phe Met Pro Thr

755 760 765
Asp Phe Lys Asn Glu Trp Lys Gly Glu Gln His Ser Leu Leu Gln Lys
770 775 780
Ser Leu Ala Tyr Tyr Glu Gln Cys Lys Glu Glu Leu Lys Asn Leu Leu
785 790 795 800
Pro Glu Lys Val Phe Gln His Leu Pro Phe Lys Leu Gly Gly Tyr Phe
805 810 815
Gln Gln Lys Tyr Leu Tyr Gln Phe Tyr Thr Cys Tyr Leu Asp Lys Arg

820 825 830
Leu Glu Tyr Ile Ser Gly Leu Val Gln Gln Ala Glu Asn Phe Lys Ser
835 840 845
Glu Asn Lys Val Phe Lys Lys Val Glu Asn Glu Cys Phe Lys Phe Leu
850 855 860
Lys Lys Gln Asn Tyr Thr His Lys Glu Leu Asp Ala Arg Val Gln Ser
865 870 875 880
Ile Leu Gly Tyr Pro Ile Phe Leu Glu Arg Gly Phe Met Asp Glu Lys

885 890 895
Pro Thr Ile Ile Lys Gly Lys Thr Phe Lys Gly Asn Glu Ala Leu Phe
900 905 910
Ala Asp Trp Phe Arg Tyr Tyr Lys Glu Tyr Gln Asn Phe Gln Thr Phe
915 920 925
Tyr Asp Thr Glu Asn Tyr Pro Leu Val Glu Leu Glu Lys Lys Gln Ala
930 935 940
Asp Arg Lys Arg Lys Thr Lys Ile Tyr Gln Gln Lys Lys Asn Asp Val

945 950 955 960
Phe Thr Leu Leu Met Ala Lys His Ile Phe Lys Ser Val Phe Lys Gln
965 970 975
Asp Ser Ile Asp Gln Phe Ser Leu Glu Asp Leu Tyr Gln Ser Arg Glu

980 985 990

Glu Arg Leu Gly Asn Gln Glu Arg Ala Arg Gln Thr Gly Glu Arg Asn

995 1000 1005

Thr Asn Tyr Ile Trp Asn Lys Thr Val Asp Leu Lys Leu Cys Asp

1010 1015 1020

Gly Lys Ile Thr Val Glu Asn Val Lys Leu Lys Asn Val Gly Asp

1025 1030 1035

Phe Ile Lys Tyr Glu Tyr Asp Gln Arg Val Gln Ala Phe Leu Lys

1040 1045 1050

Tyr Glu Glu Asn Ile Glu Trp Gln Ala Phe Leu Ile Lys Glu Ser

1055 1060 1065

Lys Glu Glu Glu Asn Tyr Pro Tyr Val Val Glu Arg Glu Ile Glu

1070 1075 1080

Gln Tyr Glu Lys Val Arg Arg Glu Glu Leu Leu Lys Glu Val His

1085 1090 1095

Leu Ile Glu Glu Tyr Ile Leu Glu Lys Val Lys Asp Lys Glu Ile

1100 1105 1110

Leu Lys Lys Gly Asp Asn Gln Asn Phe Lys Tyr Tyr Ile Leu Asn

1115 1120 1125

Gly Leu Leu Lys Gln Leu Lys Asn Glu Asp Val Glu Ser Tyr Lys

1130 1135 1140

Val Phe Asn Leu Asn Thr Glu Pro Glu Asp Val Asn Ile Asn Gln

1145 1150 1155

Leu Lys Gln Glu Ala Thr Asp Leu Glu Gln Lys Ala Phe Val Leu

1160 1165 1170

Thr Tyr Ile Arg Asn Lys Phe Ala His Asn Gln Leu Pro Lys Lys

1175 1180 1185

Glu Phe Trp Asp Tyr Cys Gln Glu Lys Tyr Gly Lys Ile Glu Lys

1190 1195 1200

Glu Lys Thr Tyr Ala Glu Tyr Phe Ala Glu Val Phe Lys Lys Glu

1205 1210 1215

Lys Glu Ala Leu Ile Lys

1220

<210> 234

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 234

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp

35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn

50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu

65 70 75 80

Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95

Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu

100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile

115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445
Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460
Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480
Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510
Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560
Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575
Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605
Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620
Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640
Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655
Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn
660 665 670
Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu

770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr

885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly

900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys

930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp

945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu

965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu

980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn

995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala

1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala

1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr

1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val

1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 235

<211> 1174

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 235

Met Thr Glu Gln Ser Glu Arg Pro Tyr Asn Gly Thr Tyr Tyr Thr Leu

1 5 10 15

Glu Asp Lys His Phe Trp Ala Ala Phe Leu Asn Leu Ala Arg His Asn

20 25 30

Ala Tyr Ile Thr Leu Thr His Ile Asp Arg Gln Leu Ala Tyr Ser Lys

35 40 45

Ala Asp Ile Thr Asn Asp Gln Asp Val Leu Ser Phe Lys Ala Leu Trp

50 55 60

Lys Asn Leu Asp Asn Asp Leu Glu Arg Lys Ser Arg Leu Arg Ser Leu

65 70 75 80

Ile Leu Lys His Phe Ser Phe Leu Glu Gly Ala Ala Tyr Gly Lys Lys

85 90 95

Leu Phe Glu Ser Lys Ser Ser Gly Asn Lys Ser Ser Lys Asn Lys Glu

100 105 110

Leu Thr Lys Lys Glu Lys Glu Glu Leu Gln Ala Asn Ala Leu Ser Leu

115 120 125

Asp Asn Leu Lys Ser Ile Leu Phe Asp Phe Leu Gln Lys Leu Lys Asp

130 135 140

Phe Arg Asn Tyr Tyr Ser His Tyr Arg His Ser Gly Ser Ser Glu Leu

145 150 155 160

Pro Leu Phe Asp Gly Asn Met Leu Gln Arg Leu Tyr Asn Val Phe Asp

165 170 175

Val Ser Val Gln Arg Val Lys Arg Asp His Glu His Asn Asp Lys Val

180 185 190

Asp Pro His Tyr His Phe Asn His Leu Val Arg Lys Gly Lys Lys Asp

195 200 205

Arg Tyr Gly His Asn Asp Asn Pro Ser Phe Lys His His Phe Val Asp

210 215 220

Ser Glu Gly Met Val Thr Glu Ala Gly Leu Leu Phe Phe Val Ser Leu

225 230 235 240

Phe Leu Glu Lys Arg Asp Ala Ile Trp Met Gln Lys Lys Ile Arg Gly

245 250 255

Phe Lys Gly Gly Thr Gly Pro Tyr Glu Gln Met Thr Asn Glu Val Phe

260 265 270

Cys Arg Ser Arg Ile Ser Leu Pro Lys Leu Lys Leu Glu Ser Leu Arg
275 280 285
Thr Asp Asp Trp Met Leu Leu Asp Met Leu Asn Glu Leu Val Arg Cys
290 295 300
Pro Lys Pro Leu Tyr Asp Arg Leu Arg Glu Lys Asp Arg Ala Cys Phe
305 310 315 320

Arg Val Pro Val Asp Ile Leu Pro Asp Glu Asp Asp Thr Asp Gly Gly
325 330 335
Gly Glu Asp Pro Phe Lys Asn Thr Leu Val Arg His Gln Asp Arg Phe
340 345 350
Pro Tyr Phe Ala Leu Arg Tyr Phe Asp Leu Lys Lys Val Phe Thr Ser
355 360 365
Leu Arg Phe His Ile Asp Leu Gly Thr Tyr His Phe Ala Ile Tyr Lys
370 375 380

Lys Met Ile Gly Glu Gln Pro Glu Asp Arg His Leu Thr Arg Asn Leu
385 390 395 400
Tyr Gly Phe Gly Arg Ile Gln Asp Phe Ala Glu Glu His Arg Pro Glu
405 410 415
Glu Trp Lys Arg Leu Val Arg Asp Leu Asp Tyr Leu Glu Thr Gly Asp
420 425 430
Lys Pro Tyr Ile Ser Gln Thr Thr Pro His Tyr His Ile Glu Lys Gly
435 440 445

Lys Ile Gly Leu Arg Phe Val Pro Glu Gly Gln His Leu Trp Pro Ser
450 455 460
Pro Glu Val Gly Thr Thr Arg Thr Gly Arg Ser Lys Cys Ala Gln Asp
465 470 475 480
Lys Arg Leu Thr Ala Glu Ala Phe Leu Ser Val His Glu Leu Met Pro
485 490 495
Met Met Phe Tyr Tyr Phe Leu Leu Arg Glu Lys Tyr Ser Glu Glu Val
500 505 510

Ser Ala Glu Lys Val Gln Gly Arg Ile Lys Arg Val Ile Glu Asp Val

515 520 525

Tyr Ala Ile Tyr Asp Ala Phe Ala Arg Asp Glu Ile Asn Thr Leu Lys

530 535 540

Glu Leu Asp Thr Cys Leu Ala Asp Lys Gly Ile Arg Arg Gly His Leu

545 550 555 560

Pro Lys Gln Met Ile Thr Ile Leu Ser Gln Glu Arg Lys Asp Met Lys

565 570 575

Glu Lys Ile Arg Lys Lys Leu Gln Glu Met Ile Ala Asp Thr Asp His

580 585 590

Arg Leu Asp Met Leu Asp Arg Gln Thr Asp Arg Lys Ile Arg Ile Gly

595 600 605

Arg Lys Asn Ala Gly Leu Pro Lys Ser Gly Val Ile Ala Asp Trp Leu

610 615 620

Val Arg Asp Met Met Arg Phe Gln Pro Val Ala Lys Asp Ala Ser Gly

625 630 635 640

Lys Pro Leu Asn Asn Ser Lys Ala Asn Ser Thr Glu Tyr Arg Met Leu

645 650 655

Gln Arg Ala Leu Ala Leu Phe Gly Gly Glu Lys Glu Arg Leu Thr Pro

660 665 670

Tyr Phe Arg Gln Met Asn Leu Thr Gly Gly Asn Asn Pro His Pro Phe

675 680 685

Leu His Glu Thr Arg Trp Glu Ser His Thr Asn Ile Leu Ser Phe Tyr

690 695 700

Arg Ser Tyr Leu Arg Ala Arg Lys Ala Phe Leu Glu Arg Ile Gly Arg

705 710 715 720

Ser Asp Arg Val Glu Asn Cys Pro Phe Leu Leu Leu Lys Glu Pro Lys

725 730 735

Thr Asp Arg Gln Thr Leu Val Ala Gly Trp Lys Asp Glu Phe His Leu

740 745 750

Pro Arg Gly Ile Phe Thr Glu Ala Val Arg Asp Cys Leu Ile Glu Met

755 760 765

Gly Tyr Asp Glu Val Gly Ser Tyr Arg Glu Val Gly Phe Met Ala Lys
770 775 780
Ala Val Pro Leu Tyr Phe Glu Arg Ala Cys Glu Asp Arg Val Gln Pro
785 790 795 800
Phe Tyr Asp Ser Pro Phe Asn Val Gly Asn Ser Leu Lys Pro Lys Lys
805 810 815
Gly Arg Phe Leu Ser Lys Glu Asp Arg Ala Glu Glu Trp Glu Arg Gly
820 825 830

Met Glu Arg Phe Arg Asp Leu Glu Ala Trp Ser His Ser Ala Ala Arg
835 840 845
Arg Ile Lys Asp Ala Phe Ala Gly Ile Glu Tyr Ala Ser Pro Gly Asn
850 855 860
Lys Lys Lys Ile Glu Gln Leu Leu Arg Asp Leu Ser Leu Trp Glu Ala
865 870 875 880
Phe Glu Ser Lys Leu Lys Val Arg Ala Asp Lys Ile Asn Leu Ala Lys
885 890 895

Leu Lys Lys Glu Ile Leu Glu Ala Gln Glu His Pro Tyr His Asp Phe
900 905 910
Lys Ser Trp Gln Lys Phe Glu Arg Glu Leu Arg Leu Val Lys Asn Gln
915 920 925
Asp Ile Ile Thr Trp Met Met Cys Arg Asp Leu Met Glu Glu Asn Lys
930 935 940
Val Glu Gly Leu Asp Thr Gly Thr Leu Tyr Leu Lys Asp Ile Arg Pro
945 950 955 960

Asn Val Gln Glu Gln Gly Ser Leu Asn Val Leu Asn Arg Val Lys Pro
965 970 975
Met Arg Leu Pro Val Val Val Tyr Arg Ala Asp Ser Arg Gly His Val
980 985 990
His Lys Glu Ala Pro Leu Ala Thr Val Tyr Ile Glu Glu Arg Asn Thr
995 1000 1005
Lys Leu Leu Lys Gln Gly Asn Phe Lys Ser Phe Val Lys Asp Arg

1010 1015 1020

Arg Leu Asn Gly Leu Phe Ser Phe Val Asp Thr Gly Gly Leu Ala
1025 1030 1035
Met Glu Gln Tyr Pro Ile Ser Lys Leu Arg Val Glu Tyr Glu Leu
1040 1045 1050
Ala Lys Tyr Gln Thr Ala Arg Val Cys Val Phe Glu Leu Thr Leu
1055 1060 1065
Arg Leu Glu Glu Ser Leu Leu Ser Arg Tyr Pro His Leu Pro Asp
1070 1075 1080

Glu Ser Phe Arg Glu Met Leu Glu Ser Trp Ser Asp Pro Leu Leu
1085 1090 1095
Ala Lys Trp Pro Glu Leu His Gly Lys Val Arg Leu Leu Ile Ala
1100 1105 1110
Val Arg Asn Ala Phe Ser His Asn Gln Tyr Pro Met Tyr Asp Glu
1115 1120 1125
Ala Val Phe Ser Ser Ile Arg Lys Tyr Asp Pro Ser Ser Pro Asp
1130 1135 1140

Ala Ile Glu Glu Arg Met Gly Leu Asn Ile Ala His Arg Leu Ser
1145 1150 1155
Glu Glu Val Lys Gln Ala Lys Glu Thr Val Glu Arg Ile Ile Gln
1160 1165 1170
Ala

<210> 236
<211> 1103
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 236
Met Glu Lys Pro Leu Pro Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Thr Thr Pro Pro Asn Asp
35 40 45
Asp Lys Ile Ala Asp Val Val Cys Gly Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80

Lys His Phe Pro Phe Leu Ala Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly Ser Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Asn Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Glu Leu Ile
115 120 125
Lys Ala Leu Lys Thr Leu Val Lys Gln Leu Arg Thr Leu Arg Asn Tyr
130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175
Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Gln Asp Phe Ala His
180 185 190
Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Lys Phe Asp Arg
195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe
210 215 220
Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys
225 230 235 240
Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Ser Glu Lys Met Thr
245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu
260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu
275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Lys Asp
290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu
305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Ala Leu Ile Arg His Gln Asp Arg
325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys
340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr
355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr
370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415

Lys Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445

Leu Glu Val Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460

Ser Asp Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser

565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Asp

580 585 590

Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala Tyr Asp Val

595 600 605

Gln Asn Gln Pro Ile Glu Ser Ser Lys Ala Asn Ser Thr Glu Phe Gln

610 615 620

Leu Ile Gln Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys Asn Arg Leu

625 630 635 640

Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr Asn Pro His

645 650 655

Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn Leu Val Asp

660 665 670

Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu Glu Ala Ile

675 680 685

Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu Leu Lys Ile

690 695 700

Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu Gln Gly Gly

705 710 715 720

Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg Glu Thr Leu

725 730 735

Ser Glu Asp Leu Thr Leu Ser Lys Pro Ile Arg Lys Glu Ile Lys Lys

740 745 750

His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu Tyr Phe Arg
755 760 765

Glu Arg Tyr Gln Asp Asp His Gln Ser Phe Tyr Asn Leu Pro Tyr Glu
770 775 780

Leu Glu Ala Lys Ala Ser Thr Pro Lys Pro Pro Leu Pro Lys Lys Arg
785 790 795 800

Glu Tyr Val Leu Arg Ala Glu His Tyr Glu Tyr Trp Gln Gln Asn Lys
805 810 815

Pro Gln Ser Pro Thr Glu Leu Gln Arg Leu Glu Leu His Thr Ser Asp
820 825 830

Arg Trp Lys Asp Tyr Leu Leu Tyr Lys Arg Trp Gln His Leu Glu Lys
835 840 845

Lys Leu Arg Leu Tyr Arg Asn Gln Asp Val Met Leu Trp Leu Met Thr
850 855 860

Leu Glu Leu Thr Lys Asn His Phe Lys Glu Leu Lys Leu Asn Tyr His
865 870 875 880

Gln Leu Lys Leu Glu Asn Leu Ala Val Asn Val Gln Glu Ala Asp Ala
885 890 895

Lys Leu Asn Pro Leu Asn Gln Thr Leu Pro Met Val Leu Pro Val Lys
900 905 910

Val Tyr Pro Ala Thr Ala Phe Gly Glu Val Gln Tyr Gln Glu Thr Pro
915 920 925

Ile Arg Thr Val Tyr Ile Arg Glu Glu Gln Thr Lys Ala Leu Lys Met
930 935 940

Gly Asn Phe Lys Ala Leu Val Lys Asp Arg Arg Leu Asn Gly Leu Phe
945 950 955 960

Ser Phe Ile Lys Glu Glu Asn Asp Thr Gln Lys His Pro Ile Ser Gln
965 970 975

Leu Arg Leu Arg Arg Glu Leu Glu Ile Tyr Gln Ser Leu Arg Val Asp
980 985 990

Ala Phe Lys Glu Thr Leu Ser Leu Glu Glu Lys Leu Leu Asn Lys His

995 1000 1005

Ala Ser Leu Ser Ser Leu Glu Asn Glu Phe Arg Thr Leu Leu Glu

1010 1015 1020

Glu Trp Lys Lys Lys Tyr Ala Ala Ser Ser Met Val Thr Asp Glu

1025 1030 1035

His Ile Ala Phe Ile Ala Ser Val Arg Asn Ala Phe Cys His Asn

1040 1045 1050

Gln Tyr Pro Phe Tyr Lys Glu Thr Leu His Ala Pro Ile Leu Leu

1055 1060 1065

Phe Thr Val Ala Gln Pro Thr Thr Glu Glu Lys Asp Gly Leu Gly

1070 1075 1080

Ile Ala Glu Ala Leu Leu Arg Val Leu Arg Glu Tyr Cys Glu Ile

1085 1090 1095

Val Lys Ser Gln Ile

1100

<210> 237

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 237

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp

35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn

50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu

65 70 75 80

Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125
Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His
180 185 190
Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg
195 200 205
Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe
210 215 220
Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys
225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr
245 250 255
Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu
260 265 270
Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu
275 280 285
Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn
290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu
305 310 315 320
Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser

435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser

565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn
660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg
725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His
785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln
805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr

885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly

900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys

930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp

945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu

965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu

980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn

995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala

1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala

1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr

1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val

1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 238

<211> 1224

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 238

Met Glu Asn Lys Thr Ser Leu Gly Asn Asn Ile Tyr Tyr Asn Pro Phe

1 5 10 15

Lys Pro Gln Asp Lys Ser Tyr Phe Ala Gly Tyr Phe Asn Ala Ala Met

20 25 30

Glu Asn Thr Asp Ser Val Phe Arg Glu Leu Gly Lys Arg Leu Lys Gly

35 40 45

Lys Glu Tyr Thr Ser Glu Asn Phe Phe Asp Ala Ile Phe Lys Glu Asn

50 55 60

Ile Ser Leu Val Glu Tyr Glu Arg Tyr Val Lys Leu Leu Ser Asp Tyr

65 70 75 80

Phe Pro Met Ala Arg Leu Leu Asp Lys Lys Glu Val Pro Ile Lys Glu

85 90 95

Arg Lys Glu Asn Phe Lys Lys Asn Phe Lys Gly Ile Ile Lys Ala Val

100 105 110

Arg Asp Leu Arg Asn Phe Tyr Thr His Lys Glu His Gly Glu Val Glu

115 120 125

Ile Thr Asp Glu Ile Phe Gly Val Leu Asp Glu Met Leu Lys Ser Thr

130 135 140

Val Leu Thr Val Lys Lys Lys Lys Val Lys Thr Asp Lys Thr Lys Glu

145 150 155 160

Ile Leu Lys Lys Ser Ile Glu Lys Gln Leu Asp Ile Leu Cys Gln Lys

165 170 175

Lys Leu Glu Tyr Leu Arg Asp Thr Ala Arg Lys Ile Glu Glu Lys Arg

180 185 190

Arg Asn Gln Arg Glu Arg Gly Glu Lys Glu Leu Val Ala Pro Phe Lys

195 200 205

Tyr Ser Asp Lys Arg Asp Asp Leu Ile Ala Ala Ile Tyr Asn Asp Ala

210 215 220

Phe Asp Val Tyr Ile Asp Lys Lys Lys Asp Ser Leu Lys Glu Ser Ser

225 230 235 240

Lys Ala Lys Tyr Asn Thr Lys Ser Asp Pro Gln Gln Glu Glu Gly Asp

245 250 255

Leu Lys Ile Pro Ile Ser Lys Asn Gly Val Val Phe Leu Leu Ser Leu

260 265 270

Phe Leu Thr Lys Gln Glu Ile His Ala Phe Lys Ser Lys Ile Ala Gly

275 280 285

Phe Lys Ala Thr Val Ile Asp Glu Ala Thr Val Ser Glu Ala Thr Val

290 295 300

Ser His Gly Lys Asn Ser Ile Cys Phe Met Ala Thr His Glu Ile Phe

305 310 315 320

Ser His Leu Ala Tyr Lys Lys Leu Lys Arg Lys Val Arg Thr Ala Glu

325 330 335

Ile Asn Tyr Gly Glu Ala Glu Asn Ala Glu Gln Leu Ser Val Tyr Ala

340 345 350

Lys Glu Thr Leu Met Met Gln Met Leu Asp Glu Leu Ser Lys Val Pro

355 360 365

Asp Val Val Tyr Gln Asn Leu Ser Glu Asp Val Gln Lys Thr Phe Ile

370 375 380

Glu Asp Trp Asn Glu Tyr Leu Lys Glu Asn Asn Gly Asp Val Gly Thr

385 390 395 400

Met Glu Glu Glu Gln Val Ile His Pro Val Ile Arg Lys Arg Tyr Glu

405 410 415

Asp Lys Phe Asn Tyr Phe Ala Ile Arg Phe Leu Asp Glu Phe Ala Gln
420 425 430
Phe Pro Thr Leu Arg Phe Gln Val His Leu Gly Asn Tyr Leu His Asp
435 440 445
Ser Arg Pro Lys Glu Asn Leu Ile Ser Asp Arg Arg Ile Lys Glu Lys
450 455 460
Ile Thr Val Phe Gly Arg Leu Ser Glu Leu Glu His Lys Lys Ala Leu

465 470 475 480
Phe Ile Lys Asn Thr Glu Thr Asn Glu Asp Arg Glu His Tyr Trp Glu
485 490 495
Ile Phe Pro Asn Pro Asn Tyr Asp Phe Pro Lys Glu Asn Ile Ser Val
500 505 510
Asn Asp Lys Asp Phe Pro Ile Ala Gly Ser Ile Leu Asp Arg Glu Lys
515 520 525
Gln Pro Val Ala Gly Lys Ile Gly Ile Lys Val Lys Leu Leu Asn Gln

530 535 540
Gln Tyr Val Ser Glu Val Asp Lys Ala Val Lys Ala His Gln Leu Lys
545 550 555 560
Gln Arg Lys Ala Ser Lys Pro Ser Ile Gln Asn Ile Ile Glu Glu Ile
565 570 575
Val Pro Ile Asn Glu Ser Asn Pro Lys Glu Ala Ile Val Phe Gly Gly
580 585 590
Gln Pro Thr Ala Tyr Leu Ser Met Asn Asp Ile His Ser Ile Leu Tyr

595 600 605
Glu Phe Phe Asp Lys Trp Glu Lys Lys Lys Glu Lys Leu Glu Lys Lys
610 615 620
Gly Glu Lys Glu Leu Arg Lys Glu Ile Gly Lys Glu Leu Glu Lys Lys
625 630 635 640
Ile Val Gly Lys Ile Gln Ala Gln Ile Gln Gln Ile Ile Asp Lys Asp
645 650 655
Thr Asn Ala Lys Ile Leu Lys Pro Tyr Gln Asp Gly Asn Ser Thr Ala

660 665 670

Ile Asp Lys Glu Lys Leu Ile Lys Asp Leu Lys Gln Glu Gln Asn Ile

675 680 685

Leu Gln Lys Leu Lys Asp Glu Gln Thr Val Arg Glu Lys Glu Tyr Asn

690 695 700

Asp Phe Ile Ala Tyr Gln Asp Lys Asn Arg Glu Ile Asn Lys Val Arg

705 710 715 720

Asp Arg Asn His Lys Gln Tyr Leu Lys Asp Asn Leu Lys Arg Lys Tyr

725 730 735

Pro Glu Ala Pro Ala Arg Lys Glu Val Leu Tyr Tyr Arg Glu Lys Gly

740 745 750

Lys Val Ala Val Trp Leu Ala Asn Asp Ile Lys Arg Phe Met Pro Thr

755 760 765

Asp Phe Lys Asn Glu Trp Lys Gly Glu Gln His Ser Leu Leu Gln Lys

770 775 780

Ser Leu Ala Tyr Tyr Glu Gln Cys Lys Glu Glu Leu Lys Asn Leu Leu

785 790 795 800

Pro Glu Lys Val Phe Gln His Leu Pro Phe Lys Leu Gly Gly Tyr Phe

805 810 815

Gln Gln Lys Tyr Leu Tyr Gln Phe Tyr Thr Cys Tyr Leu Asp Lys Arg

820 825 830

Leu Glu Tyr Ile Ser Gly Leu Val Gln Gln Ala Glu Asn Phe Lys Ser

835 840 845

Glu Asn Lys Val Phe Lys Lys Val Glu Asn Glu Cys Phe Lys Phe Leu

850 855 860

Lys Lys Gln Asn Tyr Thr His Lys Glu Leu Asp Ala Arg Val Gln Ser

865 870 875 880

Ile Leu Gly Tyr Pro Ile Phe Leu Glu Arg Gly Phe Met Asp Glu Lys

885 890 895

Pro Thr Ile Ile Lys Gly Lys Thr Phe Lys Gly Asn Glu Ala Leu Phe

900 905 910

Ala Asp Trp Phe Arg Tyr Tyr Lys Glu Tyr Gln Asn Phe Gln Thr Phe

915 920 925

Tyr Asp Thr Glu Asn Tyr Pro Leu Val Glu Leu Glu Lys Lys Gln Ala

930 935 940

Asp Arg Lys Arg Lys Thr Lys Ile Tyr Gln Gln Lys Lys Asn Asp Val

945 950 955 960

Phe Thr Leu Leu Met Ala Lys His Ile Phe Lys Ser Val Phe Lys Gln

965 970 975

Asp Ser Ile Asp Gln Phe Ser Leu Glu Asp Leu Tyr Gln Ser Arg Glu

980 985 990

Glu Arg Leu Gly Asn Gln Glu Arg Ala Arg Gln Thr Gly Glu Arg Asn

995 1000 1005

Thr Asn Tyr Ile Trp Asn Lys Thr Val Asp Leu Lys Leu Cys Asp

1010 1015 1020

Gly Lys Ile Thr Val Glu Asn Val Lys Leu Lys Asn Val Gly Asp

1025 1030 1035

Phe Ile Lys Tyr Glu Tyr Asp Gln Arg Val Gln Ala Phe Leu Lys

1040 1045 1050

Tyr Glu Glu Asn Ile Glu Trp Gln Ala Phe Leu Ile Lys Glu Ser

1055 1060 1065

Lys Glu Glu Glu Asn Tyr Pro Tyr Val Val Glu Arg Glu Ile Glu

1070 1075 1080

Gln Tyr Glu Lys Val Arg Arg Glu Glu Leu Leu Lys Glu Val His

1085 1090 1095

Leu Ile Glu Glu Tyr Ile Leu Glu Lys Val Lys Asp Lys Glu Ile

1100 1105 1110

Leu Lys Lys Gly Asp Asn Gln Asn Phe Lys Tyr Tyr Ile Leu Asn

1115 1120 1125

Gly Leu Leu Lys Gln Leu Lys Asn Glu Asp Val Glu Ser Tyr Lys

1130 1135 1140

Val Phe Asn Leu Asn Thr Glu Pro Glu Asp Val Asn Ile Asn Gln

1145 1150 1155

Leu Lys Gln Glu Ala Thr Asp Leu Glu Gln Lys Ala Phe Val Leu

1160 1165 1170

Thr Tyr Ile Arg Asn Lys Phe Ala His Asn Gln Leu Pro Lys Lys

1175 1180 1185

Glu Phe Trp Asp Tyr Cys Gln Glu Lys Tyr Gly Lys Ile Glu Lys

1190 1195 1200

Glu Lys Thr Tyr Ala Glu Tyr Phe Ala Glu Val Phe Lys Lys Glu

1205 1210 1215

Lys Glu Ala Leu Ile Lys

1220

<210> 239

<211> 948

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 239

Met Phe Phe Ser Phe His Asn Ala Gln Arg Val Ile Phe Lys His Leu

1 5 10 15

Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu Asp Tyr Lys

20 25 30

Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His Leu Asn Arg

35 40 45

Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg Tyr Arg Phe

50 55 60

Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe Phe Thr Asn

65 70 75 80

Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys Lys Val Ser

85 90 95

Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr Thr Glu Val

100 105 110

Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu Glu Ser Arg
115 120 125
Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu Leu Ser Arg
130 135 140
Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn Lys Lys His
145 150 155 160
Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu Glu Glu Gln
165 170 175

Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg Phe Pro Tyr
180 185 190
Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys Ser Ile Arg
195 200 205
Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr Asp Lys Lys
210 215 220
Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr Leu Leu Ser
225 230 235 240

Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro Gln Glu Trp
245 250 255
Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser Asn Gln Pro
260 265 270
Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp Asn Lys Ile
275 280 285
Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser Leu Glu Ile
290 295 300

Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn Ser Gly Phe
305 310 315 320
Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro Leu Met Phe
325 330 335
Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys Glu Thr Val
340 345 350

Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu Arg Ile Asn
355 360 365

Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu Pro Leu Gly
370 375 380
Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys Gln Pro Asp
385 390 395 400
Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile Ala Glu Thr
405 410 415
Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser Ser Pro Lys
420 425 430

Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val Leu Ala Asp
435 440 445
Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala Tyr Asp Ala
450 455 460
Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr Glu Phe Trp
465 470 475 480
Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys Asn Arg Leu
485 490 495

Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr Asn Pro His
500 505 510
Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn Leu Val Asp
515 520 525
Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu Glu Ala Ile
530 535 540
Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu Leu Lys Ile
545 550 555 560

Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu Gln Gly Gly
565 570 575
Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg Glu Thr Leu
580 585 590
Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu Ile Lys Lys

595 600 605

His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu Tyr Phe Lys

610 615 620

Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu Ser Tyr Lys

625 630 635 640

Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His Tyr Glu Tyr

645 650 655

Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln Arg Leu Glu

660 665 670

Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr Lys Arg Trp

675 680 685

Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln Asp Val Met

690 695 700

Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe Lys Glu Leu

705 710 715 720

Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala Val Asn Val

725 730 735

Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr Leu Pro Met

740 745 750

Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly Glu Val Gln

755 760 765

Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu Glu His Thr

770 775 780

Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys Asp Arg Arg

785 790 795 800

Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp Thr Gln Lys

805 810 815

His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu Ile Tyr Gln

820 825 830

Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu Glu Glu Lys

835 840 845

Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn Glu Phe Arg
850 855 860
Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala Ser Ser Met Val
865 870 875 880

Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val Arg Asn Ala Phe Cys
885 890 895
His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala Leu His Ala Pro Ile Pro
900 905 910
Leu Phe Thr Val Ala Gln Pro Thr Thr Glu Glu Lys Asp Gly Leu Gly
915 920 925
Ile Ala Glu Ala Leu Leu Lys Val Leu Arg Glu Tyr Cys Glu Ile Val
930 935 940

Lys Ser Gln Ile
945

<210> 240
<211> 1095
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 240
Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95

Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu

100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile

115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys
340 345 350
Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr
355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr
370 375 380
Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400
Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415
Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445
Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460
Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480
Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510
Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575
Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val

580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr

610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu

770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln
835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe
850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala
865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu
915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val
1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val

1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 241

<211> 1106

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 241

Met Glu Lys Pro Leu Pro Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Thr Thr Pro Pro Asn Asp

35 40 45

Asp Lys Ile Ala Asp Val Val Cys Gly Thr Trp Asn Asn Ile Leu Asn

50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu

65 70 75 80

Lys His Phe Pro Phe Leu Ala Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95

Glu Gly Lys Lys Lys Gly Ser Gln Lys Glu Gln Gln Lys Glu Lys Glu

100 105 110

Asn Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Glu Leu Ile

115 120 125

Lys Ala Leu Lys Thr Leu Val Lys Gln Leu Arg Thr Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Gln Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Lys Phe Asp Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Ser Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Lys Asp

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Ala Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Lys Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser

435 440 445

Leu Glu Val Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460

Ser Asp Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser

565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val

580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605

Tyr Asp Val Gln Asn Gln Pro Ile Glu Ser Ser Lys Ala Asn Ser Thr

610 615 620

Glu Phe Gln Leu Ile Gln Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685
Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700
Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720
Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735
Glu Thr Leu Ser Glu Asp Leu Thr Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750
Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765
Tyr Phe Arg Glu Arg Tyr Gln Asp Asp His Gln Ser Phe Tyr Asn Leu
770 775 780
Pro Tyr Glu Leu Glu Ala Lys Ala Ser Thr Pro Lys Pro Pro Leu Pro

785 790 795 800
Lys Lys Arg Glu Tyr Val Leu Arg Ala Glu His Tyr Glu Tyr Trp Gln
805 810 815
Gln Asn Lys Pro Gln Ser Pro Thr Glu Leu Gln Arg Leu Glu Leu His
820 825 830
Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr Lys Arg Trp Gln His
835 840 845
Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln Asp Val Met Leu Trp

850 855 860
Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe Lys Glu Leu Lys Leu
865 870 875 880
Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala Val Asn Val Gln Glu
885 890 895
Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr Leu Pro Met Val Leu
900 905 910
Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly Glu Val Gln Tyr Gln

915 920 925

Glu Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu Glu Gln Thr Lys Ala

930 935 940

Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys Asp Arg Arg Leu Asn

945 950 955 960

Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp Thr Gln Lys His Pro

965 970 975

Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu Ile Tyr Gln Ser Leu

980 985 990

Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu Glu Glu Lys Leu Leu

995 1000 1005

Asn Lys His Ala Ser Leu Ser Ser Leu Glu Asn Glu Phe Arg Thr

1010 1015 1020

Leu Leu Glu Glu Trp Lys Lys Lys Tyr Ala Ala Ser Ser Met Val

1025 1030 1035

Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val Arg Asn Ala Phe

1040 1045 1050

Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Thr Leu His Ala Pro

1055 1060 1065

Ile Leu Leu Phe Thr Val Ala Gln Pro Thr Thr Glu Glu Lys Asp

1070 1075 1080

Gly Leu Gly Ile Ala Glu Ala Leu Leu Arg Val Leu Arg Glu Tyr

1085 1090 1095

Cys Glu Ile Val Lys Ser Gln Ile

1100 1105

<210> 242

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 242

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125
Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His
180 185 190
Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg
195 200 205
Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe
210 215 220
Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys
225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser

435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510
Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575
Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605
Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640
Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655
Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn
660 665 670
Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700
Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720
Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg
725 730 735
Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His
785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln
805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr
820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln
835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe
850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala
865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu
915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020
Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val
1025 1030 1035
Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050
Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080
Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile
1085 1090 1095

<210> 243
<211> 1095
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 243
Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45
Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80

Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95

Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu

100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile

115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser

435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser

565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605
Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620
Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640
Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655
Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670
Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685
Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700
Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720
Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735
Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750
Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765
Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780
Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800
Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln
805 810 815
Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr

885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly

900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys

930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp

945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu

965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu

980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn

995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala

1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala

1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr

1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080
Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile
1085 1090 1095

<210> 244
<211> 1095
<212> PRT
<213> Unknown
<220><223> Description of Unknown:

Cas13 sequence

<400> 244

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45
Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu

770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr

885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly

900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu
915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val
1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile
1085 1090 1095

<210> 245

<211> 948

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 245

Met Phe Phe Ser Phe His Asn Ala Gln Arg Val Ile Phe Lys His Leu

1 5 10 15

Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu Asp Tyr Lys

20 25 30

Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His Leu Asn Arg

35 40 45

Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg Tyr Arg Phe

50 55 60

Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe Phe Thr Asn

65 70 75 80

Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys Lys Val Ser

85 90 95

Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr Thr Glu Val

100 105 110

Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu Glu Ser Arg

115 120 125

Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu Leu Ser Arg

130 135 140

Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn Lys Lys His

145 150 155 160

Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu Glu Glu Gln

165 170 175

Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg Phe Pro Tyr

180 185 190

Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys Ser Ile Arg

195 200 205

Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr Asp Lys Lys

210 215 220

Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr Leu Leu Ser

225 230 235 240

Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro Gln Glu Trp

245 250 255

Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser Asn Gln Pro
260 265 270
Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp Asn Lys Ile
275 280 285
Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser Leu Glu Ile

290 295 300
Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn Ser Gly Phe
305 310 315 320
Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro Leu Met Phe
325 330 335
Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys Glu Thr Val
340 345 350
Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu Arg Ile Asn

355 360 365
Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu Pro Leu Gly
370 375 380
Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys Gln Pro Asp
385 390 395 400
Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile Ala Glu Thr
405 410 415
Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser Ser Pro Lys

420 425 430
Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val Leu Ala Asp
435 440 445
Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala Tyr Asp Ala
450 455 460
Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr Glu Phe Trp
465 470 475 480
Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys Asn Arg Leu

485 490 495
Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr Asn Pro His

500 505 510

Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn Leu Val Asp

515 520 525

Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu Glu Ala Ile

530 535 540

Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu Leu Lys Ile

545 550 555 560

Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu Gln Gly Gly

565 570 575

Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg Glu Thr Leu

580 585 590

Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu Ile Lys Lys

595 600 605

His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu Tyr Phe Lys

610 615 620

Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu Ser Tyr Lys

625 630 635 640

Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His Tyr Glu Tyr

645 650 655

Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln Arg Leu Glu

660 665 670

Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr Lys Arg Trp

675 680 685

Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln Asp Val Met

690 695 700

Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe Lys Glu Leu

705 710 715 720

Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala Val Asn Val

725 730 735

Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr Leu Pro Met

740 745 750

Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly Glu Val Gln
        755   760   765
Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu Glu His Thr
    770   775   780
Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys Asp Arg Arg
785   790   795   800
Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp Thr Gln Lys

                805   810   815
His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu Ile Tyr Gln
            820   825   830
Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu Glu Glu Lys
        835   840   845
Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn Glu Phe Arg
    850   855   860
Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala Ser Ser Met Val

865   870   875   880
Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val Arg Asn Ala Phe Cys
                885   890   895
His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala Leu His Ala Pro Ile Pro
            900   905   910
Leu Phe Thr Val Ala Gln Pro Thr Thr Glu Glu Lys Asp Gly Leu Gly
        915   920   925
Ile Ala Glu Ala Leu Leu Lys Val Leu Arg Glu Tyr Cys Glu Ile Val

    930   935   940
Lys Ser Gln Ile
945

<210> 246
<211> 1008
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
      Cas13 sequence

<400> 246

Met Asp Thr Pro Asn Phe Ser Glu Arg Ile Pro Val Ser Leu Gln Ser
1 5 10 15

His Pro Tyr Tyr Phe Ala His Tyr Leu Asn Met Ala Arg His Asn Ala
20 25 30

Tyr Val Ile Leu Glu Tyr Val Asn Arg Glu Leu Ile Lys Pro Gly Lys
35 40 45

Asn Leu Asp Glu Asp Asn Leu Ile Gln Ser Thr Val Leu Lys Asp Gly
50 55 60

Tyr Phe Asp Arg Lys Pro Asp Glu Leu Ser His Arg Asn Arg Leu Leu
65 70 75 80

Val Gln His Phe Pro Phe Leu Arg Glu Ala Glu Asn Glu Gly Ala Arg
85 90 95

Thr Cys Asn Pro Val Ser Tyr Lys Leu Lys Thr Ala Leu Ala Ala Leu
100 105 110

Asn Gln Trp Arg Asn Asn Ala Ser His Tyr Pro Leu Asn Gln Asn His
115 120 125

Glu Lys Asp Phe Asp Leu Gln Pro Phe Phe Ser Phe Ala Ile Glu Ala
130 135 140

Cys Lys Lys Arg Met Arg Glu Val Phe Gln Pro Asp Asp Phe Tyr Leu
145 150 155 160

Leu Glu Thr Asn Glu Lys Gln Phe Tyr Thr Leu His Asn Glu Asn Gly
165 170 175

Phe Thr Glu Lys Gly Leu Tyr Cys Phe Ile Cys Phe Phe Leu Glu Lys
180 185 190

Lys Tyr Ala Phe Gln Phe Leu Ala Gly Ile Lys Gly Phe Lys Asn Thr
195 200 205

Thr Asp Asn Lys Phe Arg Ala Thr Leu Glu Thr Phe Thr Glu His Cys
210 215 220

Cys Arg Leu Pro Lys Pro Lys Leu Asp Ser Ser Asp Ile Lys Leu Asp
225 230 235 240

Met Leu Gly Glu Leu Ser Arg Cys Pro Ala Pro Leu Phe Asp Leu Leu
245 250 255
Asp Ile Glu Glu Arg Lys Lys Phe Ile Arg Glu Pro Glu Glu Val Lys
260 265 270
Pro Asp Glu Ser Gly Asp Arg Glu Glu Val Gln Gln Val Leu Met Lys
275 280 285
Arg Tyr Asp Asp Arg Phe Pro Tyr Phe Ala Leu Arg Tyr Phe Glu Glu

290 295 300
Lys Asn Leu Leu Lys Gly Ile Ser Phe His Ile His Ile Gly Arg Trp
305 310 315 320
Ile Lys Ser Glu His Thr Lys Lys Ile Met Gly Ala Glu Arg Asp Arg
325 330 335
Arg Leu Leu Lys Asp Ile Arg Thr Phe Gly Glu Leu Lys Glu Phe Ser
340 345 350
Pro Glu His Ala Pro Asp Tyr Trp Leu Arg Asp Gly Ile Thr Pro Asp

355 360 365
Asp Val Asp Gln Phe Ser Pro Gln Tyr Arg Ile Val Gly Asn Arg Ile
370 375 380
Gly Ile Lys Leu Asn Tyr Asn Gly His Asn Arg Trp Ser Val Pro Asp
385 390 395 400
Lys Glu Ile Asn Val Lys Pro Asp Ala Ile Ile Ser Thr Tyr Glu Phe
405 410 415
Leu Asn Leu Phe Leu Tyr Glu His Leu Tyr Gln Lys Lys Leu Thr Gly

420 425 430
Leu Ser Pro Ala Glu Phe Ile Gln Asp Tyr Leu Asp Arg Phe Asn Asn
435 440 445
Phe Leu Ser Glu Phe Lys Ala Gly His Ile Arg Pro Val Gly Asp Phe
450 455 460
Ser Leu Glu Lys Arg Arg Gly Gln Gly Asp Glu Pro Asp Leu Thr Ala
465 470 475 480
Arg Arg Lys Ser Leu Gln Lys Glu Leu Asp Arg Phe Val Leu Lys Gly

485 490 495

Lys Asp Leu Pro Asp Lys Ile Arg Glu Tyr Leu Leu Gly Tyr Lys Gln

500 505 510

Lys Ser Glu Lys Lys Gln Ala Lys Trp Ile Leu Gly Gly Met Ile Lys

515 520 525

Glu Thr Val Tyr Trp Arg Asn Lys Ala Glu Gln Ser Pro Glu Lys Met

530 535 540

Arg Ser Gly Asp Met Ala Gln Gln Leu Ala Arg Asp Ile Ile Phe Leu

545 550 555 560

Thr Pro Pro His Thr Val Lys Glu His Lys Gln Lys Leu Asn Ser Leu

565 570 575

Glu Tyr Asp Val Leu Gln Tyr Ala Leu Ala Tyr Phe Ser Ser Asn Arg

580 585 590

Glu Lys Leu Tyr Ser Phe Phe Lys Glu His Gln Leu Thr Val Lys Gly

595 600 605

Asp Arg Ala His Pro Phe Leu Tyr Lys Ile Arg Leu Asp Glu Cys Gln

610 615 620

Gly Ile Leu Asp Phe Phe Ile Val Tyr Met Gln Gln Lys Glu Lys Trp

625 630 635 640

Leu Gly Trp Leu Asp Arg Asn Leu Lys Ser Pro Arg Leu Asn Glu Glu

645 650 655

Glu Phe Phe Asn Thr Tyr Ser Tyr Phe Ile Lys Thr Asp Thr Lys Arg

660 665 670

Ala Ile Glu Met Asp Tyr Glu Ser Cys Pro Asn Tyr Leu Pro Arg Gly

675 680 685

Ile Phe Asn Glu Pro Ile Ala Lys Ala Leu Gln Lys Ala Gly Val Lys

690 695 700

Ile Lys Asp Glu Asp Asn Ala Ser Tyr Ala Leu Ser Val Tyr Ser Asn

705 710 715 720

Gly Lys Thr Gln Pro Phe Tyr Asn Lys Glu Arg Tyr Tyr Asn Lys Gly

725 730 735

Ile Phe Arg Met Glu Glu Leu Pro Glu Lys Leu Gln Pro Lys Glu Leu

740 745 750

Leu Gly Lys Ile Gln Trp Thr Ile Lys Ser Ser Gly Lys Asp Thr Glu

755 760 765

Glu Phe Arg Ser Leu Gln Asn Leu Lys Asn Arg Ile Leu Asn Thr Glu

770 775 780

Lys Glu Ile Arg Tyr Val Gln Ser Thr Asp Arg Ala Leu Trp Ile Met

785 790 795 800

Val Ala Asp Leu Phe Pro Glu Thr Phe Glu Leu Arg Pro Asp Asp Leu

805 810 815

Glu Cys Ile Gly His Asp Leu Ser Asp Asp Leu Leu Ser Arg Pro Tyr

820 825 830

Gln Met Lys Glu Lys Val Tyr Asn Tyr Thr Ile Thr Asp Tyr Leu Pro

835 840 845

Ile Lys Arg Tyr Gly Glu Phe Arg Arg Phe Leu Lys Asp Arg Arg Leu

850 855 860

Glu Asn Leu Leu Thr Tyr Phe Glu Glu Gly Val Pro Leu His Arg Glu

865 870 875 880

Ala Leu Val Ala Glu Leu Glu Ala Tyr Asp Leu Gln Arg Lys Asn Leu

885 890 895

Leu Glu Ile Ile Tyr Arg Phe Glu Lys Leu Val Phe Asp Arg His Arg

900 905 910

His Glu Leu Thr Phe Ser Gly Glu Gly Glu Asn Gln Tyr Val Asn His

915 920 925

Trp Asp Tyr Leu Asp Phe Val Ala Arg Lys Tyr Gly Leu Ser Ala Glu

930 935 940

Val Lys Glu Leu Asn Ser Glu Arg Phe Thr Glu Leu Arg Asn Lys Met

945 950 955 960

Leu His Asn Gln Ile Pro Tyr Gln Leu Trp Ile Lys Glu Ala Ile Ala

965 970 975

Ala Arg Glu Glu Asn Thr Val Cys Gly Arg Ile Met Gly Met Ile Gly

980 985 990

Glu Ile Tyr Glu Arg Met Thr Thr Glu Ile Glu Lys Gln Met Gln Val

995 1000 1005

<210> 247

<211> 1175

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 247

Met Thr Glu Gln Asn Glu Lys Pro Tyr Asn Gly Thr Tyr Tyr Thr Leu

1 5 10 15

Glu Asp Lys His Phe Trp Ala Ala Phe Leu Asn Leu Ala Arg His Asn

20 25 30

Ala Tyr Ile Thr Leu Thr His Ile Asp Arg Gln Leu Ala Tyr Ser Lys

35 40 45

Ala Asp Ile Thr Asn Asp Glu Asp Ile Leu Phe Phe Lys Gly Gln Trp

50 55 60

Lys Asn Leu Asp Asn Asp Leu Glu Arg Lys Ala Arg Leu Arg Ser Leu

65 70 75 80

Ile Leu Lys His Phe Phe Phe Leu Glu Gly Ala Ala Tyr Gly Lys Lys

85 90 95

Leu Phe Glu Ser Gln Ser Ser Gly Asn Lys Ser Ser Lys Lys Lys Glu

100 105 110

Leu Thr Lys Lys Glu Lys Glu Glu Leu Gln Ala Asn Ala Leu Ser Leu

115 120 125

Asp Asn Leu Lys Ser Ile Leu Phe Asp Phe Leu Gln Lys Leu Lys Asp

130 135 140

Phe Arg Asn Tyr Tyr Ser His Tyr Arg His Pro Glu Ser Ser Glu Leu

145 150 155 160

Pro Leu Phe Asp Gly Asn Met Leu Gln Arg Leu Tyr Asn Val Phe Asp

165 170 175

Val Ser Val Gln Arg Val Lys Arg Asp His Glu His Asn Asp Lys Val

180 185 190

Asp Pro His Arg His Phe Asn His Leu Val Arg Lys Gly Lys Lys Asp

195 200 205

Lys Tyr Gly Asn Asn Asp Asn Pro Phe Phe Lys His His Phe Val Asp

210 215 220

Arg Glu Gly Lys Val Thr Glu Ala Gly Leu Leu Phe Phe Val Ser Leu

225 230 235 240

Phe Leu Glu Lys Arg Asp Ala Ile Trp Met Gln Lys Lys Ile Arg Gly

245 250 255

Phe Lys Gly Gly Thr Glu Thr Tyr Gln Gln Met Thr Asn Glu Val Phe

260 265 270

Cys Arg Ser Arg Ile Ser Leu Pro Lys Leu Lys Leu Glu Ser Leu Arg

275 280 285

Thr Asp Asp Trp Met Leu Leu Asp Met Leu Asn Glu Leu Val Arg Cys

290 295 300

Pro Lys Ser Leu Tyr Asp Arg Leu Arg Glu Glu Asp Arg Ala Arg Phe

305 310 315 320

Arg Val Pro Val Asp Ile Leu Ser Asp Glu Asp Asp Thr Asp Gly Ala

325 330 335

Glu Glu Asp Pro Phe Lys Asn Thr Leu Val Arg His Gln Asp Arg Phe

340 345 350

Pro Tyr Phe Ala Leu Arg Tyr Phe Asp Leu Lys Lys Val Phe Thr Ser

355 360 365

Leu Arg Phe His Ile Asp Leu Gly Thr Tyr His Phe Ala Ile Tyr Lys

370 375 380

Lys Asn Ile Gly Glu Gln Pro Glu Asp Arg His Leu Thr Arg Asn Leu

385 390 395 400

Tyr Gly Phe Gly Arg Ile Gln Asp Phe Ala Glu Glu His Arg Pro Glu

405 410 415

Glu Trp Lys Arg Leu Val Arg Asp Leu Asp Tyr Phe Glu Thr Gly Asp

420 425 430

Lys Pro Tyr Ile Thr Gln Thr Thr Pro His Tyr His Ile Glu Lys Gly

435 440 445

Lys Ile Gly Leu Arg Phe Val Pro Glu Gly Gln His Leu Trp Pro Ser

450 455 460

Pro Glu Val Gly Ala Thr Arg Thr Gly Arg Ser Lys Tyr Ala Gln Asp

465 470 475 480

Lys Arg Phe Thr Ala Glu Ala Phe Leu Ser Val His Glu Leu Met Pro

485 490 495

Met Met Phe Tyr Tyr Phe Leu Leu Arg Glu Lys Tyr Ser Glu Glu Ala

500 505 510

Ser Ala Glu Arg Val Gln Gly Arg Ile Lys Arg Val Ile Glu Asp Val

515 520 525

Tyr Ala Val Tyr Asp Ala Phe Ala Arg Asp Glu Ile Asn Thr Arg Asp

530 535 540

Glu Leu Asp Ala Cys Leu Ala Asp Lys Gly Ile Arg Arg Gly His Leu

545 550 555 560

Pro Arg Gln Met Ile Ala Ile Leu Ser Gln Lys His Lys Asp Met Glu

565 570 575

Glu Lys Val Arg Lys Lys Leu Gln Glu Met Ile Ala Asp Thr Asp His

580 585 590

Arg Leu Asp Met Leu Asp Arg Gln Thr Asp Arg Lys Ile Arg Ile Gly

595 600 605

Arg Lys Asn Ala Gly Leu Pro Lys Ser Gly Val Ile Ala Asp Trp Leu

610 615 620

Val Arg Asp Met Met Arg Phe Gln Pro Val Ala Lys Asp Thr Ser Gly

625 630 635 640

Lys Pro Leu Asn Asn Ser Lys Ala Asn Ser Thr Glu Tyr Arg Met Leu

645 650 655

Gln Arg Ala Leu Ala Leu Phe Gly Gly Glu Lys Glu Arg Leu Thr Pro

660 665 670

Tyr Phe Arg Gln Met Asn Leu Thr Gly Gly Asn Asn Pro His Pro Phe

675 680 685

Leu His Glu Thr Arg Trp Glu Ser His Thr Asn Ile Leu Ser Phe Tyr

690 695 700

Arg Ser Tyr Leu Lys Ala Arg Lys Ala Phe Leu Gln Ser Ile Gly Arg

705 710 715 720

Ser Asp Arg Val Glu Asn His Arg Phe Leu Leu Leu Lys Glu Pro Lys

725 730 735

Thr Asp Arg Gln Thr Leu Val Ala Gly Trp Lys Gly Glu Phe His Leu

740 745 750

Pro Arg Gly Ile Phe Thr Glu Ala Val Arg Asp Cys Leu Ile Glu Met

755 760 765

Gly Leu Asp Glu Val Arg Ser Tyr Lys Glu Val Gly Phe Met Ala Lys

770 775 780

Ala Val Pro Leu Tyr Phe Glu Arg Ala Ser Lys Asp Arg Val Gln Pro

785 790 795 800

Phe Tyr Asp Tyr Pro Phe Asn Val Gly Asn Ser Leu Lys Pro Lys Lys

805 810 815

Gly Arg Phe Leu Ser Lys Glu Lys Arg Ala Glu Glu Trp Glu Ser Gly

820 825 830

Lys Glu Arg Phe Arg Asp Leu Glu Ala Trp Ser His Ser Ala Ala Arg

835 840 845

Arg Ile Glu Asp Ala Phe Ala Gly Ile Glu Asn Ala Ser Arg Glu Asn

850 855 860

Lys Lys Lys Ile Glu Gln Leu Leu Gln Asp Leu Ser Leu Trp Glu Thr

865 870 875 880

Phe Glu Ser Lys Leu Lys Val Lys Ala Asp Lys Ile Asn Ile Ala Lys

885 890 895

Leu Lys Lys Glu Ile Leu Glu Ala Lys Glu His Pro Tyr Leu Asp Phe

900 905 910

Lys Ser Trp Gln Lys Phe Glu Arg Glu Leu Arg Leu Val Lys Asn Gln

915 920 925

Asp Ile Ile Thr Trp Met Met Cys Arg Asp Leu Met Glu Glu Asn Lys

930 935 940

Val Glu Gly Leu Asp Thr Gly Thr Leu Tyr Leu Lys Asp Ile Arg Thr

945 950 955 960

Asp Val Gln Glu Gln Gly Ser Leu Asn Val Leu Asn His Val Lys Pro

965 970 975

Met Arg Leu Pro Val Val Val Tyr Arg Ala Asp Ser Arg Gly His Val

980 985 990

His Lys Glu Gln Ala Pro Leu Ala Thr Val Tyr Ile Glu Glu Arg Asp

995 1000 1005

Thr Lys Leu Leu Lys Gln Gly Asn Phe Lys Ser Phe Val Lys Asp

1010 1015 1020

Arg Arg Leu Asn Gly Leu Phe Ser Phe Val Asp Thr Gly Gly Leu

1025 1030 1035

Ala Met Glu Gln Tyr Pro Ile Ser Lys Leu Arg Val Glu Tyr Glu

1040 1045 1050

Leu Ala Lys Tyr Gln Thr Ala Arg Val Cys Ala Phe Glu Gln Thr

1055 1060 1065

Leu Glu Leu Glu Glu Ser Leu Leu Thr Arg Tyr Pro His Leu Pro

1070 1075 1080

Asp Lys Asn Phe Arg Lys Met Leu Glu Ser Trp Ser Asp Pro Leu

1085 1090 1095

Leu Ala Lys Trp Pro Glu Leu His Glu Lys Val Arg Leu Leu Ile

1100 1105 1110

Ala Val Arg Asn Ala Phe Ser His Asn Gln Tyr Pro Met Tyr Asp

1115 1120 1125

Glu Ala Val Phe Ser Pro Ile Arg Lys Tyr Asp Pro Ser Ser Pro

1130 1135 1140

Asp Ala Ile Glu Glu Arg Met Arg Leu Asn Ile Ala His Arg Leu

1145 1150 1155

Ser Glu Glu Val Lys Gln Ala Lys Glu Thr Val Glu Arg Ile Ile

1160 1165 1170

Gln Ala

1175

<210> 248

<211> 1008

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 248

Met Asp Thr Pro Asn Phe Ser Glu Arg Ile Pro Val Ser Leu Gln Ser

1 5 10 15

His Pro Tyr Tyr Phe Ala His Tyr Leu Asn Met Ala Arg His Asn Ala

20 25 30

Tyr Val Ile Leu Glu Tyr Val Asn Arg Glu Leu Ile Lys Pro Gly Lys

35 40 45

Asn Leu Asp Glu Asp Asn Leu Ile Gln Ser Thr Val Leu Lys Asp Gly

50 55 60

Tyr Phe Asp Arg Lys Pro Asp Glu Leu Ser His Arg Asn Arg Leu Leu

65 70 75 80

Val Gln His Phe Pro Phe Leu Arg Glu Ala Glu Asn Glu Gly Ala Arg

85 90 95

Thr Cys Asn Pro Val Ser Tyr Lys Leu Lys Thr Ala Leu Ala Ala Leu

100 105 110

Asn Gln Trp Arg Asn Asn Ala Ser His Tyr Pro Leu Asn Gln Asn His

115 120 125

Glu Lys Asp Phe Asp Leu Gln Pro Phe Phe Ser Phe Ala Ile Glu Ala

130 135 140

Cys Lys Lys Arg Met Arg Glu Val Phe Gln Pro Asp Asp Phe Tyr Leu

145 150 155 160

Leu Glu Thr Asn Glu Lys Gln Phe Tyr Thr Leu His Asn Glu Asn Gly
165 170 175
Phe Thr Glu Lys Gly Leu Tyr Cys Phe Ile Cys Phe Phe Leu Glu Lys

180 185 190
Lys Tyr Ala Phe Gln Phe Leu Ala Gly Ile Lys Gly Phe Lys Asn Thr
195 200 205
Thr Asp Asn Lys Phe Arg Ala Thr Leu Glu Thr Phe Thr Glu His Cys
210 215 220
Cys Arg Leu Pro Lys Pro Lys Leu Asp Ser Ser Asp Ile Lys Leu Asp
225 230 235 240
Met Leu Gly Glu Leu Ser Arg Cys Pro Ala Pro Leu Phe Asp Leu Leu

245 250 255
Asp Ile Glu Glu Arg Lys Lys Phe Ile Arg Glu Pro Glu Glu Val Lys
260 265 270
Pro Asp Glu Ser Gly Asp Arg Glu Glu Val Gln Gln Val Leu Met Lys
275 280 285
Arg Tyr Asp Asp Arg Phe Pro Tyr Phe Ala Leu Arg Tyr Phe Glu Glu
290 295 300
Lys Asn Leu Leu Lys Gly Ile Ser Phe His Ile His Ile Gly Arg Trp

305 310 315 320
Ile Lys Ser Glu His Thr Lys Lys Ile Met Gly Ala Glu Arg Asp Arg
325 330 335
Arg Leu Leu Lys Asp Ile Arg Thr Phe Gly Glu Leu Lys Glu Phe Ser
340 345 350
Pro Glu His Ala Pro Asp Tyr Trp Leu Arg Asp Gly Ile Thr Pro Asp
355 360 365
Asp Val Asp Gln Phe Ser Pro Gln Tyr Arg Ile Val Gly Asn Arg Ile

370 375 380
Gly Ile Lys Leu Asn Tyr Asn Gly His Asn Arg Trp Ser Val Pro Asp
385 390 395 400
Lys Glu Ile Asn Val Lys Pro Asp Ala Ile Ile Ser Thr Tyr Glu Phe

405 410 415

Leu Asn Leu Phe Leu Tyr Glu His Leu Tyr Gln Lys Lys Leu Thr Gly

420 425 430

Leu Ser Pro Ala Glu Phe Ile Gln Asp Tyr Leu Asp Arg Phe Asn Asn

435 440 445

Phe Leu Ser Glu Phe Lys Ala Gly His Ile Arg Pro Val Gly Asp Phe

450 455 460

Ser Leu Glu Lys Arg Arg Gly Gln Gly Asp Glu Pro Asp Leu Thr Ala

465 470 475 480

Arg Arg Lys Ser Leu Gln Lys Glu Leu Asp Arg Phe Val Leu Lys Gly

485 490 495

Lys Asp Leu Pro Asp Lys Ile Arg Glu Tyr Leu Leu Gly Tyr Lys Gln

500 505 510

Lys Ser Glu Lys Lys Gln Ala Lys Trp Ile Leu Gly Gly Met Ile Lys

515 520 525

Glu Thr Val Tyr Trp Arg Asn Lys Ala Glu Gln Ser Pro Glu Lys Met

530 535 540

Arg Ser Gly Asp Met Ala Gln Gln Leu Ala Arg Asp Ile Ile Phe Leu

545 550 555 560

Thr Pro Pro His Thr Val Lys Glu His Lys Gln Lys Leu Asn Ser Leu

565 570 575

Glu Tyr Asp Val Leu Gln Tyr Ala Leu Ala Tyr Phe Ser Ser Asn Arg

580 585 590

Glu Lys Leu Tyr Ser Phe Phe Lys Glu His Gln Leu Thr Val Lys Gly

595 600 605

Asp Arg Ala His Pro Phe Leu Tyr Lys Ile Arg Leu Asp Glu Cys Gln

610 615 620

Gly Ile Leu Asp Phe Phe Ile Val Tyr Met Gln Gln Lys Glu Lys Trp

625 630 635 640

Leu Gly Trp Leu Asp Arg Asn Leu Lys Ser Pro Arg Leu Asn Glu Glu

645 650 655

Glu Phe Phe Asn Thr Tyr Ser Tyr Phe Ile Lys Thr Asp Thr Lys Arg
660 665 670
Ala Ile Glu Met Asp Tyr Glu Ser Cys Pro Asn Tyr Leu Pro Arg Gly
675 680 685
Ile Phe Asn Glu Pro Ile Ala Lys Ala Leu Gln Lys Ala Gly Val Lys

690 695 700
Ile Lys Asp Glu Asp Asn Ala Ser Tyr Ala Leu Ser Val Tyr Ser Asn
705 710 715 720
Gly Lys Thr Gln Pro Phe Tyr Asn Lys Glu Arg Tyr Tyr Asn Lys Gly
725 730 735
Ile Phe Arg Met Glu Glu Leu Pro Glu Lys Leu Gln Pro Lys Glu Leu
740 745 750
Leu Gly Lys Ile Gln Trp Thr Ile Lys Ser Ser Gly Lys Asp Thr Glu

755 760 765
Glu Phe Arg Ser Leu Gln Asn Leu Lys Asn Arg Ile Leu Asn Thr Glu
770 775 780
Lys Glu Ile Arg Tyr Val Gln Ser Thr Asp Arg Ala Leu Trp Ile Met
785 790 795 800
Val Ala Asp Leu Phe Pro Glu Thr Phe Glu Leu Arg Pro Asp Asp Leu
805 810 815
Glu Cys Ile Gly His Asp Leu Ser Asp Asp Leu Leu Ser Arg Pro Tyr

820 825 830
Gln Met Lys Glu Lys Val Tyr Asn Tyr Thr Ile Thr Asp Tyr Leu Pro
835 840 845
Ile Lys Arg Tyr Gly Glu Phe Arg Arg Phe Leu Lys Asp Arg Arg Leu
850 855 860
Glu Asn Leu Leu Thr Tyr Phe Glu Glu Gly Val Pro Leu His Arg Glu
865 870 875 880
Ala Leu Val Ala Glu Leu Glu Ala Tyr Asp Leu Gln Arg Lys Asn Leu

885 890 895
Leu Glu Ile Ile Tyr Arg Phe Glu Lys Leu Val Phe Asp Arg His Arg

900 905 910

His Glu Leu Thr Phe Ser Gly Glu Gly Glu Asn Gln Tyr Val Asn His

915 920 925

Trp Asp Tyr Leu Asp Phe Val Ala Arg Lys Tyr Gly Leu Ser Ala Glu

930 935 940

Val Lys Glu Leu Asn Ser Glu Arg Phe Thr Glu Leu Arg Asn Lys Met

945 950 955 960

Leu His Asn Gln Ile Pro Tyr Gln Leu Trp Ile Lys Glu Ala Ile Ala

965 970 975

Ala Arg Glu Glu Asn Thr Val Cys Gly Arg Ile Met Gly Met Ile Gly

980 985 990

Glu Ile Tyr Glu Arg Met Thr Thr Glu Ile Glu Lys Gln Met Gln Val

995 1000 1005

<210> 249

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 249

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln

50 55 60

Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys

65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr

85 90 95

Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly

115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140
Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Met Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Ala Asn Asn Asn Asp Leu Ser Glu Lys

180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205
Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu

245 250 255
Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270
Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Ala Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe
290 295 300
Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala

305 310 315 320
Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335
Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr

340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser

355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser

370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln

385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val

405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala

420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala

435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His

450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser

465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg

485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu

500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile

515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp

530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn

545 550 555 560

Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn

565 570 575

Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn

580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro

625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Glu Lys Glu Glu
645 650 655
Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Leu Asn Tyr Phe Arg

690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720
Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp

755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780
Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys
785 790 795 800
Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu
805 810 815
Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830
Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Asn Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Phe Ser Asn Asp Ser Ser Ala

995 1000

<210> 250

<211> 1106

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 250

Met Glu Lys Pro Leu Pro Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Thr Thr Pro Pro Asn Asp
35 40 45
Asp Lys Ile Ala Asp Val Val Cys Gly Thr Trp Asn Asn Ile Leu Asn
50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Ala Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly Ser Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Asn Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Glu Leu Ile
115 120 125

Lys Ala Leu Lys Thr Leu Val Lys Gln Leu Arg Thr Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175
Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Gln Asp Phe Ala His
180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Lys Phe Asp Arg
195 200 205
Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe
210 215 220
Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys
225 230 235 240
Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Ser Glu Lys Met Thr
245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu
260 265 270
Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Lys Asp

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Ala Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Lys Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser

435 440 445

Leu Glu Val Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460

Ser Asp Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605

Tyr Asp Val Gln Asn Gln Pro Ile Glu Ser Ser Lys Ala Asn Ser Thr
610 615 620

Glu Phe Gln Leu Ile Gln Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn
660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg
725 730 735

Glu Thr Leu Ser Glu Asp Leu Thr Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765

Tyr Phe Arg Glu Arg Tyr Gln Asp Asp His Gln Ser Phe Tyr Asn Leu

770 775 780

Pro Tyr Glu Leu Glu Ala Lys Ala Ser Thr Pro Lys Pro Pro Leu Pro
785 790 795 800

Lys Lys Arg Glu Tyr Val Leu Arg Ala Glu His Tyr Glu Tyr Trp Gln
805 810 815

Gln Asn Lys Pro Gln Ser Pro Thr Glu Leu Gln Arg Leu Glu Leu His
820 825 830

Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr Lys Arg Trp Gln His
835 840 845

Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln Asp Val Met Leu Trp
850 855 860

Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe Lys Glu Leu Lys Leu
865 870 875 880

Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala Val Asn Val Gln Glu
885 890 895

Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr Leu Pro Met Val Leu
900 905 910

Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly Glu Val Gln Tyr Gln
915 920 925

Glu Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu Glu Gln Thr Lys Ala
930 935 940

Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys Asp Arg Arg Leu Asn
945 950 955 960

Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp Thr Gln Lys His Pro
965 970 975

Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu Ile Tyr Gln Ser Leu
980 985 990

Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu Glu Glu Lys Leu Leu
995 1000 1005

Asn Lys His Ala Ser Leu Ser Ser Leu Glu Asn Glu Phe Arg Thr
1010 1015 1020

Leu Leu Glu Glu Trp Lys Lys Lys Tyr Ala Ala Ser Ser Met Val
1025 1030 1035
Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val Arg Asn Ala Phe
1040 1045 1050
Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Thr Leu His Ala Pro
1055 1060 1065
Ile Leu Leu Phe Thr Val Ala Gln Pro Thr Thr Glu Glu Lys Asp
1070 1075 1080

Gly Leu Gly Ile Ala Glu Ala Leu Leu Arg Val Leu Arg Glu Tyr
1085 1090 1095
Cys Glu Ile Val Lys Ser Gln Ile
1100 1105

<210> 251
<211> 1095
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 251
Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45
Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu

100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile

115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr
355 360 365
Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr
370 375 380
Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400
Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415
Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430
Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445
Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460
Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480
Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510
Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560
Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575
Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr

610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu

770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr

885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly

900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys

930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp

945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu

965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu

980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn

995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala

1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala

1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr

1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val

1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 252

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 252

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45
Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175
Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg
195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe
210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys
225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr
245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu
260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu
275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn
290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu
305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg
325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys
340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr
355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr
370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460
Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480
Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560
Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605
Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620
Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655
Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn
660 665 670
Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu

770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr

885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly

900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940
Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975
Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990
Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005
Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val
1025 1030 1035
Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050
Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065
Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile
1085 1090 1095
<210> 253
<211> 948
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 253
Met Phe Phe Ser Phe His Asn Ala Gln Arg Val Ile Phe Lys His Leu
1 5 10 15
Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu Asp Tyr Lys

20 25 30

Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His Leu Asn Arg

35 40 45

Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg Tyr Arg Phe

50 55 60

Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe Phe Thr Asn

65 70 75 80

Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys Lys Val Ser

85 90 95

Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr Thr Glu Val

100 105 110

Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu Glu Ser Arg

115 120 125

Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu Leu Ser Arg

130 135 140

Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn Lys Lys His

145 150 155 160

Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu Glu Glu Gln

165 170 175

Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg Phe Pro Tyr

180 185 190

Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys Ser Ile Arg

195 200 205

Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr Asp Lys Lys

210 215 220

Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr Leu Leu Ser

225 230 235 240

Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro Gln Glu Trp

245 250 255

Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser Asn Gln Pro

260 265 270

Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp Asn Lys Ile
275 280 285
Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser Leu Glu Ile

290 295 300
Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn Ser Gly Phe
305 310 315 320
Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro Leu Met Phe
325 330 335
Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys Glu Thr Val
340 345 350
Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu Arg Ile Asn

355 360 365
Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu Pro Leu Gly
370 375 380
Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys Gln Pro Asp
385 390 395 400
Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile Ala Glu Thr
405 410 415
Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser Ser Pro Lys

420 425 430
Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val Leu Ala Asp
435 440 445
Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala Tyr Asp Ala
450 455 460
Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr Glu Phe Trp
465 470 475 480
Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys Asn Arg Leu

485 490 495
Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr Asn Pro His
500 505 510
Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn Leu Val Asp

515 520 525

Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu Glu Ala Ile

530 535 540

Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu Leu Lys Ile

545 550 555 560

Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu Gln Gly Gly

565 570 575

Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg Glu Thr Leu

580 585 590

Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu Ile Lys Lys

595 600 605

His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu Tyr Phe Lys

610 615 620

Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu Ser Tyr Lys

625 630 635 640

Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His Tyr Glu Tyr

645 650 655

Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln Arg Leu Glu

660 665 670

Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr Lys Arg Trp

675 680 685

Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln Asp Val Met

690 695 700

Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe Lys Glu Leu

705 710 715 720

Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala Val Asn Val

725 730 735

Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr Leu Pro Met

740 745 750

Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly Glu Val Gln

755 760 765

Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu Glu His Thr
770 775 780
Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys Asp Arg Arg
785 790 795 800
Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp Thr Gln Lys

805 810 815
His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu Ile Tyr Gln
820 825 830
Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu Glu Glu Lys
835 840 845
Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn Glu Phe Arg
850 855 860
Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala Ser Ser Met Val

865 870 875 880
Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val Arg Asn Ala Phe Cys
885 890 895
His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala Leu His Ala Pro Ile Pro
900 905 910
Leu Phe Thr Val Ala Gln Pro Thr Thr Glu Glu Lys Asp Gly Leu Gly
915 920 925
Ile Ala Glu Ala Leu Leu Lys Val Leu Arg Glu Tyr Cys Glu Ile Val

930 935 940
Lys Ser Gln Ile
945

<210> 254
<211> 1095
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 254
Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp

35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn

50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu

65 70 75 80

Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95

Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu

100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile

115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu
260 265 270
Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu
275 280 285
Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300
Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu
305 310 315 320
Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg
325 330 335
Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys
340 345 350
Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365
Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr
370 375 380
Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400
Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415
Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430
Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445
Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460
Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480
Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser

565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val

580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr

610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His
785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr
820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln
835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe
850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu
915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys

930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn

995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala

1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala

1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr

1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val

1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 255

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 255

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp

35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn

50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu

65 70 75 80

Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95

Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125
Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175
Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His
180 185 190
Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg
195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe
210 215 220
Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys
225 230 235 240
Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr
245 250 255
Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu
260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu
275 280 285
Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn
290 295 300
Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu
305 310 315 320
Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg
325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser

435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser

565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val

580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn
660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg
725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His
785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln
805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr
820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe
850 855 860
Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala
865 870 875 880
Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895
Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu
915 920 925
Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940
Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960
Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990
Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005
Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020
Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val
1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050
Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065
Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 256

<

211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 256

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp

35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn

50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu

65 70 75 80

Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95

Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu

100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile

115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser

435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser

565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val

580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr

610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685
Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700
Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720
Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg
725 730 735
Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750
Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765
Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780
Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His
785 790 795 800
Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln
805 810 815
Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830
Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln
835 840 845
Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe
850 855 860
Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala
865 870 875 880
Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr

885 890 895
Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910
Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys

930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp

945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu

965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu

980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn

995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala

1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala

1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr

1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val

1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 257

<211> 1008

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 257

Met Asp Thr Pro Asn Phe Ser Glu Arg Ile Pro Val Ser Leu Gln Ser

1 5 10 15

His Pro Tyr Tyr Phe Ala His Tyr Leu Asn Met Ala Arg His Asn Ala
20 25 30

Tyr Val Ile Leu Glu Tyr Val Asn Arg Glu Leu Ile Lys Pro Gly Lys
35 40 45
Asn Leu Asp Glu Asp Asn Leu Ile Gln Ser Thr Val Leu Lys Asp Gly
50 55 60
Tyr Phe Asp Arg Lys Pro Asp Glu Leu Ser His Arg Asn Arg Leu Leu
65 70 75 80
Val Gln His Phe Pro Phe Leu Arg Glu Ala Glu Asn Glu Gly Ala Arg
85 90 95

Thr Cys Asn Pro Val Ser Tyr Lys Leu Lys Thr Ala Leu Ala Ala Leu
100 105 110
Asn Gln Trp Arg Asn Asn Ala Ser His Tyr Pro Leu Asn Gln Asn His
115 120 125
Glu Lys Asp Phe Asp Leu Gln Pro Phe Phe Ser Phe Ala Ile Glu Ala
130 135 140
Cys Lys Lys Arg Met Arg Glu Val Phe Gln Pro Asp Asp Phe Tyr Leu
145 150 155 160

Leu Glu Thr Asn Glu Lys Gln Phe Tyr Thr Leu His Asn Glu Asn Gly
165 170 175
Phe Thr Glu Lys Gly Leu Tyr Cys Phe Ile Cys Phe Phe Leu Glu Lys
180 185 190
Lys Tyr Ala Phe Gln Phe Leu Ala Gly Ile Lys Gly Phe Lys Asn Thr
195 200 205
Thr Asp Asn Lys Phe Arg Ala Thr Leu Glu Thr Phe Thr Glu His Cys
210 215 220

Cys Arg Leu Pro Lys Pro Lys Leu Asp Ser Ser Asp Ile Lys Leu Asp
225 230 235 240
Met Leu Gly Glu Leu Ser Arg Cys Pro Ala Pro Leu Phe Asp Leu Leu
245 250 255
Asp Ile Glu Glu Arg Lys Lys Phe Ile Arg Glu Pro Glu Glu Val Lys

260 265 270

Pro Asp Glu Ser Gly Asp Arg Glu Glu Val Gln Gln Val Leu Met Lys

275 280 285

Arg Tyr Asp Asp Arg Phe Pro Tyr Phe Ala Leu Arg Tyr Phe Glu Glu

290 295 300

Lys Asn Leu Leu Lys Gly Ile Ser Phe His Ile His Ile Gly Arg Trp

305 310 315 320

Ile Lys Ser Glu His Thr Lys Lys Ile Met Gly Ala Glu Arg Asp Arg

325 330 335

Arg Leu Leu Lys Asp Ile Arg Thr Phe Gly Glu Leu Lys Glu Phe Ser

340 345 350

Pro Glu His Ala Pro Asp Tyr Trp Leu Arg Asp Gly Ile Thr Pro Asp

355 360 365

Asp Val Asp Gln Phe Ser Pro Gln Tyr Arg Ile Val Gly Asn Arg Ile

370 375 380

Gly Ile Lys Leu Asn Tyr Asn Gly His Asn Arg Trp Ser Val Pro Asp

385 390 395 400

Lys Glu Ile Asn Val Lys Pro Asp Ala Ile Ile Ser Thr Tyr Glu Phe

405 410 415

Leu Asn Leu Phe Leu Tyr Glu His Leu Tyr Gln Lys Lys Leu Thr Gly

420 425 430

Leu Ser Pro Ala Glu Phe Ile Gln Asp Tyr Leu Asp Arg Phe Asn Asn

435 440 445

Phe Leu Ser Glu Phe Lys Ala Gly His Ile Arg Pro Val Gly Asp Phe

450 455 460

Ser Leu Glu Lys Arg Arg Gly Gln Gly Asp Glu Pro Asp Leu Thr Ala

465 470 475 480

Arg Arg Lys Ser Leu Gln Lys Glu Leu Asp Arg Phe Val Leu Lys Gly

485 490 495

Lys Asp Leu Pro Asp Lys Ile Arg Glu Tyr Leu Leu Gly Tyr Lys Gln

500 505 510

Lys Ser Glu Lys Lys Gln Ala Lys Trp Ile Leu Gly Gly Met Ile Lys
515 520 525

Glu Thr Val Tyr Trp Arg Asn Lys Ala Glu Gln Ser Pro Glu Lys Met
530 535 540

Arg Ser Gly Asp Met Ala Gln Gln Leu Ala Arg Asp Ile Ile Phe Leu
545 550 555 560

Thr Pro Pro His Thr Val Lys Glu His Lys Gln Lys Leu Asn Ser Leu
565 570 575

Glu Tyr Asp Val Leu Gln Tyr Ala Leu Ala Tyr Phe Ser Ser Asn Arg
580 585 590

Glu Lys Leu Tyr Ser Phe Phe Lys Glu His Gln Leu Thr Val Lys Gly
595 600 605

Asp Arg Ala His Pro Phe Leu Tyr Lys Ile Arg Leu Asp Glu Cys Gln
610 615 620

Gly Ile Leu Asp Phe Phe Ile Val Tyr Met Gln Gln Lys Glu Lys Trp
625 630 635 640

Leu Gly Trp Leu Asp Arg Asn Leu Lys Ser Pro Arg Leu Asn Glu Glu
645 650 655

Glu Phe Phe Asn Thr Tyr Ser Tyr Phe Ile Lys Thr Asp Thr Lys Arg
660 665 670

Ala Ile Glu Met Asp Tyr Glu Ser Cys Pro Asn Tyr Leu Pro Arg Gly
675 680 685

Ile Phe Asn Glu Pro Ile Ala Lys Ala Leu Gln Lys Ala Gly Val Lys
690 695 700

Ile Lys Asp Glu Asp Asn Ala Ser Tyr Ala Leu Ser Val Tyr Ser Asn
705 710 715 720

Gly Lys Thr Gln Pro Phe Tyr Asn Lys Glu Arg Tyr Tyr Asn Lys Gly
725 730 735

Ile Phe Arg Met Glu Glu Leu Pro Glu Lys Leu Gln Pro Lys Glu Leu
740 745 750

Leu Gly Lys Ile Gln Trp Thr Ile Lys Ser Ser Gly Lys Asp Thr Glu

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        755                 760                 765
Glu Phe Arg Ser Leu Gln Asn Leu Lys Asn Arg Ile Leu Asn Thr Glu
    770                 775                 780
Lys Glu Ile Arg Tyr Val Gln Ser Thr Asp Arg Ala Leu Trp Ile Met
785                 790                 795                 800

Val Ala Asp Leu Phe Pro Glu Thr Phe Glu Leu Arg Pro Asp Asp Leu
                805                 810                 815
Glu Cys Ile Gly His Asp Leu Ser Asp Asp Leu Leu Ser Arg Pro Tyr
            820                 825                 830
Gln Met Lys Glu Lys Val Tyr Asn Tyr Thr Ile Thr Asp Tyr Leu Pro
        835                 840                 845
Ile Lys Arg Tyr Gly Glu Phe Arg Arg Phe Leu Lys Asp Arg Arg Leu
    850                 855                 860

Glu Asn Leu Leu Thr Tyr Phe Glu Glu Gly Val Pro Leu His Arg Glu
865                 870                 875                 880
Ala Leu Val Ala Glu Leu Glu Ala Tyr Asp Leu Gln Arg Lys Asn Leu
                885                 890                 895
Leu Glu Ile Ile Tyr Arg Phe Glu Lys Leu Val Phe Asp Arg His Arg
            900                 905                 910
His Glu Leu Thr Phe Ser Gly Glu Gly Glu Asn Gln Tyr Val Asn His
        915                 920                 925

Trp Asp Tyr Leu Asp Phe Val Ala Arg Lys Tyr Gly Leu Ser Ala Glu
    930                 935                 940
Val Lys Glu Leu Asn Ser Glu Arg Phe Thr Glu Leu Arg Asn Lys Met
945                 950                 955                 960
Leu His Asn Gln Ile Pro Tyr Gln Leu Trp Ile Lys Glu Ala Ile Ala
                965                 970                 975
Ala Arg Glu Glu Asn Thr Val Cys Gly Arg Ile Met Gly Met Ile Gly
            980                 985                 990

Glu Ile Tyr Glu Arg Met Thr Thr  Glu Ile Glu Lys Gln  Met Gln Val
        995                 1000                1005
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<210> 258

<211> 948

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 258

Met Phe Phe Ser Phe His Asn Ala Gln Arg Val Ile Phe Lys His Leu
1 5 10 15
Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu Asp Tyr Lys
20 25 30

Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His Leu Asn Arg
35 40 45
Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg Tyr Arg Phe
50 55 60
Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe Phe Thr Asn
65 70 75 80
Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys Lys Val Ser
85 90 95

Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr Thr Glu Val
100 105 110
Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu Glu Ser Arg
115 120 125
Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu Leu Ser Arg
130 135 140
Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn Lys Lys His
145 150 155 160

Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu Glu Glu Gln
165 170 175
Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg Phe Pro Tyr
180 185 190
Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys Ser Ile Arg

195 200 205

Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr Asp Lys Lys

210 215 220

Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr Leu Leu Ser

225 230 235 240

Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro Gln Glu Trp

245 250 255

Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser Asn Gln Pro

260 265 270

Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp Asn Lys Ile

275 280 285

Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser Leu Glu Ile

290 295 300

Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn Ser Gly Phe

305 310 315 320

Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro Leu Met Phe

325 330 335

Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys Glu Thr Val

340 345 350

Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu Arg Ile Asn

355 360 365

Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu Pro Leu Gly

370 375 380

Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys Gln Pro Asp

385 390 395 400

Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile Ala Glu Thr

405 410 415

Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser Ser Pro Lys

420 425 430

Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val Leu Ala Asp

435 440 445

Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala Tyr Asp Ala
450 455 460
Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr Glu Phe Trp
465 470 475 480

Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys Asn Arg Leu
485 490 495
Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr Asn Pro His
500 505 510
Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn Leu Val Asp
515 520 525
Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu Glu Ala Ile
530 535 540

Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu Leu Lys Ile
545 550 555 560
Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu Gln Gly Gly
565 570 575
Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg Glu Thr Leu
580 585 590
Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu Ile Lys Lys
595 600 605

His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu Tyr Phe Lys
610 615 620
Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu Ser Tyr Lys
625 630 635 640
Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His Tyr Glu Tyr
645 650 655
Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln Arg Leu Glu
660 665 670

Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr Lys Arg Trp
675 680 685
Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln Asp Val Met

690 695 700

Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe Lys Glu Leu
705 710 715 720

Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala Val Asn Val
725 730 735

Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr Leu Pro Met
740 745 750

Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly Glu Val Gln
755 760 765

Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu Glu His Thr
770 775 780

Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys Asp Arg Arg
785 790 795 800

Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp Thr Gln Lys
805 810 815

His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu Ile Tyr Gln
820 825 830

Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu Glu Glu Lys
835 840 845

Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn Glu Phe Arg
850 855 860

Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala Ser Ser Met Val
865 870 875 880

Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val Arg Asn Ala Phe Cys
885 890 895

His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala Leu His Ala Pro Ile Pro
900 905 910

Leu Phe Thr Val Ala Gln Pro Thr Thr Glu Glu Lys Asp Gly Leu Gly
915 920 925

Ile Ala Glu Ala Leu Leu Lys Val Leu Arg Glu Tyr Cys Glu Ile Val
930 935 940

Lys Ser Gln Ile

945

<210> 259

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 259

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45
Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95

Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125
Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175
Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445
Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460
Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510
Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560
Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575
Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620
Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640
Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655
Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn
660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu

770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr

885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly

900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940
Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960
Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975
Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005
Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020
Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val
1025 1030 1035
Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065
Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080
Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile
1085 1090 1095

<210> 260
<211> 1131
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 260
Met Thr Asn Thr Pro Lys Arg Arg Thr Leu His Arg His Pro Ser Tyr

1 5 10 15
Phe Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Met Ile Met

20 25 30

Glu His Leu Ser Thr Lys Tyr Asp Met Glu Asp Lys Asn Thr Leu Asp

35 40 45

Glu Ala Gln Leu Pro Asn Ala Lys Leu Phe Gly Cys Leu Lys Lys Arg

50 55 60

Tyr Gly Lys Pro Asp Val Thr Glu Gly Val Ser Arg Asp Leu Arg Arg

65 70 75 80

Tyr Phe Pro Phe Leu Asn Tyr Pro Leu Phe Leu His Leu Glu Lys Gln

85 90 95

Gln Asn Ala Glu Gln Ala Ala Thr Tyr Asp Ile Asn Pro Glu Asp Ile

100 105 110

Glu Phe Thr Leu Lys Gly Phe Phe Arg Leu Leu Asn Gln Met Arg Asn

115 120 125

Asn Tyr Ser His Tyr Ile Ser Asn Thr Asp Tyr Gly Lys Phe Asp Lys

130 135 140

Leu Pro Val Gln Asp Ile Tyr Glu Ala Ala Ile Phe Arg Leu Leu Asp

145 150 155 160

Arg Gly Lys His Thr Lys Arg Phe Asp Val Phe Glu Ser Lys His Thr

165 170 175

Arg His Leu Glu Ser Asn Asn Ser Glu Tyr Arg Pro Arg Ser Leu Ala

180 185 190

Asn Ser Pro Asp His Glu Asn Thr Val Ala Phe Val Thr Cys Leu Phe

195 200 205

Leu Glu Arg Lys Tyr Ala Phe Pro Phe Leu Ser Arg Leu Asp Cys Phe

210 215 220

Arg Ser Thr Asn Asp Ala Ala Glu Gly Asp Pro Leu Ile Arg Lys Ala

225 230 235 240

Ser His Glu Cys Tyr Thr Met Phe Cys Cys Arg Leu Pro Gln Pro Lys

245 250 255

Leu Glu Ser Ser Asp Ile Leu Leu Asp Met Val Asn Glu Leu Gly Arg

260 265 270

Cys Pro Ser Ala Leu Tyr Asn Leu Leu Ser Glu Glu Asp Gln Ala Arg
275 280 285
Phe His Ile Lys Arg Glu Glu Ile Thr Gly Phe Glu Glu Asp Pro Asp
290 295 300
Glu Glu Leu Glu Gln Glu Ile Val Leu Lys Arg His Ser Asp Arg Phe
305 310 315 320
Pro Tyr Phe Ala Leu Arg Tyr Phe Asp Asp Thr Glu Ala Phe Gln Thr

325 330 335
Leu Arg Phe Asp Val Tyr Leu Gly Arg Trp Arg Thr Lys Pro Val Tyr
340 345 350
Lys Lys Arg Ile Tyr Gly Gln Glu Arg Asp Arg Val Leu Thr Gln Ser
355 360 365
Ile Arg Thr Phe Thr Arg Leu Ser Arg Leu Leu Pro Ile Tyr Glu Asn
370 375 380
Val Lys His Asp Ala Val Arg Gln Asn Glu Glu Asp Gly Lys Leu Val

385 390 395 400
Asn Pro Asp Val Thr Ser Gln Phe His Lys Ser Trp Ile Gln Ile Glu
405 410 415
Ser Asp Asp Arg Ala Phe Leu Ser Asp Arg Ile Glu His Phe Ser Pro
420 425 430
His Tyr Asn Phe Gly Asp Gln Val Ile Gly Leu Lys Phe Ile Asn Pro
435 440 445
Asp Arg Tyr Ala Ala Ile Gln Asn Val Phe Pro Lys Leu Pro Gly Glu

450 455 460
Glu Lys Lys Asp Lys Asp Ala Lys Leu Val Asn Glu Thr Ala Asp Ala
465 470 475 480
Ile Ile Ser Thr His Glu Ile Arg Ser Leu Phe Leu Tyr His Tyr Leu
485 490 495
Ser Lys Lys Pro Ile Ser Ala Gly Asp Glu Arg Arg Phe Ile Gln Val
500 505 510
Asp Thr Glu Thr Phe Ile Lys Gln Tyr Ile Asp Thr Ile Lys Leu Phe

515 520 525

Phe Glu Asp Ile Lys Ser Gly Glu Leu Gln Pro Ile Ala Asp Pro Pro

530 535 540

Asn Tyr Gln Lys Asn Glu Pro Leu Pro Tyr Val Arg Gly Asp Lys Glu

545 550 555 560

Lys Thr Gln Glu Glu Arg Ala Gln Tyr Arg Glu Arg Gln Lys Glu Ile

565 570 575

Lys Glu Arg Arg Lys Glu Leu Asn Thr Leu Leu Gln Asn Arg Tyr Gly

580 585 590

Leu Ser Ile Gln Tyr Ile Pro Ser Arg Leu Arg Glu Tyr Leu Leu Gly

595 600 605

Tyr Lys Lys Val Pro Tyr Glu Lys Leu Ala Leu Gln Lys Leu Arg Ala

610 615 620

Gln Arg Lys Glu Val Lys Lys Arg Ile Lys Asp Ile Glu Lys Met Arg

625 630 635 640

Thr Pro Arg Val Gly Glu Gln Ala Thr Trp Leu Ala Glu Asp Ile Val

645 650 655

Phe Leu Thr Pro Pro Lys Met His Thr Pro Glu Arg Lys Thr Thr Lys

660 665 670

His Pro Gln Lys Leu Asn Asn Asp Gln Phe Arg Ile Met Gln Ser Ser

675 680 685

Leu Ala Tyr Phe Ser Val Asn Lys Lys Ala Ile Lys Lys Phe Phe Gln

690 695 700

Lys Glu Thr Gly Ile Gly Leu Ser Asn Arg Glu Thr Ser His Pro Phe

705 710 715 720

Leu Tyr Arg Ile Asp Val Gly Arg Cys Arg Gly Ile Leu Asp Phe Tyr

725 730 735

Thr Gly Tyr Leu Lys Tyr Lys Met Asp Trp Leu Asp Asp Ala Ile Lys

740 745 750

Lys Val Asp Asn Arg Lys His Gly Lys Lys Glu Ala Lys Lys Tyr Glu

755 760 765

Lys Tyr Leu Pro Ser Ser Ile Gln His Lys Thr Pro Leu Glu Leu Asp

770 775 780

Tyr Thr Arg Leu Pro Val Tyr Leu Pro Arg Gly Leu Phe Lys Lys Ala

785 790 795 800

Ile Val Lys Ala Leu Ala Ala His Ala Asp Phe Gln Val Glu Pro Glu

805 810 815

Glu Asp Asn Val Ile Phe Cys Leu Asp Gln Leu Leu Asp Gly Asp Thr

820 825 830

Gln Asp Phe Tyr Asn Trp Gln Arg Tyr Tyr Arg Ser Ala Leu Thr Glu

835 840 845

Lys Glu Thr Asp Asn Gln Leu Val Leu Ala His Pro Tyr Ala Glu Gln

850 855 860

Ile Leu Gly Thr Ile Lys Thr Leu Glu Gly Lys Gln Lys Asn Asn Lys

865 870 875 880

Leu Gly Asn Lys Ala Lys Gln Lys Ile Lys Asp Glu Leu Ile Asp Leu

885 890 895

Lys Arg Ala Lys Arg Arg Leu Leu Asp Arg Glu Gln Tyr Leu Arg Ala

900 905 910

Val Gln Ala Glu Asp Arg Ala Leu Trp Leu Met Ile Gln Glu Arg Gln

915 920 925

Lys Gln Lys Ala Glu His Glu Glu Ile Ala Phe Asp Gln Leu Asp Leu

930 935 940

Lys Asn Ile Thr Lys Ile Leu Thr Glu Ser Ile Asp Ala Arg Leu Arg

945 950 955 960

Ile Pro Asp Thr Lys Val Asp Ile Thr Asp Lys Leu Pro Leu Arg Arg

965 970 975

Tyr Gly Asp Leu Arg Arg Val Ala Lys Asp Arg Arg Leu Val Asn Leu

980 985 990

Ala Ser Tyr Tyr His Val Ala Gly Leu Ser Glu Ile Pro Tyr Asp Leu

995 1000 1005

Val Lys Lys Glu Leu Glu Glu Tyr Asp Arg Arg Arg Val Ala Phe

1010 1015 1020

Phe Glu His Val Tyr Gln Phe Glu Lys Glu Val Tyr Asp Arg Tyr

1025 1030 1035

Ala Ala Glu Leu Arg Asn Glu Asn Pro Lys Gly Glu Ser Thr Tyr

1040 1045 1050

Phe Ser His Trp Glu Tyr Val Ala Val Ala Val Lys His Ser Ala

1055 1060 1065

Asp Thr His Phe Asn Glu Leu Phe Lys Glu Lys Val Met Gln Leu

1070 1075 1080

Arg Asn Lys Phe His His Asn Glu Phe Pro Tyr Phe Asp Trp Leu

1085 1090 1095

Leu Pro Glu Val Glu Lys Ala Ser Ala Ala Leu Tyr Ala Asp Arg

1100 1105 1110

Val Phe Asp Val Ala Glu Gly Tyr Tyr Gln Lys Met Arg Lys Leu

1115 1120 1125

Met Arg Gln

1130

<210> 261

<211> 1131

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 261

Met Thr Asn Thr Pro Lys Arg Arg Thr Leu His Arg His Pro Ser Tyr

1 5 10 15

Phe Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Met Ile Met

20 25 30

Glu His Leu Ser Thr Lys Tyr Asp Met Glu Asp Lys Asn Thr Leu Asp

35 40 45

Glu Ala Gln Leu Pro Asn Ala Lys Leu Phe Gly Cys Leu Lys Lys Arg

50 55 60

Tyr Gly Lys Pro Asp Val Thr Glu Gly Val Ser Arg Asp Leu Arg Arg

65 70 75 80

Tyr Phe Pro Phe Leu Asn Tyr Pro Leu Phe Leu His Leu Glu Lys Gln

85 90 95

Gln Asn Ala Glu Gln Ala Ala Thr Tyr Asp Ile Asn Pro Glu Asp Ile

100 105 110

Glu Phe Thr Leu Lys Gly Phe Phe Arg Leu Leu Asn Gln Met Arg Asn

115 120 125

Asn Tyr Ser His Tyr Ile Ser Asn Thr Asp Tyr Gly Lys Phe Asp Lys

130 135 140

Leu Pro Val Gln Asp Ile Tyr Glu Ala Ala Ile Phe Arg Leu Leu Asp

145 150 155 160

Arg Gly Lys His Thr Lys Arg Phe Asp Val Phe Glu Ser Lys His Thr

165 170 175

Arg His Leu Glu Ser Asn Asn Ser Glu Tyr Arg Pro Arg Ser Leu Ala

180 185 190

Asn Ser Pro Asp His Glu Asn Thr Val Ala Phe Val Thr Cys Leu Phe

195 200 205

Leu Glu Arg Lys Tyr Ala Phe Pro Phe Leu Ser Arg Leu Asp Cys Phe

210 215 220

Arg Ser Thr Asn Asp Ala Ala Glu Gly Asp Pro Leu Ile Arg Lys Ala

225 230 235 240

Ser His Glu Cys Tyr Thr Met Phe Cys Cys Arg Leu Pro Gln Pro Lys

245 250 255

Leu Glu Ser Ser Asp Ile Leu Leu Asp Met Val Asn Glu Leu Gly Arg

260 265 270

Cys Pro Ser Ala Leu Tyr Asn Leu Leu Ser Glu Glu Asp Gln Ala Arg

275 280 285

Phe His Ile Lys Arg Glu Glu Ile Thr Gly Phe Glu Glu Asp Pro Asp

290 295 300

Glu Glu Leu Glu Gln Glu Ile Val Leu Lys Arg His Ser Asp Arg Phe

305 310 315 320

Pro Tyr Phe Ala Leu Arg Tyr Phe Asp Asp Thr Glu Ala Phe Gln Thr

325 330 335

Leu Arg Phe Asp Val Tyr Leu Gly Arg Trp Arg Thr Lys Pro Val Tyr

340 345 350

Lys Lys Arg Ile Tyr Gly Gln Glu Arg Asp Arg Val Leu Thr Gln Ser

355 360 365

Ile Arg Thr Phe Thr Arg Leu Ser Arg Leu Leu Pro Ile Tyr Glu Asn

370 375 380

Val Lys His Asp Ala Val Arg Gln Asn Glu Glu Asp Gly Lys Leu Val

385 390 395 400

Asn Pro Asp Val Thr Ser Gln Phe His Lys Ser Trp Ile Gln Ile Glu

405 410 415

Ser Asp Asp Arg Ala Phe Leu Ser Asp Arg Ile Glu His Phe Ser Pro

420 425 430

His Tyr Asn Phe Gly Asp Gln Val Ile Gly Leu Lys Phe Ile Asn Pro

435 440 445

Asp Arg Tyr Ala Ala Ile Gln Asn Val Phe Pro Lys Leu Pro Gly Glu

450 455 460

Glu Lys Lys Asp Lys Asp Ala Lys Leu Val Asn Glu Thr Ala Asp Ala

465 470 475 480

Ile Ile Ser Thr His Glu Ile Arg Ser Leu Phe Leu Tyr His Tyr Leu

485 490 495

Ser Lys Lys Pro Ile Ser Ala Gly Asp Glu Arg Arg Phe Ile Gln Val

500 505 510

Asp Thr Glu Thr Phe Ile Lys Gln Tyr Ile Asp Thr Ile Lys Leu Phe

515 520 525

Phe Glu Asp Ile Lys Ser Gly Glu Leu Gln Pro Ile Ala Asp Pro Pro

530 535 540

Asn Tyr Gln Lys Asn Glu Pro Leu Pro Tyr Val Arg Gly Asp Lys Glu

545 550 555 560

Lys Thr Gln Glu Glu Arg Ala Gln Tyr Arg Glu Arg Gln Lys Glu Ile
565 570 575
Lys Glu Arg Arg Lys Glu Leu Asn Thr Leu Leu Gln Asn Arg Tyr Gly

580 585 590
Leu Ser Ile Gln Tyr Ile Pro Ser Arg Leu Arg Glu Tyr Leu Leu Gly
595 600 605
Tyr Lys Lys Val Pro Tyr Glu Lys Leu Ala Leu Gln Lys Leu Arg Ala
610 615 620
Gln Arg Lys Glu Val Lys Lys Arg Ile Lys Asp Ile Glu Lys Met Arg
625 630 635 640
Thr Pro Arg Val Gly Glu Gln Ala Thr Trp Leu Ala Glu Asp Ile Val

645 650 655
Phe Leu Thr Pro Pro Lys Met His Thr Pro Glu Arg Lys Thr Thr Lys
660 665 670
His Pro Gln Lys Leu Asn Asn Asp Gln Phe Arg Ile Met Gln Ser Ser
675 680 685
Leu Ala Tyr Phe Ser Val Asn Lys Lys Ala Ile Lys Lys Phe Phe Gln
690 695 700
Lys Glu Thr Gly Ile Gly Leu Ser Asn Arg Glu Thr Ser His Pro Phe

705 710 715 720
Leu Tyr Arg Ile Asp Val Gly Arg Cys Arg Gly Ile Leu Asp Phe Tyr
725 730 735
Thr Gly Tyr Leu Lys Tyr Lys Met Asp Trp Leu Asp Asp Ala Ile Lys
740 745 750
Lys Val Asp Asn Arg Lys His Gly Lys Lys Glu Ala Lys Lys Tyr Glu
755 760 765
Lys Tyr Leu Pro Ser Ser Ile Gln His Lys Thr Pro Leu Glu Leu Asp

770 775 780
Tyr Thr Arg Leu Pro Val Tyr Leu Pro Arg Gly Leu Phe Lys Lys Ala
785 790 795 800
Ile Val Lys Ala Leu Ala Ala His Ala Asp Phe Gln Val Glu Pro Glu

805 810 815

Glu Asp Asn Val Ile Phe Cys Leu Asp Gln Leu Leu Asp Gly Asp Thr

820 825 830

Gln Asp Phe Tyr Asn Trp Gln Arg Tyr Tyr Arg Ser Ala Leu Thr Glu

835 840 845

Lys Glu Thr Asp Asn Gln Leu Val Leu Ala His Pro Tyr Ala Glu Gln

850 855 860

Ile Leu Gly Thr Ile Lys Thr Leu Glu Gly Lys Gln Lys Asn Asn Lys

865 870 875 880

Leu Gly Asn Lys Ala Lys Gln Lys Ile Lys Asp Glu Leu Ile Asp Leu

885 890 895

Lys Arg Ala Lys Arg Arg Leu Leu Asp Arg Glu Gln Tyr Leu Arg Ala

900 905 910

Val Gln Ala Glu Asp Arg Ala Leu Trp Leu Met Ile Gln Glu Arg Gln

915 920 925

Lys Gln Lys Ala Glu His Glu Glu Ile Ala Phe Asp Gln Leu Asp Leu

930 935 940

Lys Asn Ile Thr Lys Ile Leu Thr Glu Ser Ile Asp Ala Arg Leu Arg

945 950 955 960

Ile Pro Asp Thr Lys Val Asp Ile Thr Asp Lys Leu Pro Leu Arg Arg

965 970 975

Tyr Gly Asp Leu Arg Arg Val Ala Lys Asp Arg Arg Leu Val Asn Leu

980 985 990

Ala Ser Tyr Tyr His Val Ala Gly Leu Ser Glu Ile Pro Tyr Asp Leu

995 1000 1005

Val Lys Lys Glu Leu Glu Glu Tyr Asp Arg Arg Arg Val Ala Phe

1010 1015 1020

Phe Glu His Val Tyr Gln Phe Glu Lys Glu Val Tyr Asp Arg Tyr

1025 1030 1035

Ala Ala Glu Leu Arg Asn Glu Asn Pro Lys Gly Glu Ser Thr Tyr

1040 1045 1050

Phe Ser His Trp Glu Tyr Val Ala Val Ala Val Lys His Ser Ala

1055 1060 1065

Asp Thr His Phe Asn Glu Leu Phe Lys Glu Lys Val Met Gln Leu

1070 1075 1080

Arg Asn Lys Phe His His Asn Glu Phe Pro Tyr Phe Asp Trp Leu

1085 1090 1095

Leu Pro Glu Val Glu Lys Ala Ser Ala Ala Leu Tyr Ala Asp Arg

1100 1105 1110

Val Phe Asp Val Ala Glu Gly Tyr Tyr Gln Lys Met Arg Lys Leu

1115 1120 1125

Met Arg Gln

1130

<210> 262

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 262

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp

35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn

50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu

65 70 75 80

Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95

Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu

100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile

115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr
355 360 365
Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr
370 375 380
Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400
Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415
Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430
Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445
Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460
Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480
Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510
Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560
Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575
Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val

580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr

610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu

770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe
850 855 860
Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala
865 870 875 880
Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895
Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly

900 905 910
Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu
915 920 925
Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940
Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960
Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu

965 970 975
Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990
Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005
Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020
Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035
Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050
Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065
Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080
Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 263

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 263

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125
Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His
180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg
195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe
210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys
225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr
245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu
260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu
275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn
290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu
305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg
325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys
340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr
355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr
370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser

435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser

565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val

580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr

610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700
Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720
Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg
725 730 735
Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765
Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780
Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His
785 790 795 800
Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln
805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr
820 825 830
Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln
835 840 845
Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe
850 855 860
Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala
865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895
Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910
Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu
915 920 925
Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys

930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960
Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975
Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu
980 985 990
Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020
Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val
1025 1030 1035
Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala
1040 1045 1050
Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080
Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile
1085 1090 1095

<210> 264
<211> 1095
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 264
Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp

35 40 45

Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn

50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu

65 70 75 80

Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95

Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu

100 105 110

Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile

115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser

435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser

565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val

580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr

610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780
Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800
Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln
805 810 815
Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr
820 825 830
Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln
835 840 845
Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860
Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala
865 870 875 880
Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895
Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910
Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925
Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940
Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960
Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975
Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu

980 985 990
Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005
Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala

1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala

1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr

1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val

1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 265

<211> 1115

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 265

Met Glu Ser Ile Lys Asn Ser Gln Lys Ser Thr Gly Lys Thr Leu Gln

1 5 10 15

Lys Asp Pro Pro Tyr Phe Gly Leu Tyr Leu Asn Met Ala Leu Leu Asn

20 25 30

Val Arg Lys Val Glu Asn His Ile Arg Lys Trp Leu Gly Asp Val Ala

35 40 45

Leu Leu Pro Glu Lys Ser Gly Phe His Ser Leu Leu Thr Thr Asp Asn

50 55 60

Leu Ser Ser Ala Lys Trp Thr Arg Phe Tyr Tyr Lys Ser Arg Lys Phe

65 70 75 80

Leu Pro Phe Leu Glu Met Phe Asp Ser Asp Lys Lys Ser Tyr Glu Asn

85 90 95

Arg Arg Glu Thr Thr Glu Cys Leu Asp Thr Ile Asp Arg Gln Lys Ile

100 105 110

Ser Ser Leu Leu Lys Glu Val Tyr Gly Lys Leu Gln Asp Ile Arg Asn
115 120 125

Ala Phe Ser His Tyr His Ile Asp Asp Gln Ser Val Lys His Thr Ala
130 135 140
Leu Ile Ile Ser Ser Glu Met His Arg Phe Ile Glu Asn Ala Tyr Ser
145 150 155 160
Phe Ala Leu Gln Lys Thr Arg Ala Arg Phe Thr Gly Val Phe Val Glu
165 170 175
Thr Asp Phe Leu Gln Ala Glu Glu Lys Gly Asp Asn Lys Lys Phe Phe
180 185 190

Ala Ile Gly Gly Asn Glu Gly Ile Lys Leu Lys Asp Asn Ala Leu Ile
195 200 205
Phe Leu Ile Cys Leu Phe Leu Asp Arg Glu Glu Ala Phe Lys Phe Leu
210 215 220
Ser Arg Ala Thr Gly Phe Lys Ser Thr Lys Glu Lys Gly Phe Leu Ala
225 230 235 240
Val Arg Glu Thr Phe Cys Ala Leu Cys Cys Arg Gln Pro His Glu Arg
245 250 255

Leu Leu Ser Val Asn Pro Arg Glu Ala Leu Leu Met Asp Met Leu Asn
260 265 270
Glu Leu Asn Arg Cys Pro Asp Ile Leu Phe Glu Met Leu Asp Glu Lys
275 280 285
Asp Gln Lys Ser Phe Leu Pro Leu Leu Gly Glu Glu Glu Gln Ala His
290 295 300
Ile Leu Glu Asn Ser Leu Asn Asp Glu Leu Cys Glu Ala Ile Asp Asp
305 310 315 320

Pro Phe Glu Met Ile Ala Ser Leu Ser Lys Arg Val Arg Tyr Lys Asn
325 330 335
Arg Phe Pro Tyr Leu Met Leu Arg Tyr Ile Glu Glu Lys Asn Leu Leu
340 345 350
Pro Phe Ile Arg Phe Arg Ile Asp Leu Gly Cys Leu Glu Leu Ala Ser

355 360 365

Tyr Pro Lys Lys Met Gly Glu Glu Asn Asn Tyr Glu Arg Ser Val Thr

370 375 380

Asp His Ala Met Ala Phe Gly Arg Leu Thr Asp Phe His Asn Glu Asp

385 390 395 400

Ala Val Leu Gln Gln Ile Thr Lys Gly Ile Thr Asp Glu Val Arg Phe

405 410 415

Ser Leu Tyr Ala Pro Arg Tyr Ala Ile Tyr Asn Asn Lys Ile Gly Phe

420 425 430

Val Arg Thr Gly Gly Ser Asp Lys Ile Ser Phe Pro Thr Leu Lys Lys

435 440 445

Lys Gly Gly Glu Gly His Cys Val Ala Tyr Thr Leu Gln Asn Thr Lys

450 455 460

Ser Phe Gly Phe Ile Ser Ile Tyr Asp Leu Arg Lys Ile Leu Leu Leu

465 470 475 480

Ser Phe Leu Asp Lys Asp Lys Ala Lys Asn Ile Val Ser Gly Leu Leu

485 490 495

Glu Gln Cys Glu Lys His Trp Lys Asp Leu Ser Glu Asn Leu Phe Asp

500 505 510

Ala Ile Arg Thr Glu Leu Gln Lys Glu Phe Pro Val Pro Leu Ile Arg

515 520 525

Tyr Thr Leu Pro Arg Ser Lys Gly Gly Lys Leu Val Ser Ser Lys Leu

530 535 540

Ala Asp Lys Gln Glu Lys Tyr Glu Ser Glu Phe Glu Arg Arg Lys Glu

545 550 555 560

Lys Leu Thr Glu Ile Leu Ser Glu Lys Asp Phe Asp Leu Ser Gln Ile

565 570 575

Pro Arg Arg Met Ile Asp Glu Trp Leu Asn Val Leu Pro Thr Ser Arg

580 585 590

Glu Lys Lys Leu Lys Gly Tyr Val Glu Thr Leu Lys Leu Asp Cys Arg

595 600 605

Glu Arg Leu Arg Val Phe Glu Lys Arg Glu Lys Gly Glu His Pro Val
610 615 620
Pro Pro Arg Ile Gly Glu Met Ala Thr Asp Leu Ala Lys Asp Ile Ile
625 630 635 640

Arg Met Val Ile Asp Gln Gly Val Lys Gln Arg Ile Thr Ser Ala Tyr
645 650 655
Tyr Ser Glu Ile Gln Arg Cys Leu Ala Gln Tyr Ala Gly Asp Asp Asn
660 665 670
Arg Arg His Leu Asp Ser Ile Ile Arg Glu Leu Arg Leu Lys Asp Thr
675 680 685
Lys Asn Gly His Pro Phe Leu Gly Lys Val Leu Arg Pro Gly Leu Gly
690 695 700

His Thr Glu Lys Leu Tyr Gln Arg Tyr Phe Glu Glu Lys Lys Glu Trp
705 710 715 720
Leu Glu Ala Thr Phe Tyr Pro Ala Ala Ser Pro Lys Arg Val Pro Arg
725 730 735
Phe Val Asn Pro Pro Thr Gly Lys Gln Lys Glu Leu Pro Leu Ile Ile
740 745 750
Arg Asn Leu Met Lys Glu Arg Pro Glu Trp Arg Asp Trp Lys Gln Arg
755 760 765

Lys Asn Ser His Pro Ile Asp Leu Pro Ser Gln Leu Phe Glu Asn Glu
770 775 780
Ile Cys Arg Leu Leu Lys Asp Lys Ile Gly Lys Glu Pro Ser Gly Lys
785 790 795 800
Leu Lys Trp Asn Glu Met Phe Lys Leu Tyr Trp Asp Lys Glu Phe Pro
805 810 815
Asn Gly Met Gln Arg Phe Tyr Arg Cys Lys Arg Arg Val Glu Val Phe
820 825 830

Asp Lys Val Val Glu Tyr Glu Tyr Ser Glu Glu Gly Gly Asn Tyr Lys
835 840 845
Lys Tyr Tyr Glu Ala Leu Ile Asp Glu Val Val Arg Gln Lys Ile Ser

850 855 860

Ser Ser Lys Glu Lys Ser Lys Leu Gln Val Glu Asp Leu Thr Leu Ser

865 870 875 880

Val Arg Arg Val Phe Lys Arg Ala Ile Asn Glu Lys Glu Tyr Gln Leu

885 890 895

Arg Leu Leu Cys Glu Asp Asp Arg Leu Leu Phe Met Ala Val Arg Asp

900 905 910

Leu Tyr Asp Trp Lys Glu Ala Gln Leu Asp Leu Asp Lys Ile Asp Asn

915 920 925

Met Leu Gly Glu Pro Val Ser Val Ser Gln Val Ile Gln Leu Glu Gly

930 935 940

Gly Gln Pro Asp Ala Val Ile Lys Ala Glu Cys Lys Leu Lys Asp Val

945 950 955 960

Ser Lys Leu Met Arg Tyr Cys Tyr Asp Gly Arg Val Lys Gly Leu Met

965 970 975

Pro Tyr Phe Ala Asn His Glu Ala Thr Gln Glu Gln Val Glu Met Glu

980 985 990

Leu Arg His Tyr Glu Asp His Arg Arg Arg Val Phe Asn Trp Val Phe

995 1000 1005

Ala Leu Glu Lys Ser Val Leu Lys Asn Glu Lys Leu Arg Arg Phe

1010 1015 1020

Tyr Glu Glu Ser Gln Gly Gly Cys Glu His Arg Arg Cys Ile Asp

1025 1030 1035

Ala Leu Arg Lys Ala Ser Leu Val Ser Glu Glu Glu Tyr Glu Phe

1040 1045 1050

Leu Val His Ile Arg Asn Lys Ser Ala His Asn Gln Phe Pro Asp

1055 1060 1065

Leu Glu Ile Gly Lys Leu Pro Pro Asn Val Thr Ser Gly Phe Cys

1070 1075 1080

Glu Cys Ile Trp Ser Lys Tyr Lys Ala Ile Ile Cys Arg Ile Ile

1085 1090 1095

Pro Phe Ile Asp Pro Glu Arg Arg Phe Phe Gly Lys Leu Leu Glu
1100 1105 1110

Gln Lys
1115

<210> 266

<211> 1099

<212> PRT

<213> Unknown

<220><223> Description of Unknown:
Cas13 sequence

<400> 266

Met Glu Lys Pro Leu Pro Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Thr Thr Pro Pro Asn Asp
35 40 45

Asp Lys Ile Ala Asp Val Val Cys Gly Thr Trp Asn Asn Ile Leu Asn
50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80

Lys His Phe Pro Phe Leu Ala Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95

Glu Gly Lys Lys Lys Gly Ser Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110

Lys Glu Lys Glu Asn Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro
115 120 125

Ser Glu Leu Ile Lys Val Leu Lys Thr Ile Val Lys Gln Leu Arg Thr
130 135 140

Leu Arg Asn Tyr Tyr Ser His His Ser His Lys Lys Pro Asp Thr Glu
145 150 155 160

Lys Asp Ile Phe Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg

165 170 175

Met Val Lys Glu Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg

180 185 190

Asp Phe Ala His Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro

195 200 205

Asp Phe Asn Arg Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser

210 215 220

Gly Leu Leu Phe Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr

225 230 235 240

Trp Met Leu Lys Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg

245 250 255

Glu Lys Met Thr Thr Glu Val Phe Cys Arg Ser His Ile Leu Leu Pro

260 265 270

Lys Leu Arg Leu Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp

275 280 285

Met Leu Ser Glu Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu

290 295 300

Ser Glu Glu Asn Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu

305 310 315 320

Asp Glu Ile Glu Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg

325 330 335

His Gln Asp Arg Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn

340 345 350

Glu Ser Phe Lys Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His

355 360 365

Tyr Cys Ile Tyr Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His

370 375 380

Leu Thr Arg Thr Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu

385 390 395 400

Ile Asn Arg Pro Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr

405 410 415

Lys Glu Thr Ser Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr
420 425 430
His Ile Thr Asp Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu
435 440 445
Leu Tyr Pro Ser Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys
450 455 460

Tyr Pro Tyr Asn Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His
465 470 475 480
Glu Leu Leu Pro Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu
485 490 495
Asp Leu Leu Lys Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp
500 505 510
Phe Glu Glu Glu Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn
515 520 525

Gln Gly Arg Leu Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu
530 535 540
Leu Gln Asn Lys Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile
545 550 555 560
Glu Lys Leu Ile Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr
565 570 575
Lys Leu Lys Ser Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile
580 585 590

Lys Thr Gly Val Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe
595 600 605
Gln Pro Val Ala Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys
610 615 620
Ala Asn Ser Thr Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr
625 630 635 640
Gly Gly Glu Lys Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu
645 650 655

Ile Gly Asn Thr Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys

660 665 670

Ala Cys Arg Asn Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg

675 680 685

Glu Lys Phe Leu Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln

690 695 700

Tyr Cys Leu Leu Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val

705 710 715 720

Lys Gly Trp Glu Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr

725 730 735

Glu Ala Ile Arg Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro

740 745 750

Ile Arg Lys Glu Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg

755 760 765

Ala Ile Thr Leu Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser

770 775 780

Phe Tyr Asn Leu Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys

785 790 795 800

Arg Glu Glu His Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro

805 810 815

Thr Glu Ser Gln Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp

820 825 830

Tyr Leu Leu Tyr Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu

835 840 845

Tyr Arg Asn Gln Asp Ile Met Leu Trp Leu Met Thr Leu Glu Leu Thr

850 855 860

Lys Asn His Phe Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu

865 870 875 880

Glu Asn Leu Ala Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro

885 890 895

Leu Asn Gln Thr Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala

900 905 910

Thr Ala Phe Gly Glu Val Gln Tyr Gln Glu Thr Pro Ile Arg Thr Val
915 920 925

Tyr Ile Arg Glu Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys
930 935 940

Ala Leu Val Lys Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys
945 950 955 960

Glu Glu Asn Asp Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg
965 970 975

Arg Glu Leu Glu Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu
980 985 990

Thr Leu Asp Leu Glu Glu Lys Leu Leu Lys Lys His Thr Ser Leu Ser
995 1000 1005

Ser Leu Glu Asn Lys Phe Arg Ile Leu Leu Glu Glu Trp Lys Lys
1010 1015 1020

Glu Tyr Ala Ala Ser Ser Met Val Thr Asp Glu His Ile Ala Phe
1025 1030 1035

Ile Ala Ser Val Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe
1040 1045 1050

Tyr Glu Glu Ala Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala
1055 1060 1065

Gln Gln Thr Thr Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala
1070 1075 1080

Leu Leu Arg Val Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln
1085 1090 1095

Ile

<210> 267
<211> 948
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence

<400> 267

Met Phe Phe Ser Phe His Asn Ala Gln Arg Val Ile Phe Lys His Leu
1 5 10 15

Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu Asp Tyr Lys
20 25 30

Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His Leu Asn Arg
35 40 45

Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg Tyr Arg Phe
50 55 60

Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe Phe Thr Asn
65 70 75 80

Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys Lys Val Ser
85 90 95

Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr Thr Glu Val
100 105 110

Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu Glu Ser Arg
115 120 125

Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu Leu Ser Arg
130 135 140

Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn Lys Lys His
145 150 155 160

Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu Glu Glu Gln
165 170 175

Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg Phe Pro Tyr
180 185 190

Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys Ser Ile Arg
195 200 205

Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr Asp Lys Lys
210 215 220

Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr Leu Leu Ser
225 230 235 240

Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro Gln Glu Trp
245 250 255
Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser Asn Gln Pro
260 265 270
Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp Asn Lys Ile
275 280 285
Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser Leu Glu Ile
290 295 300

Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn Ser Gly Phe
305 310 315 320
Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro Leu Met Phe
325 330 335
Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys Glu Thr Val
340 345 350
Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu Arg Ile Asn
355 360 365

Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu Pro Leu Gly
370 375 380
Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys Gln Pro Asp
385 390 395 400
Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile Ala Glu Thr
405 410 415
Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser Ser Pro Lys
420 425 430

Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val Leu Ala Asp
435 440 445
Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala Tyr Asp Ala
450 455 460
Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr Glu Phe Trp
465 470 475 480
Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys Asn Arg Leu

485 490 495

Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr Asn Pro His
500 505 510
Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn Leu Val Asp
515 520 525
Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu Glu Ala Ile
530 535 540
Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu Leu Lys Ile
545 550 555 560

Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu Gln Gly Gly
565 570 575
Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg Glu Thr Leu
580 585 590
Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu Ile Lys Lys
595 600 605
His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu Tyr Phe Lys
610 615 620

Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu Ser Tyr Lys
625 630 635 640
Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His Tyr Glu Tyr
645 650 655
Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln Arg Leu Glu
660 665 670
Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr Lys Arg Trp
675 680 685

Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln Asp Val Met
690 695 700
Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe Lys Glu Leu
705 710 715 720
Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala Val Asn Val
725 730 735

Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr Leu Pro Met
740 745 750

Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly Glu Val Gln
755 760 765

Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu Glu His Thr
770 775 780

Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys Asp Arg Arg
785 790 795 800

Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp Thr Gln Lys
805 810 815

His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu Ile Tyr Gln
820 825 830

Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu Glu Glu Lys
835 840 845

Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn Glu Phe Arg
850 855 860

Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala Ser Ser Met Val
865 870 875 880

Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val Arg Asn Ala Phe Cys
885 890 895

His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala Leu His Ala Pro Ile Pro
900 905 910

Leu Phe Thr Val Ala Gln Pro Thr Thr Glu Glu Lys Asp Gly Leu Gly
915 920 925

Ile Ala Glu Ala Leu Leu Lys Val Leu Arg Glu Tyr Cys Glu Ile Val
930 935 940

Lys Ser Gln Ile
945

<210> 268

<211> 1099

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 268

Met Glu Lys Pro Leu Pro Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Thr Thr Pro Pro Asn Asp
35 40 45

Asp Lys Ile Ala Asp Val Val Cys Gly Thr Trp Asn Asn Ile Leu Asn
50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80

Lys His Phe Pro Phe Leu Ala Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95

Glu Gly Lys Lys Lys Gly Ser Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110

Lys Glu Lys Glu Asn Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro
115 120 125

Ser Glu Leu Ile Lys Val Leu Lys Thr Ile Val Lys Gln Leu Arg Thr
130 135 140

Leu Arg Asn Tyr Tyr Ser His His Ser His Lys Lys Pro Asp Thr Glu
145 150 155 160

Lys Asp Ile Phe Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg
165 170 175

Met Val Lys Glu Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg
180 185 190

Asp Phe Ala His Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro
195 200 205

Asp Phe Asn Arg Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser
210 215 220

Gly Leu Leu Phe Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr
225 230 235 240

Trp Met Leu Lys Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg
245 250 255

Glu Lys Met Thr Thr Glu Val Phe Cys Arg Ser His Ile Leu Leu Pro
260 265 270

Lys Leu Arg Leu Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp
275 280 285

Met Leu Ser Glu Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu
290 295 300

Ser Glu Glu Asn Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu
305 310 315 320

Asp Glu Ile Glu Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg
325 330 335

His Gln Asp Arg Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn
340 345 350

Glu Ser Phe Lys Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His
355 360 365

Tyr Cys Ile Tyr Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His
370 375 380

Leu Thr Arg Thr Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu
385 390 395 400

Ile Asn Arg Pro Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr
405 410 415

Lys Glu Thr Ser Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr
420 425 430

His Ile Thr Asp Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu
435 440 445

Leu Tyr Pro Ser Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys
450 455 460

Tyr Pro Tyr Asn Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His

465 470 475 480

Glu Leu Leu Pro Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu

485 490 495

Asp Leu Leu Lys Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp

500 505 510

Phe Glu Glu Glu Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn

515 520 525

Gln Gly Arg Leu Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu

530 535 540

Leu Gln Asn Lys Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile

545 550 555 560

Glu Lys Leu Ile Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr

565 570 575

Lys Leu Lys Ser Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile

580 585 590

Lys Thr Gly Val Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe

595 600 605

Gln Pro Val Ala Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys

610 615 620

Ala Asn Ser Thr Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr

625 630 635 640

Gly Gly Glu Lys Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu

645 650 655

Ile Gly Asn Thr Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys

660 665 670

Ala Cys Arg Asn Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg

675 680 685

Glu Lys Phe Leu Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln

690 695 700

Tyr Cys Leu Leu Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val

705 710 715 720

Lys Gly Trp Glu Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr
725 730 735
Glu Ala Ile Arg Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro
740 745 750

Ile Arg Lys Glu Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg
755 760 765
Ala Ile Thr Leu Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser
770 775 780
Phe Tyr Asn Leu Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys
785 790 795 800
Arg Glu Glu His Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro
805 810 815

Thr Glu Ser Gln Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp
820 825 830
Tyr Leu Leu Tyr Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu
835 840 845
Tyr Arg Asn Gln Asp Ile Met Leu Trp Leu Met Thr Leu Glu Leu Thr
850 855 860
Lys Asn His Phe Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu
865 870 875 880

Glu Asn Leu Ala Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro
885 890 895
Leu Asn Gln Thr Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala
900 905 910
Thr Ala Phe Gly Glu Val Gln Tyr Gln Glu Thr Pro Ile Arg Thr Val
915 920 925
Tyr Ile Arg Glu Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys
930 935 940

Ala Leu Val Lys Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys
945 950 955 960
Glu Glu Asn Asp Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg

965 970 975

Arg Glu Leu Glu Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu

980 985 990

Thr Leu Asp Leu Glu Glu Lys Leu Leu Lys Lys His Thr Ser Leu Ser

995 1000 1005

Ser Leu Glu Asn Lys Phe Arg Ile Leu Leu Glu Glu Trp Lys Lys

1010 1015 1020

Glu Tyr Ala Ala Ser Ser Met Val Thr Asp Glu His Ile Ala Phe

1025 1030 1035

Ile Ala Ser Val Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe

1040 1045 1050

Tyr Glu Glu Ala Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala

1055 1060 1065

Gln Gln Thr Thr Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala

1070 1075 1080

Leu Leu Arg Val Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln

1085 1090 1095

Ile

<210> 269

<211> 1003

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 269

Met Gly Ala Ile Glu Asn Lys His Ile Phe Ala Ala Tyr Ala Asn Leu

1 5 10 15

Ala Ile Asp Gly Leu Ile Lys Thr Leu Asn Phe Ile Ala Lys Lys Leu

20 25 30

Asp Thr Gln Lys Gln Leu Ser Ser Trp Asp Ile Lys His Val Ile Thr

35 40 45

Leu Ile Asp Ser Ile Phe Asp Gln Asn Pro Gln Asn Asn Leu Glu Gln
50 55 60
Val Val Glu Gly Tyr Leu Pro Trp Ile Lys Pro Ile Ile Glu Met Lys
65 70 75 80

Thr Pro Lys Lys Gly Glu Arg Gln Ser Asp Lys Leu Cys Ile Glu Tyr
85 90 95
Lys Thr Ile Ile Thr Ala Phe Ala Ser Leu Leu Asn Asp Val Arg Asn
100 105 110
Tyr Tyr Thr His Tyr Tyr His Asp Pro Ile Cys Ile Tyr Pro Gly Gly
115 120 125
Tyr Asp Ile Pro Ser Ser Leu Asn Cys Ile Tyr Asp Ser Ala Ile Asn
130 135 140

Ile Ile Lys Glu Arg Phe Gln Ala Glu Glu Lys Glu Ile Glu His Leu
145 150 155 160
Arg Arg Tyr Thr Arg Lys Lys Gly Arg Val Val Leu Lys Thr Glu Asp
165 170 175
Asp His Phe Tyr Tyr Thr Leu Val Asn Asn Asn Asp Leu Ser Glu Lys
180 185 190
Gly Tyr Ala Phe Phe Ile Ser Met Phe Leu Glu Arg Lys Tyr Ser Tyr
195 200 205

Leu Phe Leu Lys Lys Leu Ser Gly Phe Lys Arg Gly Asp Ser Leu Gln
210 215 220
Tyr Arg Leu Thr Leu Glu Val Phe Thr Ala Leu Ser Thr Lys Pro Pro
225 230 235 240
Val Glu Arg Leu Arg Thr Thr Lys Asp Thr Lys Gln Asp Arg Ala Leu
245 250 255
Asp Ile Leu Asn Glu Leu Ser Arg Ile Pro Ile Glu Leu Tyr Gln Thr
260 265 270

Leu Glu Pro Lys Tyr Arg Glu Met Tyr Asn Glu Thr Leu Gln Pro Thr
275 280 285
Asp Ala Glu Asp Pro Tyr Gly Leu Pro Asp Arg Ser Arg Ile Arg Phe

290 295 300

Arg Ser Arg Phe Glu Ala Phe Ala Leu His Phe Leu Asp Lys Gln Ala
305 310 315 320

Asp Phe Lys Glu Ile Gly Phe Tyr Thr Tyr Leu Gly Asn Tyr Phe His
325 330 335

Asn Gly Tyr Gln Lys Thr Arg Val Asp Arg Glu Thr Lys Asp Arg Tyr
340 345 350

Ile Asn Phe Gln Leu Ala Gly Phe Cys Lys Asn Ile Gln Asp Ile Ser
355 360 365

Ala Lys Lys Leu Ser Glu Ala Leu Asn Val Lys Ser Ile Asp Ile Ser
370 375 380

Thr Asp Ser Ile Pro Asp Ile Asn Ser Phe Glu Pro Tyr Leu Val Gln
385 390 395 400

Ser Thr Pro His Tyr Ile Val Asn Gly Asn Asn Ile Gly Ile Lys Val
405 410 415

Leu Pro Glu Gly Lys Asp Thr Tyr Pro Thr Ile Asp Glu Lys Gly Ala
420 425 430

Lys Met Pro Ile Ala Asp Phe Trp Leu Ser Lys Tyr Glu Leu Pro Ala
435 440 445

Met Leu Phe Tyr Thr Tyr Leu Arg Asn Asn Asn Ile His Lys Ser His
450 455 460

Cys Pro Leu Ser Val Lys Asp Ile Ile Glu Arg Ser Ile His Lys Ser
465 470 475 480

Thr Lys Gln Lys His Pro Glu Glu Arg Ser Glu Leu Met Leu Arg Arg
485 490 495

Val Met Lys Ala Ile Phe Trp Thr Asp Ser Lys Leu Asn Glu Val Glu
500 505 510

Arg Ile Lys Ser Gln Lys Ser Ala Phe Gly Lys Arg Gln His Glu Ile
515 520 525

Leu Lys Ala Gly Arg Ile Ala Glu Thr Leu Val Arg Asp Met Leu Trp
530 535 540

Leu Gln Pro Ser Lys Asn Asn Gly Arg Asp Lys Val Thr Glu Pro Asn
545 550 555 560
Phe Gln Ala Ile Gln Val Ser Leu Ala Tyr Phe Gly Ile Arg Arg Asn
565 570 575
Asp Leu Thr Glu Ile Phe Thr Arg Ala Gly Leu Ile Asn Ser Ser Asn
580 585 590

Pro His Pro Phe Leu Ala Gln Ile Gly Thr Asn Tyr Thr Ser Leu Ile
595 600 605
Glu Phe Tyr Ile Ala Tyr Leu Lys Glu Arg Lys Val Tyr Phe Ser Arg
610 615 620
Ile Gln Lys Lys Ile Leu Gln Gly Lys Leu Asn Ile Gln Cys His Pro
625 630 635 640
Leu Arg Asp Leu Gln Arg Glu Pro Asn Lys Pro Gln Asp Lys Glu Glu
645 650 655

Ala Ile Phe Leu Pro Arg Gly Leu Phe Asn Glu Ala Ile Ile Asn Cys
660 665 670
Leu Lys Lys Ser Lys Leu Lys Gln Leu Ile Glu Ser Pro Thr Arg Glu
675 680 685
Lys Ser Pro Ala Leu Asn Val Ser Tyr Leu Ile Gln Asn Tyr Phe Arg
690 695 700
Thr Tyr Phe Glu Asp Gln Ser Gln Glu Phe Tyr Ala Gln Pro Arg Asn
705 710 715 720

Tyr Arg Leu Phe Asp Lys Leu Ser Pro Asn Lys Gly Lys Ser Lys Ser
725 730 735
Tyr Leu Ser Leu Glu Gln Arg Ile Lys Lys Met Glu Glu Leu Arg Pro
740 745 750
Ser Lys Ile Pro Val Ala Glu Ala Asn Lys Leu Leu Glu Lys Glu Asp
755 760 765
Arg Leu Tyr Arg Lys Asn Tyr Asn Glu Ile Cys Asp Asn Glu Ser Ile
770 775 780

Ile Arg Leu Tyr Gln Ile Gln Asp Ile Leu Leu Phe Met Met Thr Lys

785 790 795 800

Glu Tyr Leu Pro Ser Asp Leu Tyr Asn Arg Ile Asn Lys Tyr Lys Leu

805 810 815

Glu Asn Val Lys Gly Ile Leu Asn Glu Arg Val Ser Tyr Leu Ile Asp

820 825 830

Leu Asn Pro Leu Lys Ile Gln Gly Glu Asp Ile Lys Ile Lys Asp Tyr

835 840 845

Gly Lys Leu Phe Tyr Ile His His Asp Thr Arg Ile Ser Ser Leu Asn

850 855 860

Lys Val Leu Ser Lys Val Lys Arg Asn Asn Ser Ile Ser Ser Ser Val

865 870 875 880

Lys Ile Gln Pro Tyr Glu Asn Tyr Lys Arg Glu Cys Leu Asp Phe Glu

885 890 895

Glu Ala Gln Ile Gln Ile Ile Pro Ile Ile His Ser Phe Glu Ile Ala

900 905 910

Met Val Ser Met Phe Pro Asp Leu Lys Lys Ala Thr Pro Gly Asn Tyr

915 920 925

Tyr Asp Phe Asn Glu Leu Ile Thr Glu Tyr Glu Lys Arg Thr Lys Gln

930 935 940

Lys Ile Asp Ser Ser Phe Leu Ile Lys Thr Arg Asn Met Phe Leu His

945 950 955 960

Asp Lys Tyr Glu Ala Glu Cys Ile Lys Glu Ile Ser Asp Asp Phe Val

965 970 975

Tyr Ala Lys Lys Ile Ile Ala Glu Phe Lys Met Lys Ile Glu Asn Ile

980 985 990

Lys Leu Glu Asp Leu Ser Asn Asp Ser Ser Ala

995 1000

<210> 270

<211> 1095

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 270

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45
Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys

85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125
Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175
Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His
180 185 190
Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg
195 200 205
Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220
Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro

385 390 395 400

Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415

Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp

420 425 430

Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser

435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn

450 455 460

Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510
Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560
Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575
Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605
Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620
Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640
Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655
Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670
Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685
Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700
Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Asp Trp Glu
705 710 715 720
Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu

770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr

885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly

900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys

930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp

945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu

965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu

980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn

995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala

1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala

1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr

1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val

1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 271

<211> 1106

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 271

Met Glu Lys Pro Leu Pro Pro Asn Val Tyr Thr Leu Lys His Lys Phe

1 5 10 15

Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr

20 25 30

Ile Cys His Ile Asn Glu Gln Leu Gly Leu Thr Thr Pro Pro Asn Asp

35 40 45

Asp Lys Ile Ala Asp Val Val Cys Gly Thr Trp Asn Asn Ile Leu Asn

50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Ala Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly Ser Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Asn Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Glu Leu Ile
115 120 125

Lys Ala Leu Lys Thr Leu Val Lys Gln Leu Arg Thr Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175
Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Gln Asp Phe Ala His
180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Lys Phe Asp Arg
195 200 205
Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe
210 215 220
Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys
225 230 235 240
Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Ser Glu Lys Met Thr
245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu
260 265 270
Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu
275 280 285
Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Lys Asp
290 295 300
Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Ala Leu Ile Arg His Gln Asp Arg
325 330 335
Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys
340 345 350
Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr
355 360 365
Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr
370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400
Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415
Lys Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430
Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445

Leu Glu Val Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460
Ser Asp Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro
465 470 475 480
Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys
530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala
595 600 605

Tyr Asp Val Gln Asn Gln Pro Ile Glu Ser Ser Lys Ala Asn Ser Thr
610 615 620

Glu Phe Gln Leu Ile Gln Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys
625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr
645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn
660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu
675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu
690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu
705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg
725 730 735

Glu Thr Leu Ser Glu Asp Leu Thr Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765

Tyr Phe Arg Glu Arg Tyr Gln Asp Asp His Gln Ser Phe Tyr Asn Leu
770 775 780

Pro Tyr Glu Leu Glu Ala Lys Ala Ser Thr Pro Lys Pro Pro Leu Pro
785 790 795 800

Lys Lys Arg Glu Tyr Val Leu Arg Ala Glu His Tyr Glu Tyr Trp Gln

805 810 815

Gln Asn Lys Pro Gln Ser Pro Thr Glu Leu Gln Arg Leu Glu Leu His

820 825 830

Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr Lys Arg Trp Gln His

835 840 845

Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln Asp Val Met Leu Trp

850 855 860

Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe Lys Glu Leu Lys Leu

865 870 875 880

Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala Val Asn Val Gln Glu

885 890 895

Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr Leu Pro Met Val Leu

900 905 910

Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly Glu Val Gln Tyr Gln

915 920 925

Glu Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu Glu Gln Thr Lys Ala

930 935 940

Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys Asp Arg Arg Leu Asn

945 950 955 960

Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp Thr Gln Lys His Pro

965 970 975

Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu Ile Tyr Gln Ser Leu

980 985 990

Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu Glu Glu Lys Leu Leu

995 1000 1005

Asn Lys His Ala Ser Leu Ser Ser Leu Glu Asn Glu Phe Arg Thr

1010 1015 1020

Leu Leu Glu Glu Trp Lys Lys Lys Tyr Ala Ala Ser Ser Met Val

1025 1030 1035

Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val Arg Asn Ala Phe

1040 1045 1050

Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Thr Leu His Ala Pro
1055 1060 1065
Ile Leu Leu Phe Thr Val Ala Gln Pro Thr Thr Glu Glu Lys Asp
1070 1075 1080

Gly Leu Gly Ile Ala Glu Ala Leu Leu Arg Val Leu Arg Glu Tyr
1085 1090 1095
Cys Glu Ile Val Lys Ser Gln Ile
1100 1105

<210> 272
<211> 1095
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas13 sequence
<400> 272

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45
Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60
Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125
Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr

130 135 140

Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe

145 150 155 160

Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu

165 170 175

Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His

180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg

195 200 205

Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe

210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys

225 230 235 240

Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr

245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu

260 265 270

Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu

275 280 285

Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn

290 295 300

Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu

305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg

325 330 335

Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys

340 345 350

Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr

355 360 365

Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr

370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400
Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser

405 410 415
Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430
Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445
Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460
Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480
Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys
485 490 495
Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu
500 505 510
Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu
515 520 525
Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540
Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile
545 550 555 560
Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser
565 570 575
Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val
580 585 590
Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605
Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr
610 615 620
Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg

725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu

740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu

755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu

770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His

785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln

805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr

820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln

835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe

850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala

865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895
Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910
Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu

915 920 925
Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940
Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960
Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu
965 970 975
Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu

980 985 990
Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn
995 1000 1005
Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala
1010 1015 1020
Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val
1025 1030 1035
Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala

1040 1045 1050
Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr
1055 1060 1065
Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val
1070 1075 1080
Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile
1085 1090 1095

<210> 273
<211> 1095
<212> PRT
<213> Unknown

<220><223> Description of Unknown:

Cas13 sequence

<400> 273

Met Glu Lys Pro Leu Leu Pro Asn Val Tyr Thr Leu Lys His Lys Phe
1 5 10 15
Phe Trp Gly Ala Phe Leu Asn Ile Ala Arg His Asn Ala Phe Ile Thr
20 25 30
Ile Cys His Ile Asn Glu Gln Leu Gly Leu Lys Thr Pro Ser Asn Asp
35 40 45
Asp Lys Ile Val Asp Val Val Cys Glu Thr Trp Asn Asn Ile Leu Asn
50 55 60

Asn Asp His Asp Leu Leu Lys Lys Ser Gln Leu Thr Glu Leu Ile Leu
65 70 75 80
Lys His Phe Pro Phe Leu Thr Ala Met Cys Tyr His Pro Pro Lys Lys
85 90 95
Glu Gly Lys Lys Lys Gly His Gln Lys Glu Gln Gln Lys Glu Lys Glu
100 105 110
Ser Glu Ala Gln Ser Gln Ala Glu Ala Leu Asn Pro Ser Lys Leu Ile
115 120 125

Glu Ala Leu Glu Ile Leu Val Asn Gln Leu His Ser Leu Arg Asn Tyr
130 135 140
Tyr Ser His Tyr Lys His Lys Lys Pro Asp Ala Glu Lys Asp Ile Phe
145 150 155 160
Lys His Leu Tyr Lys Ala Phe Asp Ala Ser Leu Arg Met Val Lys Glu
165 170 175
Asp Tyr Lys Ala His Phe Thr Val Asn Leu Thr Arg Asp Phe Ala His
180 185 190

Leu Asn Arg Lys Gly Lys Asn Lys Gln Asp Asn Pro Asp Phe Asn Arg
195 200 205
Tyr Arg Phe Glu Lys Asp Gly Phe Phe Thr Glu Ser Gly Leu Leu Phe
210 215 220

Phe Thr Asn Leu Phe Leu Asp Lys Arg Asp Ala Tyr Trp Met Leu Lys
225 230 235 240
Lys Val Ser Gly Phe Lys Ala Ser His Lys Gln Arg Glu Lys Met Thr
245 250 255

Thr Glu Val Phe Cys Arg Ser Arg Ile Leu Leu Pro Lys Leu Arg Leu
260 265 270
Glu Ser Arg Tyr Asp His Asn Gln Met Leu Leu Asp Met Leu Ser Glu
275 280 285
Leu Ser Arg Cys Pro Lys Leu Leu Tyr Glu Lys Leu Ser Glu Glu Asn
290 295 300
Lys Lys His Phe Gln Val Glu Ala Asp Gly Phe Leu Asp Glu Ile Glu
305 310 315 320

Glu Glu Gln Asn Pro Phe Lys Asp Thr Leu Ile Arg His Gln Asp Arg
325 330 335
Phe Pro Tyr Phe Ala Leu Arg Tyr Leu Asp Leu Asn Glu Ser Phe Lys
340 345 350
Ser Ile Arg Phe Gln Val Asp Leu Gly Thr Tyr His Tyr Cys Ile Tyr
355 360 365
Asp Lys Lys Ile Gly Asp Glu Gln Glu Lys Arg His Leu Thr Arg Thr
370 375 380

Leu Leu Ser Phe Gly Arg Leu Gln Asp Phe Thr Glu Ile Asn Arg Pro
385 390 395 400
Gln Glu Trp Lys Ala Leu Thr Lys Asp Leu Asp Tyr Lys Glu Thr Ser
405 410 415
Asn Gln Pro Phe Ile Ser Lys Thr Thr Pro His Tyr His Ile Thr Asp
420 425 430
Asn Lys Ile Gly Phe Arg Leu Gly Thr Ser Lys Glu Leu Tyr Pro Ser
435 440 445

Leu Glu Ile Lys Asp Gly Ala Asn Arg Ile Ala Lys Tyr Pro Tyr Asn
450 455 460
Ser Gly Phe Val Ala His Ala Phe Ile Ser Val His Glu Leu Leu Pro

465 470 475 480

Leu Met Phe Tyr Gln His Leu Thr Gly Lys Ser Glu Asp Leu Leu Lys

485 490 495

Glu Thr Val Arg His Ile Gln Arg Ile Tyr Lys Asp Phe Glu Glu Glu

500 505 510

Arg Ile Asn Thr Ile Glu Asp Leu Glu Lys Ala Asn Gln Gly Arg Leu

515 520 525

Pro Leu Gly Ala Phe Pro Lys Gln Met Leu Gly Leu Leu Gln Asn Lys

530 535 540

Gln Pro Asp Leu Ser Glu Lys Ala Lys Ile Lys Ile Glu Lys Leu Ile

545 550 555 560

Ala Glu Thr Lys Leu Leu Ser His Arg Leu Asn Thr Lys Leu Lys Ser

565 570 575

Ser Pro Lys Leu Gly Lys Arg Arg Glu Lys Leu Ile Lys Thr Gly Val

580 585 590

Leu Ala Asp Trp Leu Val Lys Asp Phe Met Arg Phe Gln Pro Val Ala

595 600 605

Tyr Asp Ala Gln Asn Gln Pro Ile Lys Ser Ser Lys Ala Asn Ser Thr

610 615 620

Glu Phe Trp Phe Ile Arg Arg Ala Leu Ala Leu Tyr Gly Gly Glu Lys

625 630 635 640

Asn Arg Leu Glu Gly Tyr Phe Lys Gln Thr Asn Leu Ile Gly Asn Thr

645 650 655

Asn Pro His Pro Phe Leu Asn Lys Phe Asn Trp Lys Ala Cys Arg Asn

660 665 670

Leu Val Asp Phe Tyr Gln Gln Tyr Leu Glu Gln Arg Glu Lys Phe Leu

675 680 685

Glu Ala Ile Lys Asn Gln Pro Trp Glu Pro Tyr Gln Tyr Cys Leu Leu

690 695 700

Leu Lys Ile Pro Lys Glu Asn Arg Lys Asn Leu Val Lys Gly Trp Glu

705 710 715 720

Gln Gly Gly Ile Ser Leu Pro Arg Gly Leu Phe Thr Glu Ala Ile Arg
725 730 735

Glu Thr Leu Ser Glu Asp Leu Met Leu Ser Lys Pro Ile Arg Lys Glu
740 745 750

Ile Lys Lys His Gly Arg Val Gly Phe Ile Ser Arg Ala Ile Thr Leu
755 760 765

Tyr Phe Lys Glu Lys Tyr Gln Asp Lys His Gln Ser Phe Tyr Asn Leu
770 775 780

Ser Tyr Lys Leu Glu Ala Lys Ala Pro Leu Leu Lys Arg Glu Glu His
785 790 795 800

Tyr Glu Tyr Trp Gln Gln Asn Lys Pro Gln Ser Pro Thr Glu Ser Gln
805 810 815

Arg Leu Glu Leu His Thr Ser Asp Arg Trp Lys Asp Tyr Leu Leu Tyr
820 825 830

Lys Arg Trp Gln His Leu Glu Lys Lys Leu Arg Leu Tyr Arg Asn Gln
835 840 845

Asp Val Met Leu Trp Leu Met Thr Leu Glu Leu Thr Lys Asn His Phe
850 855 860

Lys Glu Leu Asn Leu Asn Tyr His Gln Leu Lys Leu Glu Asn Leu Ala
865 870 875 880

Val Asn Val Gln Glu Ala Asp Ala Lys Leu Asn Pro Leu Asn Gln Thr
885 890 895

Leu Pro Met Val Leu Pro Val Lys Val Tyr Pro Ala Thr Ala Phe Gly
900 905 910

Glu Val Gln Tyr His Lys Thr Pro Ile Arg Thr Val Tyr Ile Arg Glu
915 920 925

Glu His Thr Lys Ala Leu Lys Met Gly Asn Phe Lys Ala Leu Val Lys
930 935 940

Asp Arg Arg Leu Asn Gly Leu Phe Ser Phe Ile Lys Glu Glu Asn Asp
945 950 955 960

Thr Gln Lys His Pro Ile Ser Gln Leu Arg Leu Arg Arg Glu Leu Glu

965 970 975

Ile Tyr Gln Ser Leu Arg Val Asp Ala Phe Lys Glu Thr Leu Ser Leu

980 985 990

Glu Glu Lys Leu Leu Asn Lys His Thr Ser Leu Ser Ser Leu Glu Asn

995 1000 1005

Glu Phe Arg Ala Leu Leu Glu Glu Trp Lys Lys Glu Tyr Ala Ala

1010 1015 1020

Ser Ser Met Val Thr Asp Glu His Ile Ala Phe Ile Ala Ser Val

1025 1030 1035

Arg Asn Ala Phe Cys His Asn Gln Tyr Pro Phe Tyr Lys Glu Ala

1040 1045 1050

Leu His Ala Pro Ile Pro Leu Phe Thr Val Ala Gln Pro Thr Thr

1055 1060 1065

Glu Glu Lys Asp Gly Leu Gly Ile Ala Glu Ala Leu Leu Lys Val

1070 1075 1080

Leu Arg Glu Tyr Cys Glu Ile Val Lys Ser Gln Ile

1085 1090 1095

<210> 274

<211> 1335

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12a sequence

<400> 274

Met Lys Ser Leu Ala Gln Phe Gln Asn Leu Tyr Ala Leu Gln Lys Thr

1 5 10 15

Leu Arg Phe Glu Leu Lys Pro Glu Gly His Thr Arg Glu Thr Phe Asn

20 25 30

Arg Trp Leu Glu Glu Ile Glu Lys Glu Gln Ala Ser Glu Asn Glu Asn

35 40 45

Ile Val Tyr Gln Asp Leu Leu Arg Ala Lys Lys Tyr Glu Lys Ile Lys

50 55 60

Ile Ile Leu Asp Glu Tyr His Lys Asp Phe Ile Glu Gln Ala Leu Ala
65 70 75 80
Tyr Ala Asn Leu Thr Glu Leu Glu Lys Tyr Glu Glu Leu Tyr Arg Lys
85 90 95
Ser Asn Arg Thr Ser Glu Glu Glu Glu Glu Phe Glu Asn Thr Lys Glu

100 105 110
Ser Leu Arg Lys Gln Ile Ala Asn Ile Phe Ile Lys Asn Pro Asn Lys
115 120 125
Thr Val Gln Glu Arg Trp Lys Phe Leu Phe Ser Lys Lys Leu Ile Gln
130 135 140
Asn Glu Leu Ile Val Trp Val Lys Gly Asn Tyr Glu Leu Leu Ser Glu
145 150 155 160
Lys Leu Lys Asn Glu Phe Pro Asp Glu Ser Ser Ile Ile Ser Thr Ile

165 170 175
Glu Asp Phe Lys Tyr Phe Thr Thr Tyr Phe Arg Asn Tyr His Glu Asn
180 185 190
Arg Lys Asn Leu Tyr Ser Asn Glu Asp Lys Phe Ser Thr Ile Ala His
195 200 205
Arg Leu Ile His Glu Asn Leu Pro Lys Phe Ile Asp Asn Ile Ala Ile
210 215 220
Tyr Gln Lys Ala Lys Ala Val Leu Asn Ile Asn Glu Val Glu Lys Glu

225 230 235 240
Leu Gly Leu Pro Glu Asp Thr Leu Asp Lys Ile Phe Ser Leu Asp Phe
245 250 255
Phe Ser Lys Ala Leu Thr Gln Lys Gly Ile Asp Gln Tyr Asn Tyr Phe
260 265 270
Leu Gly Gly Lys Thr Glu Asn Glu Val Lys Lys Ile Lys Gly Leu Asn
275 280 285
Glu Phe Ile Asn Leu Tyr Asn Gln Gln Gln Gln Asp Lys Asn Gln Arg

290 295 300
Leu Pro Phe Leu Lys Val Leu Tyr Lys Leu Pro Leu Phe Glu Arg Thr

305 310 315 320

Ser Thr Ser Phe Arg Phe Glu Pro Ile Glu Asn Asp Arg Asp Leu Ile

325 330 335

Glu Arg Ile Gly Lys Phe Tyr Tyr Asn Asp Leu Lys Gln Tyr Arg Asp

340 345 350

Asp Ser Gln Gly Asp Thr Thr Asp Ile Leu Ser Gly Ile Asn Thr Leu

355 360 365

Leu Arg His Val His Asp Tyr Arg Asp Gly Leu Tyr Val Asn Gly Gly

370 375 380

Ile Thr Leu Thr Gln Ile Ser Gln Lys Ile Phe Gly Ser Trp Ser Tyr

385 390 395 400

Ile Asn Asn Ala Leu Ala Tyr Phe Tyr Asp Thr Tyr Ile Asp Ala Ser

405 410 415

Gly Val Asp His Gln Gly Glu Arg Lys Pro Lys Lys Gln Lys Gln Ile

420 425 430

Gln Glu Lys Thr Lys Trp Leu Lys Gln Lys Gln Phe Pro Val Ile Leu

435 440 445

Val Glu Lys Ala Leu Ser Glu Tyr Lys Ser Ile Glu Thr Asn Glu Asp

450 455 460

Leu Lys Thr Arg Ile Ser Asp Thr Thr Leu Cys Asp Phe Phe Lys Arg

465 470 475 480

Cys Gly Asn Asp Asp Asn Gly Gln Asp Leu Phe Asp Arg Ile Glu Ala

485 490 495

Arg Leu Arg Glu Lys Asn Glu Glu Gly Tyr Ser Leu Glu Asp Leu Leu

500 505 510

Lys Lys Glu Phe Thr Thr Glu Arg Lys Leu Met Gln Asp Lys Thr Lys

515 520 525

Thr Leu Leu Ile Lys Asn Phe Leu Asp Val Ile Gln Gly Asp Lys Asp

530 535 540

Asp Ile Thr Ala Gly Leu Leu His Phe Val Lys Cys Leu Ile Pro Arg

545 550 555 560

Thr Glu Ile Ser Glu Lys Asn Glu Leu Phe Tyr Ser Gly Met Glu Lys
565 570 575
Tyr Leu Asn Ile Leu Ser Glu Val Thr Pro Leu Tyr Asn Lys Ala Arg
580 585 590
Asn Tyr Leu Thr Gln Lys Pro Tyr Ser Ile Glu Lys Val Lys Leu Asn
595 600 605
Phe Glu Asn Ser Thr Leu Leu Asp Gly Trp Asp Glu Asn Glu Glu Ser

610 615 620
Asp Asn Ser Cys Val Leu Leu Arg Lys Arg Gly Tyr Tyr Tyr Leu Gly
625 630 635 640
Ile Met Asn Lys Lys His Asn Met Ile Phe Asp Arg Lys Ile Tyr Pro
645 650 655
Lys Ala Thr Glu Gly Glu Ala Tyr Tyr Glu Lys Met Ile Tyr Lys Leu
660 665 670
Leu Pro Gly Ala Tyr Lys Met Leu Pro Lys Val Phe Phe Ser Glu Lys

675 680 685
Asn Ile Asp Tyr Phe Lys Pro Ser Glu Glu Ile Leu Arg Ile Arg Asn
690 695 700
Thr Ala Ser Tyr Ser Lys Asn Gly Gln Pro Gln Glu Gly Tyr Gln Lys
705 710 715 720
Ala Ser Phe Ser Ile Glu Asp Cys Arg Lys Tyr Ile Asp Phe Phe Lys
725 730 735
Lys Cys Ile Ala Asn His Trp Asp Trp Gln Lys Phe Asn Phe Asn Phe

740 745 750
Ser Pro Thr Glu Tyr Tyr Gln Ser Ile Asp Glu Phe Tyr Arg Glu Ile
755 760 765
Glu Arg Gln Gly Tyr Lys Ile Asp Phe Val Lys Ile Pro Glu Ser Tyr
770 775 780
Ile Asn Gln Leu Ile Lys Glu Asn Lys Leu Tyr Leu Phe Lys Ile Tyr
785 790 795 800
Asn Lys Asp Phe Ser Glu Lys Lys Lys Ser Lys Gly Lys Asp Asn Leu

805 810 815

His Thr Leu Tyr Trp Lys Met Leu Phe Asp Glu Lys Asn Leu Lys Asp

820 825 830

Val Val Leu Lys Leu Asn Gly Glu Ala Glu Val Phe Phe Arg Gln Lys

835 840 845

Ser Ile Leu Tyr Asn Glu Glu Ile Trp Asn Lys Gly His His Tyr Ser

850 855 860

Glu Leu Lys Asp Arg Phe Ser Tyr Pro Ile Ile Ser Asn Lys Arg Tyr

865 870 875 880

Ala Glu Asp Lys Phe Phe Leu His Val Pro Ile Thr Leu Asn Phe Lys

885 890 895

Ala Asp Gly Ile Asn Asn Val Asn Asn Met Val Asn Glu Phe Ile Lys

900 905 910

Asp Asn Arg Asp Ile His Ile Ile Gly Ile Asp Arg Gly Glu Arg His

915 920 925

Leu Leu Tyr Val Ser Val Ile Asn Gln Lys Gly Asp Ile Val Glu Gln

930 935 940

Cys Ser Leu Asn Glu Ile Val Thr Glu Tyr Asn Gly Lys Ile Phe Lys

945 950 955 960

Lys Asn Tyr His Glu Glu Leu Asp Asn Leu Glu Lys Glu Arg Asp Arg

965 970 975

Ala Arg Lys Asp Trp Gln Thr Ile Ala Asn Ile Lys Glu Leu Lys Glu

980 985 990

Gly Tyr Leu Ser His Val Ile His Lys Ile Ser Lys Leu Ile Leu Lys

995 1000 1005

Tyr Asn Ala Ile Val Val Met Glu Asp Leu Asn Ser Gly Phe Lys

1010 1015 1020

Arg Gly Arg Gln Lys Val Glu Lys Gln Val Tyr Gln Asn Phe Glu

1025 1030 1035

Lys Gln Leu Ile Glu Lys Leu Asn Tyr Leu Val Leu Lys Glu Ser

1040 1045 1050

Asn Val Asp Glu Pro Gly Gly Val Leu Arg Ala Tyr Gln Leu Ala

1055 1060 1065

Asn Lys Phe Glu Thr Phe Lys Lys Leu Gly Lys Gln Ser Gly Ile

1070 1075 1080

Ile Phe Tyr Val Pro Ala Ala Tyr Thr Ser Ala Ile Asp Pro Val

1085 1090 1095

Thr Gly Tyr Ile Gln Tyr Leu Tyr Pro Leu Lys Gln Ala Asp Ser

1100 1105 1110

Val Glu Lys Ala Arg Lys Phe Tyr Ser Gln Phe Lys Arg Ile Ser

1115 1120 1125

Tyr Asn Pro His Lys Gln Trp Phe Glu Phe Ser Phe Asp Tyr Asn

1130 1135 1140

Asp Phe Asn Ile Ile Tyr His Gly Lys Ser Ser Trp Thr Ile Cys

1145 1150 1155

Thr Thr Asn Thr Glu Arg Tyr Met Trp Asn Arg Leu Leu Asn Asn

1160 1165 1170

Gly His Gly Gly Glu Glu Leu Val Tyr Val Thr Asn Glu Leu Glu

1175 1180 1185

Leu Leu Phe Gly Glu Tyr Asn Ile Ile Tyr Gly Asp Gly Lys Asp

1190 1195 1200

Ile Lys Gln Gln Ile Thr Asp Val Gln Asp Ile Asp Val Asp Arg

1205 1210 1215

Thr Ala Lys Gln Phe Tyr Lys Arg Ile Asn Glu Leu Leu Asn Leu

1220 1225 1230

Thr Leu Lys Leu Arg His Asn Asn Gly Lys Lys Gly Ala Asp Glu

1235 1240 1245

Glu Asp Tyr Ile Leu Ser Pro Val Glu Pro Tyr Phe Asp Ser Arg

1250 1255 1260

Phe Glu Ser Arg Lys Pro Ser Met Gln Gln Thr Leu Pro Ile Asn

1265 1270 1275

Ala Asp Ala Asn Gly Ala Phe Asn Ile Ala Arg Lys Gly Leu Leu

1280 1285 1290

Leu Leu Glu Arg Leu Asn Gln Leu Gly Val Glu Glu Phe Glu Lys

1295 1300 1305

Thr Lys Lys Ser Asn Asn Lys Lys Thr Gln Trp Leu Pro His Glu

1310 1315 1320

Leu Trp Val Glu Tyr Ala Gln Asn His Thr Arg Lys

1325 1330 1335

<210> 275

<211> 1273

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12a sequence

<400> 275

Met Gln Asp Lys Thr Gly Trp Ser Ser Phe Thr Asn Lys Tyr Ser Leu

1 5 10 15

Ser Lys Thr Leu Arg Phe Glu Leu Lys Pro Val Gly Asn Thr Gln Lys

20 25 30

Met Leu Glu Asp Asp Gly Val Phe Gln Lys Asp Arg Glu Arg Gln Glu

35 40 45

Asn Tyr Lys Lys Val Lys Pro Phe Met Asp Lys Leu His Arg Glu Phe

50 55 60

Ile Lys Glu Ala Leu Asn Asn Leu Lys Leu Glu Gly Leu Thr Glu Tyr

65 70 75 80

Phe Glu Ile Phe Lys Lys Phe Arg Lys Asp Lys Asn Asn Lys Glu Leu

85 90 95

Lys Asn Ala Glu Lys Lys Leu Arg Gln Ile Ile Gly Arg Cys Tyr Thr

100 105 110

Glu Thr Ala Gln Ile Trp Val Glu Lys Tyr Lys Glu Phe Gly Phe Lys

115 120 125

Lys Lys Asn Ile Gly Phe Leu Phe Glu Glu Gly Val Phe Glu Leu Met

130 135 140

Lys Leu Lys Tyr Gly Asn Asp Glu Ala Ser Gln Ile Glu Lys Asn Gly
145 150 155 160
Glu Val Leu Ser Ile Phe Asp Gly Trp Lys Gly Phe Leu Gly Tyr Phe
165 170 175
Lys Lys Phe Phe Glu Thr Arg Asn Asn Phe Tyr Lys Asp Asp Gly Thr
180 185 190
Ser Thr Ala Val Ser Thr Arg Ile Ile Asn Glu Asn Leu Lys Ile Tyr
195 200 205

Leu Asp Asn Leu Ile Lys Tyr Asn Lys Ile Lys Asp Lys Val Asp Phe
210 215 220
Lys Glu Ala Asp Ile Leu Gln Glu Asn Lys Leu Asn Leu Ser Asp Phe
225 230 235 240
Phe Asn Val Glu Ser Tyr Ala Lys Tyr Ser Leu Gln Lys Gly Ile Asp
245 250 255
Tyr Tyr Asn Glu Ile Leu Gly Gly Lys Thr Leu Lys Asn Gly Thr Lys
260 265 270

Leu Lys Gly Leu Asn Glu Val Ile Asn Glu Tyr Lys Gln Lys Asn Lys
275 280 285
Ser Gly Glu Leu Ser Lys Phe Lys Met Leu Lys Lys Gln Ile Leu Gly
290 295 300
Glu Gly Glu Asp Arg Thr Leu Phe Glu Glu Ile Glu Asn Glu Asp Glu
305 310 315 320
Leu Lys Asp Val Leu Lys Asp Phe Phe Tyr Asn Ala Asp Pro Lys Ile
325 330 335

Thr Leu Phe Lys Thr Leu Leu Glu Asp Phe Phe Ser Asn Thr Glu Lys
340 345 350
Tyr Lys Asp Glu Leu Asp Lys Ile Tyr Phe Asn Thr Val Ala Ile Asn
355 360 365
Gly Ile Leu His Arg Trp Val Asp Asp Ser Gly Val Phe Gln Lys Tyr
370 375 380

Leu Phe Glu Val Leu Lys Ser Asn Lys Leu Val Lys Ser Asn His Tyr
385 390 395 400

Asp Lys Lys Glu Asp Ser Tyr Lys Phe Pro Asp Phe Ile Ser Phe Glu
405 410 415
His Ile Lys Val Ala Leu Glu Asn Cys Glu Arg Asp Gly Leu Lys Asp
420 425 430
Lys Phe Trp Lys Glu Lys Tyr Tyr Thr Lys Glu Cys Leu Thr Glu Asn
435 440 445
Gly Leu Ala Asn Leu Trp Gln Glu Phe Leu Glu Ile Tyr Lys Cys Glu
450 455 460

Phe Lys Lys Leu Tyr Asp Tyr Lys Thr Asp Asp Asn Asp Cys Tyr Leu
465 470 475 480
Gln Tyr Arg Asp Asn Tyr Lys Lys Tyr Ile Leu Asp Ala Asn Phe Asn
485 490 495
Pro Lys Glu Lys Ser Ala Lys Asp Ile Ile Lys Asp Tyr Leu Asp Ser
500 505 510
Val Leu Ser Ile Tyr Gln Leu Ala Lys Tyr Phe Ala Leu Glu Lys Lys
515 520 525

Lys Val Trp Thr Thr Asp Tyr Glu Thr Gly Asp Phe Tyr Tyr Glu Tyr
530 535 540
Ile Lys Phe Tyr Glu Asp Thr Tyr Glu Gln Ile Ile Lys Pro Tyr Asn
545 550 555 560
Leu Val Arg Asn Tyr Leu Thr Arg Lys Pro Ile Asn Thr Ala Lys Lys
565 570 575
Trp Lys Leu Asn Phe Asp Asn Ala Tyr Leu Ala Ser Gly Trp Asp Lys
580 585 590

Asp Lys Glu Val Ser Asn Leu Thr Val Ile Leu Arg Arg Asp Glu Gln
595 600 605
Tyr Tyr Leu Ala Ile Met Lys Lys Gly Lys Asn Lys Ile Phe Glu Lys
610 615 620
Lys Phe Ser Cys Gly Glu Phe Glu Lys Met Glu Tyr Lys Gln Ile Ala

625 630 635 640

Glu Ala Ser Ser Asp Ile His Asn Leu Val Leu Met Asn Asp Gly Ser

645 650 655

Cys Arg Arg Cys Ile Lys Met His Asp Lys Arg Lys Tyr Trp Pro Leu

660 665 670

Asp Ile Ser Ile Ile Lys Glu Lys Lys Ser Tyr Ala Lys Glu Asn Phe

675 680 685

Val Arg Arg Asp Phe Glu Arg Phe Val Asn Tyr Met Lys Lys Cys Ser

690 695 700

Leu Leu Tyr Trp Lys Glu Tyr Asp Leu Lys Phe Ser Asp Thr Ser Thr

705 710 715 720

Tyr Lys Asn Ile Asn Asp Phe Thr Asn Glu Ile Ala Ser Gln Gly Tyr

725 730 735

Lys Leu Ser Phe Ser Ala Ile Pro Glu Ser Tyr Ile Asn Glu Lys Asn

740 745 750

Asn Asn Gly Glu Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Gly

755 760 765

Ile Lys Thr Glu Gly Asn Lys Asn Leu His Thr Met Tyr Trp Glu Ser

770 775 780

Ile Phe Ser Glu Glu Asn Arg Phe Arg Asn Phe Ile Val Lys Leu Asn

785 790 795 800

Gly Lys Ala Glu Ile Phe Tyr Arg Pro Lys Ser Glu Gln Val Glu Lys

805 810 815

Glu Gln Arg Asn Phe Thr Arg Glu Ile Ile Lys Asn Arg Arg Tyr Thr

820 825 830

Glu Asn Lys Ile Tyr Phe His Cys Pro Ile Thr Leu Asn Arg Ile Ser

835 840 845

Arg Glu Asn Val Lys Lys Phe Asn Asn Gly Ile Asn Asn Tyr Ile Ala

850 855 860

Thr Asn Pro Asn Ile Asn Ile Leu Gly Val Asp Arg Gly Glu Lys His

865 870 875 880

Leu Val Tyr Tyr Ala Ile Val Asp Gln Asp Gly Lys Leu Ile Asp Ala
885 890 895
Glu Asp Ala Thr Gly Ser Phe Asn Thr Ile Gly Ser Thr Asp Tyr His
900 905 910

Arg Leu Leu Glu Glu Lys Ala Lys Asp Arg Glu Lys Glu Arg Lys Asp
915 920 925
Trp Asp Leu Ile Arg Gly Ile Lys Asp Leu Lys Lys Gly Tyr Ile Ser
930 935 940
Leu Val Val Arg Lys Ile Ala Asp Leu Ala Ile Lys Tyr Asn Ala Ile
945 950 955 960
Ile Ile Phe Glu Asp Leu Asn Thr Arg Phe Lys Gln Ile Arg Gly Gly
965 970 975

Met Glu Lys Ser Val Tyr Gln Gln Leu Glu Lys Ala Leu Ile Asn Lys
980 985 990
Leu Ser Phe Leu Val Asn Lys Gly Glu Lys Asp Pro Glu Gln Ala Gly
995 1000 1005
His Leu Leu Lys Ala Tyr Gln Leu Ala Ala Pro Phe Gln Thr Phe
1010 1015 1020
Asp Lys Met Gly Arg Gln Thr Gly Ile Ile Phe Tyr Thr Gln Ala
1025 1030 1035

Ser Tyr Thr Ser Lys Ile Asp Pro Ile Thr Gly Trp Arg Pro Asn
1040 1045 1050
Leu Tyr Leu Lys Tyr Arg Asn Ile Asp Asp Ser Lys Glu Ser Ile
1055 1060 1065
Lys Lys Phe Lys Ser Ile Leu Phe Asn Lys Glu Lys Asn Arg Phe
1070 1075 1080
Glu Phe Thr Tyr Asp Leu Lys Asp Phe Val Asp Phe Glu Glu Asp
1085 1090 1095

Lys Ile Pro Glu Lys Thr Glu Trp Thr Leu Cys Ser Ser Val Glu
1100 1105 1110
Arg His Lys Trp Asn Arg His Met Asn Asn Asn Lys Gly Gly Tyr

1115 1120 1125

Glu Val Tyr Lys Asp Leu Thr Glu Asn Phe Tyr Lys Leu Phe Asp

1130 1135 1140

Glu Asn Asn Ile Ser Met Asn Lys Asp Ile Val Asp Gln Val Glu

1145 1150 1155

Ser Ile Ser Asn Gly Asn Phe Phe Arg Gln Phe Ile Tyr Leu Phe

1160 1165 1170

Asn Leu Val Cys Gln Ile Arg Asn Thr Asp Glu Lys Ala Glu Asp

1175 1180 1185

Val Asp Lys Arg Asp Phe Ile Leu Ser Pro Val Glu Pro Phe Phe

1190 1195 1200

Asp Ser Arg Arg Ala Lys Asp Phe Lys Ala Tyr Gly Asp Asn Leu

1205 1210 1215

Pro Lys Asn Gly Asp Glu Asn Gly Ala Tyr Asn Ile Ala Arg Lys

1220 1225 1230

Gly Val Leu Ile Ile Lys Lys Ile Lys Glu Tyr Tyr Asn Gln Asn

1235 1240 1245

Gly Ser Cys Asp Lys Leu Gly Trp Gly Asp Leu Ser Ile Ser His

1250 1255 1260

Lys Glu Trp Asp Asp Phe Ala Thr Asn Asn

1265 1270

<210> 276

<211> 1301

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12a sequence

<400> 276

Met Asp Ser Tyr Glu Gln Phe Thr Lys Leu Tyr Pro Ile Gln Lys Thr

1 5 10 15

Ile Arg Phe Glu Leu Lys Pro Gln Gly Arg Thr Lys Glu His Phe Asp

20 25 30

Asn Ser Asn Phe Leu Glu Lys Asp Arg Glu Arg Asp Asp Asn Tyr Lys

35 40 45

Ile Leu Lys Glu Val Ile Asp Asp Tyr His Arg Glu Phe Ile Asp Glu

50 55 60

Cys Leu Ser Asn Ile Gln Leu Asn Trp Asp Asp Leu Lys Lys Phe Ser

65 70 75 80

Glu Glu Tyr Arg Arg Ser Lys Glu Lys Lys Asn Asn Arg Asp Ser Glu

85 90 95

Ser Glu Gln Lys Arg Met Ser Thr Thr Ser Glu Thr Arg Ala Ile Asn

100 105 110

Lys Lys Asn Leu Glu Ala Glu Gln Lys Arg Met Arg Gly Glu Ile Val

115 120 125

Ser Ala Phe Lys Lys Asp Asp Arg Phe Lys His Leu Phe Ser Glu Lys

130 135 140

Leu Phe Ser Ile Leu Leu Lys Asn Gln Ile Tyr Glu Lys Gly Thr Leu

145 150 155 160

Glu Glu Ile Glu Ala Phe Asp Cys Phe Asn Lys Phe Ser Gly Tyr Phe

165 170 175

Lys Ser Phe His Glu Asn Arg Lys Asn Met Tyr Ser Asp Glu Asp Lys

180 185 190

Glu Thr Ala Ile Ser Tyr Arg Ile Ile Asn Glu Asn Phe Pro Lys Leu

195 200 205

Leu Asp Asn Phe Glu Lys Tyr Gln Tyr Val Cys Arg Glu Tyr Pro Glu

210 215 220

Gln Ile Arg Glu Ala Glu Ser Thr Leu Ala Glu Ala Gly Cys Tyr Ile

225 230 235 240

Lys Met Asp Glu Ile Phe Ser Ile Asp Asn Phe Asn Asn Val Met Met

245 250 255

Gln Gly Gly Lys Glu Ser Gly Ile Ser Arg Tyr Asn Leu Ala Ile Gly

260 265 270

Gly Ile Val Gln Gly Thr Gly Glu Lys Pro Lys Gly Leu Asn Glu Phe

275 280 285

Leu Asn Leu Ala Tyr Gln Asn Glu Pro Asn Gly Arg Lys Lys Ile Arg

290 295 300

Met Glu Pro Leu Tyr Lys Gln Ile Leu Ser Lys Glu Glu Ser Phe Ser

305 310 315 320

Tyr Arg Leu Glu Ala Phe Thr Asp Asp Ser Gln Leu Leu Ser Ala Ile

325 330 335

Arg Ser Phe Phe Asp Ile Val Glu Lys Asp Lys Asn Gly Asn Ile Phe

340 345 350

Asp Arg Ala Val Asn Leu Met Ser Ser Phe Ser Asn Tyr Asp Thr Ser

355 360 365

Lys Ile Tyr Ile Arg Lys Ala Tyr Leu Asn Gln Val Ser Lys Glu Ile

370 375 380

Phe Gly Tyr Arg Gly Lys Ser Asp Ser Lys Pro Ala Lys Thr Ala Asp

385 390 395 400

Glu Ser Leu Asn Lys Ser Gly Gly Trp Glu Lys Leu Gly Gln Met Leu

405 410 415

Arg Asp Tyr Lys Ala Asp Ser Ile Gly Asp Arg Asn Leu Glu Lys Thr

420 425 430

Cys Lys Lys Val Asp Lys Trp Leu Asp Ser Asp Glu Phe Thr Leu Ser

435 440 445

Asp Ile Leu Gly Ala Ile Ser Leu Ala Gly Ser Asn Glu Thr Phe Glu

450 455 460

Ala Tyr Val Ser Glu Ile Cys Val Ala Arg Arg Asn Ile Asp Lys Glu

465 470 475 480

Lys Glu Lys Glu Lys Asn Ile Asn Val Glu Lys Ile Ser Gly Asp Thr

485 490 495

Glu Ser Ile Gln Ile Ile Lys Ala Leu Leu Asp Ser Val Gln Glu Phe

500 505 510

Phe His Leu Leu Ser Pro Phe Gln Leu His Pro Asn Thr Pro His Asp

515 520 525

Trp Thr Phe Tyr Ala Glu Phe Asn Asp Ile Tyr Asp Lys Leu Ser Ala
530 535 540
Ile Thr Pro Leu Tyr Asn Gln Ala Arg Asn His Leu Thr Lys Lys Asn
545 550 555 560
Leu Asp Thr Ser Lys Ile Lys Leu Asn Phe Asn Asn Pro Thr Leu Ala

565 570 575
Asn Gly Trp Asp Val Asn Lys Glu Tyr Glu Asn Thr Ala Val Ile Leu
580 585 590
Ile Arg Asp Gly Lys Tyr Tyr Leu Gly Ile Met Asn Pro Lys Asn Lys
595 600 605
Arg Lys Ile Lys Phe Asp Glu Gly Ser Gly Ala Gly Pro Phe Tyr Gln
610 615 620
Lys Met Val Tyr Lys Leu Leu Pro Gly Pro Tyr Arg Met Leu Pro Lys

625 630 635 640
Val Phe Phe Ala Lys Lys Asn Ile Asp Tyr Tyr Asn Pro Ser Gln Glu
645 650 655
Ile Arg Glu Gly Tyr Lys Ala Gly Lys His Lys Lys Gly Lys Glu Phe
660 665 670
Asp Lys Gly Phe Cys His Lys Leu Ile Asp Phe Phe Lys Glu Ser Ile
675 680 685
Gln Lys Asn Glu Asn Trp Lys Val Phe Asp Phe Lys Phe Ser Pro Thr

690 695 700
Glu Ser Tyr Asp Asp Ile Ser Glu Phe Tyr Gln Glu Val Glu Lys Gln
705 710 715 720
Gly Tyr Arg Met Tyr Phe Val Asn Ile Pro Ser Asp Thr Ile Asp Arg
725 730 735
Tyr Val Glu Gly Gly Asp Met Phe Leu Phe Gln Ile Tyr Asn Lys Asp
740 745 750
Phe Ala Lys Gly Ala Lys Gly Asn Lys Asp Met His Thr Leu Tyr Trp

755 760 765
Asn Ala Val Phe Ser Glu Glu Asn Leu Gln Lys Gly Val Met Lys Leu

770 775 780

Ser Gly Glu Ala Glu Leu Phe Tyr Arg Lys Lys Ser Asp Ile Lys Asp

785 790 795 800

Pro Pro His Arg Glu Gly Glu Ile Leu Val Asn Arg Thr Tyr Ile Asp

805 810 815

Arg Thr His Val Ser Gly Val Met Gly Glu Gln Asn Thr Val Lys Glu

820 825 830

Ser Arg Ile Pro Val Pro Asp Glu Ile His Lys Asn Leu Phe Asp Tyr

835 840 845

Tyr Asn His Gly Arg Glu Leu Thr Lys Glu Glu Lys Glu Tyr Cys Asp

850 855 860

Lys Val Gly Ser Phe Lys Ala Tyr Tyr Gly Ile Val Lys Asp Arg Arg

865 870 875 880

Tyr Leu Glu Asn Lys Met Tyr Phe His Val Pro Leu Thr Leu Asn Phe

885 890 895

Lys Ala Ile Gly Glu Lys Arg Ile Asn Lys Met Ala Ile Glu Lys Phe

900 905 910

Leu Thr Asp Glu Asn Ala Cys Ile Ile Gly Ile Asp Arg Gly Glu Arg

915 920 925

Asn Leu Leu Tyr Tyr Ser Ile Ile Asp Arg Asn Gly Lys Ile Ile Asp

930 935 940

Gln Lys Ser Leu Asn Val Ile Asp Gly Phe Asp Tyr His Glu Lys Leu

945 950 955 960

Ser Gln Arg Gln Thr Glu Arg Glu Val Ala Arg Gln Ser Trp Asn Ser

965 970 975

Ile Gly Lys Ile Lys Asp Leu Lys Glu Gly Tyr Leu Ala Lys Ala Val

980 985 990

His Glu Ile Ser Lys Met Ala Ile Lys Tyr Asn Ala Ile Val Val Leu

995 1000 1005

Glu Asp Leu His Phe Gly Phe Lys Lys Gly Arg Leu Lys Val Glu

1010 1015 1020

Lys Gln Ile Tyr Gln Lys Phe Glu Glu Met Leu Ile Asn Lys Leu
1025 1030 1035
Asn Tyr Leu Val Phe Lys Asp Val Ser Asp Ser Ser Asp Ala Gly
1040 1045 1050
Gly Val Leu Asn Ala Tyr Gln Leu Thr Ala Pro Leu Glu Ser Phe
1055 1060 1065
Ser Lys Leu Gly Lys Gln Ser Gly Ile Leu Phe Tyr Val Pro Ala

1070 1075 1080
Ala Phe Thr Ser Val Ile Asp Pro Thr Thr Gly Phe Val Asp Leu
1085 1090 1095
Phe Asn Ser Ser Ser Ile Thr Ser Thr Gln Lys Lys Lys Glu Phe
1100 1105 1110
Leu Gln Arg Phe Glu Ser Ile Val Tyr Ser Ala Arg Asp Gly Gly
1115 1120 1125
Ile Phe Ala Phe Thr Phe Asp Tyr Arg Asn Phe Ser Lys Ile Ala

1130 1135 1140
Thr Asp His Arg Asn Met Trp Thr Val Tyr Thr His Gly Glu Arg
1145 1150 1155
Ile Arg Tyr Val Arg Asp Glu Lys Cys Tyr Lys Thr Thr Asp Pro
1160 1165 1170
Thr Lys Arg Ile Lys Glu Ala Leu Ser Gly Ile Glu Tyr Asp Asp
1175 1180 1185
Gly Ser Asp Ile Arg Asp Lys Ile Thr Gln Ser Gly Asp Asn Asn

1190 1195 1200
Leu Ile Asn Thr Val Tyr His Ser Phe Met Asp Thr Ile Lys Met
1205 1210 1215
Arg Asn Lys Asp Gly Arg Ile Asp Tyr Ile Ile Ser Pro Val Lys
1220 1225 1230
Asn Arg Asn Gly Glu Phe Phe Arg Ser Asp Tyr Lys His Arg Asp
1235 1240 1245
Phe Pro Val Asp Ala Asp Ala Asn Gly Ala Tyr His Ile Ala Leu

1250 1255 1260

Lys Gly Glu Leu Leu Met Arg Met Ile Gly Lys Thr Tyr Asp Ser

1265 1270 1275

Asn Ser Asp Lys Met Pro Lys Leu Glu His Lys Asp Trp Phe Glu

1280 1285 1290

Phe Met Gln Thr Arg Gly Asp Gln

1295 1300

<210> 277

<211> 1188

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12b sequence

<400> 277

Met Cys Val Ser Arg Leu Pro Trp Phe Asn Ile Thr Leu Thr Gly Lys

1 5 10 15

Leu Asn Arg Gln Arg Leu Asn Gln Met Cys Val Ser Arg Leu Pro Trp

20 25 30

Phe Cys Thr Pro Lys Gly Gln Leu Ala Ala Thr Pro Lys Thr Val Val

35 40 45

Ala Gln Gln Glu Asn Ala Met Leu Ala Ile Ile Arg Asp Val His Glu

50 55 60

Ala Ala Pro Ala Asp Leu Lys Thr Val Ala Gln Arg Leu Glu Pro Gly

65 70 75 80

Tyr Phe Val Thr Gln Phe Pro Lys Gln Gln Met Thr Gly Asp Glu Ala

85 90 95

Arg Ala Glu Ala Glu Arg Leu Phe Ala Ala Cys Gln Lys Lys Phe Lys

100 105 110

Glu Leu Ala Glu Tyr Glu Asp Gly Tyr Arg Gln Cys Leu Asp Ala Leu

115 120 125

Gly Pro Asn Leu Ser Leu Pro Arg Leu Gly Arg Lys Pro Lys Gly Ala

130 135 140

Tyr Pro Tyr Ala Val Val Phe Lys Leu Met Pro Thr Asn Ala Thr Trp
145 150 155 160
Glu Cys Phe Lys Arg Val Thr Ala Ser Leu Tyr Lys Arg Ala Gln Lys
165 170 175
Gly Val Val Ser Pro Val Ser Ala Asp Ser Ile Ala Asp Val Arg Thr
180 185 190

Asn Asp Glu Pro Leu Phe Glu Tyr Phe Thr Asn Leu Ala Leu Val Arg
195 200 205
Pro Pro Gly Asn Lys Asp Arg Ala Val Trp Phe Glu Phe Asp Leu Ala
210 215 220
Ala Phe Ile Glu Ala Ile Lys Ser Pro His Gln Phe Phe Gln Asp Thr
225 230 235 240
Ile Lys Arg Glu Gln Ala Val Ala Gln Ile Lys Ala Lys Leu Asp Ala
245 250 255

Met Asp Gly Gln Gly Arg Ala Ala Ser Gly Glu Glu Asp Ala Leu Pro
260 265 270
Gly Phe Glu Gly Asp Asp Arg Ile Thr Leu Leu Arg Glu Leu Val Thr
275 280 285
Asp Thr Leu Gly Tyr Leu Ala Glu Ala Asp Ala Ser Thr Ser Pro Gly
290 295 300
Gly Lys Ile Glu Tyr Ser Ile Gln Glu Arg Thr Val Arg Gly Phe Ala
305 310 315 320

Glu Val Lys Arg Arg Trp Arg Asp Leu Val Glu Lys Gly Lys Ala Thr
325 330 335
Glu Asp Ala Leu Leu Lys Val Leu Ala Glu Glu Gln Thr Glu His Arg
340 345 350
Asp Asp Phe Gly Ser Ala Thr Leu Tyr Arg Glu Leu Ala Lys Pro Lys
355 360 365
Phe Gln Pro Ile Trp Arg Asp Pro Gly Thr Gln Pro Trp His Ala Asp
370 375 380

Asp Pro Leu Arg Ala Trp Leu Glu Tyr Arg Glu Leu Gly Arg Glu Leu

385 390 395 400

Glu Asp Lys Gln Arg Pro Ile Arg Phe Thr Pro Val His Pro Val His

405 410 415

Ser Pro Arg Phe Phe Ile Phe Pro Lys Lys Lys Gly Gly Gly Arg Phe

420 425 430

Gly Thr Val His Glu Pro Gly Gln Leu Arg Val Met Ala Gly Ile Val

435 440 445

Ala Gln Thr Gln His Gly Trp Glu Pro Val Pro Val Arg Ile Thr Tyr

450 455 460

Ala Ala Pro Arg Leu Arg Arg Asp Gln Leu Arg Asp Asp Val Glu Thr

465 470 475 480

Asp Leu Glu Ser Arg Pro Trp Leu Gln Pro Met Met Gln Ala Leu Gly

485 490 495

Leu Pro Glu Pro Asp Thr Ala Asp Phe Ser Asn Cys Arg Val Thr Leu

500 505 510

Gln Pro Ser Ala Pro Asp Asp Ile Gln Leu Thr Phe Pro Val Asp Val

515 520 525

Ser Ala Asp Lys Leu Thr Thr Ala Ile Gly Lys Ala Ala Arg Trp Ala

530 535 540

Lys Gln Phe Asn Leu Phe Pro Asp Gly Asp Asn Phe Tyr Asn Ala Ser

545 550 555 560

Leu Arg Trp Pro His Glu Lys Lys Pro Ser Lys Pro Pro Val Pro Trp

565 570 575

His Glu Ala Leu Asp Asn Phe Ser Val Leu Ala Ala Asp Leu Gly Gln

580 585 590

Arg Cys Ala Gly Ala Phe Ala Arg Leu Glu Val Arg Ala Asn Asp Asp

595 600 605

Phe Ala Gly Lys Pro Ser Arg Phe Ile Gly Glu Thr Pro Gly Lys Lys

610 615 620

Trp Arg Ala Ala Leu Val Ala Ala Gly Met Leu Arg Leu Pro Gly Glu

625 630 635 640

Glu Gln Thr Val Trp Arg Pro Gly Ala Thr Gly Pro Asn Phe His Thr
645 650 655
Glu Leu Ser Gly Ser Arg Gly Arg Met Ala Arg Pro His Glu Ala Asp
660 665 670
Asp Thr Ala Asp Leu Leu Arg Ala Phe Asp Cys Pro Glu Glu Ser Leu
675 680 685
Met Pro Ala Asp Trp Arg Thr Ser Leu Ser Phe Pro Glu Gln Asn Asp
690 695 700

Lys Leu Leu Val Ala Ala Arg Arg Tyr Gln Ser Arg Leu Ala Arg Leu
705 710 715 720
His Arg Trp Cys Trp Phe Leu Thr Asp Glu Lys Lys Arg Gln Thr Ala
725 730 735
Leu Asp Glu Ile Arg Glu Ala Glu Asp Met Pro Ala Ala Asp Asp Pro
740 745 750
Gln Leu Thr Asp Lys Leu Arg Ala Leu Leu Leu Gln Lys Gln Ala Ala
755 760 765

Leu Pro Gly Leu Leu Val Arg Leu Ala Asn Arg Ile Leu Pro Leu Arg
770 775 780
Gly Arg Ser Trp Gln Trp Glu Thr His Pro Asp Lys Ala Asp Cys His
785 790 795 800
Leu Leu Thr Gln Thr Gly Pro Ala Leu Pro Asp Val Trp Ile Arg Gly
805 810 815
Gln Arg Gly Leu Ser Met Gln Arg Ile Glu Gln Ile Glu Glu Leu Arg
820 825 830

Arg Arg Phe Gln Ser Leu Asn Gln Met Gln Arg Arg Glu Ile Gly Gly
835 840 845
Lys Pro Pro Ile Arg Arg Asp Asp Ser Ile Pro Asp Cys Cys Pro Asp
850 855 860
Leu Leu Asp Lys Leu Asp Gln Ile Lys Glu Gln Arg Ala Asn Gln Ala
865 870 875 880
Ala His Met Ile Leu Ala Glu Ala Leu Gly Leu Arg Leu Ala Pro Pro

885 890 895

Pro Ala Asp Lys Arg Gln Leu Arg Ala Ser Arg Asp Val His Gly Gln
900 905 910
Tyr Val Lys Ser Arg Glu Pro Val Asp Phe Ile Val Ile Glu Asp Leu
915 920 925
Ser Arg Tyr Arg Ser Ser Gln Gly Arg Ala Pro Arg Glu Asn Ser Arg
930 935 940
Leu Met Lys Trp Cys His Arg Ala Val Arg Asp Lys Leu Arg Glu Leu
945 950 955 960

Cys Glu Pro Phe Gly Ile Pro Val Val Glu Thr Pro Ala Ala Tyr Ser
965 970 975
Ser Arg Phe Cys Ser Arg Ser Gly Val Ala Gly Phe Arg Ala Val Glu
980 985 990
Val Gly Pro Gly Phe Asp Arg Glu Phe Pro Trp Met Met Leu Lys Asp
995 1000 1005
Arg Glu Asp Glu Gly Glu Pro Val Arg Gln Leu Ile Leu Gln Val
1010 1015 1020

Ala Thr Leu Asn Gln Gly Arg Asp Gly Lys Pro Pro Arg Thr Leu
1025 1030 1035
Leu Ala Pro Leu Ala Gly Gly Pro Ile Phe Val Pro Ile Val Asp
1040 1045 1050
Lys Leu Asn Gly Ala Asp Ile Gln Pro Ala Leu Ala Gln Ala Asp
1055 1060 1065
Ile Asn Ala Ala Ile Asn Leu Gly Leu Arg Ala Ile Ala Asp Pro
1070 1075 1080

Arg Leu Trp Ser Ile His Pro Arg Cys Arg Thr Gln Arg Gln Gly
1085 1090 1095
Asp Gln Met Leu Thr Arg Glu Lys Arg Lys Phe Gly Glu Thr Gly
1100 1105 1110
Gln Pro Leu Ala Val His Arg Ala Asp Gly Val Lys Pro Asp Asp
1115 1120 1125

Thr Arg Asn Pro Asn Phe Phe Ala Asp Ile Ser Gly Ser Leu Pro
1130 1135 1140

Ala Trp Glu Ser Ala Thr Leu Asp Gly Gln His Leu Leu Ser Gly
1145 1150 1155
Arg Cys Leu Arg Ser Glu Ile Lys Lys Arg Gln Trp Gln Arg Cys
1160 1165 1170
Ala Glu Ile Asn Asp Arg Arg Met Asn Arg Trp Met Lys Gly Glu
1175 1180 1185

<210> 278
<211> 1518
<212> PRT
<213> Unknown
<220><223> Description of Unknown:
Cas12b sequence
<400> 278

Met Thr Glu Leu Gln Thr Gln Arg Ala Tyr Thr Leu Arg Leu Lys Gly
1 5 10 15
Ile Asp Glu Lys Asp Gln Ser Trp Arg Asp Ala Leu Trp Lys Thr His
20 25 30
Glu Ala Val Asn Lys Gly Ala Lys Val Phe Gly Asp Trp Leu Leu Thr
35 40 45
Leu Arg Gly Gly Leu Asp His Thr Leu Ala Asp Ala Glu Ile Pro Gly
50 55 60

Glu Lys Gly Lys Pro Asp Arg Ala Pro Thr Gln Glu Glu Arg Lys His
65 70 75 80
Arg Arg Ile Leu Leu Ala Leu Ser Trp Leu Ser Val Glu Ser Glu Arg
85 90 95
Gly Ala Pro Glu Glu Phe Ile Val Ala Thr Gly Lys Glu Pro Ala Ala
100 105 110
Thr Arg Asn Asp Lys Val Ile Ala Ala Leu Lys Asp Ile Leu Arg Gly
115 120 125

Arg Asn Leu Thr Glu Glu Lys Ile Ser Glu Trp Thr Glu Val Cys Thr
130 135 140
Pro Ser Leu Ser Ala Ala Ile Arg Glu Asp Ala Val Trp Val Asn Arg
145 150 155 160
Ser Arg Ala Phe Asp Glu Ala Val Lys Arg Ile Gly Ser Ser Leu Thr
165 170 175
Arg Glu Glu Val Trp Asp Met Leu Glu Cys Phe Phe Gly Ser Arg Asn
180 185 190

Ala Tyr Leu Ala Pro Val Lys Ile Ser Glu Asp Glu Ser Ser Asp Gly
195 200 205
Glu Gln Glu Glu Lys Ala Lys Asp Leu Val Gln Lys Ala Gly Gln Trp
210 215 220
Leu Ser Ser Arg Phe Gly Thr Gly Glu Gly Ala Asp Phe Ala Lys Met
225 230 235 240
Ala Ala Val Tyr Ala Lys Ile Ala Ala Trp Ala Gly Asn Ala Gln Ala
245 250 255

Gly Thr Thr Gly Asn Glu Val Ile Asn Asn Leu Ala Thr Ala Leu Arg
260 265 270
Glu Phe Thr Pro Lys Ser Asn Asp Leu Lys Gly Val Leu Asp Leu Ile
275 280 285
Ser Gly Pro Gly Tyr Lys Ser Ala Thr Arg Asn Leu Leu Lys Gln Ile
290 295 300
Ala Asn Thr Lys Thr Val Thr Arg Glu Asp Ile Ser Lys Leu Gln Glu
305 310 315 320

Thr Ala Gly Glu Asp Ser Glu Glu Cys Ala Thr Lys Thr Gly Ser Lys
325 330 335
Gly Lys Arg Ala Tyr Ala Asp Ala Ile Leu Lys Asp Val Glu Ser Val
340 345 350
Cys Gly Phe Thr Tyr Arg Ile Asp Lys Asp Gly Gln Pro Val Ser Val
355 360 365
Ala Asp Tyr Ser Lys Tyr Asp Glu Asp Tyr Lys Trp Gly Ser Ser Arg

370 375 380

His Lys Glu Phe Ala Val Met Leu Asp His Ala Ala Arg Arg Val Ser
385 390 395 400
Leu Ala His Thr Trp Ile Lys Arg Ala Glu Ala Glu Arg Arg Lys Phe
405 410 415
Glu Glu Asp Ser Lys Lys Ile Met Gln Val Pro Gln Ala Ala Lys Asp
420 425 430
Trp Leu Asp Ala Tyr Cys Ala Gln Arg Ser Glu Ala Ser Gly Ala Leu
435 440 445

Glu Pro Tyr Arg Ile Arg Lys Arg Ala Ile Gln Gly Trp Lys Glu Ile
450 455 460
Ile Ala Ser Trp Asn Lys Pro Asp Cys Lys Thr Ala Glu Asp Arg Ile
465 470 475 480
Ala Ala Ala Arg Gln Leu Gln Asp Asp Pro Glu Ile Glu Lys Phe Gly
485 490 495
Asp Ile Gln Leu Phe Glu Ala Leu Ala Glu Asp Asp Ala Gln Cys Val
500 505 510

Trp Lys Lys Glu Asp Gly Thr Leu Asp Pro Glu Ile Leu Ile Asn Tyr
515 520 525
Thr Leu Ala Ser Glu Ala Met Phe Lys Lys Gln His Phe Lys Val Pro
530 535 540
Ser Tyr Arg His Pro Asp Ala Phe Leu Tyr Pro Val Phe Cys Asp Phe
545 550 555 560
Gly Asn Ser Arg Trp Glu Leu Asp Phe Ser Ile Arg Glu Ala Ala Thr
565 570 575

Lys Leu Lys Glu Ile Glu Ala Lys Ile Glu Lys Gln Arg Gln Glu Val
580 585 590
His Lys Val Gln Gln Ala Leu Glu Lys Cys Glu Asn Asp Glu Lys Arg
595 600 605
Pro Lys Met Glu Glu Arg Leu Lys Glu Ala Gln Lys Lys Leu Gln Glu
610 615 620

Ser Gln Asn Tyr Gly Glu Tyr Leu His Ser Asn Asn Lys Ile Thr Met
625 630 635 640

Val Leu Phe Asp Gly Thr Phe Val Lys Lys His Ile Phe Ala Trp Gln
645 650 655
Ser Lys Arg Leu Thr Lys Asp Leu Ala Leu Tyr Gln Glu Pro Ser Ala
660 665 670
Asp Pro Lys Asn Val Val Ser Arg Ala Asp Arg Leu Gly Arg Ala Val
675 680 685
Ala Ser Val Gly Ile Asn Asp Ala Val Lys Val Ala Gly Leu Phe Glu
690 695 700

Gln Glu Asn Trp Asn Gly Arg Leu Gln Ala Pro Arg Gln Gln Leu Glu
705 710 715 720
Ala Ile Ala Gln Tyr Val Glu Lys His Gly Trp Asp Asn Lys Ala Glu
725 730 735
Lys Met Arg Ala Ser Ile Lys Trp Phe Ile Thr Phe Ser Ala Lys Leu
740 745 750
Gln Ser Lys Gly Pro Trp Asn Glu Phe Ala Arg Lys His Gly Leu Lys
755 760 765

Glu Asp Pro His Tyr Trp Pro His Ala Glu Lys Asn Glu Asn Arg Thr
770 775 780
Ala His Ser Arg Leu Ile Leu Ser Arg Leu Pro Gly Leu Arg Val Leu
785 790 795 800
Ser Val Asp Leu Gly His Arg Tyr Ala Ala Ala Cys Ala Val Trp Glu
805 810 815
Ala Leu Gly Ser Glu Ala Phe Lys Lys Asp Ile Glu Gly Lys Arg Ile
820 825 830

Ile Arg Gly Asp Thr Asp Glu Asn Ala Leu Tyr Cys His Thr Glu His
835 840 845
Glu Ala Asn Gly Lys Lys His Ile Thr Ile Tyr Arg Arg Ile Gly Ala
850 855 860
Asp Thr Leu Pro Asp Gly Ala His His Pro Ala Pro Trp Ala Arg Leu

865 870 875 880

Asp Arg Gln Phe Leu Ile Lys Leu Gln Gly Glu Asp Glu Gln Ala Arg

885 890 895

Glu Ala Ser Asn Glu Glu Ile Trp Lys Val His Gln Leu Glu Asn Thr

900 905 910

Leu Gly Arg Arg Thr Pro Leu Ile Asp Arg Leu Ile Ala Gly Gly Trp

915 920 925

Gly Tyr Thr Glu Lys Gln Lys Ala Arg Leu Glu Val Leu Thr Asn Leu

930 935 940

Gly Trp Cys Pro Thr Asn Lys Thr Asp Asn Gln Glu Glu Gly Asp Glu

945 950 955 960

Glu Glu Thr Ala Ile Leu Ser Lys Pro Ser Leu Leu Val Asp Asp Leu

965 970 975

Met Phe Ser Ala Val Arg Thr Leu Arg Leu Ala Leu Lys Arg His Gly

980 985 990

Asp Arg Ala Arg Ile Ala His Tyr Leu Ile Thr Asp Glu Lys Thr Lys

995 1000 1005

Pro Gly Gly Val Lys Glu Lys Leu Asp Lys Asn Gly Arg Val Glu

1010 1015 1020

Leu Leu Leu Asp Ala Leu Gly Leu Trp His Asp Leu Phe Ser Ser

1025 1030 1035

Pro Gly Trp His Asp Glu Lys Ala Lys Gln Leu Trp Asn Ala Tyr

1040 1045 1050

Ile Ala Gly Leu Leu Pro Glu Gly Glu Leu Gln Gln Ala Lys Ser

1055 1060 1065

Val Thr Thr Ser Ala Ala Leu Gly Gly Gln Gln Lys Lys Glu Lys

1070 1075 1080

Lys Glu Lys Leu Arg Ala Val Ala Glu Ala Leu Tyr Leu Asn Ser

1085 1090 1095

Asp Leu Cys His Ser Leu Asn Glu Val Trp Arg Lys Arg Trp Glu

1100 1105 1110

Glu Asp Asp Lys Gln Trp Arg Ile Tyr Ile Arg Trp Phe Lys Asp
1115 1120 1125
Trp Ile Met Pro Arg Gly Ala Asn Ala Lys Ser Pro Ala Ile Arg
1130 1135 1140

His Val Gly Gly Leu Ser Leu Thr Arg Leu Ala Thr Leu Thr Glu
1145 1150 1155
Phe Arg Arg Lys Val Gln Val Gly Phe Phe Thr Arg Leu His Pro
1160 1165 1170
Asp Gly Thr Lys Thr Glu Thr Arg Glu Asp Phe Gly Gln Lys Thr
1175 1180 1185
Leu Asp Thr Leu Glu His Leu Arg Glu Gln Arg Val Lys Gln Leu
1190 1195 1200

Ala Ser Arg Ile Val Glu Ala Ala Leu Gly Ile Gly Ser Glu Asp
1205 1210 1215
Lys Arg His Trp Asp Gly Lys Lys Arg Pro Arg Gln Arg Ile Ala
1220 1225 1230
Asp Pro Arg Phe Val Pro Cys His Ala Val Val Ile Glu Asn Leu
1235 1240 1245
Thr His Tyr Arg Pro Glu Glu Thr Arg Thr Arg Arg Glu Asn Arg
1250 1255 1260

Gln Ile Met Glu Trp Ala Ser Ser Lys Val Lys Lys Tyr Leu Ser
1265 1270 1275
Glu Ile Cys Gln Leu His Gly Leu His Leu Arg Glu Val Ser Ala
1280 1285 1290
Ala Tyr Thr Ser His Gln Asp Ser Arg Thr Gly Ala Pro Gly Ile
1295 1300 1305
Arg Cys Gln Asp Val Ser Leu Ile Glu Phe Met Lys Ser Pro Phe
1310 1315 1320

Trp Arg Lys Gln Val Ala Gln Ala Glu Lys Lys Gln Lys Glu Gly
1325 1330 1335
Lys Gly Asp Ala Val Glu Arg Tyr Leu Cys Glu Leu Asn Gln Lys

1340 1345 1350

Trp Lys Gly Ala Ser Glu Glu Glu Trp Arg Lys Ala Gly Phe Val

1355 1360 1365

Arg Ile Pro Leu Arg Gly Gly Glu Ile Phe Val Ser Ala Ala Gly

1370 1375 1380

His Asp Ser Pro Ala Ala Lys Gly Ile His Ala Asp Leu Asn Ala

1385 1390 1395

Ala Ala Asn Ile Gly Leu Arg Ala Leu Leu Asp Pro Asp Trp Ser

1400 1405 1410

Gly Lys Trp Trp Tyr Val Pro Cys Asn Ser Ser Thr Met Cys Pro

1415 1420 1425

Ala Arg Asp Lys Val Thr Gly Ser Ala Ala Val Asn Pro Gly Gln

1430 1435 1440

Pro Leu Gln Val Ser Ala Gln Leu Glu Ser Asp Asp Ala Ala Lys

1445 1450 1455

Asp Thr Lys Lys Arg Lys Lys Lys Gly Asp Gly Lys Ser Lys Glu

1460 1465 1470

Ile Ile Asn Leu Trp Arg Asp Ile Ser Ser Tyr Pro Leu Glu Asp

1475 1480 1485

Thr Arg Gly Gly Thr Trp Ser Asn Lys Thr Val Tyr Trp Asn Arg

1490 1495 1500

Val Gln Ser Asn Val Val His Ile Leu Gln Asn Gln Met Lys Gly

1505 1510 1515

<210> 279

<211> 1374

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12b sequence

<400> 279

Met Pro Glu Thr Thr Gln Arg Ala Tyr Thr Leu Arg Leu Gln Gly His

1 5 10 15

Asp Pro Lys Asp Ala Ser Trp Arg Glu Ala Leu Trp Lys Thr His Glu
20 25 30

Ala Val Asn Arg Gly Ala Lys Ala Phe Gly Asp Trp Leu Leu Thr Leu
35 40 45
Arg Gly Gly Leu Asp His Ser Leu Ala Asp Glu Gly Ala Pro Gly Gln
50 55 60
Thr Pro Thr Glu Glu Gln Arg Lys Gln Arg Arg Ile Leu Leu Ala Leu
65 70 75 80
Ser Trp Leu Ser Val Glu Ser Glu Asn Gly Ala Pro Gln Glu Tyr Ile
85 90 95

Val Pro His Asp Arg Asp Asn Glu Ser Gly Ala Arg Gln Asn Trp Lys
100 105 110
Thr Arg Glu Ala Leu Arg Glu Ile Leu Lys Asn Arg Gly Cys Arg Asp
115 120 125
Asp Glu Ile Glu Ser Trp Cys His Asp Cys Glu Pro Ser Leu Thr Ser
130 135 140
Ala Ile Arg Lys Asp Ala Val Trp Val Asn Arg Ser Lys Ala Phe Asp
145 150 155 160

Asn Ala Val Gln Ser Ile Pro Asn Phe Ser Arg Glu Glu Ile Trp Asp
165 170 175
Leu Leu Gly Cys Phe Phe Val Ser Ser Gln Ala Tyr Leu Ala Pro Leu
180 185 190
Glu Ser Pro Lys Asp Asp Lys Pro Asp Ala Ser Lys Lys Asp Ser Ser
195 200 205
Lys Asp Leu Ile Gln Ser Ala Gly Gln Trp Leu Ser Arg Arg Phe Gly
210 215 220

Arg Gly Lys Gly Leu Asn Phe Ala Arg Leu Ala Glu Thr Tyr Glu Ala
225 230 235 240
Ile Ala Arg Trp Ala Ser Val Ala Asn Pro Gly Asp Thr Asn Asp Leu
245 250 255
Ile Ala Asp Leu Ala Lys Thr Leu Asn Ala Glu Thr Pro Glu Leu Asp

260 265 270

Gly Ile Leu Lys Val Val Ser Gly Pro Gly His Lys Ser Lys Thr Arg

275 280 285

Asn Leu Leu Arg Ser Leu Ser Ala Val Asn His Ile Thr Lys Asp Thr

290 295 300

Leu Gln Arg Leu Lys Asp Thr Ala Asn Glu Asp Ala Lys Lys Ala Lys

305 310 315 320

Leu Lys Lys Gly Glu Lys Gly His Arg Ala Tyr Ala Tyr Lys Val Leu

325 330 335

Glu Ala Val Glu Asp Ala Cys Gly Phe Thr Tyr Leu Gln Glu Gly Asp

340 345 350

Arg Ala Lys His Cys Glu Phe Ala Val Met Leu Asp His Ala Ala Arg

355 360 365

Arg Val Ser Ser Leu His Thr Trp Ile Lys Arg Ala Glu Ala Glu Arg

370 375 380

Arg Arg Phe Glu Ile Asp Thr Lys Lys Lys Asp Gln Leu Pro Pro Ser

385 390 395 400

Val Lys Glu Trp Leu Asp Thr Tyr Cys Gln Lys Arg Ser Lys Glu Thr

405 410 415

Gly Ala Val Glu Pro Tyr Arg Ile Arg Arg Gly Ala Ile Glu Gly Trp

420 425 430

Lys Glu Ile Val Glu Ala Trp Ser Lys Ala Gly Thr Thr Thr Ala Glu

435 440 445

Asp Arg Lys His Glu Ala Arg Arg Leu Pro Asp Asn Pro His Ile Asp

450 455 460

Lys Ser Gly Asp Ile Lys Leu Phe Glu Asp Leu Ala Leu Glu Asp Ala

465 470 475 480

Leu Pro Val Trp His Ala Asn Gly Asp Pro Asn Asn Pro Pro Asp Pro

485 490 495

Gln Leu Leu Ile Asp Tyr Val Glu Gly Ser Glu Ala Glu Phe Lys Lys

500 505 510

Arg Ala Phe Lys Val Pro Thr Tyr Cys His Pro Asp Pro Leu Val His
515 520 525
Pro Val Phe Cys Asp Tyr Gly Cys Ser Arg Trp Asn Val Ser Phe Ala
530 535 540

Ile Gln Pro Val Lys Lys Gln Lys Leu Ser Ser Glu Glu Lys Leu Pro
545 550 555 560
Ala Lys Gly Leu Leu Leu Asp Leu Leu His Gly Thr Ala Ile Arg Pro
565 570 575
Val Ala Leu Arg Trp Gln Ser Lys Arg Phe Ala Arg Asp Leu Ala Leu
580 585 590
Asn Thr Thr Asp Ser Ser Asp Lys Pro Asn Glu Val Thr Arg Ala Asp
595 600 605

Arg Phe Gly Cys Ala Leu Ala Lys Cys Pro Ser Ser Gln Lys Ile Arg
610 615 620
Ile Arg Gly Leu Phe Glu Glu Lys Tyr Trp Asn Gly Arg Leu Gln Ala
625 630 635 640
Pro Arg Pro Glu Leu Thr Ala Leu Ala Lys Arg Val Ala Lys Tyr Gly
645 650 655
Trp Asp Lys Lys Ala Arg Lys Leu Arg Asn Ser Leu Asn Trp Phe Ile
660 665 670

Thr Phe Ser Ala Asn Leu Arg Pro Ser Gly Pro Trp Glu Glu Tyr Thr
675 680 685
Lys Tyr Ala Glu Lys Ala Phe Ser Ser Asn Ala Ser Ala Lys Pro Ser
690 695 700
Val Ser Arg Gly Gly Phe Trp Val Val His Ala Ser Pro Asn Lys Arg
705 710 715 720
Gly Lys Met Ala Gln Leu Arg Leu Cys Arg Leu Pro Glu Leu Arg Val
725 730 735

Leu Ser Val Asp Leu Gly His Arg Tyr Ala Ala Ala Cys Ala Val Trp
740 745 750
Glu Thr Leu Ser Lys Ser Ala Phe Glu Gln Glu Ile His Glu Arg Lys

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        755                 760                 765
Ile Leu Arg Gly Gly Thr Gly Pro Asn Asp Leu Phe Cys His Thr Gln
    770                 775                 780
His Asp Thr Asn Gly Gln Ser Lys Val Thr Ile Tyr Arg Arg Ile Gly
785                 790                 795                 800

Ala Asp Thr Leu Pro Asn Gly Thr Pro His Pro Ala Pro Trp Ala Arg
                805                 810                 815
Leu Asp Arg Gln Phe Leu Ile Lys Leu Pro Gly Glu Glu Arg Glu Ala
            820                 825                 830
Arg Lys Ala Ser Pro Thr Glu Leu Ala Asn Val Glu Lys Leu Glu Lys
        835                 840                 845
Glu Leu Gly Leu Lys Thr Ser Glu Asn Arg Val Lys Arg Ile Asp Asp
    850                 855                 860

Leu Met Ser Asp Thr Leu Arg Thr Val Arg Gln Ala Leu Arg Arg His
865                 870                 875                 880
Ser Leu Arg Ala Arg Ile Ala Phe Asn Leu Ala Thr Leu Arg Asp Gln
                885                 890                 895
Ser Asp Gly Asp Glu Glu Ser Gln Ser Lys Gln Lys Arg Asp Thr Arg
            900                 905                 910
Trp Asn Asn Thr Val Lys Ile Trp His Ser Leu Leu Glu Ser Asn Glu
        915                 920                 925

Trp Thr Asp Asp Trp Ala Lys Ala Leu Trp Asp Glu Leu Gly Pro Leu
    930                 935                 940
Ser Asp Pro Gln Lys Ala Asp Asp Ala Glu Trp Leu Lys Leu Ala Ala
945                 950                 955                 960
Glu Lys Phe Tyr Thr Arg Trp Gln Glu Asp Glu Gln Thr Trp Arg Glu
                965                 970                 975
Arg Leu Arg Trp Leu Arg Arg Trp Ile Leu Pro Arg Gly Ser Gln Ala
            980                 985                 990

Ala Ser Gln Lys Gly Ser Ile Arg  His Val Gly Gly Leu  Ser Leu Thr
        995                 1000                1005
```

Arg Leu Ala Thr Ile Lys Thr Leu Tyr Gln Val Leu Lys Ala Tyr
1010 1015 1020
His Met Arg Leu Lys Pro Asp Asn Ser Arg Lys Asn Ile Pro Ala
1025 1030 1035
Glu Gly Asp Glu Ala Leu Gln Asn Phe Gly Gln Lys Ile Leu Asp
1040 1045 1050

Asp Leu Glu His Met Arg Glu Gln Arg Val Lys Gln Leu Ala Ser
1055 1060 1065
Arg Ile Val Glu Ala Ala Leu Gly Leu Gly Arg Met Lys Gln Val
1070 1075 1080
Thr Ile Gly Lys Asp Pro Lys Arg Pro Arg Glu Pro Val Asp Gln
1085 1090 1095
Ser Cys His Ala Val Val Ile Glu Asn Leu Thr His Tyr Arg Pro
1100 1105 1110

Glu Lys Arg Gln Thr Arg Arg Glu Asn Arg Gln Leu Met Asp Trp
1115 1120 1125
Ser Ala Ala Lys Val Lys Lys Tyr Leu Lys Glu Cys Cys Gln Leu
1130 1135 1140
His Gly Leu His Leu Val Glu Val Ser Ala Ser Tyr Thr Ser Arg
1145 1150 1155
Gln Asp Ser Arg Thr Gly Ala Pro Gly Ile Arg Cys Gln Glu Val
1160 1165 1170

Pro Leu Thr Asp Phe Leu Lys Lys Asn Phe Trp Arg Glu Gln Val
1175 1180 1185
Lys Gln Ala Lys Gln Arg Leu Ser Glu Gly Lys Ala Asn Ala Arg
1190 1195 1200
Asp Arg Tyr Leu Cys Gln Leu Asn Glu Arg Trp Gly Asn Ala Pro
1205 1210 1215
Ala Pro Val Thr Gln Thr Ala Ile Arg Leu Arg Ile Pro Leu Asn
1220 1225 1230

Gly Gly Glu Leu Phe Val Ser Ala Asp Gln Asn Ser Pro Ala Ser

1235 1240 1245

Lys Gly Ile Gln Ala Asp Leu Asn Ala Ala Ala Asn Ile Gly Leu

1250 1255 1260

Arg Ala Ile Thr Asp Pro Asp Trp Pro Gly Ala Trp Trp Tyr Val

1265 1270 1275

Pro Cys Glu Ala Asn Thr Phe Lys Pro Val Lys Asp Lys Val Ala

1280 1285 1290

Gly Ser Ala Ala Ile Asp Ser Asn Val Ser Leu Lys Lys Asp Ser

1295 1300 1305

Pro Asn Ser Glu Lys Pro Ala Ser Asp Arg Lys Ser Arg Thr Ser

1310 1315 1320

Lys Ser Met Ile Asn Leu Trp Cys Asp Thr Ser Ser Lys Ser Leu

1325 1330 1335

Ser Glu Lys Asp Gln Trp Gln Glu Ser Ala Pro Tyr Trp Glu Asp

1340 1345 1350

Val Ala Ala Arg Thr Ile Asn Ile Leu Gln Ala Ser Leu Ala Cys

1355 1360 1365

Ser Thr Thr Asn Ser Gln

1370

<210> 280

<211> 1335

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12a sequence

<400> 280

Met Lys Ser Leu Ala Gln Phe Gln Asn Leu Tyr Ala Leu Gln Lys Thr

1 5 10 15

Leu Arg Phe Glu Leu Lys Pro Glu Gly His Thr Arg Glu Thr Phe Asn

20 25 30

Arg Trp Leu Glu Glu Ile Glu Lys Glu Gln Ala Ser Glu Asn Glu Asn

35 40 45

Ile Val Tyr Gln Asp Leu Leu Arg Ala Lys Lys Tyr Glu Lys Ile Lys
50 55 60
Ile Ile Leu Asp Glu Tyr His Lys Asp Phe Ile Glu Gln Ala Leu Ala
65 70 75 80
Tyr Ala Asn Leu Thr Glu Leu Glu Lys Tyr Glu Glu Leu Tyr Arg Lys
85 90 95

Ser Asn Arg Thr Ser Glu Glu Glu Glu Glu Phe Glu Asn Thr Lys Glu
100 105 110
Ser Leu Arg Lys Gln Ile Ala Asn Ile Phe Ile Lys Asn Pro Asn Lys
115 120 125
Thr Val Gln Glu Arg Trp Lys Phe Leu Phe Ser Lys Lys Leu Ile Gln
130 135 140
Asn Glu Leu Ile Val Trp Val Lys Gly Asn Tyr Glu Leu Leu Ser Glu
145 150 155 160

Lys Leu Lys Asn Glu Phe Pro Asp Glu Ser Ser Ile Ile Ser Thr Ile
165 170 175
Glu Asp Phe Lys Tyr Phe Thr Thr Tyr Phe Arg Asn Tyr His Glu Asn
180 185 190
Arg Lys Asn Leu Tyr Ser Asn Glu Asp Lys Phe Ser Thr Ile Ala His
195 200 205
Arg Leu Ile His Glu Asn Leu Pro Lys Phe Ile Asp Asn Ile Ala Ile
210 215 220

Tyr Gln Lys Ala Lys Ala Val Leu Asn Ile Asn Glu Val Glu Lys Glu
225 230 235 240
Leu Gly Leu Pro Glu Asp Thr Leu Asp Lys Ile Phe Ser Leu Asp Phe
245 250 255
Phe Ser Lys Ala Leu Thr Gln Lys Gly Ile Asp Gln Tyr Asn Tyr Phe
260 265 270
Leu Gly Gly Lys Thr Glu Asn Glu Val Lys Lys Ile Lys Gly Leu Asn
275 280 285

Glu Phe Ile Asn Leu Tyr Asn Gln Gln Gln Gln Asp Lys Asn Gln Arg

290 295 300

Leu Pro Phe Leu Lys Val Leu Tyr Lys Leu Pro Leu Phe Glu Arg Thr
305 310 315 320

Ser Thr Ser Phe Arg Phe Glu Pro Ile Glu Asn Asp Arg Asp Leu Ile
325 330 335

Glu Arg Ile Gly Lys Phe Tyr Tyr Asn Asp Leu Lys Gln Tyr Arg Asp
340 345 350

Asp Ser Gln Gly Asp Thr Thr Asp Ile Leu Ser Gly Ile Asn Thr Leu
355 360 365

Leu Arg His Val His Asp Tyr Arg Asp Gly Leu Tyr Val Asn Gly Gly
370 375 380

Ile Thr Leu Thr Gln Ile Ser Gln Lys Ile Phe Gly Ser Trp Ser Tyr
385 390 395 400

Ile Asn Asn Ala Leu Ala Tyr Phe Tyr Asp Thr Tyr Ile Asp Ala Ser
405 410 415

Gly Val Asp His Gln Gly Glu Arg Lys Pro Lys Lys Gln Lys Gln Ile
420 425 430

Gln Glu Lys Thr Lys Trp Leu Lys Gln Lys Gln Phe Pro Val Ile Leu
435 440 445

Val Glu Lys Ala Leu Ser Glu Tyr Lys Ser Ile Glu Thr Asn Glu Asp
450 455 460

Leu Lys Thr Arg Ile Ser Asp Thr Thr Leu Cys Asp Phe Phe Lys Arg
465 470 475 480

Cys Gly Asn Asp Asp Asn Gly Gln Asp Leu Phe Asp Arg Ile Glu Ala
485 490 495

Arg Leu Arg Glu Lys Asn Glu Glu Gly Tyr Ser Leu Glu Asp Leu Leu
500 505 510

Lys Lys Glu Phe Thr Thr Glu Arg Lys Leu Met Gln Asp Lys Thr Lys
515 520 525

Thr Leu Leu Ile Lys Asn Phe Leu Asp Val Ile Gln Gly Asp Lys Asp
530 535 540

Asp Ile Thr Ala Gly Leu Leu His Phe Val Lys Cys Leu Ile Pro Arg
545 550 555 560
Thr Glu Ile Ser Glu Lys Asn Glu Leu Phe Tyr Ser Gly Met Glu Lys
565 570 575
Tyr Leu Asn Ile Leu Ser Glu Val Thr Pro Leu Tyr Asn Lys Ala Arg
580 585 590
Asn Tyr Leu Thr Gln Lys Pro Tyr Ser Ile Glu Lys Val Lys Leu Asn
595 600 605

Phe Glu Asn Ser Thr Leu Leu Asp Gly Trp Asp Glu Asn Glu Glu Ser
610 615 620
Asp Asn Ser Cys Val Leu Leu Arg Lys Arg Gly Tyr Tyr Tyr Leu Gly
625 630 635 640
Ile Met Asn Lys Lys His Asn Met Ile Phe Asp Arg Lys Ile Tyr Pro
645 650 655
Lys Ala Thr Glu Gly Glu Ala Tyr Tyr Glu Lys Met Ile Tyr Lys Leu
660 665 670

Leu Pro Gly Ala Tyr Lys Met Leu Pro Lys Val Phe Phe Ser Glu Lys
675 680 685
Asn Ile Asp Tyr Phe Lys Pro Ser Glu Glu Ile Leu Arg Ile Arg Asn
690 695 700
Thr Ala Ser Tyr Ser Lys Asn Gly Gln Pro Gln Glu Gly Tyr Gln Lys
705 710 715 720
Ala Ser Phe Ser Ile Glu Asp Cys Arg Lys Tyr Ile Asp Phe Phe Lys
725 730 735

Lys Cys Ile Ala Asn His Trp Asp Trp Gln Lys Phe Asn Phe Asn Phe
740 745 750
Ser Pro Thr Glu Tyr Tyr Gln Ser Ile Asp Glu Phe Tyr Arg Glu Ile
755 760 765
Glu Arg Gln Gly Tyr Lys Ile Asp Phe Val Lys Ile Pro Glu Ser Tyr
770 775 780
Ile Asn Gln Leu Ile Lys Glu Asn Lys Leu Tyr Leu Phe Lys Ile Tyr

785 790 795 800

Asn Lys Asp Phe Ser Glu Lys Lys Lys Ser Lys Gly Lys Asp Asn Leu
805 810 815
His Thr Leu Tyr Trp Lys Met Leu Phe Asp Glu Lys Asn Leu Lys Asp
820 825 830
Val Val Leu Lys Leu Asn Gly Glu Ala Glu Val Phe Phe Arg Gln Lys
835 840 845
Ser Ile Leu Tyr Asn Glu Glu Ile Trp Asn Lys Gly His His Tyr Ser
850 855 860

Glu Leu Lys Asp Arg Phe Ser Tyr Pro Ile Ile Ser Asn Lys Arg Tyr
865 870 875 880
Ala Glu Asp Lys Phe Phe Leu His Val Pro Ile Thr Leu Asn Phe Lys
885 890 895
Ala Asp Gly Ile Asn Asn Val Asn Asn Met Val Asn Glu Phe Ile Lys
900 905 910
Asp Asn Arg Asp Ile His Ile Ile Gly Ile Asp Arg Gly Glu Arg His
915 920 925

Leu Leu Tyr Val Ser Val Ile Asn Gln Lys Gly Asp Ile Val Glu Gln
930 935 940
Cys Ser Leu Asn Glu Ile Val Thr Glu Tyr Asn Gly Lys Ile Phe Lys
945 950 955 960
Lys Asn Tyr His Glu Glu Leu Asp Asn Leu Glu Lys Glu Arg Asp Arg
965 970 975
Ala Arg Lys Asp Trp Gln Thr Ile Ala Asn Ile Lys Glu Leu Lys Glu
980 985 990

Gly Tyr Leu Ser His Val Ile His Lys Ile Ser Lys Leu Ile Leu Lys
995 1000 1005
Tyr Asn Ala Ile Val Val Met Glu Asp Leu Asn Ser Gly Phe Lys
1010 1015 1020
Arg Gly Arg Gln Lys Val Glu Lys Gln Val Tyr Gln Asn Phe Glu
1025 1030 1035

Lys Gln Leu Ile Glu Lys Leu Asn Tyr Leu Val Leu Lys Glu Ser
1040 1045 1050

Asn Val Asp Glu Pro Gly Gly Val Leu Arg Ala Tyr Gln Leu Ala
1055 1060 1065
Asn Lys Phe Glu Thr Phe Lys Lys Leu Gly Lys Gln Ser Gly Ile
1070 1075 1080
Ile Phe Tyr Val Pro Ala Ala Tyr Thr Ser Ala Ile Asp Pro Val
1085 1090 1095
Thr Gly Tyr Ile Gln Tyr Leu Tyr Pro Leu Lys Gln Ala Asp Ser
1100 1105 1110

Val Glu Lys Ala Arg Lys Phe Tyr Ser Gln Phe Lys Arg Ile Ser
1115 1120 1125
Tyr Asn Pro His Lys Gln Trp Phe Glu Phe Ser Phe Asp Tyr Asn
1130 1135 1140
Asp Phe Asn Ile Ile Tyr His Gly Lys Ser Ser Trp Thr Ile Cys
1145 1150 1155
Thr Thr Asn Thr Glu Arg Tyr Met Trp Asn Arg Leu Leu Asn Asn
1160 1165 1170

Gly His Gly Gly Glu Glu Leu Val Tyr Val Thr Asn Glu Leu Glu
1175 1180 1185
Leu Leu Phe Gly Glu Tyr Asn Ile Ile Tyr Gly Asp Gly Lys Asp
1190 1195 1200
Ile Lys Gln Gln Ile Thr Asp Val Gln Asp Ile Asp Val Asp Arg
1205 1210 1215
Thr Ala Lys Gln Phe Tyr Lys Arg Ile Asn Glu Leu Leu Asn Leu
1220 1225 1230

Thr Leu Lys Leu Arg His Asn Asn Gly Lys Lys Gly Ala Asp Glu
1235 1240 1245
Glu Asp Tyr Ile Leu Ser Pro Val Glu Pro Tyr Phe Asp Ser Arg
1250 1255 1260
Phe Glu Ser Arg Lys Pro Ser Met Gln Gln Thr Leu Pro Ile Asn

1265 1270 1275

Ala Asp Ala Asn Gly Ala Phe Asn Ile Ala Arg Lys Gly Leu Leu

1280 1285 1290

Leu Leu Glu Arg Leu Asn Gln Leu Gly Val Glu Glu Phe Glu Lys

1295 1300 1305

Thr Lys Lys Ser Asn Asn Lys Lys Thr Gln Trp Leu Pro His Glu

1310 1315 1320

Leu Trp Val Glu Tyr Ala Gln Asn His Thr Arg Lys

1325 1330 1335

<210> 281

<211> 1520

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12b sequence

<400> 281

Met Ala Tyr Gln Asn Gly Lys Glu Gln Pro Thr Val Thr Asn Gln Arg

1 5 10 15

Ala Tyr Thr Leu Arg Leu Ser Gly Thr Asn Asp Gln Asp Ser Ile Trp

20 25 30

Arg Asn Arg Leu Trp His Thr His Glu Ala Val Asn Lys Gly Ala Lys

35 40 45

Thr Phe Gly Asp Trp Leu Leu Thr Met Arg Gly Gly Leu Cys His Thr

50 55 60

Leu Ala Glu Ala Asp Val Pro Gly Lys Gly Asn Lys Pro Ala Arg His

65 70 75 80

Pro Thr Pro Gln Glu Ile Arg Ser Arg Arg Val Val Leu Ala Leu Ser

85 90 95

Trp Leu Ser Val Glu Ser Gln His Gly Ala Pro Glu Arg His Leu Val

100 105 110

Ser His Asp Leu Asp Ile Ala Thr Gly Glu Arg Lys Asn Trp Lys Thr

115 120 125

Val Glu Ala Leu Arg Glu Ile Leu His Gly Arg Cys Leu Cys Lys Glu

130 135 140

Leu Ile Asp Glu Trp Ala Asn Asp Cys Arg Asp Ser Leu Ser Ala Thr
145 150 155 160
Ile Arg Glu Asp Ala Val Trp Val Asn Arg Ser Lys Ala Phe Asp Leu
165 170 175
Ala Ala Lys Lys Ile Gly Ala Ser Leu Thr Arg Glu Glu Leu Trp Asp
180 185 190
Phe Leu Gln Pro Phe Phe Ala Asn Lys His Gly Tyr Leu Gln Met Asp

195 200 205

Thr Val Ala Gly Val Thr Asn Gly Asp Ser Glu Thr Asp Ala Glu Glu
210 215 220
Ala Lys Glu Asp Ser Ser Glu Glu Lys Ala Lys Asp Leu Ser Gln Lys
225 230 235 240
Ala Gly Gln Trp Leu Ser Ser Arg Phe Gly Thr Gly Thr Gly Ala Asp
245 250 255
Phe Ser Arg Phe Ser Lys Val Tyr Glu Val Leu Ala Ala Arg Cys Gly

260 265 270

Ser Val Ala Val Gly Val Ser Gly Val Glu Ala Ile Arg Ile Leu Ala
275 280 285
Gly Thr Leu Ala Asp Phe Ser Pro Gly Ser Asn Asp Ile Glu Gly Met
290 295 300
Leu Gly Leu Met Ser Gly Pro Gly Tyr Lys Ser Ala Thr Arg Asn Ile
305 310 315 320
Leu Gln Lys Ile Asn Thr Leu Gln Thr Val Ser Gln Gln Asp Leu Asp

325 330 335

Arg Leu Arg Glu Ala Ser Glu Lys Asp Ala Leu Gln Ser Lys Gln Lys
340 345 350
Val Gly Gly Lys Gly Ser Arg Pro Tyr Ala Asn Ala Ile Leu Gln Asp
355 360 365
Val Glu Ala Ala Cys Gly Ile Cys Tyr Ala Gly Thr Gly Glu Ser Pro

370 375 380

Ala Arg His Trp Gln Tyr Ala Val Ile Leu Asp His Ala Ala Arg Arg

385 390 395 400

Val Ser Met Ala His Ser Trp Ile Lys Arg Ala Glu Glu Gln Arg Ser

405 410 415

Lys Phe Glu Ile Glu Lys Asp Lys Leu Asp His Val Pro Lys Asp Ala

420 425 430

Leu Ala Trp Leu Asp Ala Phe Cys Ala Arg Arg Ser Ser Glu Ser Gly

435 440 445

Ala Ser Asp Ala Tyr Arg Ile Arg Arg Ser Ala Val Asp Gly Trp Lys

450 455 460

Gln Val Val Ala Ala Trp Ala Ala Leu Pro Pro Lys Pro Glu Asn Gln

465 470 475 480

Gly Ser Glu Leu Leu Ser Asp Ala Glu Ser Ala Arg Ile Gln Ala Ala

485 490 495

Arg Glu Leu Gln Asp Thr Val Glu Lys Phe Gly Asp Ile Gln Leu Phe

500 505 510

Glu Ala Leu Ser Leu Thr Gly Ala Lys Cys Val Trp Gln Pro Asp Gly

515 520 525

Arg Pro Asp Ala Gln Pro Leu Leu Asp Tyr Val Ala Gly Thr Asp Ala

530 535 540

Ile Ser Lys Lys Gln Arg Phe Lys Val Pro Ala Tyr Arg His Pro Asp

545 550 555 560

Ala Leu Leu His Pro Val Phe Cys Asp Phe Gly Asn Ser Arg Trp Asn

565 570 575

Ile Asn Tyr Ala Ile His Arg Ala Pro Glu Lys Leu Thr Pro Ala Gln

580 585 590

Gln Leu Leu Glu Lys Lys Lys Ala Glu Ile Asp Lys Ala Glu Leu Thr

595 600 605

Leu Ala Lys Ala Gly Asp Ala Ala Lys Gln Ala Asn Ile Ser Glu Lys

610 615 620

Ile Asn Gly Leu Arg Ala Ala Phe Ile Gln Gln Gln Glu Lys Val Ala
625 630 635 640
Trp Leu Asn Ser Arg His Ala Met Thr Met Ser Leu Trp Asp Gly Thr

645 650 655
His Ile Glu Asp Thr Pro Leu Ile Trp Gln Ser Lys Arg Phe Gly Ser
660 665 670
Asp Ile Gly Gln Pro Val Glu Ala Gln Pro Leu Pro Val Ser Arg Ala
675 680 685
Asp Arg Phe Gly Arg Ala Val Ala Leu Ala Gln Asp Asn Val Pro Val
690 695 700
Ile Pro Ser Gly Leu Phe Asp Leu Ser Asp Trp Asn Gly Arg Leu Gln

705 710 715 720
Ala Pro Arg Arg Gln Leu Glu Ala Ile Ala Ala Ile Arg Asp Ser Ala
725 730 735
Lys Leu Ser Val Asn Glu Lys Gln Gln Leu Val Ala Lys Arg Ile Gln
740 745 750
Ser Ile Arg Trp Leu Leu Thr Phe Ser Ala Lys Leu Gln Ser His Gly
755 760 765
Pro Phe Ile Ala Tyr Ala Ala Gln His Gly Phe Asp Trp Arg Tyr Gly

770 775 780
Ala His Gly Pro Glu Asn Lys Ser Arg Gln Gly Leu Ala Lys Leu Ile
785 790 795 800
Leu Cys Arg Leu Pro Gly Leu Arg Ile Leu Ser Val Asp Leu Gly His
805 810 815
Arg Tyr Ala Ala Ala Cys Ala Val Trp Glu Thr Leu Asn Ala Gly Gln
820 825 830
Ile Gln Lys Ala Cys Leu Asp Ala Gly Lys Glu Ala Pro Gly Pro Cys

835 840 845
Thr Leu Tyr Leu His Leu Lys Gln Ile Ala Asn Gly Lys Glu Lys Lys
850 855 860
Thr Ile Phe Arg Arg Ile Ala Ala Asp Thr Leu Pro Asp Gly Ser Pro

865 870 875 880

His Pro Ala Pro Trp Ala Arg Leu Asp Arg Gln Phe Leu Ile Lys Leu

885 890 895

Gln Gly Glu Asp Arg Asp Ala Arg Leu Ala Thr Ser Glu Glu Ile Ala

900 905 910

Ala Val Glu Gln Met Glu Asn Glu Leu Gly Val Val Arg Gln Leu Lys

915 920 925

Arg Lys Gly Arg Glu Leu Leu Val Asp Glu Leu Met Ser Asp Ala Leu

930 935 940

Arg Thr Leu Arg Leu Gly Leu Arg Arg His Gly Val Arg Ala Arg Ile

945 950 955 960

Ala Phe Asn Leu Thr Ala Asn Lys Arg Ile Arg Pro Gly Gly Lys Glu

965 970 975

Glu Val Leu Asp Gln Glu Gly Arg Val Leu Leu Leu Thr Glu Thr Leu

980 985 990

Leu Ala Trp Tyr Glu Leu Tyr Thr Ala Glu Arg Trp Thr Asp Glu Pro

995 1000 1005

Ala Arg Glu Leu Trp Asn Arg His Ile Gln Pro Leu Leu Gly Ala

1010 1015 1020

Thr Ile Leu Gln Asn Thr Val Asn Gln Glu Asp Thr Pro Ser Ala

1025 1030 1035

Ala Lys Arg Arg Lys Leu Arg Glu Glu Thr Ser Gly Lys Leu Lys

1040 1045 1050

His Val Ala Glu Glu Ile Ala Lys Asn Asp Ser Leu Cys Arg Gln

1055 1060 1065

Leu His Val Leu Trp Ser Ala Gln Trp Gln Thr Glu Asp Val Ile

1070 1075 1080

Trp Arg Thr Arg Leu Arg Met Met Arg Arg Trp Leu Leu Pro Arg

1085 1090 1095

Gly Val Lys Arg Asn Ala Gln Leu Arg Ile Ser Ile Arg Asp Val

1100 1105 1110

Gly Gly Leu Ser Leu Thr Arg Ile Ala Ser Phe Lys Ser Leu Tyr

1115 1120 1125

Gln Val Gln Lys Ala Tyr Gln Met Arg Pro His Pro Glu Asp Pro

1130 1135 1140

Arg Leu Asn Ile Pro Glu Arg Gly Asp Ser Arg Leu Glu Asn Phe

1145 1150 1155

Gly Gln Arg Val Leu Asp Ala Met Glu Arg Met Arg Glu Asn Arg

1160 1165 1170

Val Lys Gln Leu Ala Ser Arg Ile Ala Glu Ala Ala Leu Gly Ile

1175 1180 1185

Gly Gly Glu Thr Gly Ile Ser Ser Lys Asp Gly Ser Gln Lys Lys

1190 1195 1200

Arg Pro Thr Glu Arg Ser Ser Asp Pro Arg Phe Ala Pro Cys His

1205 1210 1215

Ala Val Val Ile Glu Asp Leu Thr His Tyr Arg Pro Asp Glu Thr

1220 1225 1230

Gln Thr Arg Arg Glu Asn Arg Gln Leu Met Ser Trp Ser Ser Ser

1235 1240 1245

Lys Val Lys Lys Tyr Leu Gly Glu Ala Cys Glu Leu Asn Gly Leu

1250 1255 1260

Tyr Leu Arg Glu Val Ser Pro Ala Tyr Thr Ser Arg Gln Asp Ser

1265 1270 1275

Arg Thr Gly Ala Pro Gly Leu Arg Cys Asn Asp Val Thr Val Val

1280 1285 1290

Glu Phe Asn Asn Ser Pro Phe Trp Arg Lys Gln Val Gly Ala Ala

1295 1300 1305

Glu Lys Asn Gln Lys Glu Gly Asn Lys Gly Asp Ala Arg Glu Arg

1310 1315 1320

Tyr Leu Leu Ser Ile Glu Glu Gly Ile Arg Gly Ala Ala Asn Asp

1325 1330 1335

Arg Asp Ile Phe Arg Ile Pro Val Lys Gly Gly Glu Ile Phe Val

1340 1345 1350

Ser Ala Cys Ile Thr Asp Gly Gly Asn Asn Ala Lys Lys Asn Ala

1355 1360 1365

Pro Pro Gly Leu Gln Ala Asp Leu Asn Ala Ala Ala Asn Ile Gly

1370 1375 1380

Leu Arg Ala Ile Phe Asp Pro Asp Trp Glu Gly Arg Trp Trp Tyr

1385 1390 1395

Ile Pro Cys Asp Ala Ala Thr Leu Cys Pro Asp Ala Lys Lys Phe

1400 1405 1410

Ile Gly Cys Lys Ala Val Asp Pro Thr Lys Pro Leu Arg Val Val

1415 1420 1425

Ala Glu Glu Gly Ala Ile Ser Ala Ser Gly Ile Gly Ser Lys Lys

1430 1435 1440

Ser Gly Arg Lys Lys Asn Ala Ala Thr Asp Gly Thr Arg Ile Val

1445 1450 1455

Asn Leu Trp Arg Asp Pro Ser Gly Ala Pro Ile His Arg Asp Val

1460 1465 1470

Leu Arg Ser Pro Glu Trp Gln Asp Tyr Ala Gly Tyr Trp Asn Glu

1475 1480 1485

Val Gln His Arg Val Ile Arg Asn Leu Lys Thr Cys Tyr Glu Gln

1490 1495 1500

Thr Ser Gln Gln Glu Asp Pro Phe Val Ser Gln Asp Ala Asp Lys

1505 1510 1515

Pro Phe

1520

<210> 282

<211> 1180

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12b sequence

<400> 282

Met Lys Arg Leu Ala Glu Thr Ala Leu Ala Asp Lys Val Lys Cys Glu
1 5 10 15
Thr Asn Ser Arg Pro Lys Gly Glu Arg Ala Tyr Ala Asn Ser Ile Leu
20 25 30
His Asp Val Glu Ser Ala Cys Gly Phe Thr Tyr Arg Val Asp Lys Gly

35 40 45
Glu Gln Pro Val Pro Val Ser Asp Tyr Ser His Tyr Ala Asn Asp Tyr
50 55 60
Arg Trp Gly Pro Ala Asn His Ser Glu Phe Ala Val Met Leu Asp His
65 70 75 80
Ala Ala Arg Arg Val Ser Leu Ala His Thr Trp Ile Lys Arg Ala Glu
85 90 95
Ala Glu Arg Arg Gln Phe Glu Glu Asn Ala Lys Lys Ile Asp Lys Val

100 105 110
Pro Lys Val Ala Arg Glu Trp Leu Asp Ser Leu Cys Ala Glu Arg Ser
115 120 125
Ile Val Leu Gly Ala Leu Glu Pro Tyr Arg Ile Arg Arg Arg Ala Val
130 135 140
Asp Gly Trp Lys His Val Val Ala Ala Trp Ser Lys Ser Asp Cys Lys
145 150 155 160
Thr Ala Gln Asp Arg Ile Thr Ala Ala Arg Leu Leu Gln Glu Asp Pro

165 170 175
Glu Ile Asp Lys Phe Gly Asp Ile Gln Leu Phe Glu Ala Leu Ala Glu
180 185 190
Asp His Ala Val Cys Val Trp Gln Arg Asp Gly Glu Ala Gly Lys Thr
195 200 205
Ser Asp Pro Gln Leu Leu Ile Asp Tyr Ala Leu Ala Ala Glu Ala Glu
210 215 220
Phe Lys Lys Arg His Phe Lys Val Pro Ala Tyr Arg His Pro Glu Ala

225 230 235 240
Phe Trp His Pro Val Phe Cys Asp Phe Gly Gln Ser Arg Trp Lys Ile

245 250 255

Cys Phe Asp Val His Lys Asn Arg Gln Ser Arg Arg Gln Arg Ala Cys

260 265 270

Ala Asn Arg Ile Ser Arg Lys Ile Cys Phe Asp Val His Lys Lys Arg

275 280 285

Gln Thr Leu Arg Leu Ser Leu Glu Val Trp Thr Gly Ser Lys Met Leu

290 295 300

Asp Met Pro Leu Cys Trp Gln Cys Lys Arg Leu Ala Arg Asp Leu Ala

305 310 315 320

Leu Gly Gln Asp His Lys Lys Asp Arg Ser Cys Gln Val Thr Arg Ala

325 330 335

Asp Arg Leu Gly Arg Ala Val Ser Asn Val Ala Arg Asn Gln Glu Val

340 345 350

Gln Ile Leu Gly Leu Phe Glu Gln Glu Tyr Trp Asn Gly Arg Leu Gln

355 360 365

Ala Pro Arg Pro Gln Leu Glu Ala Leu Gly Arg Tyr Ile Glu Lys His

370 375 380

Gly Trp Asp Ala Lys Ala Gln Lys Ser Cys Arg Ala Ile Arg Trp Met

385 390 395 400

Ile Ser Phe Ser Pro Arg Leu Gln Pro Ala Gly Pro Trp Gly Lys Phe

405 410 415

Ala Glu Lys Leu Gln Leu Asn Pro Asn Pro Lys Tyr Trp Pro His Ala

420 425 430

Glu Asp Asn Lys Asp Arg Gly Ser Arg Ser Lys Leu Ile Leu Cys Arg

435 440 445

Leu Pro Gly Leu Arg Val Leu Ser Val Asp Leu Gly His Arg Tyr Ala

450 455 460

Ala Ala Cys Ala Val Trp Glu Ala Val Asp Ala Glu Gln Val Lys Glu

465 470 475 480

Ala Cys Gln Ala Ala Gly His Arg Glu Pro Asn Glu Asn Asp Leu Tyr

485 490 495

Leu His Leu Lys Lys Arg Thr Thr Lys Gln Lys Lys Gly Ser Gln Gly
500 505 510
Val Val Glu Glu Thr Thr Ile Tyr Arg Arg Ile Gly Ala Asp Thr Leu
515 520 525
Pro Asp Cys Thr Pro His Pro Ala Pro Trp Ala Arg Leu Asp Arg Gln
530 535 540
Phe Leu Ile Arg Leu Gln Gly Glu Glu Asp Glu Ala Arg Ala Ala Ser

545 550 555 560
Asn Glu Glu Val Trp Ala Val His Lys Leu Glu Ala Glu Leu Gly Arg
565 570 575
Thr Ile Pro Leu Ile Asp Arg Leu Leu Gly Ala Gly Trp Gly Gln Thr
580 585 590
Glu Lys Gln Lys Ala Arg Leu Lys Ala Leu Arg Glu Leu Gly Trp Thr
595 600 605
Pro Ala Asn Lys Cys Gln Ala Phe Asn Ser Thr Asp Glu Thr Glu Leu

610 615 620
Arg Arg Pro Ser Leu Ala Val Asp Glu Leu Met Leu Asp Ala Val Gly
625 630 635 640
Thr Leu Arg Leu Ala Leu Lys Arg His Gly Asp Arg Ala Arg Ile Ala
645 650 655
Arg Tyr Leu Ile Thr Asp Glu Arg Thr Lys Pro Gly Gly Val Lys Glu
660 665 670
Lys Leu Asp Glu Asn Gly Arg Ile Glu Leu Leu Gln Asp Ala Leu Ile

675 680 685
Ile Trp His Gly Leu Phe Ser Ser Pro Arg Trp Arg Asp Asp Ala Ala
690 695 700
Lys Gln Leu Trp Asn Glu His Ile Ala Lys Leu Val Gly Glu Gln Asn
705 710 715 720
Leu Val Glu Val Ser Glu Asp Ala Ser Gly Ser Glu Arg Arg Thr Lys
725 730 735
Gln Lys Gln Asn Arg Glu Lys Leu Arg Glu Ala Ala Lys Ala Leu Val

740 745 750

Asp Asp Val Ala Leu Arg Gln Ala Leu His Asp Met Trp Lys Arg Arg

755 760 765

Trp Glu Glu Glu Asp Arg Glu Trp Arg Arg Arg Leu Arg Trp Phe Lys

770 775 780

Asp Trp Val Leu Pro Arg Arg Glu Gln Ala Arg Lys Ala Tyr Ser Arg

785 790 795 800

Pro Ala Glu Thr Gly Ser Ser Ser His Pro Lys Arg Arg Ala Arg Tyr

805 810 815

Ala Ala Ile Arg Arg Val Gly Gly Leu Ser Leu Thr Arg Leu Ala Thr

820 825 830

Leu Thr Glu Phe Arg Arg Lys Val Gln Val Gly Phe Phe Thr Arg Leu

835 840 845

Lys Pro Asp Gly Thr Lys Ala Glu Ala Lys Glu Gly Phe Gly Gln Ser

850 855 860

Thr Leu Asp Ala Leu Glu His Leu Arg Ala Gln Arg Val Lys Gln Leu

865 870 875 880

Ala Ser Arg Ile Val Glu Ala Ala Leu Gly Val Gly Arg Ile Arg Arg

885 890 895

Phe Pro Gly Val Lys Asn Pro Lys Arg Pro Asp Thr Pro Val Asp Lys

900 905 910

Pro Cys His Ala Ile Val Ile Glu Asn Leu Thr His Tyr Arg Pro Glu

915 920 925

Glu Thr Arg Thr Arg Arg Glu Asn Arg Gln Leu Met Thr Trp Ser Ser

930 935 940

Ser Lys Ile Lys Lys Tyr Leu Ala Glu Ala Cys Gln Leu Tyr Gly Leu

945 950 955 960

His Leu Arg Glu Val Thr Ala Ala Tyr Thr Ser Arg Gln Asp Ser Arg

965 970 975

Thr Gly Ala Pro Gly Leu Arg Cys Gln Asp Val Pro Val Lys Glu Phe

980 985 990

Met Arg Ser Leu Phe Trp Arg Lys Glu Val Ala Gln Ala Glu Lys Lys

995 1000 1005

Leu Thr Ala Gly Lys Gly Ser Ser Tyr Glu Arg Leu Leu Cys Glu

1010 1015 1020

Leu Asn Gln Arg Trp Lys Asp Asn Ser Pro Gly Asp Gly Lys Arg

1025 1030 1035

Ala Glu Leu Leu Arg Leu Pro His Lys Gly Gly Glu Ile Phe Val

1040 1045 1050

Ser Ala Ala Pro Asp Ser Pro Ala Ala Arg Gly Leu Gln Ala Asp

1055 1060 1065

Leu Asn Ala Ala Ala Asn Ile Gly Leu Arg Ala Leu Thr Asp Pro

1070 1075 1080

Asp Trp Pro Gly Lys Trp Trp His Val Pro Cys Asn Ala Val Thr

1085 1090 1095

Phe Arg Pro Val Glu Asp Lys Val Lys Gly Ser Ala Ala Val Lys

1100 1105 1110

Leu Asp Gln Ser Leu Arg Gln Val Ala His Pro Gln Ser Lys Asp

1115 1120 1125

Pro Gly Ala Lys Lys Ser Lys Glu Ile Val Asn Leu Trp Cys Asp

1130 1135 1140

Ile Ser Ser Leu Pro Leu Glu His Arg Glu Trp Lys Leu Asp Trp

1145 1150 1155

Glu Pro Tyr Pro Ala Tyr Trp Asn Asn Val Gln Cys Arg Val Ile

1160 1165 1170

Arg Val Leu Gln Gly Lys Val

1175 1180

<210> 283

<211> 1546

<212> PRT

<213> Unknown

<220><223> Description of Unknown:

Cas12b sequence

<400> 283

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Leu Asn Ala Pro Ser Asp Thr Thr Asp Arg Ser Pro Leu Trp His Arg
            20                  25                  30
Ile Phe Arg Thr His Tyr Ala Ile Cys Cys Gly Ala Arg Glu Phe Gly
        35                  40                  45

Lys Leu Leu Leu Asp Leu Arg Gly Gly Leu Pro Thr Ser Leu Ala Gln
    50                  55                  60
Leu Gly Glu Gly Ile Ala Glu Asn Asp Arg Arg Gln Thr Gln Arg Gly
65                  70                  75                  80
Thr Arg Arg Ile Leu Ala Leu Gly Trp Leu Ser Val Glu Asp Leu Asp
                85                  90                  95
His Ala Arg Asn Asp Pro His Arg Val Gln Asp Thr Ala Pro Gly Ser
            100                 105                 110

Pro Leu Asp Gln Asp Leu Ala Glu Lys Ile Leu Arg Lys Ile Leu Ile
        115                 120                 125
Thr Lys Gly Ile Lys Ser Glu Glu Glu Gln Ser Asn Trp Ile Ser Asp
    130                 135                 140
Cys Leu Pro Ala Leu Thr Ala Asn Ile Arg Pro Asp Ala Val Trp Val
145                 150                 155                 160
Asn Arg Ala Glu Ser Phe Ala Gln Trp Gln Arg Gly Thr Gln Pro Gly
                165                 170                 175

Ala Gln Pro Pro Thr Pro Glu Glu Ala Gln Gln Ile Leu Phe Ser Leu
            180                 185                 190
Cys Gly Glu Ser Leu Val Thr Leu Thr Leu Pro Glu Gln Pro Ala Ala
        195                 200                 205
Ala Gly Gln Lys Gln Pro Asp Gln Glu Thr Ser Pro Asp Pro Glu Glu
    210                 215                 220
Gln Thr Asp Arg Pro Pro Ala Ala Pro Ser Ala Asp Asp Glu Met Asp
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225 230 235 240

Pro Ser Asn Ala Ser Arg Gly Ile Phe Gly Asp Leu Phe Gly Glu Asn
245 250 255
Ala Glu Gly Lys Arg Ser Arg Ser Gln Gly Lys Asp Asn Phe Ala Cys
260 265 270
Ala Val Arg Asp Phe Leu Cys Ala Asn Pro Thr Pro Ser Ala Asp Ala
275 280 285
Ile Thr Glu Phe Arg Glu Lys Gln Lys Pro Arg Glu Pro Asn Pro Pro
290 295 300

Gly Pro Glu Lys Tyr Pro Pro Glu Val Ser Thr Ser Gly Ala Pro Thr
305 310 315 320
Ala Val Ala Lys Arg Tyr Arg Lys Leu Leu Val Cys Ala Gly Leu Trp
325 330 335
Pro Lys Ser Ala Asp Glu Asp Gly Ser Ser Arg Asn Ser Ala Lys Thr
340 345 350
Lys Phe Ala Asp Pro Lys Glu Pro Gln Lys Thr Glu Ile Gln Ile Asn
355 360 365

Ala Leu Asp Leu Ile Asp Ala Cys Asn Gln Ala Ala Pro Ala Asp Asp
370 375 380
Ser Gly Thr Ser Pro Lys Ala Gly Arg Val Phe Ala Pro Ala Trp Ala
385 390 395 400
Ser Asn Ile Ala Glu Lys Val Ala Ser Ala Thr Gln Met Pro Ala Asn
405 410 415
Ala Lys Ser Leu Asn Glu Phe Lys Arg Leu Met Phe Ala Leu Ala Ala
420 425 430

Arg Arg Phe Ser Gln Thr Gln Ser Trp Thr Arg Arg Asn Glu Ala Glu
435 440 445
Arg His Met Ala Ala Ala Arg Gln Asp Ala Ala Val Ala Arg Leu Arg
450 455 460
Glu Ile Asp Pro Asp His Lys Ala Gln Asp Trp Leu Arg Gly Tyr Glu
465 470 475 480

Gln Arg Arg Ala Asp Gln Ser Gly Ser Asn Gly Glu Phe Arg Ile Thr
485 490 495

Arg Arg Met Ile Gly Glu Ala Glu Ala Val Phe Lys Ala Trp Ala Gly
500 505 510
Thr Asn Ser Ala Ala Glu Arg Glu Leu Lys Thr Val Ala Val Gln Thr
515 520 525
Thr Ala Glu Lys Phe Gly Asp Ala Ala Leu Tyr Ser Glu Ile Ala Arg
530 535 540
Asn Thr Ala Ala Glu Ala Val Trp Arg Ser Gly Ser Ala Pro Glu Ile
545 550 555 560

Leu Asp Gln Trp Val Lys Leu Arg Lys Ala Gln Ser Asp Gln Gln Arg
565 570 575
Thr Arg Val Pro Arg Phe Cys His Pro Asn Ala Phe Arg His Pro Thr
580 585 590
Trp Cys Glu Phe Gly Glu Ser Ser Lys Pro Gly Val Trp Tyr Ala Trp
595 600 605
Asn Pro Lys Ser Lys Pro Arg Lys Pro Glu Val Gly Gly Glu Gly Asp
610 615 620

Gly Thr Arg Arg Leu Trp Val Leu Leu Pro Asp Phe Asn Ser Gly Ile
625 630 635 640
Gly Gln Ala Val Pro Leu Arg Trp Arg Ser Lys Arg Leu Ser Lys Asp
645 650 655
Leu Gly Glu Ala Leu Gln Pro Ser Asp Ala Pro Ile Pro Arg Ala Asp
660 665 670
Arg Val Ser Ile Ala Ala Ala Gly Leu Asn Leu Glu Gly Ala Asn Gly
675 680 685

Val Pro Ala Arg Tyr Arg Pro Ser Leu Pro Phe Ser Glu Asn Thr Lys
690 695 700
Gly Trp Asn Ala Arg Leu Gln Ala Asn Arg Thr Ala Leu Leu His Leu
705 710 715 720
Glu Ser Lys Trp Asp Ala Glu Ala Ala Thr Trp Arg Asp Gly Gly Arg

725 730 735

Ser Leu Leu Ala Leu Lys Trp Phe Thr Thr Phe Ser Pro Glu Leu Ala

740 745 750

Met Ser Glu Gly Pro Gly Arg Ala Ile His Pro Lys Leu Gly Trp Asn

755 760 765

Ser Glu Pro His Ser Asp Leu Asn Arg Ala Gln Lys Arg Gly Gly Asn

770 775 780

Ala Lys Leu Ile Leu Ser Arg Leu Pro Gly Leu Arg Val Leu Ser Val

785 790 795 800

Asp Leu Gly His Arg Tyr Ala Ala Ala Cys Ala Val Trp Glu Thr Leu

805 810 815

Thr Thr Glu Gln Met Asn Ala Ala Cys Gln Ala Lys Asn His Thr Gln

820 825 830

Pro Ala Glu Ser Asp Met Tyr Val His Leu Ala His Pro Thr Glu Arg

835 840 845

Val Val Lys Ser Gly Arg Lys Lys Gly Gln Asn Leu Ile Gln Thr Thr

850 855 860

Val Tyr Arg Arg Ile Ala Ala Asp Thr Leu Pro Asp Gly Thr Pro His

865 870 875 880

Pro Ala Pro Trp Gly Arg Leu Asp Arg Gln Phe Leu Ile Lys Leu Gln

885 890 895

Gly Glu Gln Arg Pro Thr Arg Ala Ala Ser Lys Asn Glu Ala Asp Leu

900 905 910

Ala Asn Ala Leu Phe His Arg Leu Gly Leu Arg Ser Asp Ala Asp Ser

915 920 925

Glu Asn Lys Ser Arg Ala Val Asp Lys Leu Met Ala Arg Thr Val Arg

930 935 940

Val Ala Thr Leu Gly Leu Lys Arg His Ala Arg Arg Ala Lys Ile Ala

945 950 955 960

Tyr Ala Leu Asp Pro Asn Thr Lys Ala Ile Pro Gly Met Gly Gly Ser

965 970 975

Ser Ala Ala Phe Thr Pro Gly Asp Glu Pro His Ile His Leu Leu Thr
980 985 990

Asp Ala Leu Phe Asp Trp Gln Ser Leu Ala Thr Asp Ala Lys Trp Asp
995 1000 1005

Asp Ala His Ala Arg Ser Leu Trp Asn His His Ile Ala Thr Leu
1010 1015 1020

Pro Gly Gly Phe His Leu Glu Asn Pro Thr Pro Arg Asp Glu Ser
1025 1030 1035

Ala His Glu Pro Ser Arg Gln Arg Gln Arg Ser Gly Asp Asp Ala
1040 1045 1050

Leu Arg Ala Thr Leu Lys Pro Ile Ala Glu Lys Leu Ser Lys Ala
1055 1060 1065

Asp Arg Gln Glu Val His Ala Ala Trp Lys Lys Tyr Trp Gly Asp
1070 1075 1080

Ser Asp Gly Gln Ser Ala Ile Val Pro Lys Val Leu Gln Gly Gln
1085 1090 1095

Arg Gly Pro Glu Lys Thr Thr Pro Ser Ala Ser Ala Ser Gly Trp
1100 1105 1110

His Gly Lys Ile Arg Trp Ile Thr Asp Trp Ile Met Gly Lys Tyr
1115 1120 1125

Leu Glu Gly Cys Thr Gly His Ala Trp Lys His Asp Val Gly Gly
1130 1135 1140

Leu Ser Val Ser Arg Ile Thr Thr Met Lys Ser Leu Tyr Gln Leu
1145 1150 1155

His Lys Ala Phe Ala Met Arg Ala Thr Pro Glu Lys Pro Arg Gly
1160 1165 1170

Ala Pro Glu Lys Gly Glu Ser Asn Leu Gly Ala Ala Gln Gly Ile
1175 1180 1185

Leu Thr Ala Met Glu Ser Met Arg Gln Gln Arg Val Lys Gln Leu
1190 1195 1200

Ala Ser Arg Ile Ala Glu Ala Ala Leu Gly Ala Gly Ile Glu Arg

1205 1210 1215

Arg Ser Asp Asn Gly Arg Glu Leu Gln Arg Pro Arg Glu Arg Val

1220 1225 1230

Asp Asp Pro Arg Phe Ala Ala Cys His Ala Val Val Val Glu Asp

1235 1240 1245

Leu Thr Asn Tyr Arg Pro Asp Glu Met Gln Thr Arg Arg Glu Asn

1250 1255 1260

Arg Gln Leu Met Gln Trp Ala Ser Ser Lys Val Lys Lys Tyr Leu

1265 1270 1275

Ser Glu Ala Cys Gln Leu His Gly Leu Tyr Leu Arg Gly Val Pro

1280 1285 1290

Ala Gly Tyr Thr Ser Arg Gln Asp Ser Arg Thr Gly Ala Pro Gly

1295 1300 1305

Val Arg Cys Gly Asp Ile Pro Val Glu Glu Leu Met Ala Ala Pro

1310 1315 1320

Arg Trp Arg Arg Gln Ile Leu Thr Ala Glu Lys Thr Arg Arg Glu

1325 1330 1335

Asn Asn Thr Gly Thr Ala Arg Asp Arg Tyr Ile Leu Thr Leu Asp

1340 1345 1350

Glu Lys Tyr Arg Leu Leu Thr Ala Glu Gln Arg Lys Lys Thr Pro

1355 1360 1365

Pro Ala Arg Ile Pro Val Lys Gly Gly Asp Leu Phe Val Ser Ala

1370 1375 1380

Asp Pro Asp Ser Pro Ala Ala Ser Gly Ile Gln Ala Asp Leu Asn

1385 1390 1395

Ala Ala Ala Asn Ile Gly Leu Lys Ala Leu Ile Asp Pro Asp Trp

1400 1405 1410

Pro Gly Arg Trp Trp Tyr Ile Pro Cys Asp Ala Thr Thr His Lys

1415 1420 1425

Pro Ser Pro Glu Arg Thr Arg Gly Ser Ala Ala Val Asp Cys Asp

1430 1435 1440

Val Pro Leu Gly Pro Asp Ser Thr Gly Thr Pro Glu Asp Arg Asp
1445 1450 1455
Ala Lys Pro Lys Lys Asn Gln Arg Asn Ser Lys Ile Ala Gly Arg
1460 1465 1470
Gly Gln Ser Ala Ile Ile Asn Leu Trp Arg Asp Pro Thr His Leu
1475 1480 1485

Pro Ile Lys Glu Asn Pro Ser Ala Trp Cys Glu Ser Lys Lys Tyr
1490 1495 1500
Trp Asn Gln Val Glu His Asn Val Val Lys Val Ile Glu Ser Lys
1505 1510 1515
Gly Gln Lys Leu Thr Gln Thr Ala Glu Ala Ala Thr Gly Glu Ser
1520 1525 1530
Ala Ser Ser Pro Pro Ile Ala Pro Thr Asp Val Pro Trp
1535 1540 1545

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284
<211> 91
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic
oligonucleotide
<400> 284
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tgcaacccct atagtgagtc gtattaattt c 91
<210> 285
<211> 91
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic
oligonucleotide
<400> 285
agtgtctttg caggaaagaa cacagatctt gagggttgca gtctccgcct acatgggagt 60

tgtgacccct atagtgagtc gtattaattt c 91

<210> 286

<211> 91

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 286

tctttgcagg aaagaacaca gatcttgagg ggtgtagttc ccctcaattt ggggatgaac 60

gtcgacccct atagtgagtc gtattaattt c 91

<210> 287

<211> 91

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 287

tctttgcagg aaagaacaca gatcttgagg gtcgacgttc atccccaaat tgaggggaac 60

tacacccct atagtgagtc gtattaattt c 91

<210> 288

<211> 136

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 288

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acctggaaag tggccattgg cacacccgtt gaaaaattct gtcctctaga cccctatagt 120

gagtcgtatt aatttc 136

<210> 289

<211> 82

<212> DNA

<213> Artificial Sequence

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oligonucleotide

<400> 289

ttccggctcg tatgttgtgt ggaattgtga gcggagtgcc acttctcaga ccgctcgccc 60

tatagtgagt cgtattaatt tc 82

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<211> 113

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 290

cgagcggtca tcttgaagcc aacggggtgt ttgctcttgg aaagagcaca ttggcacttc 60

ccgttgtcct cgccgtccta tagacgaccc ctatagtgag tcgtattaat ttc 113

<210> 291

<211> 60

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 291

aattgtgagc ggataaacac aggtgctaat gcctccccta tagtgagtcg tattaatttc 60

<210> 292

<211> 105

<212> DNA

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polynucleotide

<400> 292

gagacatcgt ccagcaatag gagtttctca caccctgcag cacttatagc tagacggttg 60

tcctgaccaa aagacagaac ccctatagtg agtcgtatta atttc 105

<210> 293

<211> 84

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 293

atggtcatag ctgtttcctg tgtttatccg ctcagtgcta atcacattta attcatctac 60

cctatagtga gtcgtattaa tttc 84

<210> 294

<211> 105

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 294

gataaataat gtaatcctgt ggttgaatgg atttttttcca tccttagcac acgcacagta 60

ttctttgccc tttaggcaaa ccctatagtg agtcgtatta atttc 105