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(71) 출원인
퀀텀-에스아이 인코포레이티드
미국 06437 코네티컷주 길포드 올드 화이트필드
스트리트 530
(72) 발명자
로스버그, 조나단, 엠.
미국 06437 코네티컷주 길포드 운카스 포인트 로
드 215
리드, 브라이언
미국 06443 코네티컷주 매디슨 홀 로드 94
(뒷면에 계속)
(74) 대리인
양영준, 김영

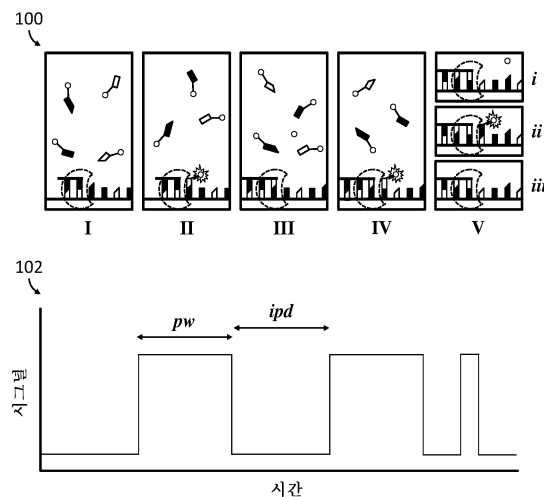
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(54) 발명의 명칭 시퀀싱 반응을 위한 중합 효소

(57) 요약

변형된 제조합 중합 효소를 포함하는 조성물이, 이러한 변형된 중합 효소를 코딩하는 핵산 분자와 함께 제공된다. 일부 측면에서, 핵산 분자를 합성하거나 또는 핵산 주형을 시퀀싱하기 위해 이러한 중합 효소를 사용하는 방법이 제공된다.

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(72) 발명자

부이야, 모함마드, 와두드

미국 06437 코네티컷주 길포드 화이트필드 스트리트 329

판데이, 만줄라

미국 06437 코네티컷주 길포드 화이트 버치 드라이브 460

크리스티안, 토마스

미국 06512 코네티컷주 뉴헤이븐 코브 스트리트 103 아파트먼트 비

래키, 제레미

미국 06437 코네티컷주 길포드 노튼타운 로드 636

명세서

청구범위

청구항 1

표 1로부터 선택된 제1 중합 효소에 기초한 재조합 중합 효소이며, 여기서 제1 중합 효소의 적어도 하나의 아미노산 절편이 표 1로부터 선택된 제2 중합 효소로부터의 상응하는 아미노산 절편으로 대체되었고, 제1 중합 효소와 제2 중합 효소가 상이하고, 임의로 재조합 중합 효소가 표 1의 제1 및/또는 제2 중합 효소의 서열과 비교하여 하나 이상의 아미노산 삽입, 결실, 또는 치환을 추가로 포함하는 것인 재조합 중합 효소.

청구항 2

제1항에 있어서, 제1 중합 효소가 $\Phi 29$ 폴리머라제 (서열식별번호: 1)이고, 제2 중합 효소가 서열식별번호: 2-19 중 어느 하나로부터 선택되는 것인 재조합 중합 효소.

청구항 3

제1항 또는 제2항에 있어서, 제1 중합 효소의 적어도 1 내지 3개의 추가의 아미노산 절편이 표 1의 하나 이상의 중합 효소로부터의 상응하는 아미노산 절편으로 대체되었고, 표 1의 하나 이상의 중합 효소가 제1 중합 효소와 상이하고, 임의로 상응하는 아미노산 절편 중 하나 이상이 표 1 내에서의 그의 서열과 비교하여 하나 이상의 아미노산 삽입, 결실, 또는 치환을 포함하는 것인 재조합 중합 효소.

청구항 4

제1항 내지 제3항 중 어느 한 항에 있어서, 절편 중 하나 이상이 표 1의 중합 효소의 도메인을 포함하는 것인 재조합 중합 효소.

청구항 5

제1항 내지 제4항 중 어느 한 항에 있어서, 아미노산 절편 중 하나 이상이 표 1의 중합 효소의 도메인의 부분을 포함하는 것인 재조합 중합 효소.

청구항 6

제4항 또는 제5항에 있어서, 아미노산 절편 중 하나 이상이 표 1의 중합 효소 내의 도메인 또는 그의 부분을 플랭킹하는 하나 이상의 아미노산을 포함하는 것인 재조합 중합 효소.

청구항 7

제1항 내지 제6항 중 어느 한 항에 있어서, 적어도 하나의 아미노산 삽입, 결실, 또는 치환이 표 1의 상이한 자연 발생 중합 효소 내에서 발견된 아미노산 삽입, 결실, 또는 치환에 상응하는 것인 재조합 중합 효소.

청구항 8

제1항 내지 제7항 중 어느 한 항에 있어서, 적어도 하나의 아미노산 삽입, 결실, 또는 치환이 표 1의 자연 발생 중합 효소 내에서 발견되지 않는 아미노산 삽입, 결실, 또는 치환에 상응하는 것인 재조합 중합 효소.

청구항 9

제1항 내지 제8항 중 어느 한 항에 있어서, 하나 이상의 상응하는 아미노산 절편이 M2Y 폴리머라제로부터의 아미노산 1-51, 이. 파에시움(*E. faecium*) 폴리머라제로부터의 아미노산 271-375, 이. 파에시움 폴리머라제로부터의 아미노산 72-89, 및/또는 이. 파에시움 폴리머라제로부터의 아미노산 445-449로 이루어진 군으로부터 선택되는 것인 재조합 중합 효소.

청구항 10

제1항 내지 제9항 중 어느 한 항에 있어서, 적어도 하나의 아미노산 삽입, 결실, 또는 치환이 $\Phi 29$ 폴리머라제

내의 위치: M8, V51, N62, I71, L107, K131, K135, L142, G197, Y224, E239, V250, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, A437, A444, E466, D476, A484, E508, D510, K512, E515, K539, D570, 및 T571로부터 선택된 위치에 상응하는 위치에 있는 것인 재조합 중합 효소.

청구항 11

제10항에 있어서, M8R, V51A, N62D, I71V, L107I, K131E, K135Q, L142K, G197D, Y224K, E239G, V250A, V250I, L253A, L253H, Y281H, I288L, T301C, R306Q, R308L, D325E, D341E, K354R, T368F, E375Y, A437G, A444T, E466K, D476H, A484E, E508R, D510K, D510R, K512Y, E515Q, K539E, D570S, 및 T571V로부터 선택된 하나 이상의 아미노산 치환을 포함하는 재조합 중합 효소.

청구항 12

제1항 내지 제11항 중 어느 한 항에 있어서, 서열식별번호: 1 내의 I71, L107, K135, L142, G197, Y224, E239, V250, L253, E375, A437, A444, E466, D476, A484, E508, D510, K512, E515, K539, D570, 및 T571에 상응하는 위치에 하나 이상의 아미노산 치환을 포함하는 재조합 중합 효소.

청구항 13

제12항에 있어서, 하나 이상의 아미노산 치환이 서열식별번호: 1 내의 I71V, L107I, K135Q, L142K, G197V, Y224K, E239G, V250I, L253A, E375Y, A437G, A444V, E466K, D476H, A484E, E508R, D510R, K512Y, E515Q, K539E, D570S, 및 T571V로부터 선택되는 것인 재조합 중합 효소.

청구항 14

제1항 내지 제13항 중 어느 한 항에 있어서, 서열식별번호: 1 내의 K131, K135, L142, Y148, Y224, E239, V250, L253, R306, R308, E375, A437, E466, D476, A484, E508, D510, K512, E515, K539, D570, 및 T571에 상응하는 위치에 하나 이상의 아미노산 치환을 포함하는 재조합 중합 효소.

청구항 15

제14항에 있어서, 하나 이상의 아미노산 치환이 서열식별번호: 1 내의 K131E, K135Q, L142K, Y148I, Y224K, E239G, V250A, V250I, L253A, L253H, R306Q, R308L, E375Y, A437G, E466K, D476H, A484E, E508R, D510K, D510R, K512Y, E515Q, K539E, D570E, D570S, 및 T571V로부터 선택되는 것인 재조합 중합 효소.

청구항 16

제4항에 있어서, 하나 이상의 아미노산 치환이 서열식별번호: 1 내의 K131E, L142K, Y148I, Y224K, E239G, V250A, L253H, E375Y, A437G, A484E, E508R, D510K, K512Y, E515Q, 및 D570E로부터 선택되는 것인 재조합 중합 효소.

청구항 17

제1항 내지 제16항 중 어느 한 항에 있어서, 치환된 절편 중 적어도 하나가 엑소뉴클레아제 영역, 팜(palm) 영역, TPR1 영역, 핑거 영역, TPR2 영역, 섬(thumb) 영역, 또는 그의 어느 하나의 부분을 포함하고, 하나 이상의 플랭킹 아미노산을 임의로 포함하는 재조합 중합 효소.

청구항 18

표 1의 아미노산 서열과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 아미노산 서열을 갖고 표 2-5의 하나 이상의 아미노산 변형을 포함하는 재조합 중합 효소.

청구항 19

제18항에 있어서, 하나 이상의 아미노산 변형이 적어도 하나의 아미노산 돌연변이를 포함하는 것인 재조합 중합 효소.

청구항 20

제18항에 있어서, 하나 이상의 아미노산 변형이 적어도 하나의 도메인 치환을 포함하는 것인 재조합 중합 효소.

청구항 21

제18항에 있어서, 하나 이상의 아미노산 변형이 적어도 하나의 도메인 치환 및 적어도 하나의 아미노산 돌연변이를 포함하는 것인 재조합 중합 효소.

청구항 22

제18항에 있어서, 표 2로부터 선택된 서열을 갖는 재조합 중합 효소.

청구항 23

제18항에 있어서, 표 3으로부터 선택된 서열을 갖는 재조합 중합 효소.

청구항 24

제1항 내지 제23항 중 어느 한 항에 있어서, 정제 태그를 추가로 포함하는 재조합 중합 효소.

청구항 25

제24항에 있어서, 정제 태그가 C-말단 태그인 재조합 중합 효소.

청구항 26

제24항에 있어서, 정제 태그가 N-말단 태그인 재조합 중합 효소.

청구항 27

제24항 내지 제26항 중 어느 한 항에 있어서, 정제 태그가 His 태그인 재조합 중합 효소.

청구항 28

제1항 내지 제27항 중 어느 한 항에 있어서, 커플링 기를 추가로 포함하는 재조합 중합 효소.

청구항 29

제28항에 있어서, 커플링 기가 재조합 중합 효소의 C-말단 단부에 부착되는 것인 재조합 중합 효소.

청구항 30

제28항에 있어서, 커플링 기가 재조합 중합 효소의 N-말단 단부에 부착되는 것인 재조합 중합 효소.

청구항 31

제28항 내지 제30항 중 어느 한 항에 있어서, 커플링 기가 비오틀화 서열인 재조합 중합 효소.

청구항 32

제1항 내지 제31항 중 어느 한 항에 있어서, His 태그 및 비오틀화 서열을 포함하는 재조합 중합 효소.

청구항 33

제18항에 있어서, 표면 상에 고정화되는 재조합 중합 효소.

청구항 34

제33항에 있어서, 표면이 나노개구를 포함하는 것인 재조합 중합 효소.

청구항 35

제18항의 재조합 중합 효소를 코딩하는 단리된 핵산 분자.

청구항 36

제18항의 재조합 중합 효소를 포함하는 조성물.

청구항 37

제18항의 재조합 중합 효소를 시퀀싱 반응 혼합물과 접촉시키는 것을 포함하는, 핵산을 시퀀싱하는 방법.

청구항 38

표 1의 아미노산 서열과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 아미노산 서열을 갖고, 표 1 또는 표 2의 상이한 중합 효소로부터의 엑소뉴클레아제 영역과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 엑소뉴클레아제 영역을 포함하는 재조합 중합 효소.

청구항 39

표 1의 아미노산 서열과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 아미노산 서열을 갖고, 표 1 또는 표 2의 상이한 중합 효소로부터의 팜 영역과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 팜 영역을 포함하는 재조합 중합 효소.

청구항 40

표 1의 아미노산 서열과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 아미노산 서열을 갖고, 표 1 또는 표 2의 상이한 중합 효소로부터의 TPR1 영역과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 TPR1 영역을 포함하는 재조합 중합 효소.

청구항 41

표 1의 아미노산 서열과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 아미노산 서열을 갖고, 표 1 또는 표 2의 상이한 중합 효소로부터의 핑거 영역과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 핑거 영역을 포함하는 재조합 중합 효소.

청구항 42

표 1의 아미노산 서열과 적어도 80% 동일한 아미노산 서열을 갖고, 표 1 또는 표 2의 상이한 중합 효소로부터의 TPR2 영역과 적어도 80% 동일한 TPR2 영역을 포함하는 재조합 중합 효소.

청구항 43

표 1의 아미노산 서열과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 아미노산 서열을 갖고, 표 1 또는 표 2의 상이한 중합 효소로부터의 섬 영역과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 섬 영역을 포함하는 재조합 중합 효소.

청구항 44

표 1의 아미노산 서열과 적어도 60%, 60-70%, 70-80%, 또는 적어도 80% 동일한 아미노산 서열을 갖고, 제38항 내지 제43항 중 어느 한 항의 2개 이상의 영역을 포함하는 재조합 중합 효소.

청구항 45

제1항 내지 제34항 및 제38항 내지 제44항 중 어느 한 항의 하나 이상의 폴리머라제를 사용하여 시퀀싱 반응을 수행하는 것을 포함하는 시퀀싱 방법.

발명의 설명

기술 분야

관련 출원

본 출원은 35 U.S.C. § 119(e) 하에, 2016년 12월 19일에 출원된 미국 가출원 번호 62/436,410을 우선권 주장하며, 이 가출원은 그 전문이 본원에 참조로 포함된다.

[0003] **본 출원의 분야**

[0004] 본 출원은 일반적으로, 생물학적 및/또는 화학적 샘플의 시퀀싱 분석을 위한 방법 및 조성물에 관한 것이다.

배경 기술

[0005] DNA 폴리머라제는 모든 생물체의 게놈 복제에 필수적인 뉴클레오티드 중합 효소이다. DNA 폴리머라제는 복제 및 복구 동안 게놈 무결성을 유지하는 역할 이외에도, DNA 클로닝, 돌연변이 유발, 및 시퀀싱을 포함하여 시험관 내에서의 DNA 조작을 위해 널리 사용되고 있다. 주형 DNA에 따라 상보적 가닥을 합성할 수 있는 DNA 폴리머라제의 기본적인 능력은 보존되지만, 효소 간에는 전진성(processivity), 충실도, 및 기질 뉴클레오티드 선택성을 포함한 특이적 특성이 상이하다.

발명의 내용

[0006] 본원에 개시된 기술의 측면은 시험관내 중합 반응을 시행하기 위해 사용될 수 있는 변형된 중합 효소 (예를 들어, 폴리머라제)에 관한 것이다. 일부 측면에서, 본원에 기재된 폴리머라제는 시퀀싱 반응 (예를 들어, 핵산 시퀀싱)에 사용하기 적합하다. 일부 측면에서, 본 개시내용은 하나 이상의 변형을 갖는 재조합 폴리머라제를 제공한다. 일부 실시양태에서, 본 개시내용의 재조합 폴리머라제는 아미노산 돌연변이 또는 도메인 치환 중 적어도 하나를 포함한다.

[0007] 일부 측면에서, 본 개시내용은 자연 발생 폴리머라제 (예를 들어, 표 1로부터 선택됨)에 기초하고 하나 이상의 아미노산 돌연변이 및/또는 절편 치환을 포함하는 아미노산 서열을 갖는 변형된 중합 효소 (예를 들어, 핵산 중합 효소, 또는 핵산 폴리머라제)를 제공한다. 일부 실시양태에서, 변형된 중합 효소는 하나 이상의 절편 치환 (예를 들어, 여기서 폴리머라제의 하나 이상의 절편이 상이한 폴리머라제로부터의 하나 이상의 상응하는 절편으로 대체된다), 하나 이상의 아미노산 부가, 결실, 및/또는 치환, 또는 그의 조합을 포함한다. 일부 실시양태에서, 절편은 폴리머라제의 규정된 영역 (예를 들어, 구조적 또는 기능적 도메인 또는 서브 도메인), 또는 그의 부분을 포함하며, 이는 하나 이상의 플랭킹 아미노산 (예를 들어, 표 1의 자연 발생 폴리머라제 내의 특정 영역 또는 그의 부분의 어느 한쪽 상의 아미노산 1 내지 50개, 1 내지 40개, 1 내지 30개, 1 내지 20개, 5 내지 10개, 5 내지 25개, 또는 이들 범위 내의 임의의 정수)을 임의로 포함한다. 일부 실시양태에서, 하나 이상의 아미노산 삽입, 결실, 또는 치환은 하나 이상의 위치에서 2개의 자연 발생 폴리머라제 간의 자연 발생 차이에 상응한다. 일부 실시양태에서, 하나 이상의 아미노산 삽입, 결실, 또는 치환은 새로운 비-자연 발생 변화이다. 일부 실시양태에서, 아미노산 치환은 보존적 아미노산 치환 (예를 들어, 하나의 아미노산을 유사한 특성, 예를 들어 유사한 하전, 극성, 소수성, 친수성, 및/또는 다른 유사한 특성, 예컨대 유사한 크기를 갖는 또 다른 아미노산으로 대체시킨다)이다. 일부 실시양태에서, 아미노산 치환은 비-보존적 아미노산 치환이다. 일부 실시양태에서, 하나 이상의 아미노산 삽입, 결실, 또는 치환은 상이한 폴리머라제로부터의 하나 이상의 교환된 절편 내 및/또는 원래의 폴리머라제의 절편 내를 포함하여, 변형된 폴리머라제 내의 임의의 위치(들)에서 일어날 수 있다.

[0008] 따라서, 일부 실시양태에서 본 개시내용은 표 1로부터 선택된 아미노산 서열 (또는 표 1로부터 선택된 아미노산 서열에 대해 적어도 50%, 적어도 60%, 적어도 70%, 적어도 80%, 80-90%, 90-95%, 95-99%, 또는 그 초과)의 아미노산 서열 동일성을 갖는 아미노산 서열)을 갖고, 표 2, 표 3, 표 4, 또는 표 5로부터의 하나 이상의 아미노산 변형을 포함하는 재조합 중합 효소를 제공한다. 일부 실시양태에서, 하나 이상의 아미노산 변형은 적어도 하나의 아미노산 돌연변이 (예를 들어, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25개, 또는 그 초과)의 아미노산 돌연변이를 포함한다. 일부 실시양태에서, 하나 이상의 아미노산 변형은 적어도 1개 내지 5개 이하의 아미노산 돌연변이, 적어도 1개 내지 10개 이하의 아미노산 돌연변이, 적어도 1개 내지 15개 이하의 아미노산 돌연변이, 적어도 1개 내지 25개 이하의 아미노산 돌연변이, 적어도 1개 내지 50개 이하의 아미노산 돌연변이, 또는 적어도 1개 내지 100개 이하의 아미노산 돌연변이를 포함한다. 일부 실시양태에서, 하나 이상의 아미노산 변형은 적어도 하나의 도메인 치환 (예를 들어, 전체 도메인의 치환, 또는 특정 도메인 또는 특정 도메인의 부분을 포괄하는 절편의 치환)을 포함한다. 일부 실시양태에서, 적어도 하나의 도메인 치환은 엑소뉴클레아제 도메인 치환 및 폴리머라제 도메인 치환 중 적어도 하나를 포함한다. 일부 실시양태에서, 엑소뉴클레아제 도메인 치환은 엑소뉴클레아제 루프 치환을 포함한다. 일부 실시양태에서, 폴리머라제 도메인 치환은 팜(palm) 서브 도메인 치환, TPR1 서브 도메인 치환, 핑거 서브 도메인 치환, TPR2 서브 도메인 치환, 또는 섬/thumb 서브 도메인 치환 중 어느 하나 (예를 들어, 전체의 폴리머라제, 팜, TPR1, 핑거, TPR2, 또는 섬 도메인 또는 서브 도메인, 또는 하나 이상의 플랭킹 아미노산을 임의로 포함한 그 중 어느 하나의 부분의 치환)를 포함한다. 일부 실시양

태에서, 하나 이상의 아미노산 변형은 적어도 하나의 도메인 치환 및 적어도 하나의 아미노산 돌연변이를 포함한다. 일부 실시양태에서, 아미노산 돌연변이는 아미노산 삽입, 결실, 또는 치환일 수 있다.

[0009] 일부 실시양태에서, 본 개시내용의 재조합 중합 효소는 표 2로부터 선택된 서열을 갖는다. 일부 실시양태에서, 본 개시내용은 표 3으로부터 선택된 서열을 갖는 재조합 중합 효소를 제공한다.

[0010] 일부 실시양태에서, 재조합 중합 효소는 정제 태그를 추가로 포함한다. 일부 실시양태에서, 정제 태그는 중합 효소 서열 내의 영역과 공유 결합된다. 일부 실시양태에서, 정제 태그는 중합 효소 서열의 말단 단부와 공유 결합된다. 일부 실시양태에서, 정제 태그는 C-말단 태그이다. 일부 실시양태에서, 정제 태그는 N-말단 태그이다. 일부 실시양태에서, 정제 태그는 His 태그 (예를 들어, 반복 히스티딘 잔기의 서열, 예컨대 헥사히스티딘 서열)이다.

[0011] 일부 실시양태에서, 재조합 중합 효소는 커플링 기를 추가로 포함한다. 일부 실시양태에서, 커플링 기는 중합 효소 서열 내의 영역에 부착된다. 일부 실시양태에서, 커플링 기는 중합 효소의 말단 단부에 부착된다. 일부 실시양태에서, 커플링 기는 재조합 중합 효소의 C-말단 단부에 부착된다. 일부 실시양태에서, 커플링 기는 재조합 중합 효소의 N-말단 단부에 부착된다. 일부 실시양태에서, 커플링 기는 비오틴화 서열이다. 일부 실시양태에서, 재조합 중합 효소는 펩티드 링커 (예를 들어, 5 내지 15개의 아미노산 또는 그 초과 길이)와 직접적으로 연결되거나 또는 이러한 링커에 의해 분리된 정제 태그 (예를 들어, His 태그)와 커플링 기 (예를 들어, 비오틴화 서열)를 포함한다 (예를 들어, 그의 C 말단에 포함한다).

[0012] 일부 실시양태에서, 재조합 중합 효소는 특정 표면 상에 고정화된다. 일부 실시양태에서, 이러한 표면은 재조합 중합 효소와 결합하도록 설정된 커플링 기를 포함한다. 일부 실시양태에서, 상기 표면은 나노개구를 포함한다. 일부 실시양태에서, 상기 표면은 샘플 웰의 바닥면을 포함한다. 일부 실시양태에서, 샘플 웰은 표면 (예를 들어, 칩 또는 통합 장치의 표면) 상의 복수 개의 샘플 웰 사이에 배치된다. 일부 실시양태에서, 복수 개의 샘플 웰 각각은 재조합 중합 효소를 수용하도록 설정된다. 일부 실시양태에서, 재조합 중합 효소를 포함하는 복수 개의 샘플 웰 각각은 단일 분자 시퀀싱 반응을 시행할 수 있다.

[0013] 일부 측면에서, 본 개시내용은 본원에 기재된 재조합 중합 효소를 코딩하는 단리된 핵산 분자를 제공한다. 일부 실시양태에서, 이러한 단리된 핵산 분자는 RNA를 포함한다. 일부 실시양태에서, 단리된 핵산 분자는 DNA를 포함한다. 일부 실시양태에서, 단리된 핵산 분자는 바이러스 벡터를 포함한다. 일부 실시양태에서, 단리된 핵산 분자는 발현 벡터를 포함한다. 일부 실시양태에서, 단리된 핵산 분자는 플라스미드를 포함한다. 일부 실시양태에서, 단리된 핵산은 프로모터 (예를 들어, 유도성 프로모터)를 포함한다. 일부 실시양태에서, 단리된 핵산은 재조합 중합 효소를 발현할 수 있는 숙주 세포 내에 있다. 일부 실시양태에서, 재조합 중합 효소는 숙주 세포로부터 (예를 들어, 바이오리액터에서의 성장 및 유도성 프로모터의 유도 후, 예를 들어 숙주 세포 체제로부터) 단리된다.

[0014] 일부 측면에서, 본 개시내용은 본 출원에 기재된 재조합 중합 효소를 포함하는 조성물을 제공한다. 일부 실시양태에서, 이러한 조성물은 핵산을 시퀀싱하는 방법에 사용된다. 일부 실시양태에서, 상기 조성물은 시퀀싱 반응 혼합물을 추가로 포함한다. 일부 실시양태에서, 시퀀싱 반응 혼합물은 뉴클레오타이드 폴리포스페이트 (예를 들어, 2개 이상의 포스페이트 기를 포함하는 뉴클레오타이드, 예컨대 뉴클레오타이드 또는 뉴클레오타이드 헥사포스페이트), 시퀀싱될 주형 핵산, 상보적 가닥 합성을 위한 출발점으로서 제공되는 핵산 프라이머, 2가 금속 이온, 완충제 성분, 및 염 중 하나 이상을 포함할 수 있다. 일부 실시양태에서, 뉴클레오타이드 폴리포스페이트는 검출 가능한 모이어티 (예를 들어, 발광 표지)를 포함한다.

[0015] 일부 측면에서, 본 개시내용은 본 출원에 기재된 재조합 중합 효소를 시퀀싱 반응 혼합물과 접촉시킴으로써 핵산을 시퀀싱하는 방법을 제공한다. 일부 실시양태에서, 시퀀싱 반응 혼합물은 뉴클레오타이드 폴리포스페이트 (예를 들어, 2개 이상의 포스페이트 기를 포함하는 뉴클레오타이드, 예컨대 뉴클레오타이드 또는 뉴클레오타이드 헥사포스페이트), 시퀀싱될 주형 핵산, 상보적 가닥 합성을 위한 출발점으로서 제공되는 핵산 프라이머, 2가 금속 이온, 완충제 성분, 및 염 중 하나 이상을 포함할 수 있다. 일부 실시양태에서, 뉴클레오타이드 폴리포스페이트는 발광 표지를 포함한다. 일부 실시양태에서, 상기 방법은 주형 핵산에 상보적인 성장 가닥 내의 하나 이상의 뉴클레오타이드 폴리포스페이트의 혼입을 검출하는 것을 추가로 포함한다. 일부 실시양태에서, 검출하는 것은 혼입 이벤트에 관여하는 발광성 표지된 뉴클레오타이드 폴리포스페이트의 하나 이상의 발광 특성 (예를 들어, 수명, 세기, 광자 도착 시간, 양자 수율)을 측정하는 것을 포함한다.

[0016] 일부 측면에서, 본 개시내용은 표 1에서의 재조합 중합 효소 중 어느 하나의 엑소뉴클레아제 영역 또는 그의 부

분 (및 임의로, 한쪽 또는 양쪽 상의 플랭킹 아미노산)을 포함하는 절편을 포함하는 재조합 중합 효소를 제공한다. 일부 측면에서, 본 개시내용은 표 1에서의 재조합 중합 효소 중 어느 하나의 팜 영역 또는 그의 부분 (및 임의로, 한쪽 또는 양쪽 상의 플랭킹 아미노산)을 포함하는 절편을 포함하는 재조합 중합 효소를 제공한다. 일부 측면에서, 본 개시내용은 표 1에서의 재조합 중합 효소 중 어느 하나의 TPR1 영역 또는 그의 부분 (및 임의로, 한쪽 또는 양쪽 상의 플랭킹 아미노산)을 포함하는 절편을 포함하는 재조합 중합 효소를 제공한다. 일부 측면에서, 본 개시내용은 표 1에서의 재조합 중합 효소 중 어느 하나의 핑거 영역 또는 그의 부분 (및 임의로, 한쪽 또는 양쪽 상의 플랭킹 아미노산)을 포함하는 절편을 포함하는 재조합 중합 효소를 제공한다. 일부 측면에서, 본 개시내용은 표 1에서의 재조합 중합 효소 중 어느 하나의 TPR2 영역 또는 그의 부분 (및 임의로, 한쪽 또는 양쪽 상의 플랭킹 아미노산)을 포함하는 절편을 포함하는 재조합 중합 효소를 제공한다. 일부 측면에서, 본 개시내용은 표 1에서의 재조합 중합 효소 중 어느 하나의 섬 영역 또는 그의 부분 (및 임의로, 한쪽 또는 양쪽 상의 플랭킹 아미노산)을 포함하는 절편을 포함하는 재조합 중합 효소를 제공한다. 일부 측면에서, 본 개시내용은 본원에 기재된 바와 같은 2개 이상의 절편을 포함하는 재조합 중합 효소를 제공한다.

[0017] 따라서, 일부 실시양태에서, 재조합 중합 효소는 상이한 중합 효소로부터의 (예를 들어, 상이한 종으로부터의) 하나 이상의 아미노산 절편을 포함하는 키메라 효소이다. 일부 실시양태에서, 키메라 폴리머라제는 하나 이상의 절편을 상이한 중합 효소로부터의 절편(들)으로 대체시킨 제1 중합 효소로부터의 아미노산 서열을 포함한다. 일부 실시양태에서, 상이한 중합 효소로부터의 하나 이상의 절편은 M2Y 폴리머라제로부터의 아미노산 1-51을 포함하는 절편, 이. 파에시움(*E. faecium*) 폴리머라제로부터의 아미노산 271-375를 포함하는 절편, 이. 파에시움 폴리머라제로부터의 아미노산 72-89를 포함하는 절편, 및/또는 이. 파에시움 폴리머라제로부터의 아미노산 445-449를 포함하는 절편일 수 있다. 일부 실시양태에서, M2Y 폴리머라제로부터의 1-51 절편이 상응하는 자연 발생 폴리머라제 절편 (예를 들어, Φ 29 폴리머라제의 아미노산 1-54)을 대체한다. 일부 실시양태에서, 이. 파에시움 폴리머라제로부터의 271-375 절편이 상응하는 자연 발생 폴리머라제 절편 (예를 들어, Φ 29 폴리머라제의 아미노산 260-359)을 대체한다. 일부 실시양태에서, 이. 파에시움 폴리머라제로부터의 72-89 절편이 상응하는 자연 발생 폴리머라제 절편 (예를 들어, Φ 29 폴리머라제의 아미노산 75-91)을 대체한다. 일부 실시양태에서, 이. 파에시움 폴리머라제로부터의 445-449 절편이 상응하는 자연 발생 폴리머라제 절편 (예를 들어, Φ 29 폴리머라제의 아미노산 429-433)을 대체한다.

[0018] 일부 실시양태에서, 재조합 중합 효소는 Φ 29 내에서의 하기 치환에 상응하는 하나 이상의 치환을 포함한다: M8R, V51A, N62D, I71V, L107I, K131E, K135Q, L142K, G197D, Y224K, E239G, V250A/I, L253A/H, Y281H, I288L, T301C, R306Q, R308L, D325E, D341E, K354R, T368F, E375Y, A437G, A444T, E466K, D476H, A484E, E508R, D510K/R, K512Y, E515Q, K539E, D570S, 및 T571V.

[0019] 일부 실시양태에서, 변형된 폴리머라제는 본원에 기재된 절편 치환 및/또는 아미노산 삽입, 결실, 및/또는 치환 중 하나 이상을 포함하고, 또한 하나 이상의 (예를 들어, 1-5, 5-10, 10-25, 25-50, 50-75, 75-100, 100-125, 125-150개의) 부가의 아미노산 삽입, 결실, 및/또는 치환 (예를 들어, 보존적 또는 비-보존적 아미노산 치환)을 포함한다. 따라서, 일부 실시양태에서, 표 2 또는 표 3의 변형된 폴리머라제는 하나 이상의 (예를 들어, 1-5, 5-10, 10-25, 25-50, 50-75, 75-100, 100-125, 125-150개의) 부가의 아미노산 삽입, 결실, 및/또는 치환 (예를 들어, 보존적 또는 비-보존적 아미노산 치환)을 포함할 수 있다.

[0020] 이들 및 다른 측면은 하기 상세한 설명에 보다 상세하게 기재되고 비-제한적 도면 및 실시예에 의해 예시된다.

도면의 간단한 설명

[0021] 통상의 기술자는 본원에 기재된 도면이 단지 예시하기 위한 것임을 이해할 것이다. 일부 경우에, 본 발명의 이해를 용이하게 하기 위하여, 본 발명의 다양한 측면이 과장되거나 또는 확대되어 보여질 수 있음을 이해해야 한다. 본 도면에서, 유사한 참조 문자는 일반적으로, 다양한 도면 전반에 걸쳐 유사한 특색, 기능적으로 유사하고/하거나 구조적으로 유사한 요소를 지칭한다. 본 도면은 반드시 축척된 것은 아니며, 대신 교시의 원리를 예시하는 것에 중점을 둔다. 본 도면은 어떤 방식으로든 본 교시의 범위를 제한하지 않는다.

본 발명의 특색 및 이점은 도면과 연계하여 후술되는 상세한 설명으로부터 더욱 명백해질 것이다.

본 도면과 관련하여 실시양태를 설명할 때, 방향에 대한 언급 ("위", "아래", "상단", "하단", "좌측", "우측", "수평", "수직" 등)을 이용할 수 있다. 이러한 언급은 단지 정상적인 배향으로 본 도면을 보는 독자를 돕기 위한 것이다. 이들 방향 언급은 구체화된 장치의 선호되거나 또는 유일한 배향을 기재하기 위한 것이 아니다. 장치는 다른 배향으로 구체화될 수 있다.

상세한 설명으로부터 명백한 바와 같이, 본 도면 (예를 들어, 도 1 내지 도 7)에 도시되고 본 출원 전반에 걸쳐 예시의 목적으로 추가로 기재된 예들은 비-제한적 실시양태를 설명하고, 일부 경우에는 특정 프로세스를 단순화하거나 또는 더 명확하게 예시하기 위하여 특색 또는 단계를 생략할 수 있다.

도 1은 단일 분자 프로세스를 모니터링하기 위한 비-제한적 프로세스에서 시그널 판독정보와 관련하여 중합 반응의 진행을 예시하는 개략도이다.

도 2는 $\Phi 29$ 폴리머라제의 구조 및 이러한 폴리머라제의 도메인 및 서브 도메인을 도시하는 비-제한적 예시이다.

도 3은 폴리펩티드 가닥의 도메인 및 서브 도메인 내에 돌연변이 부위를 수반한 선택된 돌연변이 변이체의 비-제한적 예를 도시한다.

도 4는 폴리펩티드 가닥 내로 치환된 상이한 도메인 및 서브 도메인을 갖는 선택된 키메라 폴리머라제 변이체의 비-제한적 예를 도시한다.

도 5a는 $\Phi 29$ 폴리머라제의 엑소뉴클레아제 도메인 내의 루프 영역을 도시하는 비-제한적 예시이다.

도 5b는 $\Phi 29$ 폴리머라제의 엑소뉴클레아제 영역과 다른 폴리머라제의 비-제한적 세트 간의 서열 상동성 정렬을 도시한다.

도 6은 하나 이상의 부위 특이적 돌연변이를 포함하는 키메라 폴리머라제 변이체의 비-제한적 일반적인 예를 도시한다.

도 7은 이. 콜라이(*E. coli*)에서 발현된 폴리머라제의 순도를 평가하기 위해 시행된 SDS-PAGE의 그림이다.

발명을 실시하기 위한 구체적인 내용

[0022] 본 개시내용의 측면은 변형된 중합 효소 및 그의 조성물에 관한 것이다. 일부 측면에서, 본 개시내용은 변형된 재조합 중합 효소를 사용하는 방법 및 이러한 효소를 포함하는 조성물을 제공한다. 일부 실시양태에서, 본 개시내용은 시험관내 중합 반응을 시행하기 위해 사용될 수 있는 변형된 재조합 중합 효소 및 조성물을 제공한다. 일부 측면에서, 본원에 기재된 중합 효소는 변형된 재조합 핵산 폴리머라제, 예를 들어, 변형된 재조합 DNA 폴리머라제이다. 일부 실시양태에서, 본 개시내용에 의해 제공된 변형된 재조합 DNA 폴리머라제는 DNA의 조작 (예를 들어, DNA 시퀀싱)과 관련된 시험관내 반응을 위해 사용될 수 있다.

[0023] 다른 측면 중에서, 본 개시내용은 시험관내 중합 반응을 시행하기 위해 사용될 수 있는 변형된 중합 효소 (예를 들어, 폴리머라제)를 제공한다. 일부 실시양태에서, 본원에 기재된 폴리머라제는 개별적으로 또는 조합하여, 시퀀싱 반응을 시행하는 데 유용한 하나 이상의 변형을 포함한다. 일부 실시양태에서, 본원에 기재된 변형 중 하나 이상을 활용하여, 시퀀싱 반응을 시행하는 데 유용한 하나 이상의 특성, 예를 들어, 폴리머라제 전진성, 충실도 (예를 들어, 정확도), 기질 (예를 들어, 뉴클레오시드 폴리포스페이트) 결합 친화성, 기질 활용률 (예를 들어, 뉴클레오시드 폴리포스페이트가 주형 가닥에 상보적인 성장 가닥 내로 혼입되는 비율), 변형된 기질 (예를 들어, 표지된 뉴클레오시드 폴리포스페이트)과의 폴리머라제 상호 작용, 또는 그의 일부 조합과 같은 특성을 갖는 폴리머라제를 생산할 수 있다. 일부 실시양태에서, 상기 변형 중 하나 이상은 폴리머라제의 교정 능력을 최소화하거나 또는 없앤다. 예를 들어, 일부 실시양태에서, 하나 이상의 변형은 폴리머라제의 엑소뉴클레아제 활성 상의 손실을 초래하는 폴리머라제의 엑소뉴클레아제 도메인에 대해 이루어질 수 있다.

[0024] 일부 측면에서, 본 출원은 단일 분자 핵산 시퀀싱 기술에 유리한 변경된 생화학적 특성을 갖는 변형된 폴리머라제에 관한 것이다. 일부 실시양태에서, 본원에 기재된 변이체 폴리머라제는 단일 분자 시퀀싱 반응에서 개선된 시그널 판독정보를 제공하도록 변형되었다. 도 1은 실시간 시그널 판독정보와 관련하여 시퀀싱 반응의 진행을 예시하는 예를 제공한다. 이론에 얽매이고자 한 것은 아니지만, 일부 단일 분자 핵산 시퀀싱 반응은 계획 (100)에 따라서 진행되는 것으로 여겨진다.

[0025] 반응의 시작에서 (패널 I), 폴리머라제 (파선)는 관찰 영역에 한정되고 주형 가닥 및 프라이머 가닥과 결합된다. 도시된 바와 같이, 상이한 유형의 검출 가능한 표지를 각각 갖는 상이한 유형의 뉴클레오티드 (예를 들어, A, G, T, C, U)가 동일한 반응 혼합물에 존재한다. 폴리머라제가 발광성 표지된 뉴클레오티드와 연합되면 (패널 II), 이러한 표지는 일정 기간 동안 관찰 영역에 한정된다. 혼입 이벤트 동안에는, 예를 들어, 이러한 기간이 상기 표지가 관찰 영역에서의 그의 존재를 검출하고 확인하기에 충분한 양의 에너지를 수용 및/또는 방출하기에 충분할 수 있다. 시그널 판독정보 (102)와 관련하여 계획 (100)의 패널 I 및 II에 의해 예시된 바

와 같이, 혼입 이벤트는 펄스 폭 (pw)에 상응하는 일정 기간 동안 시그널 펄스와 연관될 수 있다.

- [0026] 일부 실시양태에서, 혼입 이벤트와 연관된 개별 시그널 펄스는 혼입되는 뉴클레오티드의 유형 또는 특이적 시점에서의 폴리머라제의 활성과 같은 각종 조건에 의해 영향을 받을 수 있다는 것을 인지해야 한다. 일부 실시양태에서, 개별 시그널 펄스는 약 10밀리초 내지 약 10초의 개별 펄스 폭을 가질 수 있다. 따라서, 일부 실시양태에서, 개별 펄스 폭은 비교 목적을 위한 파라미터를 제공하기 위해 평균될 수 있다. 본원에 사용된 바와 같이, 일부 실시양태에서, "펄스 폭"은 각각의 개별 시그널 펄스가 개별 펄스 폭을 갖는 복수 개의 개별 시그널 펄스의 평균에 상응하는 값을 지칭한다.
- [0027] 일부 실시양태에서, 본 출원의 변형된 중합 효소는 약 10밀리초 내지 약 10초의 펄스 폭을 생산한다. 일부 실시양태에서, 펄스 폭은 적어도 10밀리초 내지 10초 이하, 적어도 10밀리초 내지 5초 이하, 적어도 10밀리초 내지 1초 이하, 또는 약 10밀리초 내지 약 1초이다. 일부 실시양태에서, 펄스 폭은 약 10 내지 약 500밀리초, 약 10 내지 약 200밀리초, 약 10 내지 약 100밀리초, 약 10 내지 약 50밀리초, 약 50밀리초 내지 약 1초, 약 50 내지 약 500밀리초, 약 50 내지 약 200밀리초, 약 50 내지 약 100밀리초, 약 100밀리초 내지 약 1초, 약 100 내지 약 500밀리초, 약 100 내지 약 200밀리초, 약 200밀리초 내지 약 1초, 약 200 내지 약 500밀리초, 또는 약 500밀리초 내지 약 1초이다.
- [0028] 뉴클레오티드가 성장 가닥 내로 혼입되고 발광 표지가 절단된 후, 이러한 표지는 조명 용적으로부터 확산되어 관찰 영역에서 더 이상 검출 가능하지 않다 (패널 III). 또한, 패널 III에 예시된 바와 같이, 혼입 이벤트 후, 폴리머라제는 주형 가닥을 따라 진행하여 후속의 발광성 표지된 뉴클레오티드와 연합될 수 있다. 패널 I에서 패널 II로의 진행과 유사하게, 시그널 트레이스 (102)에서 패널 III에서 패널 IV로의 진행에 상응하는 시그널은 비교적 낮은 세기 수준에서부터 연합 이벤트를 표시하는 시그널 펄스로 그 세기가 증가한다. 시그널 트레이스 (102)의 관점에서, 혼입 이벤트와 후속 연합 이벤트 사이의 기간은 인터펄스 거리 (ipd)와 연관될 수 있다.
- [0029] 펄스 폭과 관련하여 전술한 바와 같이, 일부 실시양태에서, 제1 시그널 펄스와 제2 시그널 펄스 사이의 기간과 연관된 개별 인터펄스 거리는 특이적 시점에서의 폴리머라제의 활성 또는 전진성과 같은 각종 조건에 의해 영향을 받을 수 있다. 일부 실시양태에서, 개별 인터펄스 거리는 약 10밀리초 내지 약 1분 이상 (예를 들어, 약 1 내지 약 60초, 약 1 내지 약 30초, 약 1 내지 약 20초, 약 1 내지 약 10초, 또는 약 1초 미만)의 기간에 상응한다. 따라서, 일부 실시양태에서, 개별 인터펄스 거리는 비교 목적을 위한 파라미터를 제공하기 위해 평균될 수 있다. 본원에 사용된 바와 같이, 일부 실시양태에서, "인터펄스 거리"는 복수 개의 개별 인터펄스 거리의 평균에 상응하는 값을 지칭한다.
- [0030] 일부 실시양태에서, 본 출원의 변형된 중합 효소는 약 10밀리초 내지 약 10초의 인터펄스 거리를 초래한다. 일부 실시양태에서, 인터펄스 거리는 적어도 10밀리초 내지 10초 이하, 적어도 10밀리초 내지 5초 이하, 적어도 10밀리초 내지 1초 이하, 또는 약 10밀리초 내지 약 1초이다. 일부 실시양태에서, 인터펄스 거리는 약 10 내지 약 500밀리초, 약 10 내지 약 200밀리초, 약 10 내지 약 100밀리초, 약 10 내지 약 50밀리초, 약 50밀리초 내지 약 1초, 약 50 내지 약 500밀리초, 약 50 내지 약 200밀리초, 약 50 내지 약 100밀리초, 약 100밀리초 내지 약 1초, 약 100 내지 약 500밀리초, 약 100 내지 약 200밀리초, 약 200밀리초 내지 약 1초, 약 200 내지 약 500밀리초, 또는 약 500밀리초 내지 약 1초이다.
- [0031] 펄스 폭 및/또는 인터펄스 거리의 특징은, 일부 실시양태에서, 특이적 발광 표지를 확인하기 위해 사용될 수 있다. 일부 실시양태에서, 본 개시내용의 변형된 폴리머라제는 주형 가닥의 뉴클레오티드 서열을 결정하기 위해 발광성 표지된 뉴클레오티드의 연합을 표시하는 일련의 펄스 폭을 관찰함으로써 시퀀싱 반응에 사용될 수 있다. 일부 실시양태에서, 이러한 프로세스에서의 인공물은 부정확한 시퀀싱 정보를 야기할 수 있다. 예를 들어, 패널 V는 발광성 표지된 뉴클레오티드가 시그널 펄스를 발생시키기에 충분한 기간 동안 관찰 영역에 한정되지만 혼입 이벤트가 없는 결합 및 방출 이벤트를 예시한다.
- [0032] 패널 V에 제시된 바와 같이, 패널 IV에서 검출된 혼입 후에, 절단된 발광 표지는 관찰 가능한 영역 밖으로 확산한다 (i). 추가로 발광성 표지된 뉴클레오티드는 관찰 가능한 영역에서 폴리머라제와 연합하여 검출 가능한 시그널을 발생시킨다 (ii). 성장 가닥 내로 혼입되기 보다는, 발광성 표지된 뉴클레오티드가 폴리머라제로부터 해리되어 다시 반응 혼합물 내로 확산된다 (iii). 따라서, 동일한 유형의 뉴클레오티드의 후속적으로 성공적인 혼입 후 (도시되지 않음), 패널 V에 상응하는 시그널 펄스는 시퀀싱 정보 관독에 명백한 삽입을 초래할 것이다. 따라서, 일부 실시양태에서, 본 출원의 변형된 폴리머라제는 이들 및 다른 인공물 이벤트로부터의 진실한 혼입 이벤트를 판별하기에 충분한 길이의 펄스 폭을 갖는다. 일부 실시양태에서, 본 출원의 변형된 폴리머라제는 폴리머라제 활성 부위로부터의 조기 기질 방출 가능성을 감소시키는 하나 이상의 변형을 갖는다. 일부 실시양태

에서, 본 출원의 변형된 폴리머라제는 일단 기질이 폴리머라제 활성 부위와 연합되면 기질 혼입의 가능성을 증가시키는 하나 이상의 변형을 갖는다.

[0033] 일부 실시양태에서, 본 개시내용에 의해 제공된 변형된 폴리머라제는 하나 이상의 변형을 수반한 표 1에 제시된 야생형 폴리머라제 서열 [서열식별번호 (SEQ ID NO): 1-19]에 따르는 폴리머라제 서열을 포함한다 (예를 들어, 표 2-5에 예시된 바와 같거나, 또는 그의 2개 이상의 조합).

[0034] <표 1>

[0035] 야생형 폴리머라제 아미노산 서열

명칭	SEQ ID NO.	서열
Φ29	<u>1</u>	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLK VQADLYFHNLKFDGAFFIINWLERNGFKWSADGLPNTYNTIISRMGQWYIMIDIC LGYGKGRKRIHTVIYDSLKKLPFPVKKIADFKLTVLKGDIDYHKERPVGKYKIT PEEYAYIKNDIQIIAEALIIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVF TSLSLGLDKEVRYAYRGGFTWLNDRFKEKEIGEGMVFVDNSLYPAQMYSRLLPY GEPIVFEGKYVWDEDYPLHIQHIRCEFELKEGYIPTIQIKRSRFYKNEYLKS SGGEIADLWLSNVDELMEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIK TTSEGAIKQLAKLMLNSLYGKFASNPDVTKVPYLYKENGALGFRGEEETKDP VYTPMGVFITAWARYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDP KKLGYWAHESTFKRAKYLQKTYIQDIYMKEVDGKLVEGSPDDYTDIKFSVKC AGMTDKIKKEVTFENFKVGFSSRMKPKPVQVPGGVVLVDFTTIK
M2Y	<u>2</u>	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQA DLYFHDLLKFDGAFFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYIMIDICFGY KGKRLHTVIYDSLKKLPFPVKKIADFKQLPLKGDIDYHTERPVGHEITPEE YEYIKNDIEI IARALDIQFKQGLDRMTAGSDSLKGFKDILSTKKFNKVPKLS LPMDEIRKAYRGGFTWLNDRFKEKEIGEGMVFVDNSLYPSQMYSRLLPYGAP IVFQGYEKDEQYPLYIQRIRFEFELKEGYIPTIQIKKNPFFKNEYLKNNGV EPELYLTNVDLELIQEHYELYNVEYIDGFKFREKTGLFKDFIDKWTYVKT EGAKKQLAKLMLNSLYGKFASNPDVTKVPYLYKDDGSLGFRVGDDEYKDPVYT PMGVFITAWARFTTITAAQACYDRIIYCDTDSIHLTGTEVPEI IKDIVDPKKL GYWAHESTFKRAKYLQKTYIQDIYVKEVDGKLKECSPDEATTKFSVKCAGM TDTIKKKVTFDNFAVGFSMGMKPKPVQVNGGVVLVDVSVFTIK
루실리아 쿠프리나 WT	<u>3</u>	MARKRPIRITKNDRAEYKRLSKNAKSKLNRTVKNYGIDLSNDVDIPKLSDFKT RKEFNDWKQKITSFTSRNQEQFRKNEYGVVASVKELNEIKRNTKKAQKIAK EKIDKAMKLDYVEGERQGVKDRIKLMKKEEVAGVSVVPVDFDKIQTRKRL EDKAGFMEERATGDYRKKDIQMKENFISMI EQGFNSDADEVIKKLLKIPDD FVELTIVTDEIDFRNYGSKNEGGINDEDKLEELNNTLNDYFNETTTDVNDCRV WAYGWMEIGKTSNYKIGTDFNEFMEWMIHSSRLYFHNLFKDGSIIVNWLLHN GYTWTKRPSKEGQFSTLISKMGQWYGITICSGRDGRKKLTTIHDSLKKLPFP VRKIGKDFKLVNLKGDIDYHKPRPIGYEIDDEEYQYIKNDIQIIAEALEVQTV QGLTGMTNGKDALDEFVNMSGKLYEKLFPVFSLELNEEIRKAYRGGFTWLN PVYGTKKYVKDGI VFDVNSLYPSQMYDRDLPCGVPIPFEGEYVYDKSHPLYIQKL TFEFELKENYIPTIQLKNSRFGFKGNEYLSSSNGERITISVSSVDWELIREHY HUYDVEFEKGWKFRTKQAFRQYIDKWLKVNMSAGAKKAIKLMNSLYGKF ATNPDI TGKRPYLREDGSGNFELMEEEFRDPVYTPVGIFITSWARYTTITSAQ KCYDRIIYCDTDSMHLEGLDVPESIKDIVADDVLGYWKKEGQFKQKGFIRQKT YMEEYYAKYVRDENG EIKYDDEKPIKTI CDKEESDTTIEIKCAGMPDNIKKH VTFDNFDIGFTMEGKLKPKQVYGGVVLVEETYTMK

[0036]

명칭	SEQ ID NO.	서열
루실리아 쿠프리나 mod.	<u>4</u>	MKHMPRKMYSCDFETTTDVNDCRVWAYGWMEIGKTSNYKIGTDFNEFMEWMIH SSSRLYFHDLKFDGSFIVNWLLHNGYTWTKRPSKEGQFSTLISKMGQWYGITI CSGRDGRKKLLTTIHDSLKKLPFPVRKIGKDFKLVNKGIDIDYHKPRPIGYEI DDEEYQYIKNDIQIAEALEVQTVQGLTGMTNGKDALDEFVNMSGKLYEKLFP VFSLELNEEIRKAYRGGFTWLNVPVYGTKKYVKDGI VFDVNSLYPSQMYDRDLP CGVPIPFEGEYVYDKSHPLYIQKLTFFEFELKENYIPTIQLKNSRFGFKGNEYL SSSNGERITISVSSVDWELIREHYHVYDVEFEKGWKFRSTKQAFRQYIDKMWL VKNMSAGAKKAIKMLNLSYKGFATNPDITGKRPLYREDGSGNFELMEEEF DPVYTPVGIFITSWARYTTITSAQKCYDRIICYDSDMSHLEGLDVPESIKDIV ADDVLGYWKKEGQFKQKFI RQKTYMEEYAKYVRDENG EIKYDDEKPIKTIC DKEESDTTII EIKCAGMPDNIKKHVTFDNFDIGFTMEGKLKPKQVYGGVVLVE ETYTMK
엔테로코쿠 스 파에시움	<u>5</u>	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLEIDSFFEWCEMQGST DIYFHDKEFDGEFMLSFLKNGFKWCKEAKEERTFSTLISNMGQWYALEICWN VKCTTTKTGKTKEKQRTIIYDSLKKYFPFVKEIAEAFNFP I KKG EIDYTKER PIGYNPTDDEWDYLNNDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKT YGKSRFKQWFFVLSLGFDKDLRKAYKGGFTWVNKVFQGKEIGEGIVFDVNSLY PSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQS SLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIHYTYGYMFK SCDMFKGWIWKWIEVKNTEGARKANAKGMLNLSYKGFGTNPDITGKVPYMG DGI VRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRCFDNIIICYDSDSIH LTGTEVPEAIEHLVDSKKLG YWKHESTFQRAKFIRQKTYVEEIDGELNVKCA GMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
바실루스 파지 VMY22	<u>6</u>	MATKKRKAYSCDFEATTSTYSETETRVWAYGWMEIGNTSHFNIGDNLDEFMLW TSKECADLYFHDLRYDGEFIVNWLLHKG YECNESGRPKTFDTVISKGGQWYKI AIHHEGKGTQIFDSLKKLPFPVKTIKAKFLPV LKGDIDYNLHRDENHVITS EEFTYIKHDI EIVARALDIQINQQLVKMTNGADSMDFIKSLDKKKKVAERI YNQYFPKMSIAMD SI FRKAYRGGFTWVNPKFKGQEVGEGMVFDVNSLYPSV MY YKPLPWGKPVFVVGKYEEDPDFLYICHIKTGFVLKEGHIPTIQIKKNPIFQ E NEYLETSGGAPVDLHVTNVDEL I KEHYELYDTEYVGWKFRRQQTGIFNNFID YWMKIKTDPKSTPAIVTLAKLQLNLSYKGFASHPDVTGKVPY LKDDGSTAFK K GLPKSKDPVYTPAGAFITAWARHMTITTAQKVYDRILYCDTDSIHILGIDIPE AIKNDIHQKELGKWAFCMFKRAKFVRQKTYVEDMYAKFMSYWEDGELNYMLK ECVKEEATARLLNVKAGMPQAVKKFVTFRTFAVGFTSDTGKLPKHVKGGOI LVDVPFTIK
바실루스 파지 GA-1	<u>7</u>	MARSVYVCDFETTTDPEDCRLWAWGMDIYNTDKWSYGEDIDSEMEWALNSNS DIYFHNLFKFDGSFILPWWRNGYVHTEEDRTNTPKEFTTTISGMGQWYAVDVC INTRGKNKNHVVFYDSLKKLPFKVEQIAKGFGLPV LKGDIDYKKYRPVGYVMD DNEIEYLKHDLLI VALALRSMFDNFTSMTVGS DALNTYKEMLGVKQWEKYFP VLSLKVNSEIRKAYKGGFTWVNPKYQGETVYGGMVFDVNSMYPAMMKNKLLPY GEPVMFKGEYKKNVEYPLYIQQVRCFFELKKDKIPCIQIKGNARFGQNEYLST SGDEYVDLYVTNVDEL I KKH YDI FEEEFIGGFMFKGFIFGFDEYIDRFMEIK NSPDSSAEQSLQAKMLNLSYKGFATNPDITGKVPYLDENGVLKFRKGELKER DPVYTPMGCFITAYARENILSNAQKLYPRFIYADTDSIHVEGLGEVDAIKDVI DPKKLGYWDHEATFQRARYVRQKTYFIETTWKENDKGKLVVCEPQDATKV KPK IACAGMSDAIKERIRFNEFKIGYSTHGS LKPKNVLGGVVLMDYFPAIK

[0037]

명칭	SEQ ID NO.	서열
악티노마이세스 파지 AV-1	<u>8</u>	MVRQSTIASPARGGVRRSHKKVPSFCADFETTTDEDDCRVWSWGIIQVGKLQN YVDGISLDGFMHSISERASHIYFHNLAFDGTFILDWLLKHGYRWTKENPGVKE FTSLISRMGKYYSITVVFETGFRVEFRDSFKKLPMSSVAIAKAFNLHDQKLEI DYEKPRPIGYIPTQEKKRYQRNDVAIVAQALEVQFAEKMTKLTAGSDSLATYK KMTGKLFIRRFPIILSPEIDTEIRKAYRGGFTYADPRYAKKLNKGSGVYDVNSL YPSVMRTALLPYGEPYSEGAERTNRPLYIASITFTAKLKPNHIPCIIKKNL SFNPTQYLEEVKEPTTVVATNIDIELWKKHYDFKIYSWNGTFEFRGSHGFDT YVDHFMEEKKNSTGGLRQIAKLHLNLSYGKFATNPDIKGKHTLKDNRVSLVM NEPETRDPVYTPMGVFITAYARKKTIISAAQDNYETFAADTDSLHLIGPTTP DSLWVDPVELGAWKHESSTKSVYIRAKQYAEIEGGKLDVHIAGMPRNVAATL TLEDMLHGWTNGKLI PVRVPGGTVLKDTTFTLKID
칸디다투스 모란박테리아	<u>9</u>	MKLKSKYVADFEATGEEQYKIDGSTHVWAVGVIDIETEETVLI SNDIAEFMNW LSKDNHNHNKNEVEFFHNLKYDGD FIVKFLLENGFKHSRERALSNEFSTLISD TGTWYEIKICFHALKTRKVEVKIHDSYKLLPFSEEKIAKAFKLTVSKGEIDYD RYRPGVYQLQEQYEVVDYLTDLIMAQALKVQMNKGLTKMTIGSNALADYKQRI SKDKFKYLPFVLDNII DADLRHAYRGGHTYLPFFYANKILENVHSYDKNSMHP SQMKNMPPYGI PVYVEGEYKNDPDYPLFIQSIEIDCKVKKGYLPTIQPRNAF RFATTEFLEDTKGEPIQLFVTSIDLMLILEHYDIHYIQYLEGFKFRSHIGLFD EYIDYWHIKETNTGPLREIAKLMLNLYGKFGTNP IARKEPIYDKTKGAVY VNLPAEEGDAVYIPMACFITAYSRYDLISTAQKFYKNVYMDTDSIKFYGISR EVIEAQIEVHDTKIGAWKYEGTAKMFKALRPKTYAYIDENDEL DVKAGLPKK AKKDITFDTFQYGFVSKEKLEIKRVKGGTILLKTKFEIKKQVDNKHIDTEYFE DEDIDIFNQL
바실루스 파지 MG-B1	<u>10</u>	MKKKRTKTKIKTYACDFETNTEAWLHEDKLRDELKTKEENPELWRKREAWKLH TGGDKAFVWSWGTEIREDMSFKGELDNFVVGKGI SEYVDWMLDGSKNVWFHN LKF DGSFIAVELLRGFKFTFDRNPAIGEFTGLIDGKKMWFEII CKEGKRGG RQFITIKDSLKKVPFGLRVAAMAFGLDVFKDDMDYDVIREPFEPIGEADYKYL KKDVEITAKI IHYQVFQSGLKKTIGSDALNEFKSTVGGDKGKKEIFPVMDFD TDSFIRKSYFGGVTQVKPGMEGKLI GEGSVFDIVSMYPWVQYTKLLPYGLPIE YNGEYTYDEEYPLYVQVVSFSFVVKDNMLPTIQLKKQNVFNYNEADDVRKFN GREFQKTSYGEIVTMYVTNVQWEQIQKHVWLDLHFKGMMFKGKIGLFKEHI DKWLKVKKQANDDGNDAKLSLAKLMLNSPYGKFGTNTIRLNVEPFLWEDDES GFRVEDDDPPADPIYTAYASFVTAYAREELVSTIMCYDRFVYCDTDSIHLI GTEIPEGIKHKIGGDLGDWEPESEFKLAKFHRAKTYCEMVYAKKVMKKDRWGD VVESLKHCSKEEWGTL PQDQKTL DKNLKCAGLQGHLDYVSFEFEIGLKINP EVNKDIMGKPLGKLMPCQVKG GTLLKVRKFSLN
에게르텔라 종	<u>11</u>	MNEYISDFETQKDPDGTGMSVWAWSI DVNDLSNIQYGNNIESWLSAIQGLPN GSLIGFHNLFKFDGSYILSYLLGVAKWEYNDKPKARKAKTVECLISSIGVHYN RINFTRKRYVKIYDTLKI FNMSVSQIAKSFGIKEQKGSIDYAI FRGYNYTMT KEVEYITNDVKI VAKAIKQFRNEGHERNTIASNAMRYKKNSSYSSNYEFLTYF PHLDDDLYHLLKRAYKGGYCYVNP KFKGPVGHGRVYDVNSLYPSVMSDPQNK YPIGTFVFFEGKYKDDPIYPLYIQFITAQFELKKGKIP TIQIKNDKRFPREY VTSTGCLM/VNLYLTNV DLEMFYECYNIKEIQYIGGYKFIGRSGIFIDYVNHFK EMKMQATIEKNAGKRSIAKLFLNSLYGKFGASNDKFVKRPYINDKGILAYQTV ETPRAKTVYVPVAAFTAYARRFIQTLFIKNVDRCCYCDTDSLHLIGDDPPE GVKISDTEFNCAHESSESRAKFLGAKLYIEEDEQGNLDVKAAGLGQNEVVK QITFDNFNTEQYFGILKSKTVQGGVELSESTFKIRERGTRE

[0038]

명칭	SEQ ID NO.	서열
스트렙토코쿠스 파지 CP-7	12	MTCYYAGDFETTNEEETEVLSCFAKVIDYDKLDTFKVNTSLEDFLKSLYLD LDKTYTETGEDEFIIFHNHFKDGSFLLSFFLNNDIECTYFINDMGVWYSITL EFPDFTLTFRDSLKILNFSIATMAGLFKMPIAKGTTPLLKHKPDEIKPEWIDY IHVDVAILARGIFAMYEEENFSKYTSASEALTEFKRIFRKSRRKFRDFFPILD EKVDDFCRKAYRGGWTFANPKTQGRTLKQLIDIYDINSMPATMLQNALPIGI PKRYKGGPKKEIKEDHYYIYHIKADFDLKRGLPTIQIKKKLDALRIGVRTSDY VTTSKNEVIDLYLTNFDLFLKHYDATIMYVETLEFQTESGLFDDYITTYRY KKENASQSPAQKQAKIMLNSLYGKFGAKIISVKKLAYLDDKGLRFRKNDDEEE VQPVYAPVALFVTSIARHFIIISNAQENYDNFLYADTDSLHLFHSDSLVLDIDP SEFGKWAHEGRAVKAKYLRSLYIEELIQEDGTHLDDVKAGMTPPEIKEKITF ENFVIGATFEGKRASKQIKGGTLIYETTFKIRETDYLV
박테로이데스 종	13	MSKKSAAKPVIIAADFETTVYPGQSTSEVWSAAWIELFTEPHVRGNIEDFLN DIFNLNKNVLCYFHNLRFDGAFIVYLLKNGYTWNARNKGMNAKEFKALISD TNKWYTVTVKPKFDTVIEFRDSVKLPMPTLDQIGSAFNTKHKLEMEYIGMRH ANCEITPEEYAYIINDIYVLKEALEVMIKSGHDKLTISSCCMDEFKNKFDAMD FKAAPNLKEIALIKYELGSDNVDQYIRKAYKGGYCYKYKQRKHITQNGMTF DVNSLYPSVMHKSNGNYPTGKPIFFEKAIPYKCLEARVYPPFYVRLRCRFLK DGFLPTVQIKGDYKYNSTQWLETSDIYYRGKYRYFTNKEGQKEEARPELTLF MTDYLLLEHYDVYDLEILDGCYFHGAIGLFDYIDHYMKIKMTTKDKGERTE AKLFLNNLYGRLAINDNSSYREPFIDPETDSIGFELHPEHEKDTLYIAAGAAV TAYARYFTITHAQANYQNFVSDTDSIHMLDDGQPVKMIKEHATELLHWKRES DWSSAIFIRQKTYAEFVQKEDGKKVTGHWEIKCAGMPEKSKKLFLASHPITDF KIGLVGGKLPKYISGGMVLVEDFYTLRAKRC
클라미디아 트라코마티스	14	MKARKFKIYAADFETTTFKGTTFTEVWSACFCELYKKDAKIMHSIQDFFNYFF SLNENIKMYFHNHFKDGSFILSYLLKDLKYEQAAYEKMADGSLVRWLETKDMK NNSIKYSISEMGQWYIIIIKKNKIIIEIRDSLKLPLPSLEAIGKSFDEHKKL KMKYEGYRYAGCEITPEEQAYIKNDVLVLKEALEIMFNEKHESLTIGSCCLNE YKTIMTKFLIERLYPNIAEYTVNVPLEFKNADYVRKSYKGGWCYLKKGCEK IYNNGTADVNLSYSSVMHSESGNYYPVGLPTFWSGNYIPEIAKEKYFFIRIK TRFYLLKRFPLPCIQVKNTRYRYKSTEWLETSDFYDKKTNKYKKYLDINGNEQN TQVILTLTMTDFELIKEHYNLVDFEILDGCYFDKEIGLFDYINKYKKIKLNS KGAKKTLAKLYLNNLYGKTATNTDSSFKVAYIKDDLSLGFYGVYACDKKPFYI PVGSAITSYARNFTIRAAQKNYKNFIYADTDSIHCKCNPAEIKGITIDDKKFL CWKLESCWDKGLFVRQKTYIEHITAENLKPIDKPFYNVVCAGMPEQCKTLFLK SIGEDVDISDLNINDDAKEFLKKKRTIKDFKAGLSVPLKLRPVQINGGVLLTE TFYTM
글로보테라 팔리다	15	MPLPRKKASSNGLSKRIYLADEFETTQAECDRVWSWGLCSVENTENVEFGDDL DSFIERISEENSITFFHNHFKDGAFLDLRFLRGYEFTDEKAPQVKEFSTLIS KMGQFYSIKVRWENGMFTEFRDSLKKLPMSVKQVAKTFKLDQAKGEIDYHYLR PVGWVMTPEEREYVKNVQIVARALKVQLQEGMTRLTVGADSLAQYKSMGKD FERHFPVLTRTIDAEIRRAYRGGWAYADERHRGKVVGAGQTFDVNSLYPSVMY SKVLPHYGEVPFYPNGLPEVTEHDHPLFITCITFTAKIRDGHLPCIQIKNSSLFT PTEYVKEVLDPITMYCTNVDELWQEHYDMDILAYNGAWLFRGIRGFFNDYID HWMRIKEESEGGKRLIAKLHLNSLYGKFATNPDPVTPKIPIFDEEKDIVRLIEG PPDERNPVYTAMGVFITSYARDLTIRTAQDHYDRFLYADTDSLHLTSDGTNN GRKSKALEVHPSKLGWKHEYDFDAGLFVRAKAYTELMTEGFHVKSKECDTP NDLHYQTHIAGMPEAIAQHITFESYRDGATFEGKLAPQVRVPGGI

[0039]

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감자 낭 선충류	16	MPLPRKKASSNGLSKRIYLADFETTTQAEDCRVWSWGLCSVENTENVEFGDGL DSFIERISEENSITFFHNLKFDGAFILDRFLRGYEFTDEKAPQVKEFSTLIS KMGQFYISIKVRWENGMFTEFRDSLKKLPMSVKQVAKTFKLDQAKGEIDYHYLR PVGWVMTPEEREYVKNVDQIVARALKVQLQEGMTRLTVGADSLAQYKSMMGKD FERHFPVLTRTIDAEIRRAYRGGWAYADERHRGKVVGAGQTFDVNSLYPSVMY SKVLPHYGEVPVFPNGLEPVTEDHPLFITCITFTAKIRDGHLPCIQIKNSSLFT PTEYVKEVLDPIITMYCTNVDLELWQEHYDMDILAYNGAWLFRGIRGFNDYID HWMRIKEESEGGKRLIAKLHLNSLYGKFATNPDPVKPIPIFDEEKDIVRLIEG PPDERNPVYTAMGVFITSYARDLTIRTAQDHYDRFLYADTDSLHLLTSDGTNN GRKSKALEVHPSKLGWYKHEYDFDAGLFVRAKAYTELMTGEFHVSKCECDTP NDLHYQTHIAGMPEAIAQHITFESYRDGATFEGKLAPQVRVPGGIVLVDDTFTI K
이베리아 스라소니 내장	17	MPSYTAADFETTTVADDCRVWAWATSRIIGNPDDVQLGNSIDTFLEWCRVHSGSR VYFHNKFDGKFIHLKILTDGKWIPDKNDCANRTFTTLISDMSQFYISIKLWF DESKSIEFLDSLKVIPLPIAAIPKAFGLEIEKLDLDYQASREVGHTEDEKE YIAHDVKIAAMAMDTMFSQGMKKITAGSNAFADYKKTIGGKKRFRDWFPEPEY DEDLRKGCGYKGGFTAVNPKIAGKKLGKGVSDVNSLYPSVMASSHGEVLPYG EPIPYDGGYEQDEDHPLYIQFIEADFAVKENRIPCLQLKGNVMFGETEYIRDS KGMQTLCLTSVDMEMLFHEYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXRTIAKLQNSLFAANPVKQSRMPYLDEGIVKYALLEPEHAEAQYLPAGAF ITSYARQFTIRAAQANYERWLYCDTDSVYLRGTEPPVDMRVDAYELGAWKKEH EFDCKAIRAKTYCFEEDGELTVHCAGMPARCHEHVTMDNFEVGASFPGLKP KDVNGGTILVEDVFTIRP*
이. 파에시움 (SK)	18	MIKKYTGFETTTDLNDCRVWSWGVCDIDNVDNITFGLDIDSFFEWCEMQGST DIYFHNKFDGEFMLSFLKNGFKWSKETKEERTFSTLISNMGQWYALEICWE VNYTTTKSGTKKEKVRTIIYDSLKKYPFPVKQIAEAFNFPICKGEIDYTKER PVGYNPTDDEWDYLKNDIQIMAMALKIQFDQGLTRMTRGSDALGDYKDWLKAT HGKSTFKQWFPILSLGFDKDLKAYKGGFTWVNKVFQKEIGDGIQVFNLSLY PSQMYVRPLPYGTPLFYEGEYKPNNDYPLYIQNIKVRFRLEKGYIPTIQVKQS SLFIQNEYLDSSVNKLGVDELIDLTLTNVDLELFFEHYDILEIHYTYGYMFKA SCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDPITGKVPYMG DGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRCFDRIIYCDTDSIH LVGTDVPEAIEHLVDPKKLGWYGHESTFQRAKFIRQKTYVEEIDGELNVKACAG MPDRIKELVTFDNFEVGFSSYKLLPKRTQGGVVLVDVTMTFTIK
바실루스 파지 하람베	19	MGNKKRKIYSCDFETTTDVNDRCRVWAYGLMEIDGKFENYKEGNNIDEFMEWTE QEQGDLYFHNLRFDGEFIVNWLHKGYRFNNTRKAGTFNAVISSMGQWYKIDI YYGREGKKVFKTSIYDSLKKLFPVKTIAKAFKLPKIEKGDIDYDAPRPVGHQI TPDESKYIKNDVEIIARALHSQNLNTAKLTMTIGSDALDGFKHS�HKSPKVS KRMVDHHPVISNAIHEEFKAYRGGFTWANPKYAGKVIGNGLVFDVNSLYPSV MYDKPLPYGLPVFPFSGEYEDETHPLFIQHIKCGFELKDGHIPITQIKKNFRF ADNEYLHSSEGNILDLHVTNVDLALIKEHYTLYEEYLYQGYKFKQVTGLFKNY IDYWSDKKINAEDPAIRQMAKMLNSLYGKFGTSIDVTGKEVFLKEDGSTGFR KGQKEERDPVYMPMGAFITAYARDVTIRTAQKCYDRILYCDTDSIHLVGTETP EAIKDRIHDKKLGWYAHSTFWRAKFIRQKTYIEDLCMRFEKEKNGEWKFKM VEEKDITKATARELSVKCAGMPAQVKQYVTFDNFVGDFKHPNDYTDEEIKRK NIKFKLKPTHRKGQVLVPTFTIK
*메타게놈 샷건 시퀀싱에서 유전자의 불완전한 서열 적용 범위로 인해 공지되지 않은 서열 정보		

[0040]

[0041]

일부 실시양태에서, 야생형 폴리머라제 서열 (예를 들어, 표 1에 제시된 바와 같음)은 하나 이상의 변형이 재조합 변이체 폴리머라제를 생성하기 위해 만들어질 수 있는 대다수의 폴리머라제 서열을 제공한다. 본원에 사용된 바와 같이, 변형된 폴리머라제의 "대다수의 폴리머라제 서열" 또는 "대다수의 서열"은 변형된 폴리머라제 서열 내에서 우세한 야생형 폴리머라제 서열을 지칭한다 (예를 들어, 변형된 폴리머라제 내의 아미노산의 적어도 50%가 대다수의 서열 내의 아미노산에 상응한다). 일부 실시양태에서, 변형된 폴리머라제 서열은 하나 이상의 아미노산 돌연변이를 추가로 포함하는 대다수의 서열을 포함한다. 일부 실시양태에서, 하나 이상의 아미노산 돌연변이는 상동 단백질 내의 위치에 상응하는 위치에 아미노산을 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 (서열식별번호: 1) 내의 A484에 상응하는 위치에 돌연변이를 포함한다. 다른 폴리머라제 내의 A484에 상응하는 아미노산은 상동성 정렬을 포함하여 관련 기술분야에 공지된 임의의 방법에 의해 결정될 수 있다. 이러한 분석의 비-제한적 예로서, 상동성 정렬은 표 1에 보고된 수많은 폴리머라제를 사용하여 시행되었으며, Φ 29 폴리머라제 내의 A484가 M2Y 내의 A481, 바실루스(*Bacillus*) 파지 VMY22 내의 A492, 엔테로코쿠스 파에시움(*Enterococcus faecium*) 내의 K500, 및 루실리아 쿠프리나(*Lucilia cuprina*) 내의 K827에 상응하는 것으로 결정되었다. 따라서, 상동성 정렬 및 관련 기술분야에 공지된 유사한 방법을 사용하여, 본원에 기재된 변형된 잔기의 위치에 상응하는 다른 폴리머라제 내의 아미노산을 확인할 수 있다. 따라서, 본 개시내용의 변형이 본원에 기재된 폴리머라제 (예를 들어, 표 1에 열거된 것)로 제한하려는 것이 아

니고, 공지된 기술을 사용하여 임의의 중합 효소로 연장될 수 있다는 것을 인지해야 한다.

[0042] 일부 실시양태에서, 변형된 폴리머라제는 표 1에 열거된 폴리머라제 중 하나 이상 (예를 들어, 서열식별번호: 1, 서열식별번호: 5, 또는 표 1에 열거된 다른 서열)에 대해 적어도 25% 아미노산 서열 동일성을 갖는다. 일부 실시양태에서, 변형된 폴리머라제는 표 1에 열거된 폴리머라제 중 하나 이상 (예를 들어, 서열식별번호: 1, 서열식별번호: 5, 또는 표 1에 열거된 다른 서열)에 대해 25-50%, 50-60%, 60-70%, 70-80%, 80-90%, 90-95%, 또는 95-99%, 또는 그 초과인 아미노산 서열 동일성을 갖는다. 일부 실시양태에서, 이러한 변형된 폴리머라제는 본 출원에 제공된 상이한 변형된 폴리머라제 입체 배치 및/또는 예의 문맥에서 기재된 아미노산 돌연변이 및/또는 도메인 치환 중 하나 이상을 포함한다.

[0043] 일부 실시양태에서, 상이한 폴리머라제로부터의 하나 이상의 절편 또는 영역은 본 출원에 기재된 특이적 서열에 대해 적어도 80% 아미노산 서열 동일성을 갖는 것으로 기재된다. 이러한 영역은, 예를 들어, 명시된 서열 (예를 들어, 표 1의 자연 발생 폴리머라제 내의 상응하는 절편 또는 영역)에 대해 80-90%, 90-95%, 95-99%, 또는 100% 서열 동일성을 가질 수 있다. 또한, 대체 실시양태에서, 이러한 절편 영역은 명시된 서열 (예를 들어, 표 1의 자연 발생 폴리머라제 내의 상응하는 절편 또는 영역)에 대해 더 낮은 서열 동일성 (예를 들어, 50-60%, 60-70%, 또는 70-80%)의 아미노산 서열 동일성을 가질 수 있다.

[0044] 2개 이상의 아미노산 서열을 비교할 목적으로, 제1 아미노산 서열과 제2 아미노산 서열 간의 "서열 동일성" (본원에서 "아미노산 동일성"으로서 지칭되기도 함)의 백분율은 [제2 아미노산 서열 내의 상응하는 위치에서의 아미노산 잔기와 동일한 제1 아미노산 서열 내의 아미노산 잔기의 수]를 [제1 아미노산 서열 내의 아미노산 잔기의 총 수]로 나누고 이에 [100%]를 곱함으로써 계산될 수 있으며, 여기서 제1 아미노산 서열과 비교해서 제2 아미노산 서열 내의 아미노산 잔기의 각각의 결실, 삽입, 치환 또는 부가는 단일 아미노산 잔기 (위치)에서의 차이로서 간주되는데, 즉 본원에 정의된 바와 같은 "아미노산 차이"로서 간주된다. 또 다른 한편으로, 두 아미노산 서열 간의 서열 동일성의 정도는 공지된 컴퓨터 알고리즘을 이용하여, 예를 들어, 문헌 [Smith and Waterman (1970) Adv. Appl. Math. 2:482c]의 국소 상동성 알고리즘에 의해, 문헌 [Needleman and Wunsch, J. Mol. Biol. (1970) 48:443]의 상동성 정렬 알고리즘에 의해, 문헌 [Pearson and Lipman. Proc. Natl. Acad. Sci. USA (1998) 85:2444]의 유사성 검색 방법에 의해, 또는 블라스트(Blast), 클러스털 오메가(Clustal Omega), 또는 다른 서열 정렬 알고리즘으로서 이용 가능한 알고리즘의 컴퓨터화된 구현에 의해, 및 예를 들어, 표준 설정을 이용하여 계산될 수 있다. 통상적으로, 상기 그 개요가 서술된 계산 방법에 따라 두 아미노산 서열 간의 "서열 동일성"의 백분율을 결정할 목적으로, 가장 많은 수의 아미노산 잔기를 갖는 아미노산 서열이 "제1" 아미노산 서열로서 간주될 것이고, 다른 아미노산 서열이 "제2" 아미노산 서열로서 간주될 것이다.

[0045] 부가적으로, 또는 또 다른 한편으로, 2개 이상의 서열은 서열 간의 동일성에 관하여 평가될 수 있다. 2개 이상의 핵산 또는 아미노산 서열의 문맥에서 용어 "동일한" 또는 퍼센트 "동일성"은 동일한 2개 이상의 서열 또는 하위 서열을 지칭한다. 2개의 서열이 하기 서열 비교 알고리즘 중 하나를 이용하거나 또는 수동 정렬 및 육안 검사에 의해 측정된 바와 같이 비교 창 또는 지명된 영역에 걸쳐 최대 상응도를 위해 비교 및 정렬되는 경우, 명시된 영역에 걸쳐 또는 전체의 서열에 걸쳐 동일한 아미노산 잔기 또는 뉴클레오티드의 명시된 백분율 (예를 들어, 적어도 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% 또는 99.9% 동일함)을 갖는 경우에 이러한 2개의 서열은 "실질적으로 동일하다". 임의로, 동일성은 적어도 약 25, 50, 75, 또는 100개 아미노산의 길이인 영역에 걸쳐, 또는 보다 바람직하게 100 내지 150, 200개 또는 그 초과인 아미노산의 길이인 영역에 걸쳐 존재한다.

[0046] 부가적으로, 또는 또 다른 한편으로, 2개 이상의 서열은 서열 간의 정렬에 관하여 평가될 수 있다. 2개 이상의 핵산 또는 아미노산 서열의 문맥에서 용어 "정렬" 또는 퍼센트 "정렬"은 동일한 2개 이상의 서열 또는 하위 서열을 지칭한다. 2개의 서열이 하기 서열 비교 알고리즘 중 하나를 이용하거나 또는 수동 정렬 및 육안 검사에 의해 측정된 바와 같이 비교 창 또는 지명된 영역에 걸쳐 최대 상응도를 위해 비교 및 정렬되는 경우, 명시된 영역에 걸쳐 또는 전체의 서열에 걸쳐 동일한 아미노산 잔기 또는 뉴클레오티드의 명시된 백분율 (예를 들어, 적어도 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% 또는 99.9% 동일함)을 갖는 경우에 이러한 2개의 서열은 "실질적으로 정렬된다". 임의로, 정렬은 적어도 약 25, 50, 75, 또는 100개 아미노산의 길이인 영역에 걸쳐, 또는 보다 바람직하게 100 내지 150, 200개 또는 그 초과인 아미노산의 길이인 영역에 걸쳐 존재한다.

[0047] 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 내의 K131, K135, L142, Y148, Y224, E239, V250, L253, R306, R308, E375, A437, E466, D476, A484, E508, D510, K512, E515, K539, D570, 및 T571에 상응하는

위치에 하나 이상 (예를 들어, 2개 이상, 5개 이상, 10개 이상, 15개 이상, 20개 이상, 예를 들어 모두)의 아미노산 돌연변이를 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제가 $\Phi 29$ 폴리머라제 대다수의 서열을 포함하는 경우, 이러한 변형된 폴리머라제는 앞서 열거된 바와 같은 위치에 하나 이상의 돌연변이를 포함한다. 일부 실시양태에서, 변형된 폴리머라제가 $\Phi 29$ 폴리머라제 대다수의 서열을 포함하지 않는 경우, 이러한 변형된 폴리머라제는, 예를 들어, 상동성 정렬 또는 관련 기술분야에 공지된 다른 방법에 의해 결정된 바와 같이, 상기 열거된 위치에 상응하는 하나 이상의 아미노산을 포함한다.

[0048] 일부 실시양태에서, 변형된 폴리머라제는 $\Phi 29$ 폴리머라제 내의 Y148, Y226, V250, N251, T368, E375, K379, Q380, A437, P477, K478, 및 A484에 상응하는 하나 이상의 위치에 돌연변이를 포함한다. 일부 실시양태에서, 본 개시내용의 변형된 폴리머라제는 Y148, Y226, V250, N251, T368, E375, K379, Q380, A437, P477, K478, 및 A484 중 하나 이상에 돌연변이를 포함하는 변형된 $\Phi 29$ 폴리머라제이다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484C 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484S 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484T 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484Q 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484N 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484E 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484D 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484K 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484R 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484H 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484Y 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Y148I, Y226F, V250A, N251R, T368F, E375K, K379R, Q380R, A437G, P477D, K478D, 및 A484X 중 하나 이상을 포함하며, 여기서 X는 본원에 기재된 바와 같은 비-자연 아미노산을 나타낸다. 본원에 사용된 바와 같은, 하나 이상은 상기 열거된 아미노산 치환 중 2개 이상, 4개 이상, 6개 이상, 8개 이상, 10개 이상, 12개 이상, 예를 들어 모두일 수 있다.

[0049] 일부 실시양태에서, 변형된 폴리머라제는 $\Phi 29$ 폴리머라제 내의 M8, V51, N62, I71, L107, K131, K135, L142, G197, Y224, E239, V250, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, A437, A444, E466, D476, A484, E508, D510, K512, E515, K539, D570, 및 T571에 상응하는 하나 이상의 위치 (예를 들어, 1 내지 35개 위치 또는 그 사이의 임의의 정수, 예를 들어 2개 이상, 5개 이상, 10개 이상, 15개 이상, 20개 이상, 예를 들어 모두)에 돌연변이를 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 $\Phi 29$ 폴리머라제 내의 M8, V51, N62, I71, L107, K131, K135, L142, G197, Y224, E239, V250, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, A437, A444, E466, D476, A484, E508, D510, K512, E515, K539, D570, 및 T571 중 하나 이상에 돌연변이를 포함하는 변형된 $\Phi 29$ 폴리머라제이다. 일부 실시양태에서, 변형된 폴리머라제는 하기 돌연변이 M8R, V51A, N62D, I71V, L107I, K131E, K135Q, L142K, G197D, Y224K, E239G, V250A, V250I, L253A, L253H, Y281H, I288L, T301C, R306Q, R308L, D325E, D341E, K354R, T368F, E375Y, A437G, A444T, E466K, D476H, A484E, E508R, D510K, D510R, K512Y, E515Q, K539E, D570S, 및 T571V 중 하나 이상 (예를 들어, 1 내지 35개 또는 그 사이의 임의의 정수, 예를 들어 2개 이상, 5개 이상, 10개 이상, 15개 이상, 20개 이상, 예를 들어 모두)을 포함한다.

[0050] 일부 실시양태에서, 변형된 폴리머라제는 $\Phi 29$ 폴리머라제 내의 K135, L142, Y224, E239, V250, L253, E375, A437, E466, D476, A484, E508, D510, K512, E515, K539, D570, 및 T571에 상응하는 하나 이상의 위치 (예를 들어, 1 내지 18개의 위치 또는 그 사이의 임의의 정수, 예를 들어 2개 이상, 5개 이상, 10개 이상, 15개 이상, 예를 들어 모두)에 돌연변이를 포함한다. 일부 실시양태에서, 본 개시내용의 변형된 폴리머라제는 K135, L142, Y224, E239, V250, L253, E375, A437, E466, D476, A484, E508, D510, K512, E515, K539, D570, 및 T571 중 하나 이상에 돌연변이를 포함하는 변형된 $\Phi 29$ 폴리머라제이다. 일부 실시양태에서, 변형된 폴리머라제는 K135Q, L142K, Y224K, E239G, V250I, L253A, E375Y, A437G, E466K, D476H, A484E, E508R, D510R, K512Y,

E515Q, K539E, D570S, 및 T571V 중 하나 이상 (예를 들어, 1 내지 18개 또는 그 사이의 임의의 정수, 예를 들어 2개 이상, 5개 이상, 10개 이상, 15개 이상, 예를 들어 모두)을 포함한다.

- [0051] 일부 실시양태에서, 본 출원의 변형된 폴리머라제는 TPR1 영역 치환을 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 (서열식별번호: 1) 내의 S260-L359에 상응하는 TPR1 영역 대신 이. 파에시움으로부터의 TPR1 영역 (예를 들어, 서열식별번호: 5 내의 V271-M375)을 포함한다.
- [0052] 일부 실시양태에서, 본 출원의 변형된 폴리머라제는 엑소뉴클레아제 영역 내의 하나 이상의 치환을 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 (서열식별번호: 1) 내의 M1-V54에 상응하는 아미노산 대신 M2Y로부터의 엑소뉴클레아제 영역의 부분 (예를 들어, 서열식별번호: 2 내의 M1-I51)을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 (서열식별번호: 1) 내의 E75-N91에 상응하는 아미노산 대신 이. 파에시움으로부터의 엑소뉴클레아제 영역의 부분 (예를 들어, 서열식별번호: 5 내의 F72-S89)을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 내의 M1-V54 및 E75-N91에 각각 상응하는 아미노산 대신 M2Y로부터의 엑소뉴클레아제 영역의 부분 및 이. 파에시움으로부터의 엑소뉴클레아제 영역의 부분을 포함한다.
- [0053] 일부 실시양태에서, 본 출원의 변형된 폴리머라제는 변형된 팜 영역을 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 (서열식별번호: 1) 내의 M429-I433에 상응하는 아미노산 대신 이. 파에시움으로부터의 팜 영역의 부분 (예를 들어, 서열식별번호: 5 내의 L445-V449)을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 내의 A444에 상응하는 위치에 알라닌에서 티민으로의 돌연변이 (예를 들어, A444T)를 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 이. 파에시움으로부터의 팜 영역의 부분 및 Φ 29 폴리머라제 내의 A444T에 상응하는 아미노산 돌연변이를 포함한다.
- [0054] 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 내의 G197, I71, 및 L107에 상응하는 하나 이상의 위치 (예를 들어, 1, 2, 또는 3개)에 돌연변이를 포함한다. 일부 실시양태에서, 본 개시내용의 변형된 폴리머라제는 G197, I71, 및 L107 중 하나 이상 (예를 들어, 1, 2, 또는 3개)에 돌연변이를 포함하는 변형된 Φ 29 폴리머라제이다. 일부 실시양태에서, 변형된 폴리머라제는 G197D, I71V, 및 L107I 중 하나 이상 (예를 들어, 1, 2, 또는 3개)을 포함한다.
- [0055] 일부 실시양태에서, 본 출원의 변형된 폴리머라제는 폴리머라제의 하나 이상의 영역 또는 절편 (예를 들어, 플랭킹 아미노산을 임의로 포함한, 도메인 또는 그의 부분) 내의 하나 이상의 아미노산 돌연변이를 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 엑소뉴클레아제 영역, 팜 영역, TPR1 영역, 핑거 영역, TPR2 영역, 및 섹 영역 중 하나 이상 내의 하나 이상의 아미노산 돌연변이를 포함한다.
- [0056] 일부 실시양태에서, 변형된 폴리머라제는 엑소뉴클레아제 영역 내의 하나 이상의 위치 (예를 들어, 엑소뉴클레아제 영역의 엑소뉴클레아제 루프)에 돌연변이를 포함한다. 일부 실시양태에서, Φ 29 폴리머라제 대다수의 서열을 갖는 변형된 폴리머라제는 엑소뉴클레아제 영역 내의 하나 이상의 위치에 돌연변이를 포함한다. 예를 들어, 일부 실시양태에서, 본 개시내용의 변형된 폴리머라제는 Φ 29 폴리머라제의 엑소뉴클레아제 영역 내의 E75, R76, S82, A83, D84, G85, L86, P87, N88, Y90, 및 N91 중 하나 이상에 돌연변이를 포함하는 변형된 Φ 29 폴리머라제이다. 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 내의 E75, R76, S82, A83, D84, G85, L86, P87, N88, Y90, 및 N91에 상응하는 위치에 하나 이상의 아미노산 돌연변이를 포함한다. 따라서, 일부 실시양태에서, 변형된 폴리머라제가 Φ 29 폴리머라제 대다수의 서열을 포함하지 않는 경우, 이러한 변형된 폴리머라제는, 예를 들어, 상동성 정렬 또는 관련 기술분야에 공지된 다른 방법에 의해 결정된 바와 같이, 상기 열거된 위치에 상응하는 하나 이상의 아미노산을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 E75F, R76K, S82C, A83K, D84E, G85A, L86K, P87E, N88R, Y90F, 및 N91S 중 하나 이상을 포함한다. 따라서, 일부 실시양태에서, 엑소뉴클레아제 도메인 또는 그의 부분을 포함하는 절편은 상이한 폴리머라제로부터의 상응하는 엑소뉴클레아제 도메인에 대해 교환된다. 예를 들어, 일부 실시양태에서, 하나의 폴리머라제의 엑소뉴클레아제 도메인의 플랭킹 아미노산 및 루프를 포함하는 절편은 또 다른 폴리머라제로부터의 상응하는 절편으로 대체된다. 예를 들어, 일부 실시양태에서, Φ 29 E75-N91 절편은 이. 파에시움으로부터의 상응하는 F72-S89 절편으로 대체된다. 일부 실시양태에서, 엑소뉴클레아제 루프를 포함하는 절편을 교환하는 것은 폴리머라제의 인터펄스 거리를 감소시킬 수 있다.
- [0057] 일부 실시양태에서, 변형된 폴리머라제는 TPR1 영역 내의 하나 이상의 위치에 돌연변이를 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 내의 Y281, I288, T301, D325, D341, 및 K354에 상응하는 하나 이상 (예를 들어, 1, 2, 3, 4, 5, 또는 6개)의 위치에 돌연변이를 포함한다. 일부 실시양태

에서, 본 개시내용의 변형된 폴리머라제는 Y281, I288, T301, D325, D341, 및 K354 중 하나 이상 (예를 들어, 1, 2, 3, 4, 5, 또는 6개)에 돌연변이를 포함하는 변형된 Φ 29 폴리머라제이다. 일부 실시양태에서, Y281, I288, T301, D325, D341, 및 K354 중 하나 이상 (예를 들어, 1, 2, 3, 4, 5, 또는 6개)에서의 아미노산은 다른 폴리머라제 (예를 들어, M2Y, 루실리아 쿠프리나, 바실루스 균주, 예를 들어 GA-1) 내의 상응하는 위치에서의 아미노산으로 변화된다. 일부 실시양태에서, 변형된 폴리머라제는 Y281H, I288L, T301C, D325E, D341E, 및 K354R 중 하나 이상 (예를 들어, 1, 2, 3, 4, 5, 또는 6개)을 포함한다. 일부 실시양태에서, Φ 29 폴리머라제 내의 Y281, I288, T301, D325, D341, 및 K354에 상응하는 하나 이상 (예를 들어, 1, 2, 3, 4, 5, 또는 6개)의 위치에서의 돌연변이는 (예를 들어, 단일 분자 시퀀싱 반응에서의) 혼입 속도를 증가시킨다.

[0058] 일부 실시양태에서, 변형된 폴리머라제는 판 영역 내의 하나 이상의 위치에 돌연변이를 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 내의 M429, G430, V431, I433, 및 A444에 상응하는 하나 이상 (예를 들어, 1, 2, 3, 4, 또는 5개)의 위치에 돌연변이를 포함한다. 일부 실시양태에서, 본 개시내용의 변형된 폴리머라제는 M429, G430, V431, I433, 및 A444 중 하나 이상 (예를 들어, 1, 2, 3, 4, 또는 5개)에 돌연변이를 포함하는 변형된 Φ 29 폴리머라제이다. 일부 실시양태에서, M429, G430, V431, I433, 및 A444 중 하나 이상 (예를 들어, 1, 2, 3, 4, 또는 5개)에서의 아미노산은 다른 폴리머라제 (예를 들어, M2Y, 루실리아 쿠프리나, 바실루스 균주, 예를 들어 GA-1) 내의 상응하는 위치에서의 아미노산으로 변화된다. 일부 실시양태에서, 변형된 폴리머라제는 M429L, G430A, V431S, I433V, 및 A444T 중 하나 이상 (예를 들어, 1, 2, 3, 4, 또는 5개)을 포함한다. 일부 실시양태에서, Φ 29 폴리머라제 내의 M429, G430, V431, I433, 및 A444에 상응하는 하나 이상 (예를 들어, 1, 2, 3, 4, 또는 5개)의 위치에서의 돌연변이는 (예를 들어, 단일 분자 시퀀싱 반응에서의) 정확도를 증가시킨다.

[0059] 일부 실시양태에서, 변형된 폴리머라제는 판 영역 내의 하나 이상의 위치 및 엑소뉴클레아제 영역 내의 하나 이상의 위치에 돌연변이를 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 내의 G197, M8, 및 V51에 상응하는 하나 이상 (예를 들어, 1, 2, 또는 3개)의 위치에 돌연변이를 포함한다. 일부 실시양태에서, 본 개시내용의 변형된 폴리머라제는 G197, M8, 및 V51 중 하나 이상 (예를 들어, 1, 2, 또는 3개)에 돌연변이를 포함하는 변형된 Φ 29 폴리머라제이다. 일부 실시양태에서, 변형된 폴리머라제는 G197D, M8R, 및 V51A 중 하나 이상 (예를 들어, 1, 2, 또는 3개)을 포함한다. 일부 실시양태에서, Φ 29 폴리머라제 내의 G197, M8, 및 V51에 상응하는 하나 이상 (예를 들어, 1, 2, 또는 3개)의 위치에서의 돌연변이는 생산 수율, 열안정성을 개선시키고/시키거나 부하 (예를 들어, 어레이의 샘플 웰 내로의 부하)의 효율을 개선시킬 수 있다.

[0060] 일부 실시양태에서, 변형된 폴리머라제는 판 영역 내의 하나 이상의 위치 및 섬 영역 내의 하나 이상의 위치에 돌연변이를 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제는 Φ 29 폴리머라제 내의 E466, D476, K539, D570, 및 T571에 상응하는 하나 이상 (예를 들어, 1, 2, 3, 4, 또는 5개)의 위치에 돌연변이를 포함한다. 일부 실시양태에서, 본 개시내용의 변형된 폴리머라제는 E466, D476, K539, D570, 및 T571 중 하나 이상 (예를 들어, 1, 2, 3, 4, 또는 5개)에 돌연변이를 포함하는 변형된 Φ 29 폴리머라제이다. 일부 실시양태에서, 변형된 폴리머라제는 E466K, D476H, K539E, D570S, 및 T571V 중 하나 이상 (예를 들어, 1, 2, 3, 4, 또는 5개)을 포함한다.

[0061] 일부 실시양태에서, 변형된 폴리머라제는 M2Y 폴리머라제 내의 N59, Y145, V247, L250, E372, A481, 및 K509에 상응하는 위치에 하나 이상 (예를 들어, 1, 2, 3, 4, 5, 6, 또는 7개)의 아미노산 돌연변이를 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제가 M2Y 폴리머라제 대다수의 서열을 포함하는 경우, 이러한 변형된 폴리머라제는 앞에 열거된 바와 같은 위치에 하나 이상의 돌연변이를 포함한다. 일부 실시양태에서, 변형된 폴리머라제가 M2Y 폴리머라제 대다수의 서열을 포함하지 않는 경우, 이러한 변형된 폴리머라제는, 예를 들어, 상동성 정렬 또는 관련 기술분야에 공지된 다른 방법에 의해 결정된 바와 같이, 상기 열거된 위치에 상응하는 하나 이상의 아미노산 돌연변이를 포함한다.

[0062] 일부 실시양태에서, 변형된 폴리머라제는 야생형 폴리머라제 (예를 들어, 표 1에 제시된 바와 같음)의 하나 이상의 절편 (예를 들어, 플랭킹 아미노산을 임의로 포함한, 도메인 또는 그의 부분)을 포함한다. 일부 실시양태에서, 엔테로코쿠스 파에시움 폴리머라제의 하나 이상의 절편 (예를 들어, 플랭킹 아미노산을 임의로 포함한, 도메인 또는 그의 부분) (예를 들어, 서열식별번호: 5의 하나 이상의 절편)이 서열식별번호: 1-4, 및 6-19 중 임의의 것의 하나 이상의 절편을 대체할 수 있다. 일부 실시양태에서, 엔테로코쿠스 파에시움 폴리머라제의 하나 이상의 절편 (예를 들어, 플랭킹 아미노산을 임의로 포함한, 도메인 또는 그의 부분)이 Φ 29 폴리머라제의 하나 이상의 절편을 대체할 수 있다. 일부 실시양태에서, 엔테로코쿠스 파에시움 폴리머라제의 하나 이상의 절편 (예를 들어, 플랭킹 아미노산을 임의로 포함한, 도메인 또는 그의 부분)이 M2Y 폴리머라제의 하나 이상의 절

편을 대체할 수 있다. 일부 실시양태에서, 엔테로코쿠스 파에시움 폴리머라제의 하나 이상의 절편 (예를 들어, 플랭킹 아미노산을 임의로 포함한, 도메인 또는 그의 부분)이 $\Phi 29$ 폴리머라제 및/또는 M2Y 폴리머라제의 하나 이상의 절편을 대체할 수 있다. 일부 실시양태에서, 엔테로코쿠스 파에시움 폴리머라제의 하나 이상의 절편 (예를 들어, 플랭킹 아미노산을 임의로 포함한, 도메인 또는 그의 부분) (예를 들어, 서열식별번호: 5의 도메인 또는 그의 변형된 형태, 예를 들어, 하나 이상의 아미노산 치환을 함유함)이 본원에 기재된 변이체 폴리머라제 (예를 들어, 표 2에 열거된 변이체 폴리머라제, 또는 표 2에 예시되거나 또는 표 3-5에 기재된 하나 이상의 아미노산 치환 또는 다른 도메인 치환을 함유하는 변이체 폴리머라제)의 하나 이상의 절편을 대체할 수 있다.

[0063] 일부 실시양태에서, 변형된 폴리머라제의 대다수의 서열은 예로서 상기 열거된 폴리머라제 내의 위치에 상응하는 하나 이상의 상동 아미노산을 포함하지 않는다. 이러한 경우, 일부 실시양태에서, 변형된 폴리머라제는 하나 이상의 돌연변이를 포함하지 않는다. 그러나, 일부 실시양태에서, 원하는 아미노산 서열을 본원에 기재된 폴리머라제 서열과 비교할 때 주변 상동 잔기가 확인 가능한 경우, 돌연변이된 아미노산은 상기 주변 상동 잔기에 기초하여 추론되는 폴리머라제 내의 특정 부위에서의 삽입으로서 상기 변형된 폴리머라제에 포함된다. 돌연변이된 폴리머라제 변이체는 본원에 기재된 실시양태에 따라서 조작되었고 표 2에 열거된다 (서열식별번호: 20-96).

[0064] <표 2>

[0065] 상동 폴리머라제 변이체

명칭	SEQ ID NO	서열
H008	20	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADKFQLPLLKGDIDHINTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDILSTKKFNKVPKLSLPMCKEIRKAYRGGFTWLND KYKEKEIGEGMVFVNLSYPSQMYSRPLPYGAPIVFQGYEKDEQYPLYIQRIRFEFE LKEGYIPTIYIKKNPFFKGNEYLKNSGVEPVVELYLTNVDLELIQEHYELYNVEYIDGF KFREKTGLFKDFIDKWTYVKTHEEGAKKQLAKMLNSLYGKFASNPVDTGKVPYLKDD GSLGFRVGDDEYKDPVYTPMGVFTAWARFTTITAAQACYDRIIYCDTDSIHLTGTEV PEI IKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYVKEVDGKLKCEPDEATTTK FSVKCAGMTDTIKKKVTFDNFAVGFSMCKPKPVQVNGGVVLVDSVFTIK
H009	21	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADKFQLPLLKGDIDHINTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDILSTKKFNKVPKLSLPMCKEIRKAYRGGFTWLND KYKEKEIGEGMVFVNLSYPSQMYSRPLPYGAPIVFQGYEKDEQYPLYIQRIRFEFE LKEGYIPTIYIKKNPFFKGNEYLKNSGVEPVVELYLTNVDLELIQEHYELYNVEYIDGF KFREKTGLFKDFIDKWTYVKTHEEGAKKQLAKMLNSLYGKFASNPVDTGKVPYLKDD GSLGFRVGDDEYKDPVYTPMGVFTAWARFTTITAAQACYDRIIYCDTDSIHLTGTEV PEI IKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYVKEVDGKLKCEPDEATTTK FSVKCAGMTDTIKKKVTFDNFAVGFSMCKPKPVQVNGGVVLVDSVFTIK
H010	22	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADKFQLPLLKGDIDHINTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDILSTKKFNKVPKLSLPMCKEIRKAYRGGFTWLND KYKEKEIGEGMVFVNLSYPSQMYSRPLPYGAPIVFQGYEKDEQYPLYIQRIRFEFE LKEGYIPTIYIKKNPFFKGNEYLKNSGVEPVVELYLTNVDLELIQEHYELYNVEYIDGF KFREKTGLFKDFIDKWTYVKTHEEGAKKQLAKMLNSLYGKFASNPVDTGKVPYLKDD GSLGFRVGDDEYKDPVYTPMGVFTAWARFTTITAAQACYDRIIYCDTDSIHLTGTEV PEI IKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYVKEVDGKLKCEPDEATTTK FSVKCAGMTDTIKKKVTFDNFAVGFSMCKPKPVQVNGGVVLVDSVFTIK
H011	23	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADKFQLPLLKGDIDYHINTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDILSTKKFNKVPKLSLPMCKEIRKAYRGGFTWLND KYKEKEIGEGMVFVNLSYPSQMYSRPLPYGAPIVFQGYEKDEQYPLYIQRIRFEFE LKEGYIPTIYIKKNPFFKGNEYLKNSGVEPVVELYLTNVDLELIQEHYELYNVEYIDGF KFREKTGLFKDFIDKWTYVKTHEEGAKKQLAKMLNSLYGKFASNPVDTGKVPYLKDD GSLGFRVGDDEYKDPVYTPMGVFTAWARFTTITAAQACYDRIIYCDTDSIHLTGTEV PEI IKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYVKEVDGKLKCEPDEATTTK FSVKCAGMTDTIKKKVTFDNFAVGFSMCKPKPVQVNGGVVLVDSVFTIK
H012	24	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLDIDSEFEWCEMGGSTDIYFH NEKFDGEFMLSFLKNGFKWCKEAKERTFSTLISNMGWYALEICWNVKTCTTKTGK TKKEKQRTIYDSLKKYFPVKEIAEAFNFIKKEIDITKERPIGYNPTDDEWDYK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTYYGKSRFKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQKKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEHYDILEIHYTYGYMFKASCDMFKGWIDKWEVKNNTTEGARKANAKGMLNSLY GKFGTNPDITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHESTFQRAKFIQKTYVEEIDG

[0066]

		ELNVKACGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H013	25	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSWSLFGKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYFPVKEIAEAFNFPKKGIDITKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTYYGKSRFKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQKKEIGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRRLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEHYDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHESTFQRAKFIQKTYVEEIDG ELNVKACGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H014	26	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSWSLFGKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYFPVKEIAEAFNFPKKGIDITKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTYYGKSRFKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQKKEIGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRRLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEHYDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTYGARKANAKGMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHESTFQRAKFIQKTYVEEIDG ELNVKACGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H016	27	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMDICFYGKGRKLHTVI YDSLKKLPFPVKIAKDFQLPLKGDIDHINTERPVGHEITPEEYIYKNDIEIARAL DIQFKQLDRMTAGSDSLKGFKDILSTKKFNKVPKLSLPMDEIRKAYRGGFTWLND KYKKEIGEGMVFDINSAYPSQMYSRPLPYGAPIVFGKYKDEQYPLYIQRIRFEFE LKEGYIPTIQIKNPPFKGNEYLKNSGVEPVLYLTNVDLELIQEHYELNVEYIDGF KFREKTGLFKDFIDKWTYVKTHEYGAKKQLAKMLNSLYGKFASNPDPVTGKVPYKDD GSLGFRVGDDEYKDPVYTPMGVFTAWGRFTTITAAQACYDRIIYCDTDSIHLTGTEV PEIHKDIDVPKKGWYWEHESTFKRAKYLRQKTYIQDIYVKEVKGYLKQCSPEATTTK FSVKACGMDTIIKKKVTDFNFAVGFSSMGKPKPVQVNGGVVLVDVSFTIK
H018	28	MKKHPRMYSCDFETTTDVNDCRVWAYGWMEIGKTSNYKIGTDFNEFMWMIHSSRL YFHDLFKDGFSFIVNWLLHNGYTWTKRPSKEGQFSTLISKMGQWYGITICSGRDGRKKK LTTIHDSLKKLPFPVRKIGKDFKLVNKGDIIDHKPRPIGYEIDDEEYQYIKNDIQII AEALEVQTVQGLTGMTNGKDALDEFVNMSGKLYEKLFPVFSLELNEEIRKAYRGGFTW LNPVYGGKYYVKDGIVFDANSAYPSQMYDRDLPCGVPIPFEGEYVYDKSHPLYIQKLT FEFELKENYIPTIQLKNSRFGFKGNEYLSSNGERITISVSSVDWELIREHYHYVDVE FEKGWKFRTKQAFRQYIDKWMLVKNMSYGAKKAIKMLNSLYGKFATNPDIITGKRP YLREDGSNGFELMEEEFDRDPVYTPVGIFITSWARYTTITSAQKCYDRIIYCDTDSMHL EGLDVPEISIKDIVADDVLGYWEKEGQFKQKFIQKTYMEEYAKYVRDENGELKYDD EKPYKTICDKESDITIIIEIKACGMPDNIIKKHVTFDNFDIGFTMEGKLKPKQVYGGVV LVEETYTMK
H020	29	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMGGSTDIYFH DEKFDGEFMLSWSLFGKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYFPVKEIAEAFNFPKKGIDITKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTYYGKSRFKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQKKEIGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRRLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEHYDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTYGARKANAKGMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHESTFQRAKFIQKTYVEEIDG ELNVKACGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK

[0067]

H022	30	MATKKRKAYSCDFEATTSTYSETETRVWAYGWMEIGNTSHFNIGDNLDEFMLWTSKEC ADLYFHDRLRYDGEFIVNWLLHKGYECNESGRPKTFDTVISKGGQWYKIAIHHEGKGT QIFDSLKKLPFPVKTIKAFKLPVLKGDIDINLHRDENHVITSEEFYIKHDIIVAR ALDIQINQQGLVKMTNGADSMDFIKSLDKKKVAERIYNQYFPKMSIAMSIFRKAY RGGFTWVNPKEKQGEVGEGMVFDANSAYPSVMYKPLPWGKVPVFGKYEEDPDFPLY ICHIKTFVLKEGHIPTIQIKKNPIFQENEYLETSGGAPVDLHVTNVDLELIKEHYEL YDTEYVGGWKFRQQTGIFNNFIDYWMKIKTDPKSTPAIVTLAKLQNLNLYGKFASHPD VTGKVPYVKDDGSTAFKKGLPKSKDPVYTPAGAFITAWARHMTITTAQKVYDRILYCD TDSIHILGIDIPEAIKNDIHQKELGKWEFECMFKRAKFVRQKTYVEDMYAKFMKYWED GELNYYLKECVKEEATARLLNVKACAGMPQAVKKFVTRTFVAVGFTSDTGKLPKHVKG GQILVDVPFTIK
H025	31	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLEIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSWSLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYFPVKEIAEAFNFPKKGIDYTKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTYYGKSRFKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQKKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEYHDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHESTFQRAKFIQKTYVEEIDG ELNVKACAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H026	32	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLEIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSWSLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYFPVKEIAEAFNFPKKGIDYTKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTYYGKSRFKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQKKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEYHDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHESTFQRAKFIQKTYVEEIDG ELNVKACAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H027	33	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLEIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSWSLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYFPVKEIAEAFNFPKKGIDYTKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTYYGKSRFKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQKKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEYHDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHESTFQRAKFIQKTYVEEIDG ELNVKACAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H028	34	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLEIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSWSLFKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYFPVKEIAEAFNFPKKGIDYTKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTYYGKSRFKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQKKEIGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEYHDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHESTFQRAKFIQKTYVEEIDG ELNVKACAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H029	35	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLEIDSFFEWCEMGGSTDIYFH

[0068]

		NEKFDGEFMLSFLKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYPPVKEIAEAFNFPKKGEIDITKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTITYGKSFRKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQGEIGEGIVFDANSAYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEYHDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHESTFQRAKFIRQKTYVEEIDG ELNVKACAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H030	36	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSFLKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYPPVKEIAEAFNFPKKGEIDITKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTITYGKSFRKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQGEIGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEYHDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTYGARKANAKGMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWKHESTFQRAKFIRQKTYVEEIDG ELNVKACAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H031	37	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSFLKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYPPVKEIAEAFNFPKKGEIDITKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTITYGKSFRKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQGEIGEGIVFDANSHYPSQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEYHDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTYGARKANAKGMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHESTFQRAKFIRQKTYVEEIDG ELNVKACAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H032	38	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSFLKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYPPVKEIAEAFNFPKKGEIDITKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTITYGKSFRKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQGEIGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEYHDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTYGARKQAKLMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDPKKLGYWEHESTFQRAKFIRQKTYVEEIDG ELNVKACAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H033	39	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSFLKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYPPVKEIAEAFNFPKKGEIDITKERPIGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTITYGKSFRKQWFPVLSLGFDDK LRKAYKGGFTWVNKVFQGEIGEGIVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENI DYPLYIQNIKVRFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVD LDLFFEYHDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTYGARKQAKLMLNSLY GKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRYTTITTAQRC FDNIIYCDTDSIHLTGTEVPEAIEHLVDSKKLGYWEHESTFQRAKFIRQKTYVEEIDG ELNVKACAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
H034	40	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLIDSFFEWCEMGGSTDIYFH NEKFDGEFMLSFLKNGFKWCKEAKEERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYPPVKEIAEAFNFPKKGEIDITKERPIGYNPTDDEWDYLK

[0069]

		NDIQIMAMALKIQFDQGLTRMTRGSDALGDYQDWVKTITYGKSRFKQWFPVLSLGFDDKDLRKAYKGGFTWVNKVFQKKEIGEGIVFDVNSLYPSQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRRLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDLFFFEHYDILEIHYTYGYMFKASCDMFKGWIDKWIEVKNTTEGARKANAKGMLNSLYGKFGTNPDIITGKVPYMGEDGIVRLTLGEEELRDPVYVPLASFVTAWGRTTITTAQRCFDNIYYCDTDSIHLTGTEVPEAIEHLVDSKLGWYKHESTFQRAKFIQKTYVEEYIMKRVKGYLVQGSPPDDYTDGELNVKACAGMPDRIKELVTFDNFEVGFSSYKLLPKRTQGGVVLVDTMFTIK
H037	41	MGNKKRKIYSCDFETTTDVNDCRVWAYGLMEIDGKFENYKEGNNIDEFMEWTEQEQGDLYFHNLRFDGEFIVNWLHLKGYRFNNTRKAGTFNAVISSMGQWYKIDIYYGREGKRVFKTSIYDSLKKLPFPVKTIKAKFKLPIEKGDIDYDAPRPVGHQITPDESKYIKNDVEIIRALHSQLNTAKLTGMTIGSDALDGFKHSKSPKVSkrmyDHHFPVISNAIHEEFKAYRGGFTWANPKYAGKVIINGLVFDVNSLYPSVMYDKPLPYGLPVFPFSGEYEDETHPLFIQHIKCGFELKDGHIPTIQIKKNFRFADNEYLHSSEGNILDLHVTNVDLALIKEHYTLYEEEEYLQGYKFKQVTGLFKNYIDYWSDDKINAEDPAIRQMAKLMLNSLYGKFGTSDVITGKEVFLKEDGSTGFRKGQKEERDPVYMPMGAFITAYARDVTIRTAKCYDRILYCDTDSIHLVGTEIPEAIKDRIHDKKLGWYAHSTFWRAKFIQKTYIEDLCMRFEQEKVNGEWFKFMVEEKDITKATARELSVKACAGMAQVQKQYVTFDNFGVDFKHPNDYTDDEIRKKNIKFKLKPTHRKGQVLVPTPTIK
Q001	42	MKHMPrKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYIMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKKEIGEGMVFDANSHPYQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIREFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGWYAHSTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKACAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
Q002	43	MKHMPrKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYIMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKKEIGEGMVFDANSHPYQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIREFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGWYAHSTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKACAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
Q003	44	MKHMPrKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYIMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKKEIGEGMVFDANSHPYQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIREFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGWYAHSTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKACAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
Q004	45	MKHMPrKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYIMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITPEEYAYIKNDIQIIA

[0070]

		EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFANDSHYPAMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDELELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEGEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
Q005	46	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFANDSHYPAMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDELELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEGEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWCHSTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
Q006	47	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFANDSHYPAMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDELELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIRQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEGEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
Q007	48	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFANDSHYPAMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDELELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKRLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEGEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
Q008	49	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFANDSHYPAMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDELELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEGEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
Q009	50	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFANDSHYPAMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC

[0071]

		EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDDPKKLGWHAESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
Q010	51	MKHMPPRMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKKGKRIH TVIYDSLKKLFFPVVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPITLSGLDKEVRKAYRGGFTW LNDRFKKEIGEEMVFDANSHPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGWHAESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
Q011	52	MKHMPPRMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKKGKRIH TVIYDSLKKLFFPVVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPITLSGLDKEVRKAYRGGFTW LNDRFKKEIGEEMVFDANSHPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGWHAESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
Q012	53	MKHMPPRMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKKGKRIH TVIYDSLKKLFFPVVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPITLSGLDKEVRKAYRGGFTW LNDRFKKEIGEEMVFDANSHPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGWHAESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
Q013	54	MKHMPPRMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKKGKRIH TVIYDSLKKLFFPVVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPITLSGLDKEVRKAYRGGFTW LNDRFKKEIGEEMVFDVNSLYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTSEGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWARYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGWHAESTFKRAKYLQKTYIQDIYMKVVDGKLVEGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDDTFITIK
Q014	55	MKHMPPRMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKKGKRIH TVIYDSLKKLFFPVVKKIAKDFKLTVLKGDIDYHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPITLSGLDKEVRKAYRGGFTW LNDRFKKEIGEEMVFDVNSLYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTSEGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL

[0072]

		KENGALGFRLGEEETKDPVYTPMGVFI TAWARYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWCHESTFKRAKYLRQKTYIQDIYMKEVDGKLVESGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q015	56	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVKKIAKDFKLTVLKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIGEGMVFDVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSEGAIKQLAKLMLNSLYGKFASNPDTVTKVPYL KENGALGFRLGEEETKDPVYTPMGVFI TAWARYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWCHSTFKRAKYLRQKTYIQDIYMKEVDGKLVESGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q016	57	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVKKIAKDFKLTVLKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIGEGMVFDVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSEGAIKQLAKLMLNSLYGKFASNPDTVTKVPYL KENGALGFRLGEEETKDPVYTPMGVFI TAWARYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWCHSTFKRAKYLRQKTYIQDIYMKEVDGKLVESGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q017	58	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVKKIAKDFKLTVLKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIGEGMVFDVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSEGAIKQLAKLMLNSLYGKFASNPDTVTKVPYL KENGALGFRLGEEETKDPVYTPMGVFI TAWARYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWCHSTFKRAKYLRQKTYIQDIYMKEVDGKLVESGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q018	59	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVKKIAKDFKLTVLKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIGEGMVFDVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSEGAIKQLAKLMLNSLYGKFASNPDTVTKVPYL KENGALGFRLGEEETKDPVYTPMGVFI TAWARYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWCHSTFKRAKYLRQKTYIQDIYMKEVDGKLVESGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q019	60	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVKKIAKDFKLTVLKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIGEGMVFDVNSLYPAQMYSRLLPYGEPIVFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSEGAIKQLAKLMLNSLYGKFASNPDTVTKVPYL KENGALGFRLGEEETKDPVYTPMGVFI TAWARYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRQKTYIQDIYMKEVDGKLVESGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK

[0073]

		DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q020	61	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIH TVIYDSLKKLFFPVVKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTKKFVKVPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDVNSHYPAQMYSRLLPYGEPVFEFGYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGNELKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHSTFKRAKYLQKTYIQDIYMKRVKGKLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETFTIK
Q021	62	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIH TVIYDSLKKLFFPVVKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTKKFVKVPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHYPAQMYSRLLPYGEPVFEFGYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGNELKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWHAHSTFKRAKYLQKTYIQDIYMKRVKGKLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETFTIK
Q022	63	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIH TVIYDSLKKLFFPVVKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTKKFVKVPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHYPAQMYSRLLPYGEPVFEFGYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGNELKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWHAHSTFKRAKYLQKTYIQDIYMKRVKGKLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETFTIK
Q023	64	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIH TVIYDSLKKLFFPVVKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTKKFVKVPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHYPAQMYSRLLPYGEPVFEFGYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGNELKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKFGYWAHSTFKRAKYLQKTYIQDIYMKRVKGKLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETFTIK
Q024	65	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIH TVIYDSLKKLFFPVVKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTKKFVKVPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHYPAQMKSRLLPYGEPVFEFGYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGNELKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHSTFKRAKYLQKTYIQDIYMKRVKGKLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETFTIK
Q025	66	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL

[0074]

		YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHYPSQMSRLLPYGEPIVEFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHASTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
Q026	67	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHPAQMSRLLPYGEPIVEFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHASTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
Q027	68	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHPAQMSRLLPYGEPIVEFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHASTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
Q028	69	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHPAQMSRLLPYGEPIVEFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQWAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHASTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
Q029	70	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHPAQMSRLLPYGEPIVEFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLFLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHASTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
Q030	71	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA

[0075]

		EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFANDSHYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGNLYKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEGEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHASTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
Q031	72	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFANDSHYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGNLYKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEGEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHASTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
Q032	73	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFANDSHYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGNLYKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWDYIKTTSYGAIKQLAKMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEGEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKKGYWAHASTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
Q033	74	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFANDSHYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGNLYKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWEYIKTTSYGAIKQLAKMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEGEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKKGYWAHASTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
Q034	75	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFANDSAYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGNLYKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEGEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
Q035	76	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFANDSAYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC

[0076]

		EFELKEGYIPTIQIKQSLFYKNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TKIPDVIKDIVHPKKLGYWEHESTFKRAKYLROKTYIQDIYMKRVRGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVETFTIK
Q036	77	MKHMPPRMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRRKI TVIYDSLKKLFFPVKKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTKKFKKVFTLSLGLDKEVRKAYRGGFTW LNDRFKKEKEIGEMVFDANSHPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWEHESTFKRAKYLROKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVETFTIK
Q037	78	MKHMPPRMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRRKI TVIYDSLKKLFFPVKKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTKKFKKVFTLSLGLDKEVRKAYRGGFTW LNDRFKKEKEIGEMVFDVNSHPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLROKTYIQDIYMKRVKGLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVETFTIK
Q038	79	MKHMPPRMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRRKI TVIYDSLKKLFFPVKKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTKKFKKVFTLSLGLDKEVRKAYRGGFTW LNDRFKKEKEIGEMVFDVNSHPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLROKTYIQDIYMKRVKGLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVETFTIK
Q039	80	MKHMPPRMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRRKI TVIYDSLKKLFFPVKKIAKDFKLTVLKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTKKFKKVFTLSLGLDKEVRKAYRGGFTW LNDRFKKEKEIGEMVFDVNSHPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLROKTYIQDIYMKVKGKLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVETFTIK
Q040	81	MKHMPPRMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRRKI TVIYDSLKKLFFPVKKIAKDFKLTVLKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTKKFKKVFTLSLGLDKEVRKAYRGGFTW LNDRFKKEKEIGEMVFDVNSHPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYL

[0077]

		KENGALGFRLGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRQKTYIQDIYMKEVDGKLVESGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMMPKPVQVPGGVVLVDETF TIK
Q041	82	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFI INWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVKKIAKDFKLTVLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDII TTKKFKKVFP TSLGLDKEVRYAYRGGFTW LNDRFKEKEIGE GMVFDVNSHYPAQMSRLLPYGEP I VFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGN EYLKSSGGEIADLWLSNVDELMLKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSEGAIKQLAKMLNSLYGKFASNP DVTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRQKTYIQDIYMKEVDGKLVESGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMMPKPVQVPGGVVLVDETF TIK
Q042	83	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFI INWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVKKIAKDFKLTVLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDII TTKKFKKVFP TSLGLDKEVRYAYRGGFTW LNDRFKEKEIGE GMVFDVNSHYPAQMSRLLPYGEP I VFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGN EYLKSSGGEIADLWLSNVDELMLKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSEGAIKQLAKMLNSLYGKFASNP DVTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRQKTYIQDIYMKEVDGKLVESGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMMPKPVQVPGGVVLVDDTF TIK
Q043	84	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFI INWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVKKIAKDFKLTVLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDII TTKKFKKVFP TSLGLDKEVRYAYRGGFTW LNDRFKEKEIGE GMVFDVNSHYPAQMSRLLPYGEP I VFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGN EYLKSSGGEIADLWLSNVDELMLKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSEGAIKQLAKMLNSLYGKFASNP DVTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRQKTYIQDIYMKEVDGKLVESGSPDDYT KIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMMPKPVQVPGGVVLVDDTF TIK
Q044	85	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFI INWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVKKIAKDFKLTVLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDII TTKKFKKVFP TSLGLDKEVRYAYRGGFTW LNDRFKEKEIGE GMVFDVNSHYPAQMSRLLPYGEP I VFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGN EYLKSSGGEIADLWLSNVDELMLKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSEGAIKQLAKMLNSLYGKFASNP DVTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRQKTYIQDIYMKHVHGKLVESGSPDDYT KIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMMPKPVQVPGGVVLVDDTF TIK
Q045	86	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFI INWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLFFPVKKIAKDFKLTVLKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDII TTKKFKKVFP TSLGLDKEVRYAYRGGFTW LNDRFKEKEIGE GMVFDVNSHYPAQMSRLLPYGEP I VFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKGN EYLKSSGGEIADLWLSNVDELMLKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSEGAIKQLAKMLNSLYGKFASNP DVTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKEVDGKLVESGSPDDYT

[0078]

		DIKLSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q046	87	MKHMPPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIH TVIYDSLKKLFFPVKKIAKDFKLTCLKGDIIDHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIEGEMVFDVNSHYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKNSRFYKGNLYLKSSGGEIADLWLSNVDELMLKEHYDLYNVEYI SGLKFKAATTLGFKDFIDKWFYIKTTSEGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKHVDGKLVESPPDDYT KIKLSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q047	88	MKHMPPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIH TVIYDSLKKLFFPVKKIAKDFKLTCLKGDIIDHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIEGEMVFDVNSHYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKNSRFYKGNLYLKSSGGEIADLWLSNVDELMLKEHYDLYNVEYI SGLKFKAATTLGFKDFIDKWFYIKTTSEGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKHVDGKLVESPPDDYT KIKLSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q048	89	MKHMPPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIH TVIYDSLKKLFFPVKKIAKDFKLTCLKGDIIDHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIEGEMVFDVNSHYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKNSRFYKGNLYLKSSGGEIADLWLSNVDELMLKEHYDLYNVEYI SGLKFKAATTLGFKDFIDKWFYIKTTSEGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKHVDGKLVESPPDDYT KIKLSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q049	90	MKHMPPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIH TVIYDSLKKLFFPVKKIAKDFKLTCLKGDIIDHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIEGEMVFDVNSHYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKNSRFYKGNLYLKSSGGEIADLWLSNVDELMLKEHYDLYNVEYI SGLKFKAATTLGFKDFIDKWFYIKTTSEGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKHVDGKLVESPPDDYT KIKLSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q050	91	MKHMPPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIH TVIYDSLKKLFFPVKKIAKDFKLTCLKGDIIDHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIEGEMVFDVNSHYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKNSRFYKGNLYLKSSGGEIADLWLSNVDELMLKEHYDLYNVEYI SGLKFKAATTLGFKDFIDKWFYIKTTSEGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKHVDGKLVESPPDDYT KIKLSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDDTFTIK
Q051	92	MKHMPPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL

[0079]

		YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYGKGRKIH TVIYDSLKKLFFPVKKIAKDFKLTKLKGDIIDHKERPVGKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIGEGMVFVDVNSHYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKNSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKHVDGKLVGSPDDYT KIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDDTFTIK
Q052	93	MKHMPPRRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYGKGRKIH TVIYDSLKKLFFPVKKIAKDFKLTKLKGDIIDHKERPVGKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIGEGMVFVDVNSHYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKNSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKHVDGKLVGSPDDYT KIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDDTFTIK
Q053	94	MKHMPPRRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYGKGRKIH TVIYDSLKKLFFPVKKIAKDFKLTKLKGDIIDHKERPVGKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIGEGMVFVDVNSHYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKNSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKHVDGKLVGSPDDYT KIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDDTFTIK
Q054	95	MKHMPPRRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYGKGRKIH TVIYDSLKKLFFPVKKIAKDFKLTKLKGDIIDHKERPVGKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIGEGMVFVDVNSHYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKNSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKHVDGKLVGSPDDYT KIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDDTFTIK
Q055	96	MKHMPPRRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYGKGRKIH TVIYDSLKKLFFPVKKIAKDFKLTKLKGDIIDHKERPVGKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRYAYRGGFTW LNDRFKEKEIGEGMVFVDVNSHYPAQMSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRC EFELKEGYIPTIQIKNSRFYKGYNEYLKSSGGEIADLWLSNVDELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRPKTYIQDIYMKHVDGKLVGSPDDYT KIKLSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDDTFTIK

[0080]

[0081]

일부 실시양태에서, 아미노산은 폴리머라제의 구조 및/또는 기능에 기초하여 변형을 위해 선택된다. 예를 들어, 도 2는 $\Phi 29$ 폴리머라제 (200)의 카톤 예시를 도시한다. 폴딩된 3차원 구조는 오버레이 (202)에 상응하는 별개의 도메인 및 서브 도메인을 포함한다: N-말단 엑소뉴클레아제 도메인 (1); 및 팜 서브 도메인 (2), 말단 단백질 영역 1 서브 도메인 (TPR1) (3), 핑거 서브 도메인 (4), TPR2 서브 도메인 (5), 및 섬 서브 도메인 (6)을 함유하는 C-말단 폴리머라제 도메인. 이들 도메인 및 서브 도메인은 N-말단에서 C-말단 방식으로 배향되는, 폴리펩티드 구축물 (204)에 따르는 폴리펩티드 가닥의 부위에 매핑된다. 도시된 바와 같이, N-말단 엑소뉴클레아제 도메인 (1)은 야생형 $\Phi 29$ 폴리머라제의 잔기 1-189에 걸쳐 있고, C-말단 폴리머라제 도메인은 잔기 190-575에 걸쳐 있다. C-말단 폴리머라제 도메인 내에서, 팜 서브 도메인 (2)은 야생형 $\Phi 29$ 폴리머라제의 잔기 190-260 및 427-530에 걸쳐 있고, TPR1 서브 도메인 (3)은 잔기 261-358에 걸쳐 있으며, 핑거 서브 도메인 (4)은 잔기 359-394에 걸쳐 있고, TPR2 서브 도메인 (5)은 잔기 395-426에 걸쳐 있으며, 섬 서브 도메인 (6)은 잔기 531-575에 걸쳐 있다. 본 출원에 기재된 상이한 폴리머라제의 등가 절편 (예를 들어, 플랭킹 아미노산을 임의로 포함한, 도메인 또는 그의 부분)이 서로 대체되어 키메라 폴리머라제를 생산할 수 있다. 예를 들어, 하나의 폴리머라제 (예를 들어, 표 1에 제시된 야생형 서열을 갖거나 또는 표 2에 예시되거나 또는 표 3-5에 기재된 하나 이상의 돌연변이를 갖는다)로부터의 엑소뉴클레아제 도메인, 팜 서브 도메인, TPR1 서브 도메인, 하나 이상의 핑거 서브 도메인, TPR2 서브 도메인, 및/또는 섬 서브 도메인 중 하나 이상이 또 다른 폴리머라제 (예를 들어, 표 1에 제시된 야생형 서열을 갖거나 또는 표 2에 예시되거나 또는 표 3-5에 기재된 하나 이상의 돌연변이를 갖는다) 내의 상응하는 도메인을 대체할 수 있다. 일부 실시양태에서, 하나 이상의 플랭킹 아미노산을

임의로 포함한, 이들 도메인 중 하나 이상의 부분을 포함하는 절편이 대체할 수 있다.

[0082]

일부 실시양태에서, 변형된 폴리머라제는 $\Phi 29$ 폴리머라제 이외의 대다수의 폴리머라제 서열을 포함한다. 이러한 실시양태에서, 대다수의 폴리머라제 서열은 (예를 들어, 상동성 정렬, 계산 모델링, 구조적 분석, 또는 임의의 적합한 방법에 기초하여) $\Phi 29$ 폴리머라제 (200)로 유추될 수 있는 하나 이상의 영역을 포함한다. 본원에 사용된 바와 같은, 폴리머라제의 "영역"은 폴리머라제 효소의 별개의 도메인 또는 서브 도메인을 지칭한다. 예를 들어, 일부 실시양태에서, 폴리머라제의 영역은 N-말단 엑소뉴클레아제 도메인 또는 C-말단 폴리머라제 도메인을 지칭한다. 일부 실시양태에서, 폴리머라제의 영역은 팜 서브 도메인, TPR1 서브 도메인, 핑거 서브 도메인, TPR2 서브 도메인, 또는 섬 서브 도메인을 지칭한다. 따라서, 일부 실시양태에서, 폴리머라제의 영역은 소정의 도메인 또는 서브 도메인을 포함하는 모든 아미노산을 지칭한다. 일부 실시양태에서, 변형된 폴리머라제는 대다수의 폴리머라제 서열의 하나 이상의 영역에 대한 변형을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 대다수의 폴리머라제 서열의 하나 이상의 부분에 대한 변형을 포함한다. 본원에 사용된 바와 같은, 폴리머라제의 "부분"은 폴리머라제 서열 내의 2개 이상의 연속되는 잔기의 연장물을 지칭한다. 일부 실시양태에서, 폴리머라제 서열의 부분은 단일 폴리머라제 도메인 또는 단일 폴리머라제 서브 도메인 내의 2개 이상의 연속되는 아미노산을 지칭한다. 일부 실시양태에서, 폴리머라제 서열의 부분은 2개 이상의 폴리머라제 도메인 및/또는 서브 도메인 전역에 걸쳐 있는 2개 이상의 연속되는 아미노산을 지칭한다. 따라서, 일부 실시양태에서, 폴리머라제 서열의 부분은 폴리머라제 서열 이내의 연속되는 아미노산의 임의의 연장물이다. 일부 실시양태에서, 부분은 5-10개의 연속되는 아미노산, 10-25개의 연속되는 아미노산, 25-50개의 연속되는 아미노산, 50-75개의 연속되는 아미노산, 75-100개의 연속되는 아미노산 또는, 예를 들어, 폴리머라제 영역 또는 도메인의 부분을 구성하는 다른 수의 연속되는 아미노산을 지칭한다.

[0083]

일부 실시양태에서, 변형된 폴리머라제는 일반적으로 도 2에 도시된 바와 같은 도메인 및/또는 서브 도메인 중 하나 이상 내에서의 하나 이상의 단일 부위 돌연변이를 포함한다. 예를 들어, 도 3은 각각의 폴리펩티드 가닥 이내의 돌연변이 부위 (화살표로 그 근차치가 제시됨)를 수반한 표 2의 선택된 돌연변이 변이체를 도시한다. M2Y 및 M2Y 돌연변이 변이체 H016 (열린 채움), 루실리아 쿠프리나 및 루실리아 쿠프리나 돌연변이 변이체 H018 (점자 채움), 엔테로코쿠스 파에시움 및 엔테로코쿠스 파에시움 돌연변이 변이체 H020 (파선 채움), 및 바실루스 파지 VMY22 및 바실루스 파지 VMY22 돌연변이 변이체 H022 (대각선 채움)에 대한 폴리펩티드 가닥이 도시된다. 그러나, 본원에 기재된 바와 같은 다른 절편 교환 및/또는 아미노산 돌연변이를 포함하는 키메라가 사용될 수도 있다.

[0084]

일부 실시양태에서, 본원에 기재된 하나 이상의 단일 부위 돌연변이 변형 이외에 또는 그에 대한 대안으로, 대다수의 폴리머라제 서열 내의 아미노산의 연장물 (예를 들어, 2개 이상의 연속되는 아미노산)이 변형된다. 일부 실시양태에서, 아미노산의 연장물은 상이한 폴리머라제 서열의 부분에 상응하는 아미노산의 연장물이다. 예를 들어, 일부 실시양태에서, 대다수의 폴리머라제 서열의 도메인/서브 도메인 (또는 그 내에서의 부분)은 상이한 폴리머라제 서열의 상응하는 도메인/서브 도메인 (또는 그 내에서의 부분)으로 교환된다. 이러한 실시양태에서, 폴리머라제는 키메라 폴리머라제, 키메라 폴리머라제 변이체, 또는 키메라로서 지칭된다. 키메라 폴리머라제는 본원에 기재된 실시양태에 따라서 조작되었고, 표 3에 열거된다 (서열식별번호: 97-516).

[0085]

<표 3>

[0086] 키메라 폴리머라제 변이체

명칭	SEQ ID NO	서열
C001	97	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTII SKMGQWYMIDICFGYKGRKKLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFDANSHYPAQMYSRLLPYGEPVIFEGKYVWDEQYPLYIQIRIFEFE LKEGYIPTIQIKKNPFFKGNEYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYIDGF KFRETTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGF SRKMMPKPVQVPGGVVLVDETF TIK
C002	98	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTII SKMGQWYMIDICFGYKGRKKLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFDANSHYPAQMYSRLLPYGEPVIFEGKYVWDEYPLHIQHIRCEFE LKEGYIPTIQIKKNPFFKGNEYLKNSGVEPVELYLTNVDLELIQEHYELYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGF SRKMMPKPVQVPGGVVLVDETF TIK
C003	99	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTII SKMGQWYMIDICFGYKGRKKLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFDANSHYPAQMYSRLLPYGEPVIFEGKYVWDEYPLHIQHIRCEFE LKEGYIPTIQIKKNPFFKGNEYLKNSGVEIADLWLSNVDLELMKEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGF SRKMMPKPVQVPGGVVLVDETF TIK
C004	100	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTII SKMGQWYMIDICFGYKGRKKLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFDANSHYPAQMYSRILPYGDPVIFDGKYVWDEYPLHIQHIRCEFE LKDGYIPTIQIKRSRFYKNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGF SRKMMPKPVQVPGGVVLVDETF TIK
C005	101	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTII SKMGQWYMIDICFGYKGRKKLHTVI

[0087]

		YDSLKLLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFANDSHYPAQMSRILPYGDPVFDGKYVWDDEYPLHIQHRCDFE LKDGYPITIQIKRSRFYKGYNEYLKSSGGDLVELWLSNVDELMEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C006	102	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKLLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFANDSHYPAQMSRILPYGDPVFDGKYVWDDEYPLHIQHRCDFE LKDGYPITIQIKRSRFYKGYNEYLKSSGGDLVELWISQVDIDLMEHYEYLYNVEYLSGI KFRATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C007	103	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEINADLYFH DLKFDGAFIVNWLEQHGFRWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKLLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFANDSHYPAQMSRLLPYGEPVFEKGKYVWDDEYPLHIQHRCDFE LKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDELMEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C008	104	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEINADLYFH DLKFDGAFIVNWLEQHGFRWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKLLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFANDSHYPAQMSRILPYGDPVFDGKYVWDDEYPLHIQHRCDFE LKDGYPITIQIKRSRFYKGYNEYLKSSGGDLVELWISQVDIDLMEHYEYLYNVEYLSGI KFRATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C009	105	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKLLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFANDSHYPAQMSRILPYGDPVFDGKYVWDDEYPLHIQHRCDFE LKDGYPITIQIKRSRFYKGYNEYLKSSGGELVELYVTNIDLDLIKEHYEYLYNVEYLSGI KFRATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C010	106	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFCEWCEMCGSSTDIYFH NEKFDGEFMLSWLKNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYIYKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND

[0088]

		RFKGEIIGEMVFDANSHYPAQMYSRLLPYGEPVFEKGKVVWDEEDYPLHIQHIRCEFE LKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLYKEN GALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C011	107	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFH NEKFDGEFMLSFLKNGFKWCKEAKERTFSTLISNMQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYPFPVKEIAEAFNFPKKGEDYTKERPIGYNPTDDEWDYLYK NDIQIMAMALKIQFDQGLDRMTAGSDSLKGFKDIIITKKFKKVFPFSLGLDKEVRKA YRGGFTWLNDRFKGKEIIGEMVFDANSHYPAQMYSRLLPYGEPVFEKGKVVWDEEDYPL HIQHIRCEFEFELKEGYIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDLELMKEHYD LYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDV TGKVPYLYKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDT DSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQ GSPPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIT IK
C012	108	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYIMIDICLYGKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPFSLGLDKEVRKAYRGGFTW LNDRFKGKEIIGEMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLY KENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDY TDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C013	109	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYIMIDICLYGKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPFSLGLDKEVRKAYRGGFTW LNDRFKGKEIIGEMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDIL EIHYYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLYKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C014	110	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFH NEKFDGEFMLSFLKNGFKWSADGLPNTYNTIISRMQWYIMIDICLYGKGRKIH YDSLKKLPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITYPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPFSLGLDKEVRKAYRGGFTWLNDR FKGKEIIGEMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQIKRSRFYKGYNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLYKEN GALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C015	111	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVDNITFGLEIDSFFEWCEMQGSTDIYFH NEKFDGEFMLSFLKNGFKWCKEAKERTFSTLISNMQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYPFPVKEIAEAFNFPKKGEDYTKERPIGYNPTDDEWDYLYK NDIQIMAMALKIQFDQGLDRMTAGSDSLKGFKDIIITKKFKKVFPFSLGLDKEVRKA YRGGFTWLNDRFKGKEIIGEMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPL

[0089]

		YIQNIKVRFLKERHIPTIQVKQSSLFIQNEYLESSVNLGVDELIDLTLTNVDLDF FEHYDILEIHYTYGYMFKASCDMFKDFIDKWYIKTTSYGAIKQAKLMLNSLYGKFA SNPDVTGKVPYLYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRI IYCDTDSIHLTGTEIPDVIKDIVDPKKLGWHESTFKRAKYLRQKTYIQDIYMKRVK GYLVQGSPPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSSRMMKPKPVQVPGGVVLV DETFTIK
C016	112	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADQFQLPLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVPFTLSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFDAHSHYPAQMYSRLLPYGEPVFEKGWVWDEYDPLHIQHIRCEFE LKEGYIPTIQIKRSRKYKNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGL KFKATTGLFKDFIDKWYIKTTSYGAIKQAKLMLNSLYGKFASNPVTGKVPYLYKEN GALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGWHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSSRMMKPKPVQVPGGVVLVDETFTIK
C017	113	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADQFQLPLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVPFTLSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFDAHSHYPAQMYSRLLPYGEPVFEKGWVWDEYDPLHIQHIRCEFE LKEGYIPTIQIKRSRKYKNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGL KFKATTGLFKDFIDKWYIKTTSYGAIKQAKLMLNSLYGKFASNPVTGKVPYLYKEN GALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGWHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSSRMMKPKPVQVPGGVVLVDETFTIK
C018	114	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHDLDKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVPFTLSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDAHSHYPAQMYSRLLPYGAPVFEQGYEKDEQYPLYIQRIRF EFELKEGYIPTIQIKKNPFFKGNEYLKNSGVEPVVELYLTNVDLELIQEHYELYNVEYI DGFKFREKTGLFKDFIDKWYIKTTSYGAIKQAKLMLNSLYGKFASNPVTGKVPYLY KENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGWHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGFSSRMMKPKPVQVPGGVVLVDETFTIK
C019	115	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADQFQLPLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVPFTLSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFDAHSHYPAQMYSRLLPYGAPVFEQGYEKDEQYPLYIQRIRFEFE LKEGYIPTIQIKKNPFFKGNEYLKNSGVEPVVELYLTNVDLELIQEHYELYNVEYIDGF KFREKTGLFKDFIDKWYIKTTSYGAIKQAKLMLNSLYGKFASNPVTGKVPYLYKEN GALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGWHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSSRMMKPKPVQVPGGVVLVDETFTIK
C020	116	MKHMPRKMYSCDFETTTDVNDCRVWAYGWMEIGKTSNYKIGTDFNEFMWMIHSSRL YFHDLDKFDGSAFIVNWLLHNGYTWTKRPSKEGQFSTLISKMGQWYGITICSGRDGRKKK LTTIHDSLKKLPFPVRKIGKDFKLVNVLKGDIDYHKPRPIGYEIDDEEYQYIKNDIQII AEALEVQTVQGLTGMTNGSDSLKGFKDIITTKKFKKVPFTLSLGLDKEVRKAYRGGFT WLNDRFKKEIGEGMVFDAHSHYPAQMYSRLLPYGEPVFEKGWVWDEYDPLHIQHIR CEFELKEGYIPTIQIKRSRKYKNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEY

[0090]

		ISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPY LKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLT GTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLQVQGGSPDDY TDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETFITIK
C021	117	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHDLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYGKRRKI TVIYDSLKKLPFPVKEIAKDFKLTVKKGDIIDHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVF DANSHYPAQMYDRDLPCGVPIPFEGEYVYDKSHPLYIQKLT EFELKENYIPTIQLKNSRF GFKGNEYLSSSNGERITISVSSVDWELIREHYHVYDVEF EKGWKFRTKQAFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPY LKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLT GTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLQVQGGSPDDY TDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETFITIK
C022	118	MKHMPRKMYSCDFETTTDNDVCRVWAYGWMEIGKTSNYKIGTDFNEFMEWMIHSSRL YFHDLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICSGRDGRKKK LTTIHDSLKKLPFPVRKIGKDFKLNVLKGDIDYHKRPPIGYEIDDEEYQYIKNDIQII AEALEVQTVQGLTGMTNGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFT WLNDRFKKEIGEGMVF DANSHYPAQMYDRDLPCGVPIPFEGEYVYDKSHPLYIQKLT FEFELKENYIPTIQLKNSRF GFKGNEYLSSSNGERITISVSSVDWELIREHYHVYDVE FEKGWKFRTKQAFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPY YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLQVQGGSPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETFITIK
C023	119	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYGKRRKI TVIYDSLKKLPFPVKEIAKDFKLTVKKGDIIDHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVF DANSHYPAQMYSRLLPYGEP IVFEGKYVWDEYPLHIQHIRC EFELKEGYIPTIQIKRSRFYKNEYLKSSSGGEIADLWLSNVDLELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPY KENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWAHESTFKRAKYLRQKTYIQDIYMKRVKGYLQVQGGSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETFITIK
C024	120	MIKKYTGD FETTTDLNDCRVWSWGVCIDIDNVNITFGLEIDSFFEWCEMGGSTDIYFH NEKFDGEFMLS WLFKNGFKWCKEAKERTFSTLISNMGQWYALEICWNVKCTTTKTGK TKKEKQRTIIYDSLKKYPFPVKEIAEAFNFP IKKGEIDYTKERP IGYNPTDDEWDYLK NDIQIMAMALKIQFDQGLTRMTRGSDALGDFKDIIITKKFKKVFP TSLGLDKEVRKA YRGGFTWLNDRFKKEIGEGMVF DANSHYPAQMYSRLLPYGEP IVFEGKYVWDEYPL HIQHIRCEFEFELKEGYIPTIQIKRSRFYKNEYLKSSSGGEIADLWLSNVDLELMKEHYD LYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPV TGKVPY LKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDT DSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLQV GSPDDYT DIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETFIT IK
C025	121	MSRKMFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLEQHGFKWSNEGLPNTYNTIISRMGQWYMIDICFGYKGRKRLHTVI YDSLKKLPFPVKKIAKDFQLPLKGDIDYHTERPVGHEITPEEYAYIKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVF DANSHYPAQMYSRLLPYGEP IVFEGKYVWDEYPLHIQHIRCEFE LKEGYIPTIQIKRSRFYKNEYLKSSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPY LKEN

[0091]

		GALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEV PEAIEHLVDSKLLGYWEHESTFQRAKFIHQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C026	122	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFGKKEIGEGMVFANDSHYPAQMYSRLLPYGEPVFEFGKYVWDEYDPLHIQHIRCEFE LKEGYIPTIQIKRSRFYKGYNEYLKSSSGGEIADLWLSNVDELMLKEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEV PEAIEHLVDPKLLGYWEHESTFQRAKFIHQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C027	123	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFGKKEIGEGMVFANDSHYPAQMYSRLLPYGEPVFEFGKYVWDEYDPLHIQHIRCEFE LKEGYIPTIQIKRSRFYKGYNEYLKSSSGGEIADLWLSNVDELMLKEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKLLGYWEHESTFKRAKYLRQKTYIQDIYVKKVRGYLVQCSPEATTTK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C028	124	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFGKKEIGEGMVFANDSHYPAQMYSRLLPYGEPVFEFGKYVWDEYDPLHIQHIRCEFE LKEGYIPTIQIKRSRFYKGYNEYLKSSSGGEIADLWLSNVDELMLKEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEV PEAIEHLVDPKLLGYWEHESTFQRAKFIHQKTYIQDIYVKKVRGYLVQCSPEATTTK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C029	125	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLIDSFFEWCEMQGSTDIYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFGKKEIGEGMVFANDSHYPAQMYSRLLPYGEPVFEFGKYVWDEYDPLHIQHIRCEFE LKEGYIPTIQIKRSRFYKGYNEYLKSSSGGEIADLWLSNVDELMLKEHYDLYNVEYISGL KFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLKEN GALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKLLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C030	126	MIKKYTGDFETTTDLNDCRVWSWGVCDIDNVNITFGLIDSFFEWCEMQGSTDIYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKRIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFGKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFEYHYDILEIH YTYGYMFKASCDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKLLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD

[0092]

		YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C031	127	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKYGKRRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPPTLSGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C032	128	MVRQSTIASPARGGVRRSHKKVPSFCADFETTTDEDDCRVWSWGIQVQKLNQYVDGI SLDGFMSHISERASHIYFHDLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQW YMIDICLGKYGKRRKIHTVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKI TPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPPTLSL GLDKEVRKAYRGGFTWLNDRFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGE YKENIDYPLYIQNIKVRFRLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTL LTNVDDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLM LNSLYGKFASNPDTVTKVPYLYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTIT AAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYI QDIYMKRVKGYLVQGSPPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPV QVPGGVVLVDETFITIK
C033	129	MNEYISDFETQKDPDTGVMSVWAWSIIVDVNDLSNIQYGNIESWLSAIQGLPNSGLIG FHDLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKYGKRRKIHT VIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPPTLSGLDKEVRKAYRGGFTWL NDRFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR FRLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILE IH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTK VPYLYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSI HLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C034	130	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWMEIQADLYFH DLKFDGAFIINWLEQHGFKWSNEGLPNTYNTIISRMQWYMIDICFGYKYGKRRKLHTVI YDSLKKLPFPVKKIAKDFQLPLKGDIDYHTERPVGHEITPEEYAYIKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPPTLSGLDKEVRKAYRGGFTWLND LDRFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C035	131	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKYGKRRKIHT TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAE BALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPPTLSGLDKEVRKAYRGGFTW LNDRFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR FRLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDIL EIH YTYGYMFKASCDMFKGVWIDKWIEVKNTTEGARKANAKGMLNSLYGKFNTNPDTV TKVPYLYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PPDDYTDIKFSVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK

[0093]

C036	132	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKI TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTW LNRDFKGEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDIL EIHYYGYMFKASCDFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDTIG KVPYMGEDGIVRLTLGEEELRDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTFITIK
C037	133	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKI TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTW LNRDFKGEIGEGMVFDANSHPAQMYRLLPYGEPYSEGAPRTNRPLYIASITFTA KLKPNHIPCIIQIKNLSFNPTQYLEEVKEPTTVVATNIDIELWKKHYDFKIYSWNGTF EFRGSHGFFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLN GALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEI PDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIK FSVKCAGMTDKIKKEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C038	134	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKI TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTW LNRDFKGEIGEGMVFDANSHPAQMYRLLPIGTVPVFFEGKYKDDPIYPLYIQFITA QFELKKGIPTIQIKNDRFNPREYVTSTGCLMVNLYLTNVDLEMFYECYNIKEIQYI GGYKFIGRSGIFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLN KENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDY TDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C039	135	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C040	136	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIHTVI YDSLKKLPFPVKKIAKDFQLPLKGDIDYHTERPVGHEITPEEYAYIKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C041	137	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLERNGFKWSNEGLPNTYNTIISRMGQWYMIDICIGYKGRKRLHTVI

[0094]

		YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
C042	138	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLERNGFKWSNEGLPNTYNTIISKMGOYIMIDICIGYKGRKRLHTVI YDSLKLLPFPVEKIAKDFQTLTKKGDIDHKERPVGYKITPEEYAYIKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
C043	139	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGOYIMIDICLGYKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYVKEVDGKKECSPDE ATDIKFSVKCAGMTDKIKKEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
C044	140	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGOYIMIDICLGYKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYVVRVDGYLVECSPE YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
C045	141	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGOYIMIDICLGYKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIIK
C046	142	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGOYIMIDICLGYKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND

[0095]

		RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTP LASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTEIPDV IKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKG YLVQGS PDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETF TIK
C047	143	MSRKMFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLPFPVEKIAKDFKLT VKKGDID IHKERPVG YKITPEEYAYIKNDIQI IAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHL TGTEIPDV IKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDE ATDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETF TIK
C048	144	MSRKMFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLPFPVEKIAKDFKLT VKKGDID IHKERPVG YKITPEEYAYIKNDIQI IAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTP LASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTEIPDV IKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDE YTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETF TIK
C049	145	MSRKMFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLPFPVEKIAKDFKLT VKKGDID IHKERPVG YKITPEEYAYIKNDIQI IAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHL TGTEIPDV IKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYVKRVDGYLVECS PDE YTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETF TIK
C050	146	MSRKMFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLPFPVEKIAKDFKLT VKKGDID IHKERPVG YKITPEEYAYIKNDIQI IAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTP LASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTEIPDV IKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYVKRVDGYLVECS PDE YTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETF TIK
C051	147	MSRKMFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIAKDFQLP LKGDIDYHTERPVGHEITPEEYAYIKNDIEI IARAL DIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEIH

[0096]

		YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLQKTYIQDIYVKEVDGKLEKCPDE ATDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C052	148	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKRLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLQKTYIQDIYVKEVDGKLEKCPDE YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C053	149	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKRLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C054	150	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKRLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C055	151	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKRLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLQKTYIQDIYVKEVDGKLEKCPDE ATDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C056	152	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKRLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL

[0097]

		TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYVKEVDGKLEKESPD ATDIKFSVKCAGMTDKIKKEVTTFENFKVGFSSRKMKPKPVQVPGGVVLVDETFTIK
C057	153	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKRLHTVI YDSLKLLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIKNIDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGEIIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPVDTGKVP YLGKENGALGFRGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIICYDTSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYVKEVDGKLEKESPD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSSRKMKPKPVQVPGGVVLVDETFTIK
C058	154	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKRLHTVI YDSLKLLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIKNIDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGEIIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPVDTGKVP YLGKENGALGFRGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIICYDTSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYVKEVDGKLEKESPD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSSRKMKPKPVQVPGGVVLVDETFTIK
C059	155	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKRLHTVI YDSLKLLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIKNIDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGEIIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPVDTGKVP YMGEDGIVRLTLGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIICYDTSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYVKEVDGKLEKESPD YTDIKFSVKCAGMPDRIKELVTFDNFEVGFSSYGLLPKRTQGGVVLVDTMFTIK
C060	156	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKRLHTVI YDSLKLLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIKNIDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGEIIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPVDTGKVP YMGEDGIVRLTLGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIICYDTSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYVKEVDGKLEKESPD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSSRKMKPKPVQVPGGVVLVDETFTIK
C061	157	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKRLHTVI YDSLKLLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYIKNIDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGEIIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPVDTGKVP YLGKENGALGFRGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIICYDTSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYVKEVDGKLEKESPD YTDIKFSVKCAGMPDRIKELVTFDNFEVGFSSYGLLPKRTQGGVVLVDTMFTIK

[0098]

C062	158	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDTGKVP YMGEDGIVRLTLGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDE ATDIKFSVKCAGMPDRIKELVTFDNFVEGVFSSYGKLLPKRTQGGVVLVDTFMTIK
C063	159	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDTGKVP YMGEDGIVRLTLGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDE ATDIKFSVKCAGMTDKIKKEVTFENFKVGFSSYGRMKPKPVQVPGGVVLVDDETFTIK
C064	160	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMGQWYMIDICFGYKGRKLHTVI YDSLKKLPFPVKKIADKDFQLPLLKGDIDYHTERPVGHEITPEEYIYKNDIEIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTGKVP YLGKENGALGFRLGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYVKEVDGKLKECSPDE ATDIKFSVKCAGMPDRIKELVTFDNFVEGVFSSYGKLLPKRTQGGVVLVDDETFTIK
C065	161	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKV FRRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDFFEHYEIL EIHFTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTG KVPYLGKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSSYGRMKPKPVQVPGGVVLVDDETFTIK
C066	162	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV FRRLKERHIPCIQVKQSSLFIQTEYLESSVNKLGVDELIELTLTNVDLDDFFEHYEIL EIHFTYGYMFRGSCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTG KVPYLGKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSSYGRMKPKPVQVPGGVVLVDDETFTIK
C067	163	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH

[0099]

		TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTW LNDRFKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKV RFRLLKERHIPCIQVKQNSLFIQTEYLENSVNKLGVDELIELTLTNVDLDDLFFEHYDIL EIHFTYGYMFRGSCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C068	164	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYIMIDICLGYKGRKRIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTW LNDRFKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKV RFRLLKERHIPCIQVKQNSLFIQTEYLENSVNKLGVDELIELTLTNVDLDDLFFEHYDIL EIHFTYGYMFRGSCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C069	165	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYIMIDICLGYKGRKRIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTW LNDRFKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKV RFRLLKERHIPCIQVKQNSLFIQTEYLENSVNKLGVDELIELTLTNVDLDDLFFEHYDIL EIHFTYGYMFKASCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C070	166	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYIMIDICLGYKGRKRIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTW LNDRFKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKV RFRLLKERHIPCIQVKQNSLFIQTEYLENSVNKLGVDELIELTLTNVDLDDLFFEHYDIL EIHFTYGYMFKASCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C071	167	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYIMIDICLGYKGRKRIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTW LNDRFKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKV RFRLLKERHIPCIQVKQNSLFIQTEYLENSVNKLGVDELIELTLTNVDLDDLFFEHYDIL EIHFTYGYMFRGSCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C072	168	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYIMIDICLGYKGRKRIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTW

[0100]

		LNDRFKKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKV RFRLLKERHIPTIQVKQNSLFIQTEYLENSVNLGVDELIELTLTVNVDLDFFEHYEIL EIHFTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLYKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C073	169	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDYPLYIQNIKVRFR LKERHIPCIQVKQSSLFIQNEYLESSVNLGVDELIELTLTVNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C074	170	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNIKVRFR LKERHIPTIQVKQNSLFIQNEYLENSVNLGVDELIDLTLTVNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C075	171	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNIKVRFR LKERHIPTIQVKQNSLFIQNEYLENSVNLGVDELIELTLTVNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C076	172	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSLFIQNEYLESSVNLGVDELIELTLTVNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C077	173	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSLFIQNEYLESSVNLGVDELIDLTLTVNVDLDFFEHYDILEIH

[0101]

		FTYGYMFKASCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C078	174	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQNEYLENSVNKLGVDELIDLTNTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C079	175	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C080	176	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFR LKERHIPCIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C081	177	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQNEYLENSVNKLGVDELIELTVTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C082	178	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFR LKERHIPCIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL

[0102]

		TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIK
C083	179	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKKIHTVI YDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFR LKERHIPCIQVKQNSLFIQNEYLENSVNKLGVDELIELTVTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIK
C084	180	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKKIHTVI YDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFR LKERHIPCIQVKQNSLFIQNEYLENSVNKLGVDELIELTVTNVDLDFFEHYEILEIH FTYGYMFRASCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIK
C085	181	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKKIH TVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL EALLIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKV RFRLLKERHIPCIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDFFEHYEIL EIHYYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPLYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIK
C086	182	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKKIH TVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL EALLIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSGLDKEVRKAYRGGFTW LNDRFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKV RFRLLKERHIPCIQVKQNSLFIQNEYLENSVNKLGVDELIELTVTNVDLDFFEHYEIL EIHYYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPLYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIK
C087	183	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSNEGLPNTYNTIISRMGQWYMIDICIGYKGRKKLHTVI YDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFIK

[0103]

C088	184	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKKGKRIHTVI YDSLKKLPFPVEKIAKDFKLTIVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLQKTYIQDIYVKEVDGKLKECSPDE ATDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMMPKPVQVPGGVVLVDETF'IK
C089	185	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMQWYMIDICFGYKKGKRLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYAYIKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYVPLASFVTAWGRYTTITTAQRCFDNIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLQKTYIQDIYVKRVDGYLVECSPE YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMMPKPVQVPGGVVLVDETF'IK
C090	186	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEQHGFKWSNEGLPNTYNTIISKMQWYMIDICFGYKKGKRLHTVI YDSLKKLPFPVKKIAKDFQLPLLKGDIDYHTERPVGHEITPEEYAYIKNDIEIIARAL DIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLQKTYIQDIYVKRVDGYLVECSPE YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMMPKPVQVPGGVVLVDETF'IK
C091	187	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKKGKRIHTVI YDSLKKLPFPVEKIAKDFKLTIVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQNEYLENSVNKLGVDELIDLTLTNVDLDDLFFEHYEILEIH FTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMMPKPVQVPGGVVLVDETF'IK
C092	188	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKKGKRIHTVI YDSLKKLPFPVEKIAKDFKLTIVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPCIQVKQSSLFIQTEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH FTYGYMFRGSCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMMPKPVQVPGGVVLVDETF'IK
C093	189	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKKGKRIHTVI

[0104]

		YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQTEYLENSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH YTYGYMFRGSCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSRKMMPKPVQVPGGVVLVDETFIIK
C094	190	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLYGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQTEYLENSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH YTYGYMFRGSCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSRKMMPKPVQVPGGVVLVDETFIIK
C095	191	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLYGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQTEYLENSVNKLGVDELIDLTVTNVDLDDLFFEHYDILEIH FTYGYMFKASCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSRKMMPKPVQVPGGVVLVDETFIIK
C096	192	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLYGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQTEYLENSVNKLGVDELIDLTVTNVDLDDLFFEHYDILEIH FTYGYMFKASCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSRKMMPKPVQVPGGVVLVDETFIIK
C097	193	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLYGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQTEYLENSVNKLGVDELIELTVTNVDLDDLFFEHYEILEIH FTYGYMFRGSCDMFKDFIDKFTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTTFENFKVGFSRKMMPKPVQVPGGVVLVDETFIIK
C098	194	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLYGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND

[0105]

		RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIQYPLYIQNLKVRFR LKERHIPTIQVKQNSLFIQTEYLENSVNKLGVDELIELTVTNVDLDFFEHYEILEIH FTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGVLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C099	195	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEKNFGKWSAEGLPNTYNTIISRMQWYMIDICFGYKGRKRIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNLKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGVLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0100	196	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEKNFGKWSAEGLPNTYNTIISRMQWYMIDICIGYKGRKRIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNLKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGVLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0101	197	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKLHTII YDSLKKLPFPVEKIAKDFKLTLLKGDIDHKERPIGYKITPDEYAYLKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNLKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGVLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0102	198	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEKNFGKWSAEGLPNTYNTIISRMQWYMIDICFGYKGRKLHTII YDSLKKLPFPVEKIAKDFKLTLLKGDIDHKERPIGYKITPDEYAYLKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNLKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGVLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0103	199	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEKNFGKWSAEGIPNTYNTIISRMQWYMIDICFGYKGRKLHTII YDSLKKLPFPVEKIAKDFKLTLLKGDIDHKERPIGYKITPDEYAYLKNDIQILAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNLKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH

[0106]

		YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0104	200	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLEQHGFKWSNEGLPNTYNTIISRMQWYMIDICLGKGRKRIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPFSLGLDKEVRKAYRGGFTWLN RFGKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0105	201	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKERTFSTIISRMQWYMIDICLGKGRKRIHTV YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPFSLGLDKEVRKAYRGGFTWLN RFGKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD DYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0106	202	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLLHNGYTWTKRPSKEGQFSTIISRMQWYMIDICLGKGRKRIHTV YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPFSLGLDKEVRKAYRGGFTWLN RFGKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD DYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0107	203	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLLHKGYECNESGRPKTFDTIISRMQWYMIDICLGKGRKRIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPFSLGLDKEVRKAYRGGFTWLN RFGKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0108	204	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLLKHGYRWTKENPGVKEFTTIISRMQWYMIDICLGKGRKRIHTV YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPFSLGLDKEVRKAYRGGFTWLN RFGKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH

[0107]

		LTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0109	205	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYIMIDICLGKGGKRIHTVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKVPYLGKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0110	206	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLKFDGAFIINWLEKNGFKWTAEGEPNTYSTIISRMQWYIMIDICLGKGGKRIHTVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKVPYLGKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0111	207	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLKFDGAFIINWLLKNGFKWTAEGLPRTYSTIISRMQWYIMIDICLGKGGKRIHTVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKVPYLGKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0112	208	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLKFDGAFIINWLFKNGYKWTAEGLPNTFSTIISRMQWYIMIDICLGKGGKRIHTVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKVPYLGKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0113	209	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLKFDGAFIINWLEKNGYKWTAEGLPKTFSTIISRMQWYIMIDICLGKGGKRIHTVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKVPYLGKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK

[0108]

C0114	210	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLLRNGYVHTEEDRTNTPKEFTTIIISRMGQWYMIDICLGKGRKRIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAE EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP T LSLGLDKEVRKAYRGGFTW LNRDFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDIL EIHITYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETF TIK
C0115	211	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLLRNGYVHTEEDRTNTPKEFTTIIISRMGQWYMIDICLGKGRKRIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAE EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP T LSLGLDKEVRKAYRGGFTW LNRDFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILE IHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGK VPYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSI HLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETF TIK
C0116	212	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLLTGWKWIPDKNDCANRTTIIISRMGQWYMIDICLGKGRKRIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAE EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP T LSLGLDKEVRKAYRGGFTW LNRDFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILE IHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGK VPYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSI HLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETF TIK
C0117	213	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLLENGFKHSRERALYSNEFTTIIISRMGQWYMIDICLGKGRKRIH TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAE EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP T LSLGLDKEVRKAYRGGFTW LNRDFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILE IHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGK VPYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSI HLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETF TIK
C0118	214	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLLGVAKWEYNDKPKARKAKTVETIIISRMGQWYMIDICLGKGRKRI HTVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQII AEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP T LSLGLDKEVRKAYRGGFT WLNRDFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIK VFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDI LEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDT GKVPYLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTD SIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS SPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVDETF TIK
C0119	215	MSRKMYSADFETTTKLDDCRVWSYGWMEVGNLDNYKIGNDIDEFMQWVMEIQSDLYFH

[0109]

		DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0120	216	MSRKMYSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNDIDEFMQWIMEIQSDLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0121	217	MSRVFTADTFETTTKLDDCRVWAYGYMEVGNLDNYKIGNSIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0122	218	MSRVYTADTFETTTKLDDCRVWAYGYMEVGNLDNYKIGNSIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0123	219	MSRMYTADTFETTTKLDDCRVWAYGYMEVGNLDNYKIGNDIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0124	220	MSRKMYSADFETTTKLDDCRVWAYGYMEVGNLDNYKIGNSIDEFMQWIMEIQSDLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL

[0110]

		LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDLIDLTLTNVDL DLF FEHYDILEIH YTYGYMFKASCDMF KDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLG YWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRMKMKPKVPQVPGGVVLVDETF TIK
C0125	221	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIH TVIYDSLKKLPFPVKKIADFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTW LNDRFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDLIDLTLTNVDL DLF FEHYDIL EIH YTYGYMFKASCDMF KDFIDKWYIKTTSEGAIKQLAKLMLNSLYGKFASNP DVTG KVPLYKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLG YWAHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRMKMKPKVPQVPGGVVLVDETF TIK
C0126	222	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIH TVIYDSLKKLPFPVKKIADFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTW LNDRFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDLIDLTLTNVDL DLF FEHYDIL EIH YTYGYMFKASCDMF KDFIDKWYIKTTSEGAIKQLAKLMLNSLYGKFASNP DVTG KVPLYKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLG YWNHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRMKMKPKVPQVPGGVVLVDETF TIK
C0127	223	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIH TVIYDSLKKLPFPVKKIADFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTW LNDRFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDLIDLTLTNVDL DLF FEHYDIL EIH YTYGYMFKASCDMF KDFIDKWYIKTTSEGAIKQLAKLMLNSLYGKFASNP DVTG KVPLYKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLG YWQHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRMKMKPKVPQVPGGVVLVDETF TIK
C0128	224	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIH TVIYDSLKKLPFPVKKIADFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTW LNDRFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDLIDLTLTNVDL DLF FEHYDIL EIH YTYGYMFKASCDMF KDFIDKWYIKTRSEGAIKQLAKLMLNSLYGKFASNP DVTG KVPLYKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLG YWAHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRMKMKPKVPQVPGGVVLVDETF TIK
C0129	225	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVI YDSLKKLPFPVEKIAKDFKLT VKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR

[0111]

		LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDVTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKGWYHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDDETFTIK
C0130	226	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDVTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVHPKKGWYHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTIK
C0131	227	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDVTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVHPKKGWYHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTIK
C0132	228	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDVTGKVP YLGKENGALGFRLGEEETKDPVYTPASFVTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVHPKKGWYHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDDETFTIK
C0133	229	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIQYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDVTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVHPKKGWYHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDDETFTIK
C0134	230	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKLLPFPVEKIAQDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKEIGEGMVFDINSHYPAQMYVRPLPYGTPLFYEGEYKENIQYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDVTGKVP

[0112]

		YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRFTTITAAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKEEVTFDNFKVGFSSRMMKPKPVQVPGGVVLVDSVFTIK
C0135	231	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFGKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKVRFR LKERHIPTIQVKQSSFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSSRMMKPKPVQVPGGVVLVDSVFTIK
C0136	232	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFGKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIQPLYIQNIKVRFR LKERHIPTIQVKQSSFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRFTTITAAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKEEVTFDNFKVGFSSRMMKPKPVQVPGGVVLVDSVFTIK
C0137	233	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAQDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFGKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIQPLYIQNIKVRFR LKERHIPTIQVKQSSFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRFTTITAAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKEEVTFDNFKVGFSSRMMKPKPVQVPGGVVLVDSVFTIK
C0138	234	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFGKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSSRMMKPKPVQVPGGVVLVDETFTIK
C0139	235	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFGKKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD

[0113]

		YTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0140	236	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKRIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDSIH TGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDD YTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0141	237	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND DRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD YTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDETFITIK
C0142	238	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND DRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD YTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDETFITIK
C0143	239	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKGRKRIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIQHPLYIQNLKVRFR LKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDSIH TGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDD YTDIKFSVKCAGMTDKIKEEVTFDNFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0144	240	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND DRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD YTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDETFITIK
C0145	241	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH

[0114]

		DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFDNFVKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0146	242	MSRRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDDANSHYPAQMYVRPLPYGTPLFYEGEYKENIQHPLYIQNLKVRF RLKERHIPCIVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRFTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFDNFVKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0147	243	MSRRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLPPFPVEKIAQDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDDINSHYPAQMYVRPLPYGTPLFYEGEYKENIQHPLYIQNLKVRF RLKERHIPCIVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRFTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFDNFVKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0148	244	MSRRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLPPFPVEKIAQDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDDINSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRF RLKERHIPCIVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRFTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFDNFVKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0149	245	MSRRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDDANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRF RLKERHIPCIVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRFTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFDNFVKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0150	246	MSRRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNSIDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA

[0115]

		LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIQHPLYIQNLKVRF RLKERHIPCIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDL DFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFR LGEEETKDPVYTPLASFVTAWGRFTTTITTAQACYDRIIYCDTDSIH LTGTYKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PD DYTDIKFSVKCAGMTDKIKKEVTFDNFKVGF SRKMKPKPVQVPGGVVLVD SVFTIK
C0151	247	MHKMSKKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADL YFHD LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIH TVIYDSLKKLPFPVEKIAKDFKLT VKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTW LND RFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDL DFFEHYDIL EIH TYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTG KV P YLKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVD EFTIK
C0152	248	MHKMSKKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADL YFHD LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIH TVIYDSLKKLPFPVEKIAKDFKLT VKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTW LND RFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDL DFFEHYDIL EIH TYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTG KV P YLKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVD EFTIK
C0153	249	MSKKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVI YDSLKKLPFPVEKIAKDFKLT VKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTW LND RFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDL DFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVD EFTIK
C0154	250	MSRKMFS CDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVI YDSLKKLPFPVEKIAKDFKLT VKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTW LND RFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDL DFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGF SRKMKPKPVQVPGGVVLVD EFTIK
C0155	251	MSRKMFS CDFETTTKLDDCRVWAYGYMELGNLDNYKIGNNIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVI YDSLKKLPFPVEKIAKDFKLT VKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTW LND RFKGEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFR

[0116]

		LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKGWYHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0156	252	MSRKMFSCDFETTTKLDDCRVWAYGYMELGNLDNYKIGNTIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKGWYHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0157	253	MSRKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNTIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKGWYHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0158	254	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNTIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKGWYHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0159	255	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNTIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLGKENGALGFRLGEEETKDPVYTPMGVFIWAGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKGWYHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0160	256	MSRKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNTIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKLLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP

[0117]

		YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSSRMMKPKPVQVPGGVVLVDETFIIK
C0161	257	MSRKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNSIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVLDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSSRMMKPKPVQVPGGVVLVDETFIIK
C0162	258	MSRKMFSCDFETTTKLDDCRVWAYGYMELGNLDNYKIGNSIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVLDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSSRMMKPKPVQVPGGVVLVDETFIIK
C0163	259	MHKMSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADL YFHD LKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIHTVI TVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL EALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTW LND RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVLDLDFFEHYDIL EIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSSRMMKPKPVQVPGGVVLVDETFIIK
C0164	260	MSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVLDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSSRMMKPKPVQVPGGVVLVDETFIIK
C0165	261	MSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVLDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDD

[0118]

		YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0166	262	MSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNTIDEFMQWIMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGKRKIHTVI YDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN RFGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0167	263	MSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGKRKIHTVI YDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN RFGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDEFTTIK
C0168	264	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLKNGFKWCKEAKEERTFSTIISRMQWYMIDICIGYKGKRKIHTV YDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0169	265	MHKMSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADL YFHD LKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGYKGKRKI HTVIYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQII AEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFT WLNDRFGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLK VRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDT GKVPY LKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTD SIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQG SPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0170	266	MHKMSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADL YFHD LKFDGAFIVNWLKNGFKWCKEAKEERTFSTIISRMQWYMIDICIGYKGKRKI HTVIYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQII AEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFT WLNDRFGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLK VRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDT GKVPY LKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTD SIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQG SPDDYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

[0119]

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C0171	267	MHKMSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFHDLFKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRRLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIHITYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVCKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQRKTYIQDIYMKRVKGYLVQGPSDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0172	268	MHKMSRKRFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWAMEIQADLYFHDLFKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRRLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIHITYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVCKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQRKTYIQDIYMKRVKGYLVQGPSDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0173	269	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLFKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRRLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIHITYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVCKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQRKTYIQDIYMKRVKGYLVQGPSDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0174	270	MHKMSKMFSCDFETTTKLDDCRVWAYGYMEVGNLDNYKIGNNIDEFMQWIMEIQADLYFHDLFKFDGAFIINWLFLKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRRLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIHITYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVCKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQRKTYIQDIYMKRVKGYLVQGPSDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0175	271	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLFKFDGAFIVNWLFLKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFRRLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIHITYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVCKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQRKTYIQDIYMKRVKGYLVQGPSDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

[0120]

		HLTGTKVPDIIKDLVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSF DDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0176	272	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFF HDLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIIISRMGQWYMIDICIGYKGRKRIHT VIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWL NDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVR FRLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILE IHITYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNLSLYGKFASNPDTVTK VPYLGKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSI HLTGTKVPDAIKDLVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSF DDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0177	273	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFF HDLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIIISRMGQWYMIDICIGYKGRKRIHT VIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWL NDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVR FRLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILE IHITYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNLSLYGKFASNPDTVTK VPYLGKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSI HLTGTKVPDAIKDLVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSF DDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0178	274	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFF HDLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIIISRMGQWYMIDICIGYKGRKRIHT VIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWL NDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVR FRLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILE IHITYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNLSLYGKFASNPDTVTK VPYLGKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSI HLTGTKVPDIIKDIVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSF DDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0179	275	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFF HDLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIIISRMGQWYMIDICIGYKGRKRIHT VIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWL NDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVR FRLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILE IHITYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNLSLYGKFASNPDTVTK VPYLGKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSI HLTGTKVPDAIKDIVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSF DDYTDGKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0180	276	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFF HDLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIIISRMGQWYMIDICIGYKGRKRIHT VIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWL NDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVR FRLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILE IHITYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNLSLYGKFASNPDTVTK VPYLGKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSI HLTGTKVPDAIKDLVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSF DDYTDGKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

[0121]

C0181	277	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFF HDLKFDGAFIVNWLFGKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHT VIYDSLKKLPPFVEKIAKDFKLTVKKGDIDIHKRPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWL NDRFKGKEIGEGMVFDANSHPYQMYVRPLPYGTPLFYQGEYKENIDHPLYQNLKVR FRLKERHIPCIVKQNSLFIQNEYLESSVNKLGVDELIEITLTNVVDLDFFEHYEILE IHYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTK VPYLGKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTTTTAQACYDRIIYCDTDSI HLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGS DDYTDIKFSVKCAGMTDKIKEEVTENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0182	278	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFF HDLKFDGAFIVNWLFGKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKLHT VIYDSLKKLPPFVEKIAKDFKLTVKKGDIDIHKRPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWL NDRFKGKEIGEGMVFDANSHPYQMYVRPLPYGTPLFYQGEYKENIDHPLYQNLKVR FRLKERHIPCIVKQNSLFIQNEYLESSVNKLGVDELIEITLTNVVDLDFFEHYEILE IHYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTK VPYLGKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTTTTAQACYDRIIYCDTDSI HLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGS DDYTDIKFSVKCAGMTDKIKEEVTENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0183	279	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFF HDLKFDGAFIVNWLFGKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKQHT VIYDSLKKLPPFVEKIAKDFKLTVKKGDIDIHKRPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWL NDRFKGKEIGEGMVFDANSHPYQMYVRPLPYGTPLFYQGEYKENIDHPLYQNLKVR FRLKERHIPCIVKQNSLFIQNEYLESSVNKLGVDELIEITLTNVVDLDFFEHYEILE IHYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTK VPYLGKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTTTTAQACYDRIIYCDTDSI HLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGS DDYTDIKFSVKCAGMTDKIKEEVTENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0184	280	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFF HDLKFDGAFIVNWLFGKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHT VIYDSLKKLPPFVEKIAKDFKLTVKKGDIDIHKRPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWL NDRFKGKEIGEGMVFDANSHPYQMYVRPLPYGTPLFYQGEYKENIDHPLYQNLKVR FRLKERHIPCIVKQNSLFIQNEYLESSVNKLGVDELIELTVTNVDLDFFEHYEILE IHYTYGYMFRGSCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTK VPYLGKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTTTTAQACYDRIIYCDTDSI HLTGTKVPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGS DDYTDIKFSVKCAGMTDKIKEEVTENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0185	281	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFF HDLKFDGAFIVNWLFGKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHT VIYDSLKKLPPFVEKIAKDFKLTVKKGDIDIHKRPVGYKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWL NDRFKGKEIGEGMVFDANSHPYQMYVRPLPYGTPLFYQGEYKENIDHPLYQNLKVR FRLKERHIPCIVKQNSLFIQNEYLESSVNKLGVDELIELTVTNVDLDFFEHYEILE IHYTYGYMFRSSCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTK VPYLGKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTTTTAQACYDRIIYCDTDSI HLTGTKVPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGS DDYTDIKFSVKCAGMTDKIKEEVTENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0186	282	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFGKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHTV

[0122]

		IYDSLKKLPPVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR RLKERHIPCIOVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKGV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTTIK
C0187	283	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLYGKGRKIHTV IYDSLKKLPPVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR RLKERHIPCIOVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKGV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTTIK
C0188	284	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLYGKGRKIHTV IYDSLKKLPPVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR RLKERHIPCIOVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKGV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTTIK
C0189	285	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWSADGLPNTYNTIISRMGQWYMIDICLYGKGRKIHTVI YDSLKKLPPVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPTIOVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYDILEIH YTYGYMFASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKGV PYLKENGALGFRGEEETKDPVYTPMGVFTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDDETFTTIK
C0190	286	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLYGKGRKIHTV IYDSLKKLPPVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR RLKERHIPCIOVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKGV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTTIK
C0191	287	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHTV IYDSLKKLPPVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLN

[0123]

		DRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0192	288	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLFKDFGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0193	289	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLFKDFGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0194	290	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLFKDFGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0195	291	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLFKDFGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0196	292	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLFKDFGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI

[0124]

		HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTQVDAIKDLVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDKGFVSKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0197	293	MSRKRFSDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDDIDHKERPVGKITPEEYAYIKNDIQIIAEAA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRF RLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIEITLTNVVDVLDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTQVDAIKDLVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDKGFVSKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0198	294	MSRKRFSDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKLHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDDIDHKERPVGKITPEEYAYIKNDIQIIAEAA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRF RLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIEITLTNVVDVLDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTQVDAIKDLVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDKGFVSKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0199	295	MSRKRFSDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKQHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDDIDHKERPVGKITPEEYAYIKNDIQIIAEAA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRF RLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIEITLTNVVDVLDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTQVDAIKDLVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDKGFVSKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0200	296	MSRKRFSDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDDIDHKERPVGKITPEEYAYIKNDIQIIAEAA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRF RLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIEITLTNVVDVLDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTQVDAIKDLVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDKGFVSKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0201	297	MSRKRFSDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDDIDHKERPVGKITPEEYAYIKNDIQIIAEAA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYVQNLKVRF RLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIEITLTNVVDVLDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH

[0125]

		LTGTVKVPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0202	298	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHITV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPICIQKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNP DVTGKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTVKVPDIIKDLVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0203	299	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHITV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPICIQKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNP DVTGKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTVKVPDAIKDLVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0204	300	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHITV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIRCEFE LKEGYIPTIQIKRSFYKNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNP DVTGKVPYLKE NGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTVKIPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0205	301	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHITV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DVNSMYPAMMKNLLPYGEPVMFKGEYKKNVEYPLYIQQVRCFFELKKDKIPICIQIKGNARFGQNEYLSTSGDEYVDLYVTNVDWELIKKH YDIFEEF IGGFMFKGFIGFFDEYIDRFMEIKNSPDSSAEQSLQAKMLNSLYGKFASNP DVTGKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTVKIPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0206	302	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHITV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKKNVEYPLYIQQVRCFFELKKDKIPICIQIKGNARFGQNEYLSTSGDEYVDLYVTNVDWELIKKH YDIFEEF IGGFMFKGFIGFFDDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNP DVTGKVPYLKE NGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTVKIPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

[0126]

C0207	303	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGRKKIHTV IYDSLKKLPPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYSRPLPYGAPIVFGKYKDEQYPLYIQIRIRFEF ELKEGYIPTIQIKKNPFFKGNEYLKNSGVEPVELYLTNVDEL IQEHYELYNVEYIDG FKFREKTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKE NGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0208	304	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGRKKIHTV IYDSLKKLPPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPITIQVKQSSLF IQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGT KIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0209	305	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGRKKIHTV IYDSLKKLPPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKPNNDYPLYIQNIKVRF RLKEGYIPTIQIKRSRKYKNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGT KIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0210	306	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGRKKIHTV IYDSLKKLPPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKEGYIPTIQIKRSRKYKNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGT KIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0211	307	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGRKKIHTV IYDSLKKLPPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKEGYIPTIQIKRSRKYKNEYLKSSGGELIELTLTNVDL DLF FEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKE NGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0212	308	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYKGRKKIHTV

[0127]

		IYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSAYPAQMYVRLLPYGTPLFYEGEYKENIDHPLYIQNLKVR RLKEGYIPTIQIKRSRFYKNEYLKSSGGELIELTLTNVDLELMKEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYLKE NGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTG IPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVTFFENFKVGFSSRMMKPKPVQVPGGVVLVDSVFTIK
C0213	309	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKIH TVIYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSAYPAQMYVRLLPYGEPLFYEGEYKENIDHPLYIQNLKVR RLKEGYIPTIQIKRSRFYKNEYLKSSGGELIELTLTNVDLELMKEHYEILEIHYTYG YMFKATTGMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYLKE NGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTG IPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVTFFENFKVGFSSRMMKPKPVQVPGGVVLVDSVFTIK
C0214	310	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKIH TVIYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSAYPAQMYVRLLPYGEPLFYEGEYKENIDHPLYIQNLKVR RLKERHIPCQVQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFKATTGMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSI HTGTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGS PPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSSRMMKPKPVQVPGGVVLVDS VFTIK
C0215	311	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKIH TVIYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSAYPAQMYVRLLPYGEPLFYEGEYKENIDHPLYIQNLKVR RLKEGYIPTIQIKRSRFYKNEYLKSSGGELIELTLTNVDLDFFEHYEILEIHYTYG YMFKATTGMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYLKE NGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTG IPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVTFFENFKVGFSSRMMKPKPVQVPGGVVLVDSVFTIK
C0216	312	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKIH TVIYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRLLPYGTPLFYEGEYKENIDHPLYIQNLKVR RLKERHIPCQVKSRLFIQNEYLESSVNELIELTLTNVDLDFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYLKE NGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTG IPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVTFFENFKVGFSSRMMKPKPVQVPGGVVLVDSVFTIK
C0217	313	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKIH TVIYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN

[0128]

		DRFKGEI GEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQKRSRLFKQNEYLESSVNELIELTLTNVDLDFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYLKE NGALGFRLEGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLQVQSPDDYTDI KFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0218	314	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGEI GEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQKRSRLFKQNEYLESSVNELIELTLTNVDLDFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYLKE NGALGFRLEGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLQVQSPDDYTDI KFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0219	315	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGEI GEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQKRSRFLYKQNEYLESSVNELIELTLTNVDLDFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYLKE NGALGFRLEGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLQVQSPDDYTDI KFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0220	316	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGEI GEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQKRSRLFKQNEYLESSVNELIELTLTNVDLDFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTVTKVPYLKE NGALGFRLEGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLQVQSPDDYTDI KFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0221	317	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGEI GEGMVFDANSHYPAQMYVRPLPYGLPVFPFSGEYEDETHPLFIQHIKCGF ELKDGHIPTIQIKNFRFADNEYLSHSEGNILDLHVTNVDLALIKEHYTLYEEYLCQ YKFKQVTGLFKNYIDYWSDKKINAEDPAIRQMAKMLNSLYGKFASNPDTVTKVPYLK ENGALGFRLEGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK KIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLQVQSPDDYTDI KFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0222	318	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYGKGRKIHTV IYDSLKKLFPFVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGEI GEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPICIQKQNSLFIQNEYLESSVNLKGVDELIELTLTNVDLDFFEHYEILEI

[0129]

		HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0223	319	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0224	320	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQNSLFIQNEYLESSVNELIELTLTNVDLDFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0225	321	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0226	322	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSAYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0227	323	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDVNSMYPAMMKNKLLPYGEPVMFKGEYKKNVEYPLYIQQVRCFF ELKKDKIPCIQIKGNARFGQNEYLSGDEYVDLYVTNVDWELIKKHDFEIEEFIGG FMFKGFIGFDEYIDRFMEIKNSPDSSAEQSLQAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK

[0130]

		TKIPDVIKDIVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYT DIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0228	324	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKSRLFIQNEYLESSVNELIELTLTNVDLDFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNLSYGKFASNPDTVTKVPYLKE NGALGFRLGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0229	325	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKSRLFKQNEYLESSVNELIELTLTNVDLDFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNLSYGKFASNPDTVTKVPYLKE NGALGFRLGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0230	326	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKSRLYKQNEYLESSVNELIELTLTNVDLDFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNLSYGKFASNPDTVTKVPYLKE NGALGFRLGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0231	327	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKSRLFYKQNEYLESSVNELIELTLTNVDLDFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNLSYGKFASNPDTVTKVPYLKE NGALGFRLGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0232	328	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKSRLFKQNEYLESSVNLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNLSYGKFASNPDTVTKV PYLKENGALGFRLGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGKIPDVIKDIVHPKKLGWHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

[0131]

C0233	329	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKEGYIPTIQIKRSRFYKNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFRLGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PD DYTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0234	330	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKEGYIPTIQIKRSRFYKNEYLKSSGGELIELTLTNVDLDDLFFEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKE NGALGFRLGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTGK IPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDI KFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0235	331	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKEGYIPTIQIKRSRFYKNEYLKSSGGELIELTLTNVDLELMKEHYEILEIHYTYG YMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKE NGALGFRLGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTGK IPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDI KFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0236	332	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DINSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQSSLF IQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFRLGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PD DYTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0237	333	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQSSLF IQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFRLGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PD DYTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0238	334	MSRRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKKIHTV

[0132]

		IYDSLKKLPPFVEKIAKDFKLTIVKKGDIIDHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRKKEHPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFITIK
C0239	335	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKYGKRRKIHTVIYDSLKKLPPFVEKIAKDFKLTIVKKGDIIDHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRKKEHPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFITIK
C0240	336	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKYGKRRKIHTVIYDSLKKLPPFVEKIAKDFKLTIVKKGDIIDHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRKKEGYIPTIQIKRSRYKGYNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFITIK
C0241	337	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKYGKRRKIHTVIYDSLKKLPPFVEKIAKDFKLTIVKKGDIIDHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRKKEGYIPTIQIKRSRYKGYNEYLESSGGELIELTLTNVDLDDLFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFITIK
C0242	338	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKYGKRRKIHTVIYDSLKKLPPFVEKIAKDFKLTIVKKGDIIDHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRKKEGYIPTIQIKRSRYKGYNEYLESSGGELIELTLTNVDLELMKEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFITIK
C0243	339	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKKIHTVIYDSLKKLPPFVEKIAKDFKLTIVKKGDIIDHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN

[0133]

		DRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTQVPDIIKDLVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0244	340	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTQVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0245	341	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTQVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0246	342	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTQVPDIIKDLVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0247	343	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDANSHYPAQMYVKNKLLPYGEPVMFKGEYKKNVEYPLYIQVQVRC FFELKKDIPICIQIKGNARFGQNEYLSTSGDEYVDLYVTNVDWELIKKHIDIFEEEF GGFMFKMGFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPLYKEN GALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKI PDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPDDYTDIK FSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0248	344	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRI HTVIYDSLKKLFPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQII AEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFT WLNDRFKGKEIGEGMVFDANSHYPAQMYSRLLPYGEPVIFEGKYVWDEYDPLHIQH IRCEFELKEGYIPTIQIKRSRFPYKGNEYLKSSGGEIADLWLSNVDELMEHYDLYNVEY

[0134]

		ISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPY LKENGALGFRLEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLT GTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDY TDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0249	345	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKRIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTTKKFKKVFTLSLGLDKEVRKAYRGGFTW LNDREFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKV RFRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDFFEHYDIL EIHYYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGKTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0250	346	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKRIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTTKKFKKVFTLSLGLDKEVRKAYRGGFTW LNDREFKGKEIGEGMVFDINSAYPAQMYSRLLPYGEPVFEKGKVVWDEDHPLHIQHLRC EFELKEGYIPTIQIKQSLFYKGYNEYLKSSSGEIAELWLSNVDLELMKEHYELYNVEYI SGLKFRATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLTG TKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDY TDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0251	347	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKRIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKGFKDITTTKKFKKVFTLSLGLDKEVRKAYRGGFTW LNDREFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKV RFRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDFFEHYEIL EIHYYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGKTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0252	348	MSRKMFSDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKRIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKGFKDITTTKKFKKVFTLSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFDINSAYPAQMYSRLLPYGEPVFEKGKVVWDEDEYPLHIQHIRCEFE LKEGYIPTIQIKQSLFYKGYNEYLKSSSGEIAIDLWLSNVDLELMKEHYDLYNVEYISGL FKKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLVKEN GALGFRLEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLTGKTI PDVVKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPDYTDIK FSVKCAGMTDKIKEEVTFFENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0253	349	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKDFGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGKGRKRI HTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQII AEALLIQFKQGLDRMTAGSDSLKGFKDITTTKKFKKVFTLSLGLDKEVRKAYRGGFT WLNDREFKGKEIGEGMVFDINSAYPAQMYSRLLPYGEPVFEKGKVVWDEDEYPLHIQH IRCEFEELKEGYIPTIQIKQSLFYKGYNEYLKSSSGEIAIDLWLSNVDLELMKEHYDLYNVEY ISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPY LKENGALGFRLEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHLT

[0135]

		GTKIPDVIKDIVHPKKLGWHEHSTFKRAKYLROKTYIQDIYMKRVRGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0254	350	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHNLFKDFGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKLKLPFPVKKIAQDFKLTVKKGDIYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TLSLGLDKEVRKAYRGGFTWLNDLDRFKGKEIGEGMVFDINSAYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIREFELKEGYIPTIQIKQSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKGVPLYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGWHEHSTFKRAKYLROKTYIQDIYMKRVRGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0255	351	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLFKDFGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKLKLPFPVKKIAQDFKLTVKKGDIYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TLSLGLDKEVRKAYRGGFTWLNDLDRFKGKEIGEGMVFDINSAYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIREFELKEGYIPTIQIKQSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKGVPLYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGWHEHSTFKRAKYLROKTYIQDIYMKRVRGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0256	352	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNLFKDFGAFIINWLFKNGFKWCKEAKERTFSTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKLKLPFPVKKIAQDFKLTVKKGDIYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TLSLGLDKEVRKAYRGGFTWLNDLDRFKGKEIGEGMVFDINSAYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIREFELKEGYIPTIQIKQSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKGVPLYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGWHEHSTFKRAKYLROKTYIQDIYMKRVRGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0257	353	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKLKLPFPVKKIAQDFKLTVKKGDIYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TLSLGLDKEVRKAYRGGFTWLNDLDRFKGKEIGEGMVFDINSAYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIREFELKEGYIPTIQIKQSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKGVPLYKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGWHEHSTFKRAKYLROKTYIQDIYMKRVRGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0258	354	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADLYFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKLKLPFPVKKIAQDFKLTVKKGDIYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFP TLSLGLDKEVRKAYRGGFTWLNDLDRFKGKEIGEGMVFDINSAYPAQMYSRLLPYGEPVIFEGKYVWDEDYPLHIQHIREFELKEGYIPTIQIKQSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYISGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKGVPLYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKVDPDAIKDLVHPKKLGWHEHSTFKRAKYLROKTYVQDIYMKRVRGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

[0136]

C0259	355	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTW LNDRFKGEIGEGLMVFINSAYPAQMYRLLPYGEPVFEFEGKYVWDEDEYPLHIQHIRC EFELKEGYIPTTIQIKQSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTG TKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPDDYT DIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0260	356	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTW LNDRFKGEIGEGLMVFINSAYPAQMYRLLPYGEPVFEFEGKYVWDEDEYPLHIQHIRC EFELKEGYIPTTIQIKQSLFYKGNEYLKSSGGEIADLWLSNVDLELMKEHYDLYNVEYI SGLKFKATTGLFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVPYL KENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHLTG TKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPDDYT DIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0261	357	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGLMVFINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPDD YTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0262	358	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTW LNDRFKGEIGEGLMVFINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RFRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDS IHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGS PPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0263	359	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGRKIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGFTWLND RFKGEIGEGLMVFINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFIITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPDD YTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0264	360	MKHMPRKMYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWVLKVQADL YFHNLFKFDGAFIINWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGRKIH

[0137]

		TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTWLNDRFKKGKEIGEGMVFDINSAYPAQMYSRLLPYGEPVFEFGKYVWDEHPLHIQHLRCFELKEGYIPCIQIKQSLFYKGYNEYLKSSGGGIAELWLSNVDELMLKEHYELYNVEYISGLKFRATTGLFKDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNPDPVTGKVPYLYKENGALGFRLGEEETKDPVYTPMGVFTITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0265	361	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHNLFKDFGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTWLNDRFKKGKEIGEGMVFDINSAYPAQMYSRLLPYGEPVFEFGKYVWDEHPLHIQHLRCFELKEGYIPCIQIKQSLFYKGYNEYLKSSGGGIAELWLSNVDELMLKEHYELYNVEYISGLKFRATTGLFKDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNPDPVTGKVPYLYKENGALGFRLGEEETKDPVYTPMGVFTITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0266	362	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTWLNDRFKKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRRLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEIHYTYGYMFKASCDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNPDPVTGKVPYLYKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0267	363	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTWLNDRFKKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRRLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEIHYTYGYMFKASCDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNPDPVTGKVPYLYKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0268	364	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHNLFKDFGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTWLNDRFKKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFRRLKERHIPCIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILIEIHYTYGYMFRASCDFIDKWYIKTTSYGAIKQLAKLMLNSLYGKFASNPDPVTGKVPYLYKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0269	365	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLFKDFGAFIINWLFKNGFKWCKEAKEERTFTIISRMGQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVEKIAKDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGFTWLNL

[0138]

		DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRKMKPKPVQVPGGVVLVDVSFTIK
C0270	366	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKRKIHTV IYDSLKKLFPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRKMKPKPVQVPGGVVLVDVSFTIK
C0271	367	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKRKIHTV IYDSLKKLFPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRKMKPKPVQVPGGVVLVDVSFTIK
C0272	368	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKRKIHTV IYDSLKKLFPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLENSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRKMKPKPVQVPGGVVLVDVSFTIK
C0273	369	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKRKIHTV IYDSLKKLFPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRKMKPKPVQVPGGVVLVDVSFTIK
C0274	370	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKRKIHTV IYDSLKKLFPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFLKERHIPICIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI

[0139]

		HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0275	371	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLVGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0276	372	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLVGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0277	373	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLVGYKGRKQHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0278	374	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLVGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDVSVFTIK
C0279	375	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLVGYKGRKIHTV IYDSLKKLFFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH

[0140]

		LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0280	376	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRV RLKERHIPCQVKQSSSLFIQNEYLESSVNKLGVDLIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0281	377	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRV RLKERHIPCQVKQSSSLFIQNEYLESSVNKLGVDLIELTLTNVDLDFFEHYEILEI HYTYGYMFRGSCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0282	378	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRV RLKERHIPCQVKQSSSLFIQNEYLESSVNKLGVDLIELTLTNVDLDFFEHYEILEI HYTYGYMFRGSCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0283	379	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRV RLKERHIPCQVKQSSSLFIQNEYLESSVNKLGVDLIELTLTNVDLDFFEHYEILEI HYTYGYMFRGSCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0284	380	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAE LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRV RLKERHIPCQVKQSSSLFIQNEYLESSVNKLGVDLIELTLTNVDLDFFEHYEILEI HYTYGYMFRGSCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

[0141]

C0285	381	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRV DGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0286	382	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRV DGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0287	383	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRF RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRV DGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0288	384	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYGKGRKIHTVI YDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN RFGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLGKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRV DGYLVQGSPDD YTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0289	385	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPICIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKV PYLKENGALGFRLGEEETKDPVYTPMGVFI TAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRV DGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0290	386	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYGKGRKIHTVI

[0142]

		YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSLF IQNEYLESSVNKLGVDELIELTLTNVDL DLF FEHYEILEIH YTYGYMFRASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHL TGTKIPDV IKDIVHPKKLGYWEHESTFKRAKYL RQKTYIQDIYMKRVKGYLVQGS PDD YTDIKFSVKCAGMTDKIKKEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0291	387	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSLF IQNEYLESSVNKLGVDELIELTLTNVDL DLF FEHYEILEIH YTYGYMFRASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDV IKDIVDPKKLGYWEHESTFKRAKYL RQKTYIQDIYMKRVKGYLVQGS PDD YTDIKFSVKCAGMTDKIKKEVT FENFKVGF SRKMKPKPVQVPGGVVLVDETFTIK
C0292	388	MSRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLEKNGFKWSADGLPNTYNTIISRMGQWYMIDICLYGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSLF IQNEYLESSVNKLGVDELIELTLTNVDL DLF FEHYEILEIH YTYGYMFRASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDV IKDIVDPKKLGYWEHESTFKRAKYL RQKTYIQDIYMKRVKGYLVQGS PDD YTDIKFSVKCAGMTDKIKKEVT FENFKVGF SRKMKPKPVQVPGGVVLVDETFTIK
C0293	389	MSRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSLF IQNEYLESSVNKLGVDELIELTLTNVDL DLF FEHYEILEIH YTYGYMFRASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDV IKDIVDPKKLGYWEHESTFKRAKYL RQKTYIQDIYMKRVKGYLVQGS PDD YTDIKFSVKCAGMTDKIKKEVT FENFKVGF SRKMKPKPVQVPGGVVLVDETFTIK
C0294	390	MSRKFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGKRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND RFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLF IQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEIH YTYGYMFKASCDMF KDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVP YLKENGALGFR LGEEETKDPVYTPMGVFI TAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDV IKDIVDPKKLGYWEHESTFKRAKYL RQKTYIQDIYMKRVKGYLVQGS PDD YTDIKFSVKCAGMTDKIKKEVT FENFKVGF SRKMKPKPVQVPGGVVLVDETFTIK
C0295	391	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLEKNGFKWSADGLPNTYNTIISRMGQWYMIDICLYGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGFTWLND

[0143]

		RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRGEEETKDPVYTPLASVTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVOGSPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0296	392	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLPPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVOGSPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0297	393	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLPPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVRFR LKERHIPTIQVKQSSSLFIQNEYLENSVNKLGVDELIDLTLTNVDLDFFEHYEILEIH YTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVOGSPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0298	394	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLEKNGFKWSAEGLPNTYNTIISRMQWYMIDICIGYKGRKIHTVI YDSLKKLPPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVOGSPDD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0299	395	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGYKGRKIHTV IYDSLKKLPPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITPEEYAYIKNDIQIAEA LLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLND DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH HYTYGYMFKASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKV PYLKENGALGFRGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIH LTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVOGSPD DYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0300	396	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKIHTVI YDSLKKLPPFPVEKIAKDFKLTVKKGDIIDHKERPVGKITPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPPLSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIH

[0144]

		YTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0301	397	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFIDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0302	398	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYGKGRKIHTVI YDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFIDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVP YLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIHL TGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD YTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0303	399	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGYGKGRKIHTV YDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFIDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKVRFR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD DYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0304	400	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGYGKGRKIHTV YDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFIDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR RLKERHIPCIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTIPDVIKDIVDPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPPD DYTDIKFSVKCAGMTDKIKKEVTFENFKVGFSRKMKPKPVQVPGGVVLVDETFITIK
C0305	401	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH DLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGYGKGRKIHTV YDSLKKLPFPVEKIAKDFKLTVKKGDIDIHKERPVGYKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFIDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR RLKERHIPCIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH

[0145]

		LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0306	402	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHDLKFDGAFIINWLFNRNGFKWCKDAKEERTFSTIISRMGQWYMIDICLGKYGKRRKIHTVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPY LKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0307	403	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLKFDGAFIINWLFNRNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIHTVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPY LKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0308	404	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHDLKFDGAFIINWLFNRNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIHTVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DANSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYEILEIHYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPY LKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTEIPDVIKDIVDPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDETFTIK
C0309	405	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNKFDGAFIINWLFNRNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIHTVIYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DINSAYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPY LKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0310	406	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFHNKFDGAFIINWLFNRNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRKIHTVIYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DINSAYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNIKVRFR LKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPY LKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLKQKTYIQDIYMKRVKGYLVQGSPPDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

[0146]

C0311	407	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHNLFKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGYKGRKRIHTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVGVKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0312	408	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHNLFKFDGAFIINWLEKNGFKWSAEGLPNTYNTIISRMQWYMIDICIGYKGRKRIHTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVGVKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0313	409	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKRIHTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVGVKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0314	410	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWMEIQADLYFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKRIHTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVGVKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0315	411	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGYKGRKRIHTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVGVKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0316	412	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFHNLFKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGYKGRKRIHTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKYKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEIHYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVGVKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPDDYTDIKFSVKCAGMTDKIKEEVTTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

[0147]

		YFHNLFKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRI HTVIYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQII AEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFT WLNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIK VRFLRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDI LEIHITYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTV GKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTD SIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGS SPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0317	413	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIVNWLEKNGFKWSAEGLPNTYNTIISRMGQWYMIDICIGYKGRKRIH TVIYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIK VRFLRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDIL EIHITYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVG KVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDS IHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGS PDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0318	414	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR FLRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVGK VPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSI HLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGS PDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0319	415	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRI HTVIYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQII AEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFT WLNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIK VRFLRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDI LEIHITYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTV GKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTD SIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYLRQKTYVQDIYMKRVRGYLVQGS SPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0320	416	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR FLRKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVGK VPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSI HLTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGS PDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0321	417	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL

[0148]

		YFHNLFKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEIHYTYGYMFKASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKENGALGFR LGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PD DYT DIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0322	418	MSRKRFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDL DLF FEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PD DYT DIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0323	419	MSRKRFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEIHYTYGYMFKASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PD DYT DIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0324	420	MSRKRFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRFR LKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDL DLF FEHYEILEIHYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PD DYT DIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0325	421	MSRKRFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTVYDSLKKLPPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLNDRFKGKEIGEGMVF DINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDL DLF FEHYDILEIHYTYGYMFKASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKENGALGFR LGEEETKDPVYTPMGVFITAWGRYTTITTAQACYDRIIYCDTDSIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PD DYT DIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0326	422	MSRKRFS CDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFHNLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV

[0149]

		IYDSLKKLFPFVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVR RLKERHIPICIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKV PYLKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0327	423	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLFPFVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVR RLKERHIPICIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKV PYLKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0328	424	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLFPFVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVR RLKERHIPICIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKV PYLKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0329	425	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLFPFVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVR RLKERHIPICIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVTKV PYLKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTGKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0330	426	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRI HTVIYDSLKKLFPFVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQII AEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSGLDKEVRKAYRGGFT WLNDRFKGKEIGEGMVFANDSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLK VRFRRLKERHIPICIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYE LEIHYTYGYMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDV TKVPLYKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTD SIHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQ GSPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTI K
C0331	427	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRI HTVIYDSLKKLFPFVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQII

[0150]

		AEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFT WLNDRFKGEIGEGMVFDANSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIK VRFRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDI LEIHITYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTV GKVPYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTD SIHLTGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQG SPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTI K
C0332	428	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRI HTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQII AEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFT WLNDRFKGEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLK VRFRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEI LEIHITYGYMFASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTV GKVPYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTD SIHLTGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQG SPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTI K
C0333	429	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRI HTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQII AEALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFT WLNDRFKGEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIK VRFRLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDI LEIHITYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTV GKVPYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTD SIHLTGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQG SPDDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTI K
C0334	430	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWFYIKTTSYGAIKQLAKMLNSLYGKFASNPDTV GKVPYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0335	431	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIHTV IYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDTV GKVPYKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVKGYLVQGS PDYTDIKFSVKCAGMTDKIKEEVTFFENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0336	432	MKHMPRKRYSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGKGRKRIH

[0151]

		TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEHYDIL EIHYYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYL RQKTYIQDIYMKRVRGYLVQGS PDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0337	433	MKHMSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMAWALKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEHYDIL EIHYYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYL RQKTYIQDIYMKRVRGYLVQGS PDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0338	434	MKHMPKRKRYSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMAWALKVQADL YFHNLFKDFGAFIINWLFKNGFKWCKEAKERTFSTIISRMGQWYMIDICLGKYGKRRIH HTVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA AEALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEHYDI LEIHYYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDT GKVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTD SIHLTGTKVPDAIKDLVHPKKLGYWEHESTFKRAKYL RQKTYIQDIYMKRVRGYLVQGS SPDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0339	435	MKHMPKRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFDINSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEHYDIL EIHYYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDS IHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYL RQKTYIQDIYMKRVRGYLVQGS PDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0340	436	MKHMPKRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFDINSHYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEHYDIL EIHYYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYL RQKTYIQDIYMKRVRGYLVQGS PDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGF SRMKPKPVQVPGGVVLVDSVFTIK
C0341	437	MKHMPKRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGKYGKRRIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIA

[0152]

		EALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP T L S L G L D K E V R K A Y R G G F T W L N D R F K G K E I G E G M V F D I N S A Y P A Q M Y V R P L P Y G T P L F Y E G E Y K E N I D Y P L Y I Q N I K V R F R L K E R H I P T I Q V K Q S S L F I Q N E Y L E S S V N K L G V D E L I D L T L T N V D L D L F F E H Y D I L E I H Y T Y G M F K A S C D M F K D F I D K W T Y I K T T S Y G A I K Q L A K L M L N S L Y G K F A S N P D V T G K V P Y L K E N A L G F R L G E E E T K D P V Y T P L A V F V T A W G R Y T T I T A A Q A C Y D R I I Y C D T D S I H L T G T K I P D V I K D I V H P K K L G Y W E H E S T F K R A K Y L R Q K T Y I Q D I Y M K R V R G Y L V Q G S P D D Y T D I K F S V K C A G M T D K I K E E V T F E N F K V G F S R K M K P K P V Q V P G G V V L V D S V F T I K
C0342	438	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIIDYHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP T L S L G L D K E V R K A Y R G G F T W L N D R F K G K E I G E G M V F D I N S A Y P A Q M Y V R P L P Y G T P L F Y E G E Y K E N I D Y P L Y I Q N I K V R F R L K E R H I P T I Q V K Q S S L F I Q N E Y L E S S V N K L G V D E L I D L T L T N V D L D L F F E H Y D I L E I H Y T Y G M F K A S C D M F K D F I D K W T Y I K T T S Y G A I K Q L A K L M L N S L Y G K F A S N P D V T G K V P Y L K E N A L G F R L G E E E T K D P V Y T P L A S F V T A W G R Y T T I T A A Q A C Y D R I I Y C D T D S I H L T G T K I P D V I K D I V H P K K L G Y W E H E S T F K R A K Y L R Q K T Y I Q D I Y M K R V R G Y L V Q G S P D D Y T D I K F S V K C A G M T D K I K E E V T F E N F K V G F S R K M K P K P V Q V P G G V V L V D S V F T I K
C0343	439	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIIDYHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP T L S L G L D K E V R K A Y R G G F T W L N D R F K G K E I G E G M V F D I N S A Y P A Q M Y V R P L P Y G T P L F Y E G E Y K E N I D Y P L Y I Q N I K V R F R L K E R H I P T I Q V K Q S S L F I Q N E Y L E S S V N K L G V D E L I D L T L T N V D L D L F F E H Y D I L E I H Y T Y G M F K A S C D M F K D F I D K W T Y I K T T S Y G A I K Q L A K L M L N S L Y G K F A S N P D V T G K V P Y L K E N A L G F R L G E E E T K D P V Y T P L A V F V T A W G R Y T T I T A A Q A C Y D R I I Y C D T D S I H L T G T K I P D V I K D I V H P K K L G Y W E H E S T F K R A K Y L R Q K T Y I Q D I Y M K R V R G Y L V Q G S P D D Y T D I K F S V K C A G M T D K I K E E V T F E N F K V G F S R K M K P K P V Q V P G G V V L V D S V F T I K
C0344	440	MKHSRKRYSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADL YFHNLFKDFGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIIDYHKERPVGYKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP T L S L G L D K E V R K A Y R G G F T W L N D R F K G K E I G E G M V F D I N S A Y P A Q M Y V R P L P Y G T P L F Y E G E Y K E N I D Y P L Y I Q N I K V R F R L K E R H I P T I Q V K Q S S L F I Q N E Y L E S S V N K L G V D E L I D L T L T N V D L D L F F E H Y D I L E I H Y T Y G M F K A S C D M F K D F I D K W T Y I K T T S Y G A I K Q L A K L M L N S L Y G K F A S N P D V T G K V P Y L K E N A L G F R L G E E E T K D P V Y T P M G V F I T A W G R Y T T I T A A Q A C Y D R I I Y C D T D S I H L T G T K I P D V I K D I V H P K K L G Y W E H E S T F K R A K Y L R Q K T Y I Q D I Y M K R V R G Y L V Q G S P D D Y T D I K F S V K C A G M T D K I K E E V T F E N F K V G F S R K M K P K P V Q V P G G V V L V D S V F T I K
C0345	441	MPRKRYSCDFETTTKVEDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIIDYHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP T L S L G L D K E V R K A Y R G G F T W L N D R F K G K E I G E G M V F D I N S A Y P A Q M Y V R P L P Y G T P L F Y E G E Y K E N I D Y P L Y I Q N I K V R F R L K E R H I P T I Q V K Q S S L F I Q N E Y L E S S V N K L G V D E L I D L T L T N V D L D L F F E H Y D I L E I H Y T Y G M F K A S C D M F K D F I D K W T Y I K T T S Y G A I K Q L A K L M L N S L Y G K F A S N P D V T G K V P Y L K E N A L G F R L G E E E T K D P V Y T P M G V F I T A W G R Y T T I T A A Q A C Y D R I I Y C D T D S I H L T G T K I P D V I K D I V H P K K L G Y W E H E S T F K R A K Y L R Q K T Y I Q D I Y M K R V R G Y L V Q G S P D D Y T D I K F S V K C A G M T D K I K E E V T F E N F K V G F S R K M K P K P V Q V P G G V V L V D S V F T I K
C0346	442	MSRKRFSCDFETTTKLDDCRVWAYGYMNIEDHSEYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMGQWYMIDICLGYKGKRKIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIIDYHKERPVGYKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP T L S L G L D K E V R K A Y R G G F T W L N D R F K G K E I G E G M V F D I N S A Y P A Q M Y V R P L P Y G T P L F Y E G E Y K E N I D Y P L Y I Q N I K V R F R

[0153]

		LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIICYDTSIHL TGTKIPDVIKDIVHPKPLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPD YTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTIK
C0347	443	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIICYDTSIHL TGTKIPDVIKDIVHPKPLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPD YTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTIK
C0348	444	MSRKRFSCDFETTTKLDDCRVWAYGYMNIEDHSEYKIGNSLDEFMAWALKVQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIICYDTSIHL TGTKIPDVIKDIVHPKPLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPD YTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTIK
C0349	445	MPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIICYDTSIHL TGTKIPDVIKDIVHPKPLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPD YTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTIK
C0350	446	MPRKRYSCDFETTTKVEDCRVWAYGYMNIEDHSEYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTGKVP YLKENGALGFRLGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIICYDTSIHL TGTKIPDVIKDIVHPKPLGYWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPD YTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDVSFTIK
C0351	447	MKHMPRKRYSCDFETTTKLDDCRVWAYGYMEIGNLSEYKIGNSLDEFMQWAMKIQADL YFHNKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIA EALLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDIL EIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPVDTG

[0154]

		KVPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLROKTYIQDIYMKRVRGYLVQGS PDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0352	448	MKHMFRKRYSCDFETTTKLDDCRVWAYGYMEIGNHSEYKIGNSLDEFMQWAMKIQADL YFHNLFKDFGAFIINWLRNFGFKWSADGLPNTYNTIISRMGQWYMIDICLGYGKGRKIH TVIYDSLKKLPPFPVKLIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAE EALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTW LNDRFKGEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDIL EIHYYTYGYMFKASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVGTG KVPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDS IHLTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLROKTYIQDIYMKRVRGYLVQGS PDDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0352 B	449	MSRKRFSDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIH TVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVR RLLKERHIPICIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDVGTGK VYLPYLKENGALGFRLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIH LTGTIKIPDVIKDIVHPKKLGYWEHESTFKRAKYLROKTYIQDIYMKRVKGYLVQGS PDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0353	450	MSRKRFSDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIH TVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVR RLLKERHIPICIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDTGK VYPMGEDGIVRLTLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIH LTGTIKIPDVIKDIVHPKKLGYWEHESTFKRAKYLROKTYIQDIYMKRVKGYLVQGS PDYTDIKFSVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
C0354	451	MSRKRFSDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIH TVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVR RLLKERHIPICIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDTGK VYPMGEDGIVRLTLGEEETKDPVYTPMGVFTAWGRYTTITAAQACYDRIIYCDTDSIH LTGTIKIPDVIKDIVHPKKLGYWEHESTFKRAKYLROKTYIQDIYMKRVKGYLVQGS PDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0355	452	MSRKRFSDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIH TVIYDSLKKLPPFPVEKIAKDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAE ALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEGMVFDANSHPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVR RLLKERHIPICIQVKQSSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDTGK VYPMGEDGIVRLTLGEEETKDPVYTPASFVTAWGRYTTITAAQACYDRIIYCDTDSIH LTGTIKIPDVIKDIVHPKKLGYWEHESTFKRAKYLROKTYIQDIYMKRVKGYLVQGS PDYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK

[0155]

		DYTDIKFSVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
C0356	453	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDI TGKVP YMGEDGIVRLTLGEEETKDPVYTPMGVITAWGRYTTITAAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPD YTDIKFSVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
C0357	454	MKHMPRKRYSCDFETTTKVEDCRVWAYGYMNI EDHSEYKIGNSLDEFMAWALKVQADL YFHNLFKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIH TVIYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIAEAL EALLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTW LNDRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKV RFRLEKRIHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDIL EIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDI TG KVPYMGEDGIVRLTLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDS IHLTGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGS PDDYTDIKFSVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
C0358	455	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDI TGKVP YMGEDGIVRLTLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPD YTDIKFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0359	456	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLERNGFKWSADGLPNTYNTIISRMQWYMIDICLGKGRKIHTVI YDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIAEAL LIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND RFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRFR LKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEIH YTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFGTNPDI TGKVP YMGEDGIVRLTLGEEETKDPVYTPASFVTAWGRYTTITTAQACYDRIIYCDTDSIHL TGTKIPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPD YTDIKFSVKCAGMPDRIKELVTFDNFEVGFSSYGKLLPKRTQGGVVLVDTMFTIK
C0360	457	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGKGRKIHTV IYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIAEA LLIQFKQGLDRMTAGSDSLKGFKDIITTKKFKKVFP TSLGLDKEVRKAYRGGFTWLND DRFKGKEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKEGYIPTIQKSLFYKGNEYLKSSGGELIDLTNTNVDLDFFEHYDILEIH YTYG YMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNP DVTGKVPYLKE NGALGFRLEETKDPVYTPMGVITAWGRYTTITAAQACYDRIIYCDTDSIHLTGK IPDVIKDIVHPKKLGWEHESTFKRAKYLRQKTYIQDIYMKRVRGYLVQGSPPDYTDI KFSVKCAGMTDKIKEEVT FENFKVGF SRKMKPKPVQVPGGVVLVDSVFTIK
C0361	458	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH

[0156]

		NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLFFPVVKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDPLYIQNLKVRF RLKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIDLTNTVDLDDLFEEHYEILEI HYTYGYMFKASCDMFKDIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0362	459	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLFFPVVKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKRSRFLFIQNEYLESSVNELIELTLTNVDLDDLFEEHYEILEIHYTYG YMFASCDMFKDIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVVPYLKE NGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0363	460	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLFFPVVKIAQDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKGFKDIIITKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKEGYIPTIQIKRSRYFKGNEYLKSSGGELIELTLTNVDLELMKEHYEILEIHYTYG YMFASCDMFKDIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKVVPYLKE NGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIHLTGTK IPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPPDDYTDI KFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0364	461	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLFFPVVEKIAKDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIIITKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDANSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFEEHYEILEI HYTYGYMFASCDMFKDIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0365	462	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLFFPVVEKIAKDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIIITKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSHYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFEEHYEILEI HYTYGYMFASCDMFKDIDKWFYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGSPPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0366	463	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICLGYGKGRKIHTV IYDSLKKLFFPVVEKIAKDFKLTVKKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEAL

[0157]

		LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKMLNSLYGKFASNPDVTKV PYLKENGALGFRLGEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGS DYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0367	464	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGEIGEGMVFDVNSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWFYIKTTSYGAIKQLAKMLNSLYGKFASNPDVTKV PYLKENGALGFRLGEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGS DYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0368	465	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGEIGEGMVFDVNSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDVTKV PYLKENGALGFRLGEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGS DYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0369	466	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDVTKV PYLKENGALGFRLGEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGS DYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0370	467	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICLGKGRKRIHTV IYDSLKKLPFPVEKIAKDFKLTVKKGDIDHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGEIGEGMVFDANSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKMLNSLYGKFASNPDVTKV PYLKENGALGFRLGEETKDPVYTPMGVFITAWGRYTTITAAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVKGYLVQGS DYTDIKFSVKCAGMTDKIKEEVTFENFKVGFSRKMKPKPVQVPGGVVLVDSVFTIK
C0371	468	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIINWLFKNGFKWCKEAKEERTFSTIISRMQWYMIDICIGYKGRKRIHTV IYDSLKKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGYKITPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKKVFTLSLGLDKEVRKAYRGGFTWLN DRFKGEIGEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI

[0158]

		HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0372	469	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRV RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0373	470	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNLKVRV RLKERHIPCIQVKQSSFLIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHYEILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0374	471	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRV RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0375	472	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRV RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKDDGSLGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0376	473	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRV RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKDDGILGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0377	474	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRV RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI

[0159]

		HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKDDGALGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0378	475	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKEDGALGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0379	476	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKEDGIVRLTLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0380	477	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKEDGIVGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0381	478	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKDDGIVGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0382	479	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKDDGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSVFTIK
C0383	480	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNFGKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRIHTV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVPPTLSGLDKEVRKAYRGGFTWLN DRFKGKEI GEGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSFLIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFFEHYDILEI

[0160]

		HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKDDGAVGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0384	481	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0385	482	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFDNFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0386	483	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFDNFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0387	484	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFDNFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0388	485	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0389	486	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI

[0161]

		HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDTIKEEVTDFNFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0390	487	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDTIKEEVTDFNFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0391	488	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDTIKEEVTDFNFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0392	489	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEIRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTDFNFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0393	490	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEIRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTDFNFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0394	491	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEIRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTDFNFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0395	492	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYQGEYKENIDHPLYIQNLKVR RLKERHIPCIQVKQNSLFIQNEYLESSVNKLGVDELIELTLTNVDLDFFEHYEILEI

[0162]

		HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0396	493	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHEYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKDDGALGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0397	494	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHEYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0398	495	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHEYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0399	496	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHEYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0400	497	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEIRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHEYEILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0401	498	MSRKRFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWAMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTLISRMGQWYMIDICIGYKGRKRIHTV IYDSLKKLFFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEIRKAYRGGFTWLN DRFKGKEIGEVMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPCIQVKQSSLFIQNEYLESSVNKLGVDELIELTLTNVDLDDLFFEHEYEILEI

[0163]

		HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDRIKEEVTDFNFKVGFGRKMKPKPVQTPGGVVLVDVSFTIK
C0402	499	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIIEGGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDHPLYIQNLKVRF RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGIVGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDRIKEEVTDFNFKVGFGRKMKPKPVQTPGGVVLVDVSFTIK
C0403	500	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIIEGGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKDDGSLGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDRIKEEVTDFNFKVGFGRKMKPKPVQTPGGVVLVDVSFTIK
C0404	501	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIIEGGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKDDGSLGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDRIKEEVTDFNFKVGFGRKMKPKPVQTPGGVVLVDVSFTIK
C0405	502	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIIEGGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDRIKEEVTDFNFKVGFGRKMKPKPVQTPGGVVLVDVSFTIK
C0406	503	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIIEGGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEI HYTYGYMFRASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRVGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDRIKEEVTDFNFKVGFGRKMKPKPVQTPGGVVLVDVSFTIK
C0407	504	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV FYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKKFKVFPFSLGLDKEVRKAYRGGFTWLN DRFKGKEIIEGGMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTNTNVDLDFFEHYDILEI

[0164]

		HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRIDGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0408	505	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRQRTI FYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRIDGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0409	506	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRKNHV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRIDGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0410	507	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRKNHV IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRIDGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0411	508	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRGTQ IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRIDGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0412	509	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRFRVE IYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRIDGEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPP DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0413	510	MSRKMFCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMQWYIMIDICIGYKGRKRFRVE FYDSLKKLFPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEAL LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSLGLDKEVRKAYRGGFTWLN DRFKGKEIGEVMFVDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVRF RLKERHIPTIQVKQSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDFFEHYDILEI

[0165]

		HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0414	511	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSGLDKVEVRKAYRGGFTWLN DKYKGEIEGEMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0415	512	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSGLDKVEVRKAYRGGFTWLN PKYKGEIEGEMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0416	513	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSGLDKVEVRKAYRGGFTWLN PKYKGEIEGEMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0417	514	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSGLDKVEVRKAYRGGFTWLN PRYKGEIEGEMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0418	515	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSGLDKVEVRKAYRGGFTWLD PKYKGEIEGEMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEEHYDILEI HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK
C0419	516	MSRKMFSCDFETTTKLDDCRVWAYGYMEIGNLDNYKIGNSLDEFMQWVMEIQADLYFH NLKFDGAFIVNWLFKNGFKWCKEAKEERTFSTIISRMGQWYMIDICIGYKGRKRIHTV IYDSLKLKLPFPVKKIAQDFKLTVKKGDIDYHKERPVGKITYPEEYAYIKNDIQIIAEA LLIQFKQGLDRMTAGSDSLKDFKDIITTKFKKVFPTLSGLDKVEVRKAYRGGFTWLD PRYKGEIEGEMVFDINSAYPAQMYVRPLPYGTPLFYEGEYKENIDYPLYIQNIKVR RLKERHIPTIQVKQSSSLFIQNEYLESSVNKLGVDELIDLTLTNVDLDDLFEEHYDILEI

		HYTYGYMFKASCDMFKDFIDKWTYIKTTSYGAIKQLAKLMLNSLYGKFASNPDTVTKV PYLKENGALGFRLGEEETKDPVYTPLASFVTAWGRYTTITTAQACYDRIIYCDTDSIH LTGTKIPDVIKDIVHPKKLGYWEHESTFKRAKYLQKTYIQDIYMKRVRGYLVQGSPD DYTDIKFSVKCAGMTDKIKEEVTFFENFKVGFGRKMKPKPVQVPGGVVLVDVSFTIK

일부 실시양태에서, 본 개시내용의 변형된 제조합 폴리머라제 효소는 표 3으로부터 선택된다. 일부 실시양태에서, 키메라 폴리머라제 변이체 (예를 들어, 표 3에 열거된 바와 같음)는 상이한 폴리머라제 서열의 영역 또는 부분으로 치환된 대다수의 서열의 영역 또는 부분을 갖는 대다수의 폴리머라제 서열을 포함한다. 일부 실시양태에서, 대다수의 폴리머라제 서열 내의 영역 (예를 들어, 도메인 및/또는 서브 도메인)을 포함하는 잔기 모두는 상이한 폴리머라제 서열 내의 상응하는 영역을 포함하는 잔기 모두로 치환된다. 일부 실시양태에서, 대다수의 폴리머라제 서열 내의 영역을 포함하는 잔기의 적어도 특정 부분은 상이한 폴리머라제 서열 내의 상응하는 영역을 포함하는 잔기의 적어도 특정 부분으로 치환된다.

일부 실시양태에서, 대다수의 서열 내의 단일 서브 도메인 만이 상이한 서열의 상응하는 서브 도메인으로 치환된다. 예를 들어, 도 4는 표 3으로부터 선택된 키메라 폴리머라제 변이체를 도시한다. 6개의 선택된 변이체가, 아미노 말단에서 카르복시 말단 배향으로 폴리펩티드 이내에 일반적으로 발생하는 바와 같이 서브 도

메인을 갖는 폴리펩티드 가닥으로서 제시된다. 도 4의 폴리펩티드 가닥 각각은 Q001의 폴리머라제 대다수의 서열 (혹색 채움)을 포함하며, 하나 이상의 도메인 및/또는 서브 도메인이 M2Y 폴리머라제 (서열식별번호: 2, 열린 채움)의 하나 이상의 상응하는 도메인 및/또는 서브 도메인 또는 루실리아 쿠프리나 (서열식별번호: 3, 점자 채움)의 하나 이상의 상응하는 도메인 및/또는 서브 도메인 및/또는 하나 이상의 플랭킹 아미노산으로 치환된다.

[0170] 일부 실시양태에서, 키메라 폴리머라제 변이체는 상이한 폴리머라제 서열로부터 치환된 엑소뉴클레아제 도메인을 갖는 대다수의 폴리머라제 서열을 포함한다. 도 4에 도시된 바와 같이, C017은 M2Y 폴리머라제 서열 (예를 들어, 서열식별번호: 2에 제시된 바와 같음)로부터 치환된 엑소뉴클레아제 도메인을 포함하는 키메라 폴리머라제 변이체이다. 유사하게, C020은 루실리아 쿠프리나 폴리머라제 서열 (예를 들어, 서열식별번호: 3에 제시된 바와 같음)로부터 치환된 엑소뉴클레아제 도메인을 포함한다. 일부 실시양태에서, 변형된 폴리머라제 변이체 내의 엑소뉴클레아제 도메인의 변형 또는 대체는 폴리머라제의 교정 능력이 바람직하지 않은 경우 (예를 들어, 시퀀싱 반응에서)에 유용할 수 있다. 그러나, 부가의 및 대안 도메인 및/또는 서브 도메인 치환이 본 개시내용의 변형된 재조합 폴리머라제를 위해 고려된다는 것을 인지해야 한다.

[0171] 일부 실시양태에서, 키메라 폴리머라제 변이체는 상이한 폴리머라제 서열로부터 치환된 엑소뉴클레아제 루프를 갖는 대다수의 폴리머라제 서열을 포함한다. 본원에 사용된 바와 같은, 일부 실시양태에서, "엑소뉴클레아제 루프"는 엑소뉴클레아제 도메인 내에 루프 영역을 형성하는 연속되는 아미노산의 연장물을 지칭한다. 예를 들어, 도 5a는 전체 투시도 (500) 및 확대 투시도 (502)에서의 $\Phi 29$ 폴리머라제의 카툰 예시를 도시한다. 전체 투시도 (500)로 도시된 박스 내에 있는 영역의 확대도인 확대 투시도 (502)는 $\Phi 29$ 폴리머라제의 엑소뉴클레아제 도메인 내의 루프 영역을 나타낸다. 선택된 루프 잔기는 잔기 N77 내지 N88에 걸쳐 있는 엑소뉴클레아제 루프를 형성하는 연속되는 아미노산의 연장물과 함께 확대 투시도 (502)의 스틱 형태로 도시된다. 이러한 엑소뉴클레아제 도메인의 영역에 대한 진화 보존 분석 결과, 루프 및 몇 개의 플랭킹 잔기가 비교적 잘 보존되지 않은 것으로 밝혀졌다. 도 5b는 $\Phi 29$ 폴리머라제의 엑소뉴클레아제 영역과 표 1로부터 선택된 다른 폴리머라제의 비-제한적 세트 간의 상동성 정렬 (504)을 도시한다. 또한, $\Phi 29$ 폴리머라제의 엑소뉴클레아제 루프 N77-N88 및 다른 폴리머라제 내의 상응하는 엑소뉴클레아제 루프를 보여주는 루프 상동성 정렬 (506)이 도시된다.

[0172] $\Phi 29$ 폴리머라제의 엑소뉴클레아제 루프 N77-N88에 상응하는 영역 내에서 비교적 낮은 보존성을 보여주는 상동성 분석에 기초하여, 이는 폴리머라제 변이체에서 바람직한 생화학적 특성 (예를 들어, 시퀀싱 반응에서 사용하기에 바람직하다)에 대한 검색에서 변이 공급원을 제공하였다. 따라서, 일부 실시양태에서, 키메라 폴리머라제 변이체는 상이한 폴리머라제 서열로부터 치환된 엑소뉴클레아제 루프를 갖는 대다수의 폴리머라제 서열을 포함하며, 여기서 "엑소뉴클레아제 루프"는 $\Phi 29$ 폴리머라제의 엑소뉴클레아제 루프 N77-N88과 상동이다 (예를 들어, 도 5b 내의 루프 상동성 정렬 (506)에 의해 도시된 바와 같음).

[0173] 도 5b 내의 예시적인 정렬에 의해 도시된 바와 같이, 서열 상동성 분석은 $\Phi 29$ 폴리머라제의 N77-N88과 상동인 엑소뉴클레아제 루프 서열을 확인하기 위해 사용될 수 있다. 한 예로서 제한 없이, 루프 상동성 정렬 (506)은 M2Y (H74-N85), 루실리아 쿠프리나 (N64-G76), 이. 파에시움 (N74-R86), 바실루스 GA-1 (N74-K88), 바실루스 VMY22 (K80-K91), 악티노마이세스(*Actinomyces*) AV-1 (H93-K105), 감자 낭 선충류 (L86-K99), 이베리아 스라소니 내장(Iberian lynx gut) (D73-R87), 칸디다투스(*Candidatus*) (N85-N98), 및 에게르텔라 종(*Eggerthella* sp.) (V73-K88)에 대한 상동 엑소뉴클레아제 루프 서열을 나타낸다. 따라서, 일부 실시양태에서, 치환된 엑소뉴클레아제 루프는 $\Phi 29$ 폴리머라제의 N77-N88과의 상동성 영역 내의 약 12개 내지 약 16개의 아미노산을 포함할 수 있다. 일부 실시양태에서, 치환된 엑소뉴클레아제 루프는 $\Phi 29$ 폴리머라제의 N77-N88과의 상동성 영역 내의 약 10개 아미노산 내지 20개 이하의 아미노산, 약 5개 아미노산 내지 15개 이하의 아미노산, 약 5개 아미노산 내지 20개 이하의 아미노산, 또는 약 5개 아미노산 내지 25개 이상의 아미노산을 포함한다.

[0174] 일부 실시양태에서, 본 출원의 변형된 폴리머라제는 $\Phi 29$ 폴리머라제의 N77-N88과의 상동성의 엑소뉴클레아제 루프를 포함하는 엑소뉴클레아제 도메인의 영역 내의 하나 이상의 아미노산 돌연변이를 포함한다. 예를 들어, 일부 실시양태에서, 본 개시내용의 변형된 폴리머라제는 $\Phi 29$ 폴리머라제 내의 E75, R76, S82, A83, D84, G85, L86, P87, N88, Y90, 및 N91 중 하나 이상에서의 돌연변이를 포함하는 변형된 $\Phi 29$ 폴리머라제이다. 일부 실시양태에서, 변형된 폴리머라제는 E75F, R76K, S82C, A83K, D84E, G85A, L86K, P87E, N88R, Y90F, 및 N91S 중 하나 이상을 포함한다. 일부 실시양태에서, 변형된 폴리머라제는 $\Phi 29$ 폴리머라제 내의 E75, R76, S82, A83, D84, G85, L86, P87, N88, Y90, 및 N91에 상응하는 위치에 하나 이상의 아미노산 돌연변이를 포함한다. 예를 들어, 일부 실시양태에서, 변형된 폴리머라제가 $\Phi 29$ 폴리머라제 대다수의 서열을 포함하지 않는 경우, 이러한 변형된 폴리머라제는, 예를 들어, 상동성 정렬 또는 관련 기술분야에 공지된 다른 방법에 의해 결정된 바와 같

이, 상기 열거된 위치에 상응하는 하나 이상의 아미노산을 포함한다.

[0175] 일부 실시양태에서, 키메라 폴리머라제 변이체는 상이한 폴리머라제 서열로부터 치환된 TPR1 서브 도메인을 갖는 대다수의 폴리머라제 서열을 포함한다. 예를 들어, C018은 M2Y 폴리머라제 서열로부터 치환된 TPR1 서브 도메인을 포함하는 키메라 폴리머라제이다. 유사하게, C021은 루실리아 쿠프리나 폴리머라제로부터 치환된 TPR1 서브 도메인을 포함한다. 일부 실시양태에서, 키메라 폴리머라제 변이체는 상이한 폴리머라제 서열로부터 치환된 팜 서브 도메인을 갖는 대다수의 폴리머라제 서열을 포함한다. 일부 실시양태에서, 키메라 폴리머라제 변이체는 상이한 폴리머라제 서열로부터 치환된 핑거 서브 도메인을 갖는 대다수의 폴리머라제 서열을 포함한다. 일부 실시양태에서, 키메라 폴리머라제 변이체는 상이한 폴리머라제 서열로부터 치환된 TPR2 서브 도메인을 갖는 대다수의 폴리머라제 서열을 포함한다. 일부 실시양태에서, 키메라 폴리머라제 변이체는 상이한 폴리머라제 서열로부터 치환된 섬 서브 도메인을 갖는 대다수의 폴리머라제 서열을 포함한다. 본원에 기재된 바와 같은, 변형된 재조합 폴리머라제는 2개 이상의 도메인 및/또는 서브 도메인 치환을 포함하는 키메라 폴리머라제 변이체를 포함한다.

[0176] 일부 실시양태에서, 대다수의 서열 내의 2개의 영역 (예를 들어, 도메인/서브 도메인)이 상이한 서열의 2개의 상응하는 영역 (예를 들어, 상응하는 도메인/서브 도메인)으로 치환된다. 예를 들어, 도 4에 도시된 바와 같이, C019는 M2Y 폴리머라제 서열의 상응하는 엑소뉴클레아제 도메인 및 TPR1 서브 도메인으로 치환된 엑소뉴클레아제 도메인 및 TPR1 서브 도메인을 포함하는 키메라 폴리머라제이다. 유사하게, C022는 루실리아 쿠프리나 폴리머라제의 상응하는 엑소뉴클레아제 도메인 및 TPR1 서브 도메인으로 치환된 엑소뉴클레아제 도메인 및 TPR1 서브 도메인을 포함한다. 일부 실시양태에서, 부가의 도메인 및/또는 서브 도메인 치환이 본원에 기재된 변형된 폴리머라제와 함께 고려된다. 예를 들어, 일부 실시양태에서, 대다수의 서열 내의 3개 이상 (예를 들어, 3개, 4개, 5개, 또는 6개)의 영역 (예를 들어, 도메인/서브 도메인)이 상이한 서열의 3개 이상 (예를 들어, 3개, 4개, 5개, 또는 6개)의 상응하는 영역으로 치환된다.

[0177] 일부 실시양태에서, 키메라 폴리머라제 변이체의 대다수의 폴리머라제 서열은 표 1-3 내의 서열로부터 선택된다. 일부 실시양태에서, 이러한 대다수의 폴리머라제 서열은 표 1-3으로부터 선택된 상이한 폴리머라제 서열로부터 치환된 하나 이상의 영역 및/또는 부분을 포함한다. 예를 들어, 표 4는 표 3으로부터 선택된 키메라 폴리머라제 변이체의 개요를 제공하고, 치환된 영역(들)/부분(들) 및 그 치환이 기초하는 서열에 관한 설명과 함께 각각에 대한 대다수의 폴리머라제 서열을 열거한다.

[0178] <표 4>

[0179] 키메라 폴리머라제 - 치환된 부분

명칭	대다수의 서열	치환된 서열의 공급원	치환된 영역(들)/부분(들)
C001	Q001	M2Y (SEQ ID NO: 2)	엑소뉴클레아제, TPR1
C002	Q001	M2Y (SEQ ID NO: 2)	엑소뉴클레아제, TPR1
C003	Q001	M2Y (SEQ ID NO: 2)	엑소뉴클레아제, TPR1
C010	Q001	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	엑소뉴클레아제
C011	Q001	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	엑소뉴클레아제
C012	Q001	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	TPR1
C013	Q001	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	TPR1
C014	Q001	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	엑소뉴클레아제, TPR1
C015	Q001	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	엑소뉴클레아제, TPR1
C016	Q002	M2Y (SEQ ID NO: 2)	엑소뉴클레아제
C017	Q001	M2Y (SEQ ID NO: 2)	엑소뉴클레아제
C018	Q001	M2Y (SEQ ID NO: 2)	TPR1
C019	Q001	M2Y (SEQ ID NO: 2)	엑소뉴클레아제, TPR1
C020	Q001	루실리아 쿠프리나 (SEQ ID NO: 3)	엑소뉴클레아제
C021	Q001	루실리아 쿠프리나 (SEQ ID NO: 3)	TPR1
C022	Q001	루실리아 쿠프리나 (SEQ ID NO: 3)	엑소뉴클레아제, TPR1

[0180]

명칭	대다수의 서열	치환된 서열의 공급원	치환된 영역(들)/부분(들)
C023	Q001	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	엑소뉴클레아제
C024	Q001	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	엑소뉴클레아제
C029	C017	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	엔테로코쿠스 파에시움에서 치환된 53개 잔기의 연장물
C030	C013	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	엔테로코쿠스 파에시움에서 치환된 56개 잔기의 연장물
C031	C013	M2Y (SEQ ID NO: 2)	M2Y에서 치환된 56개 잔기의 연장물
C032	C013	악티노마이세스 파지 AV-1 (SEQ ID NO: 8)	악티노마이세스 파지 AV-1에서 치환된 75개 잔기의 연장물
C033	C013	에제르텔라 종 (SEQ ID NO: 11)	에제르텔라 종에서 치환된 58개 잔기의 연장물
C034	Q001	M2Y (SEQ ID NO: 2), 엔테로코쿠스 파에시움 (SEQ ID NO: 5)	M2Y로부터의 엑소뉴클레아제, 엔테로코쿠스 파에시움으로부터의 TPR1
C035	Q001	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	TPR1, 핑거, 섬
C036	Q001	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	TPR1, TPR2, 섬
C037	Q001	악티노마이세스 파지 AV-1 (SEQ ID NO: 8)	TPR1
C038	Q001	에제르텔라 종 (SEQ ID NO: 11)	TPR1
C039	C013	M2Y (SEQ ID NO: 2)	M2Y에서 치환된 잔기 1-85
C040	C013	M2Y (SEQ ID NO: 2)	M2Y에서 치환된 잔기 1-85, 121-180
C041	C013	M2Y (SEQ ID NO: 2)	M2Y에서 치환된 잔기 1-56
C042	C013	M2Y (SEQ ID NO: 2)	M2Y에서 치환된 잔기 1-56
C043	C031	Q001	팜
C044	C031	Q001	팜
C045	C031	Q001	팜
C046	C031	Q001	팜
C047	C031	Q001	팜
C048	C031	Q001	팜
C049	C031	Q001	팜
C050	C031	Q001	팜
C051	C032	Q001	팜
C052	C032	Q001	팜
C053	C032	Q001	팜

[0181]

명칭	대다수의 서열	치환된 서열의 공급원	치환된 영역(들)/부분(들)
C054	C032	Q001	팜
C055	C032	Q001	팜
C056	C032	Q001	팜
C057	C032	Q001	팜
C058	C032	Q001	팜
C059	C033	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	TPR2, 섬
C060	C033	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	TPR2
C061	C033	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	섬
C062	C034	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	TPR2, 섬
C063	C034	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	TPR2
C064	C034	엔테로코쿠스 파에시움 (SEQ ID NO: 5)	섬
C0190	Q035	M2Y (SEQ ID NO: 2), 엔테로코쿠스 파에시움 (SEQ ID NO: 5)	260-359 대신 치환된 <i>이. 파에시움</i> 으로부터의 잔기 271-375; 1-54 대신 치환된 M2Y로부터의 잔기 1-51; 75- 91 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 72-89; 429-433 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 445-449
C0256	Q035	M2Y (SEQ ID NO: 2), 엔테로코쿠스 파에시움 (SEQ ID NO: 5)	1-54 대신 치환된 M2Y로부터의 잔기 1-51; 75-91 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 72-89
C0267	Q035	M2Y (SEQ ID NO: 2), 엔테로코쿠스 파에시움 (SEQ ID NO: 5)	260-359 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 271-375; 1-54 대신 치환된 M2Y로부터의 잔기 1-51; 429-433 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 445-449
C0320	Q035	M2Y (SEQ ID NO: 2), 엔테로코쿠스 파에시움 (SEQ ID NO: 5)	260-359 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 271-375; 1-54 대신 치환된 M2Y로부터의 잔기 1-51; 75-91 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 72-89; 429-433 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 445-449

[0182]

명칭	대다수의 서열	치환된 서열의 공급원	치환된 영역(들)/부분(들)
C0334	Q035	M2Y (SEQ ID NO: 2), 엔테로코쿠스 파에시움 (SEQ ID NO: 5)	260-359 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 271-375; 1-54 대신 치환된 M2Y로부터의 잔기 1-51
C0364	Q035	M2Y (SEQ ID NO: 2), 엔테로코쿠스 파에시움 (SEQ ID NO: 5)	260-359 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 271-375; 1-54 대신 치환된 M2Y로부터의 잔기 1-51; 75-91 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 72-89; 429-433 대신 치환된 <i>이.</i> <i>파에시움</i> 으로부터의 잔기 445-449

[0183]

[0184]

그러나, 예를 들어 본원의 표 중 하나 이상에 기재되고 예시된 바와 같은 다른 키메라가 사용될 수 있고/있거나 추가로 변형될 수 있다.

[0185] 일부 실시양태에서, 키메라 폴리머라제 변이체는 하나 이상의 부위 특이적 돌연변이를 추가로 포함할 수 있다. 따라서, 일부 실시양태에서, 본원에 기재된 하나 이상의 돌연변이 중 임의의 것 (예를 들어, 표 2 내의 각각의 서열에 포함된 하나 이상의 돌연변이 중 임의의 것)이 본 개시내용에 고려된 키메라 폴리머라제 (예를 들어, 상기에 언급되고 표 3에 열거된 바와 같음) 중 임의의 것에 적용될 수 있다. 도 6은 일반적으로, 하나 이상의 돌연변이를 포함하는 키메라 폴리머라제 변이체를 도시한다. 예를 들어, 돌연변이체 키메라 폴리머라제 (602)는 치환된 M2Y 엑소뉴클레아제 도메인 및 이러한 치환된 도메인 이내에서의 돌연변이를 갖는 Φ 29 폴리머라제 대다수의 서열을 포함한다. 일부 실시양태에서, 돌연변이체 키메라 폴리머라제는 2개 이상의 상이한 폴리머라제 서열에 상응하는 영역으로 치환된 2개 이상의 영역을 수반한 대다수의 서열을 포함한다. 예를 들어, 돌연변이체 키메라 폴리머라제 (604)는 치환된 엔테로코쿠스 파에시움 폴리머라제 TPR1 서브 도메인 및 치환된 M2Y 폴리머라제 TPR2 서브 도메인을 갖는 Φ 29 폴리머라제 대다수의 서열을 포함하며, 폴리머라제 서열 내의 다양한 위치에서 이루어진 부위 특이적 돌연변이를 수반한다. 일부 실시양태에서, 돌연변이체 키메라 폴리머라제는 상이한 폴리머라제에 상응하는 영역으로 치환된 2개 이상의 영역을 수반한 대다수의 서열을 포함한다. 예를 들어, 돌연변이체 키메라 폴리머라제 (606)는 치환된 엔테로코쿠스 파에시움 폴리머라제 TPR1, TPR2, 및 섬 서브 도메인을 갖는 Φ 29 폴리머라제 대다수의 서열을 포함하며, 폴리머라제 서열 내의 다양한 위치에서 이루어진 부위 특이적 돌연변이를 수반한다.

[0186] 표 5는 표 3으로부터 선택된 키메라 폴리머라제 변이체의 개요를 제공하고, 특별한 변이체가 되도록 이루어진 아미노산 돌연변이에 관한 설명과 함께 각각에 대한 대다수의 폴리머라제 서열을 제공한다.

[0187] <표 5>

[0188] 키메라 폴리머라제 - 부위 특이적 돌연변이체

명칭	대다수의 서열	설명
C004	C017	L259I, E264D, E269D, E276D, D277E, E293D
C005	C017	L259I, E264D, E269D, E276D, D277E, E288D, E293D, E319D, I320L, A321V, D322E
C006	C017	L259I, E264D, E269D, E276D, D277E, E288D, E293D, E319D, I320L, A321V, D322E L325I, N327Q, L330I, E331D, D338E, I345L, L348I, K351R, L356I
C007	C017	K15R, I37L, Q52N, I67L, K77R
C008	C017	K15R, I37L, Q52N, I67L, K77R, L259I, E264D, E269D, E276D, D277E, E288D, E293D, E319D, I320L, A321V, D322E L325I, N327Q, L330I, E331D, D338E, I345L, L348I, K351R, L356I
C009	C006	L259I, E264D, E269D, E276D, D277E, E288D, E293D, I320L, A321V, D322E, W324Y, L325V, S326T, V328I, E331D, M333I, D338E, I345L, K351R
C025	C017	I464V, D466E, V467A, K469E, D470H, I471L, P474S, K487Q, Y491F, L492I
C026	C017	I464V, D466E, V467A, K469E, D470H, I471L, K487Q, Y491F, L492I
C027	C017	M503V, R505K, K507R, G513C, D517E, Y518A, D520T, I521T
C028	C017	464-497 및 498-554 영역 내의 돌연변이

[0189]

[0190] 그러나, 다른 아미노산 돌연변이가 본원에 기재된 하나 이상의 키메라 폴리머라제 내로 혼입될 수 있다. 예를 들어, 하나 이상의 아미노산 변화가 Φ 29 폴리머라제 서열과 관련하여 위치 M8, V51, N62, I71, L107, 및/또는 K131 중 하나 이상, 및/또는 위치 K135, L142, G197, Y224, E239, V250, L253, Y281, I288, T301, R306, R308, D325, D341, K354, T368, E375, A437, A444, E466, D476, A484, E508, D510, K512, E515, K539, D570, 및 T571 중 하나 이상에 혼입될 수 있다. 예를 들어, 일부 실시양태에서, 키메라 폴리머라제는 또한, 하기 아미노산 치환: M8R, V51A, N62D, I71V, L107I, 및/또는 K131E 중 하나 이상, 및/또는 하기 아미노산 치환: K135Q, L142K, G197D, Y224K, E239G, V250A, V250I, L253A, L253H, Y281H, I288L, T301C, R306Q, R308L, D325E, D341E, K354R, T368F, E375Y, A437G, A444T, E466K, D476H, A484E, E508R, D510K, D510R, K512Y, E515Q, K539E, D570S, 및/또는 T571V 중 하나 이상을 포함할 수 있다.

[0191] 본원에 사용된 바와 같은 용어 "폴리머라제" 및 "중합 효소"는 일반적으로, 중합 반응을 촉매할 수 있는 임의의 효소를 지칭한다. 폴리머라제의 예는 DNA 폴리머라제, RNA 폴리머라제, 열 안정성 폴리머라제, 야생형 폴리머라제, 변형된 폴리머라제, 이. 콜라이 DNA 폴리머라제 I, T7 DNA 폴리머라제, 박테리오파지 T4 DNA 폴리머라제

φ29 (파이29) DNA 폴리머라제, Taq 폴리머라제, Tth 폴리머라제, Tli 폴리머라제, Pfu 폴리머라제, Pwo 폴리머라제, VENT® 폴리머라제, Deep VENT™ 폴리머라제, Ex TAQ™ 폴리머라제, LA TAQ™ 폴리머라제, Sso 폴리머라제, Poc 폴리머라제, Pab 폴리머라제, Mth 폴리머라제, ES4 폴리머라제, Tru 폴리머라제, Tac 폴리머라제, Tne 폴리머라제, Tma 폴리머라제, Tca 폴리머라제, Tih 폴리머라제, Tfi 폴리머라제, PLATINUM® Taq 폴리머라제, Tbr 폴리머라제, Tfl 폴리머라제, Tth 폴리머라제, PFUTURBO® 폴리머라제, PYROBEST™ 폴리머라제, Pwo 폴리머라제, KOD 폴리머라제, Bst 폴리머라제, Sac 폴리머라제, 클레노우 단편, 3'에서 5'로의 엑소뉴클레아제 활성을 지닌 폴리머라제, 및 그의 변이체, 변형된 산물 및 유도체를 포함하나, 이에 제한되지는 않는다. 일부 실시양태에서, 폴리머라제는 단일 서브유닛 폴리머라제이다. 폴리머라제의 부가의 예는 M2Y 폴리머라제, 루실리아 쿠프리나 폴리머라제, 엔테로코쿠스 파에시움 폴리머라제, 바실루스 파지 VMY22 폴리머라제, 바실루스 파지 GA-1 폴리머라제, 악티노마이세스 파지 AV-1 폴리머라제, 칸디다투스 모란박테리아(*Moranbacteria*) 폴리머라제, 바실루스 파지 MG-B1 폴리머라제, 에게르텔라 종 폴리머라제, 스트렙토코쿠스(*Streptococcus*) 파지 CP-7 폴리머라제, 박테로이데스 종(*Bacteroides sp.*) 폴리머라제, 클라미디아 트라코마티스(*Chlamydia trachomatis*) 폴리머라제, 및 글로보테라 팔리다(*Globodera pallida*) 폴리머라제를 포함한다. DNA 폴리머라제의 비-제한적 예 및 그의 특성은 특히, 문헌 [DNA Replication 2nd edition, Kornberg and Baker, W. H. Freeman, New York, N.Y. (1991)]에 상세히 기재되어 있다. 이러한 서열의 비-제한적 예는 표 1에서 찾을 수 있다 (서열식별번호: 1-19).

[0192] 표적 핵산의 핵 염기와 상보적인 dNTP 간의 염기쌍을 형성할 때, 폴리머라제는 새로이 합성된 가닥의 3' 히드록실 말단과 dNTP의 알파 포스페이트 간에 포스포디에스테르 결합을 형성함으로써 dNTP를 새로이 합성된 핵산 가닥 내로 혼입시킨다. 일부 실시양태에서, 폴리머라제는 높은 전진성을 지닌 폴리머라제이다. 그러나, 일부 실시양태에서, 폴리머라제는 감소된 전진성을 지닌 폴리머라제이다. 폴리머라제 전진성은 일반적으로, 핵산 주형을 방출하지 않고서도 dNTP를 핵산 주형 내로 연속적으로 혼입할 수 있는 폴리머라제의 능력을 지칭한다.

[0193] 일부 실시양태에서, 폴리머라제는 낮은 5'-3' 엑소뉴클레아제 활성 및/또는 3'-5' 엑소뉴클레아제를 수반한 폴리머라제이다. 일부 실시양태에서, 폴리머라제는 상응하는 야생형 폴리머라제와 비교하여 감소된 5'-3' 엑소뉴클레아제 활성 및/또는 3'-5' 활성을 갖는 것으로 변형된다 (예를 들어, 아미노산 치환에 의함). DNA 폴리머라제의 추가의 비-제한적 예는 9° NM™ DNA 폴리머라제 [뉴 잉글랜드 바이오랩스(New England Biolabs)], 및 클레노우 엑소-폴리머라제의 P680G 돌연변이체를 포함한다 (Tuske et al. (2000) JBC 275(31):23759-23768). 일부 실시양태에서, 감소된 전진성을 갖는 폴리머라제는 뉴클레오티드 반복 서열의 하나 이상의 연장물 (예를 들어, 동일한 유형의 2개 이상의 순차적 염기)을 함유하는 주형을 시퀀싱하기 위한 증가된 정확도를 제공한다.

[0194] 핵산 폴리머라제의 전진성, 엑소뉴클레아제 활성, 상이한 유형의 핵산에 대한 상대적 친화성, 또는 다른 특성은 상응하는 야생형 폴리머라제와 비교하여 돌연변이 또는 다른 변형에 의해 관련 기술분야의 통상의 기술자에 의해 증가되거나 또는 감소될 수 있다.

[0195] 일부 실시양태에서, 변형된 폴리머라제는 하나 이상의 비-자연 아미노산 치환을 포함한다. 본원에 사용된 바와 같은, "비-자연 아미노산"은 하기 20개의 유전적으로 코딩된 알파-아미노산 이외의 임의의 아미노산, 변형된 아미노산, 또는 아미노산 유사체를 지칭한다: 알라닌, 아르기닌, 아스파라긴, 아스파르트산, 시스테인, 글루타민, 글루탐산, 글리신, 히스티딘, 이소류신, 류신, 리신, 메티오닌, 페닐알라닌, 프롤린, 세린, 트레오닌, 트립토판, 티로신, 발린. 일부 실시양태에서, 비-자연 아미노산은 상기 20개의 알파-아미노산 이외의 자연 발생 화합물을 포함할 수 있다. 비-자연 아미노산 및 비-자연 아미노산을 단백질 서열 내로 혼입하는 방법은, 예를 들어, 미국 특허 번호 7,045,337 (그의 내용이 본원에 참조로 포함된다)에 기재된 바와 같이, 관련 기술분야에 공지되어 있다.

[0196] 본원에 기재된 바와 같은, 폴리머라제 및/또는 폴리머라제 서열은 이들이 공통 조상의 단백질 또는 단백질 서열로부터 자연적으로 또는 인공적으로 유래될 때 "상동"이다. 유사하게, 핵산 및/또는 핵산 서열은 이들이 공통 조상의 핵산 또는 핵산 서열로부터 자연적으로 또는 인공적으로 유래될 때 상동이다. 예를 들어, 임의의 자연 발생 핵산은 폴리펩티드 내의 소정의 위치에서 자연 발생하지 않는 아미노산을 코딩하는 적어도 하나의 특이적 코돈을 포함하도록 임의의 이용 가능한 돌연변이 유발 방법에 의해 변형될 수 있다. 발현될 때, 이와 같이 돌연변이 유발된 핵산은 하나 이상의 돌연변이된 아미노산을 포함하는 폴리펩티드를 코딩한다. 일부 실시양태에서, 상동성은 일반적으로, 2개 이상의 핵산 또는 단백질 (또는 그의 서열) 간의 서열 유사성으로부터 추론된다. 상동성 확립에 유용한 서열 간의 유사성의 정확한 백분율은 문제가 되는 핵산 및 단백질에 따라 다양하지만, 25% 정도의 서열 유사성이 상동성을 확립하는 데 일상적으로 사용된다. 더 높은 수준의 서열 유사성, 예를 들어, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% 또는 99% 또는 그 초과가 또한, 상동성을 확립하는 데 사용될 수

있다. 서열 유사성 백분율을 결정하는 방법은 관련 기술분야에 널리 공지되어 있다. 일부 실시양태에서, 유사성은, 예를 들어, 디폴트 파라미터를 사용하여, 예를 들어 BLASTP 및 BLASTN 알고리즘을 포함한, 상기 기재된 것과 같은 알고리즘을 사용하여 결정될 수 있다.

[0197] 일부 실시양태에서, 본 개시내용의 폴리머라제를 발현하기 위해, 이러한 폴리머라제를 코딩하는 DNA를 하나 이상의 발현 벡터 내로 삽입하여, 이와 같이 코딩된 폴리머라제가 전사 및 번역 제어 서열과 작동적으로 연결되도록 한다 [예를 들어, 미국 특허 번호 6,914,128 (그의 내용이 본원에 참조로 포함된다) 참조]. 이와 관련하여, 용어 "작동적으로 연결된"이란 폴리머라제를 코딩하는 서열이 벡터 내로 라이게이션되어 이러한 벡터 내에서의 전사 및 번역 제어 서열이 폴리머라제의 전사 및 번역을 조절하는 의도된 기능을 수행하도록 하는 것을 의미한다. 발현 벡터 및 발현 제어 서열은 사용된 발현 숙주 세포와 화합성이 되도록 선택된다. 폴리머라제-코딩 서열이 표준 방법 (예를 들어, 폴리머라제-코딩 서열 및 벡터 상의 상보적 제한 부위의 라이게이션, 및 제한 부위가 존재하지 않는 경우 평활 말단 라이게이션)에 의해 발현 벡터 내로 삽입된다.

[0198] 변형된 폴리머라제의 발현을 위하여, 변형된 폴리머라제를 코딩하는 발현 벡터를 표준 기술에 의해 숙주 세포 내로 형질감염시킬 수 있다. 용어 "형질감염"의 다양한 형태는 외인성 DNA를 원핵 또는 진핵 숙주 세포 내로 도입하는 데 흔히 사용되는 광범위한 기술, 예를 들어, 전기천공, 인산칼슘 침전, DEAE-덱스트란 형질감염 등을 포괄하는 것으로 의도된다. 본 개시내용의 폴리머라제를 발현하는 데 적합한 숙주 세포는 원핵 생물, 효모, 또는 고등 진핵 세포를 포함한다.

[0199] 이러한 목적에 적합한 원핵 생물은 유박테리아, 예컨대 그람 음성 또는 그람 양성 유기체, 예를 들어, 엔테로박테리아세아에(*Enterobacteriaceae*), 예컨대 에스케리키아(*Escherichia*), 예를 들어, 이. 콜라이, 엔테로박터(*Enterobacter*), 에르위니아(*Erwinia*), 클렙시엘라(*Klebsiella*), 프로테우스(*Proteus*), 살모넬라(*Salmonella*), 예를 들어, 살모넬라 티피무름(*Salmonella typhimurium*), 세라티아(*Serratia*), 예를 들어, 세라티아 마르세스칸스(*Serratia marcescans*), 및 시겔라(*Shigella*) 뿐만 아니라 바실루스, 예컨대 비. 서브틸리스(*B. subtilis*) 및 비. 리케니포르미스(*B. licheniformis*), 슈도모나스(*Pseudomonas*), 예컨대 피. 아에루기노사(*P. aeruginosa*), 및 스트렙토마이세스(*Streptomyces*)를 포함한다. 원핵 생물 이외에도, 진핵 미생물, 예컨대 섬유향상 진균 또는 효모가 폴리펩티드 코딩 벡터에 적합한 클로닝 또는 발현 숙주이다. 사카로마이세스 세레비시아에(*Saccharomyces cerevisiae*), 또는 일반 빵 효모가 하등 진핵 숙주 미생물 중에서 가장 흔히 사용되고 있다. 그러나, 수많은 다른 속, 종, 및 균주, 예컨대 시조사카로마이세스 폼베(*Schizosaccharomyces pombe*); 클루이베로마이세스(*Kluyveromyces*) 숙주, 예컨대, 예를 들어, 케이. 락티스(*K. lactis*), 케이. 프라길리스(*K. fragilis*), 케이. 불가리쿠스(*K. bulgaricus*), 케이. 위케라미이(*K. wickerhamii*), 케이. 왈티이(*K. waltii*), 케이. 드로소필라룸(*K. drosophilum*), 케이. 써모톨레란스(*K. thermotolerans*), 및 케이. 마르시아누스(*K. marxianus*); 피치아 파스토리스(*Pichia pastoris*); 칸디다(*Candida*); 트리코테르마 레에시아(*Trichoderma reesia*); 뉴로스포라 크라사(*Neurospora crassa*); 슈반니오마이세스(*Schwanniomyces*), 예컨대 슈반니오마이세스 옥시덴탈리스(*Schwanniomyces occidentalis*); 및 섬유향상 진균, 예컨대, 예를 들어, 뉴로스포라(*Neurospora*), 페니실륨(*Penicillium*), 톨리포클라디움(*Tolypocladium*), 및 아스페르길루스(*Aspergillus*) 숙주, 예컨대 에이. 니둘란스(*A. nidulans*) 및 에이. 니제르(*A. niger*)가 통상적으로 이용 가능하고 본원에 유용하다.

[0200] 일부 실시양태에서, 숙주 세포는 폴리머라제 생산을 위하여 상기 언급된 발현 또는 클로닝 벡터로 형질전환시키고, 프로모터를 유도하거나, 형질전환체를 선택하거나 또는 원하는 서열을 코딩하는 유전자를 증폭시키기 위해 적절하게 변형시킨 통상적인 영양 배지에서 배양한다. 폴리머라제를 생산하기 위해 사용되는 숙주 세포는 각종 배지에서 배양될 수 있다. 상업적으로 이용 가능한 배지, 예컨대 햄스(Ham's) F10™ [시그마(Sigma)], 최소 필수 배지™ (MEM) (시그마), RPMI-1640 (시그마), 및 돌베크 변형된 이글 배지™ (DMEM) (시그마)가 숙주 세포를 배양하는 데 적합하다. 배양 조건, 예컨대 온도, pH 등은 발현을 위해 선택된 숙주 세포를 이용하여 앞서 사용된 것이고, 관련 기술분야의 통상의 기술자에게 명백할 것이다.

[0201] 일부 실시양태에서, 폴리머라제 변이체는 세포 내에서, 세포질 주위 공간에서 생산되거나 또는 세포의 배지로 직접 분비될 수 있다. 폴리머라제 변이체가 세포 내에서 생산되는 실시양태에서, 숙주 세포 또는 용해된 세포 (예를 들어, 균질화로부터 생성됨)의 미립자 부스러기는 원심 분리 또는 한외 여과를 포함하지만 이에 제한되지는 않는 다양한 수단에 의해 제거될 수 있다. 폴리머라제가 배지 내로 분비되는 경우, 이러한 발현 시스템으로부터의 상등액은 상업적으로 이용 가능한 단백질 농축 필터를 사용하여 먼저 농축될 수 있으며, 그 후 하나 이상의 부가의 정제 기술을 수행할 수 있으며, 이는 단백질 친화성 크로마토그래피를 포함한 친화성 크로마토그래피, 이온 교환 크로마토그래피, 예컨대 음이온 또는 양이온 교환 크로마토그래피, 및 소수성 상호 작용 크로마

토그래피를 포함하지만, 이에 제한되지는 않는다.

- [0202] 일부 실시양태에서, 본 출원의 측면은 생물학적 샘플의 검정과 관계된 방법에 사용될 수 있다. 예시적인 실시양태에서, 본원에 제공된 방법은 샘플 내의 하나 이상의 핵산 또는 폴리펩티드의 서열을 결정하고/하거나 샘플 내의 하나 이상의 핵산 또는 폴리펩티드 변이체 (예를 들어, 관심 유전자 내의 하나 이상의 돌연변이)의 존재 또는 부재를 결정하기 위해 사용되는 기술에 유용하다. 일부 실시양태에서, 시험은 핵산 서열 정보를 제공하거나 또는 진단, 예후, 및/또는 치료 목적으로 하나 이상의 관심 핵산의 존재 또는 부재를 결정하기 위해 환자 샘플 (예를 들어, 인간 환자 샘플) 상에서 수행될 수 있다. 일부 예에서, 진단 시험은, 예를 들어 대상체의 생물학적 샘플 내의 무세포 DNA 분자 및/또는 발현 산물 (예를 들어, RNA)을 시퀀싱함으로써, 대상체의 생물학적 샘플 내의 핵산 분자를 시퀀싱하는 것을 포함할 수 있다. 예를 들어, 본 개시내용은 공동 계류중인 미국 특허 출원 번호: 14/543,865, 14/543,867, 14/543,888, 14/821,656, 14/821,686, 14/821,688, 15/161,067, 15/161,088, 15/161,125, 15/255,245, 15/255,303, 15/255,624, 15/261,697, 15/261,724, 62/289,019, 62/296,546, 62/310,398, 62/339,790, 62/343,997, 62/344,123, 및 62/426,144 (각각의 내용이 본원에 참조로 포함된다)에 기재된 기술에 유리하게 활용될 수 있는 방법 및 조성물을 제공한다.
- [0203] 본 출원의 일부 측면은 생물학적 중합체, 예컨대 핵산 및 단백질을 시퀀싱할 수 있는 기술에 유용하다. 일부 실시양태에서, 본 출원에 기재된 방법 및 조성물은 (예를 들어, 일련의 표지된 뉴클레오티드 또는 아미노산 단량체의 시간 과정에 따른 혼입을 검출함으로써) 핵산 또는 단백질 내로 혼입되는 일련의 뉴클레오티드 또는 아미노산 단량체를 확인해 주는 기술에 사용될 수 있다. 일부 실시양태에서, 본 출원에 기재된 방법 및 조성물은 중합 효소에 의해 합성된 주형 의존성 핵산 시퀀싱 반응 산물 내로 혼입되는 일련의 뉴클레오티드를 확인해 주는 기술 내로 혼입될 수 있다.
- [0204] 시퀀싱 동안, 중합 효소는 표적 핵산 분자 (예를 들어, 시퀀싱 주형의 핵산 분자)의 프라이밍 위치에 커플링 (예를 들어, 부착)될 수 있다. 프라이밍 위치는 표적 핵산 분자의 부분에 상보적인 프라이머를 포함할 수 있다. 대안으로서 프라이밍 위치는 표적 핵산 분자의 이중 가닥 절편 내에 제공되는 갭 또는 Nick(nick)이다. 갭 또는 Nick은 0 내지 적어도 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 또는 40개의 뉴클레오티드 길이일 수 있다. Nick은 이중 가닥 서열의 한 가닥에서 브레이크를 제공할 수 있으며, 이는 중합 효소, 예컨대, 예를 들어 가닥 치환 폴리머라제 효소를 위한 프라이밍 위치를 제공할 수 있다.
- [0205] 일부 경우에, 시퀀싱 프라이머는 고체 지지체에 고정화될 수 있거나 또는 고정화되지 않을 수 있는 표적 핵산 분자에 어닐링될 수 있다. 고체 지지체는, 예를 들어, 핵산 시퀀싱에 사용되는 통합 장치 상의 샘플 웰을 포함할 수 있다. 일부 실시양태에서, 시퀀싱 프라이머는 고체 지지체에 고정화될 수 있고, 표적 핵산 분자의 혼성화는 또한, 표적 핵산 분자를 고체 지지체에 고정화시킨다. 일부 실시양태에서, 폴리머라제는 고체 지지체에 고정화되고 가용성 프라이머 및 표적 핵산은 폴리머라제에 접촉된다. 그러나, 일부 실시양태에서, 폴리머라제, 표적 핵산 및 프라이머를 포함하는 복합체가 용액 중에 형성되고, 이러한 복합체는 (예를 들어, 폴리머라제, 프라이머, 및/또는 표적 핵산의 고정화를 통해) 고체 지지체에 고정화된다. 일부 실시양태에서, 샘플 웰 내의 어떠한 성분도 고체 지지체에 고정화되지 않는다. 예를 들어, 일부 실시양태에서, 폴리머라제, 표적 핵산, 및 프라이머를 포함하는 복합체가 용액 중에 형성되고, 이러한 복합체는 고체 지지체에 고정화되지 않는다.
- [0206] 적절한 조건 하에, 어닐링된 프라이머/표적 핵산에 접촉되는 폴리머라제 효소는 하나 이상의 뉴클레오티드를 프라이머 상에 부가하거나 혼입시킬 수 있으며, 뉴클레오티드는 프라이머에 5'에서 3'로의 주형 의존성 방식으로 부가될 수 있다. 이와 같이 뉴클레오티드를 (예를 들어, 폴리머라제의 작용을 통해) 프라이머 상으로 혼입하는 것은 일반적으로, 프라이머 연장 반응으로서 지칭될 수 있다. 각각의 뉴클레오티드는 핵산 연장 반응 동안 검출 및 확인될 수 있고 (예를 들어, 그의 발광 수명 및/또는 다른 특징에 기초한다), 연장된 프라이머 내로 혼입된 각각의 뉴클레오티드를 결정하고, 이에 따라 새로이 합성된 핵산 분자의 서열을 결정하는데 사용될 수 있는 검출 가능한 태그와 연합될 수 있다. 새로이 합성된 핵산 분자의 서열 상보성을 통해, 표적 핵산 분자의 서열을 결정할 수도 있다. 일부 경우에, 시퀀싱 프라이머를 표적 핵산 분자에 어닐링시키고 뉴클레오티드를 시퀀싱 프라이머에 혼입시키는 것은 유사한 반응 조건 (예를 들어, 동일하거나 또는 유사한 반응 온도) 또는 상이한 반응 조건 (예를 들어, 상이한 반응 온도)에서 발생할 수 있다. 일부 실시양태에서, 합성 방법에 의한 시퀀싱은 표적 핵산 분자의 집단 (예를 들어, 표적 핵산의 카피)의 존재 및/또는 표적 핵산의 집단을 달성하기 위한 표적 핵산의 증폭 단계를 포함할 수 있다. 그러나, 일부 실시양태에서, 합성에 의한 시퀀싱은 평가되는 각각의 반응에서 단일 분자의 서열을 결정하는데 사용된다 (그리고 핵산 증폭은 시퀀싱을 위한 표적 주형을 제조하는데 필요하지 않다). 일부 실시양태에서, 복수 개의 단일 분자 시퀀싱 반응은 본 출원의 측면에 따라서 병렬적으로 (예를 들어, 단일 통합 장치 상에서) 수행된다. 예를 들어, 일부 실시양태에서, 복수 개의 단일 분자 시퀀싱

반응은 통합 장치 상의 별도의 반응 챔버에서 각각 수행된다.

[0207] 일부 실시양태에서, 본 개시내용의 중합 효소는 상당히 작은 용적의 샘플 웰에서 시행되는 단일 분자 시퀀싱 반응에 유용하다. 예를 들어, 샘플 웰의 용적은 일부 구현에서 약 10^{-21} 리터 내지 약 10^{-15} 리터일 수 있다. 샘플 웰이 작은 용적을 갖기 때문에, 단일 샘플 이벤트 (예를 들어, 단일 분자 이벤트)의 검출이 달성 가능하다. 일부 실시양태에서, 표면 (예를 들어, 샘플 웰의 표면)은 본원에 기재된 폴리머라제를 수용하도록 설정된다. 일부 실시양태에서, 샘플 웰은 바닥면과 같은 샘플 웰의 표면 상에 배치될 수 있는 폴리머라제를 수용한다. 일부 실시양태에서, 샘플 웰은 통합 장치 내에 형성되며, 여기서 샘플 웰의 바닥면은 그것이 형성되는 통합 장치의 표면에 대해 원위이다.

[0208] 특정 실시양태에서, 본원에 기재된 기술은 샘플 웰에 부가될 수 있는 중합 효소, 및 그의 복합체에 관한 것이다. 일부 실시양태에서, 본원에 기재된 중합 효소는 샘플 웰의 표적 용적 (예를 들어, 반응 용적)에 한정될 수 있다. 일부 실시양태에서, 표적 용적은 샘플 웰 내의 영역이다. 하나 이상의 중합 효소가 바닥면 위에 고정화되어야 하는 실시양태에서, 하나 이상의 중합 효소 (예를 들어, 중합 효소 및 그의 복합체)의 부착을 허용하도록 바닥면을 기능화하는 것이 바람직할 수 있다. 일부 실시양태에서, 바닥면은 커플링 기를 포함하는 물질로 기능화된다. 예를 들어, 커플링 기는 화학적 모이어티, 예컨대 아민 기, 카르복실 기, 히드록실 기, 술폰히드릴 기, 금속, 킬레이트제 등을 포함할 수 있다. 또 다른 한편으로, 이들은 특이적 결합 요소, 예컨대 비오틴, 아비딘, 스트렙타비딘, 뉴트라비딘, 렉틴, SNAP-태그™ 또는 그에 대한 기질, 연합 또는 결합 펩티드 또는 단백질, 항체 또는 항체 단편, 핵산 또는 핵산 유사체 등을 포함할 수 있다. 부가적으로, 또는 또 다른 한편으로, 커플링 기는 일부 경우에 화학적 작용기와 특이적 결합 요소 둘 다를 포함할 수 있는 관심 분자 (예를 들어, 중합 효소 또는 그의 복합체)와 커플링 또는 결합하는데 사용되는 부가의 기와 커플링하기 위해 사용될 수 있다. 한 예로서, 커플링 기, 예를 들어, 비오틴은 기질 표면 상에 증착될 수 있고 소정의 영역에서 선택적으로 활성화될 수 있다. 이어서, 중간 결합제, 예를 들어, 스트렙타비딘이 제1 커플링 기와 커플링될 수 있다. 이러한 특별한 예에서 비오틴화될 것인 관심 분자 (예를 들어, 중합 효소 또는 그의 복합체)는 스트렙타비딘과 커플링된다. 일부 실시양태에서, 본원에 기재된 중합 효소는 폴리머라제를 표면 (예를 들어, 샘플 웰의 표면)에 고정화시키는 커플링 기와의 상호 작용을 형성할 수 있는 커플링 모이어티를 추가로 포함할 수 있다. 예를 들어, 일부 실시양태에서, 중합 효소는 아비딘 단백질과 결합할 수 있는 N-말단 또는 C-말단 비오틴화 서열을 포함한다. 일부 실시양태에서, 비오틴화 서열은 링커 서열을 추가로 포함한다. 예를 들어, 일부 실시양태에서, C-말단 링커/비오틴화 서열은 아미노산 서열 GGGSGGGSGGGSLNDFFEAQKIEWHE (서열식별번호: 517)을 포함한다.

[0209] 실시예

[0210] 실시예 1. 변형된 폴리머라제의 발현 및 평가

[0211] 재조합 폴리머라제 변이체는 이. 콜라이에서 발현되었고, 이를 His-스핀 컬럼을 사용하여 150 mL 규모의 배양물로부터 정제하였다. 단백질 순도는 SDS-PAGE에 이어 쿠마시 블루(Coomassie Blue) 염색함으로써 분석되었다 (도 7). 완충액 교환 및 단백질 농축 후, 30°C에서 30분 동안 트랩 체이스(trap chase)를 이용하여 dNTP의 존재하에 재조합 변이체를 활성화 및 전진성에 관하여 평가하였다. 키메라 폴리머라제 변이체 C017 및 C020은 트랩의 존재하에 활성화, 전진성, 및 합성 길이를 나타내었다. 변이체 폴리머라제에 의한 dNTP 유사체의 활용률을 측정하여 시퀀싱 반응에서의 폴리머라제의 적합성을 평가하였다. 상동 돌연변이체 변이체와 키메라 폴리머라제 변이체 둘 다는 dNTP의 활용률을 표시하였다. 단일 분자 시퀀싱으로부터의 결과가 하기 표 6에 제시된다.

[0212] <표 6>

[0213] 변형된 폴리머라제를 이용한 시퀀싱 결과

폴리머라제 (명칭)	판독물 수	판독물 길이	비율 (염기/s)	국소 염기 비율 (염기/s)	펄스 폭 (s)	인터 펄스 거리 (s)	정확도
Q001	90890	10205	1.82	2.41	0.07	0.36	80.9%
Q020	79366	7973	1.67	2.42	0.08	0.35	81.6%
Q035	96323	15532	2.05	3.04	0.13	0.21	88.7%
Q036	104352	8816	1.26	2.03	0.09	0.42	84.5%
C0138	16742	3486	1.47	2.30	0.11	0.34	71.4%
C0145	3982	6287	1.52	2.66	0.10	0.29	73.0%
C0173	3360	6125	1.59	2.52	0.11	0.30	70.0%
C0186	24165	11699	1.77	2.59	0.10	0.30	73.0%
C0189	60002	2880	1.77	2.47	0.11	0.32	85.2%
C0190	8729	4938	1.15	1.67	0.33	0.29	86.0%
C0239	36908	11226	1.39	1.79	0.32	0.25	84.7%
C0256	17700	14200	2.21	3.18	0.11	0.22	90.3%
C0263	9440	7640	1.96	2.81	0.10	0.27	84.4%
C0266	34395	10183	1.42	1.85	0.29	0.26	84.9%
C0267	811	6787	1.38	1.80	0.36	0.21	88.0%
C0268	23582	6638	1.47	1.95	0.27	0.26	80.7%
C0288	40472	3763	1.22	1.77	0.33	0.24	85.0%
C0289	37754	4895	1.71	2.63	0.14	0.26	85.1%
C0290	31770	4889	1.73	2.64	0.14	0.26	85.0%
C0295	36350	3110	1.48	1.99	0.21	0.31	86.1%
C0299	40027	3243	1.62	2.37	0.10	0.34	83.0%
C0303	28410	5605	1.25	1.76	0.30	0.29	85.2%
C0307	23243	3013	1.31	1.93	0.23	0.30	84.3%
C0313	1890	11676	1.41	1.87	0.29	0.26	81.9%
C0320	372	11679	1.53	2.09	0.27	0.22	87.5%
C0321	953	12311	1.3	1.75	0.31	0.27	83.9%
C0326	23	11907	2.01	2.81	0.11	0.26	77.6%
C0327	92	22355	2.12	2.93	0.09	0.27	69.5%
C0328	375	12911	1.64	2.52	0.1	0.31	81%
C0329	1409	19941	1.78	2.61	0.09	0.31	81.2%
C0333	828	20204	1.56	2.21	0.08	0.38	76.7%
C0334	859	7597	1.19	1.8	0.32	0.26	87%
C0335	664	22145	2.05	3.07	0.1	0.24	83%
C0337	943	16926	1.99	2.96	0.1	0.25	84%
C0338	511	13170	1.37	1.86	0.3	0.25	83.8%
C0352B	5269	13946	1.92	2.69	0.13	0.26	84.6%

[0214]

[0215] **등가물 및 범위**

[0216] 몇 가지 발명적 실시양태가 본원에 기재되고 예시되었지만, 관련 기술분야의 통상의 기술자는 기능을 수행하고/하거나 그 결과 및/또는 본원에 기재된 이점 중 하나 이상을 획득하기 위한 각종 다른 수단 및/또는 구조를 용이하게 구상할 것이며, 이러한 변이 및/또는 변형 각각은 본원에 기재된 발명적 실시양태의 범위 내에 있는 것으로 간주된다. 보다 일반적으로, 관련 기술분야의 통상의 기술자는 본원에 기재된 모든 파라미터, 치수, 물질, 및 입체 배치가 예시적인 것으로 의도되고 실제 파라미터, 치수, 물질, 및/또는 입체 배치가, 본 발명의 교시가 사용하는 특이적 적용(들)에 의존한다는 것을 용이하게 인지할 것이다. 관련 기술분야의 통상의 기술자는 단지 일상적인 실험을 사용하여, 본원에 기재된 특이적 발명적 실시양태에 대한 많은 등가물을 인식하거나 또는 확인할 수 있을 것이다. 따라서, 전술한 실시양태는 단지 한 예로서 제시되고, 첨부된 청구범위 및 그에 대한 등가물의 범위 내에서, 발명적 실시양태는 구체적으로 기재되고 청구된 것과 다르게 실시될 수 있다는 것을 이해해야 한다. 본 개시내용의 발명적 실시양태는 본원에 기재된 각각의 개별적인 특색, 시스템, 물품, 물질, 키트 및/또는 방법에 관한 것이다. 또한, 이러한 특색, 시스템, 물품, 물질, 키트 및/또는 방법이 서로 불일치하지 않는 경우, 이러한 특색, 시스템, 물품, 물질, 키트 및/또는 방법 중 2개 이상의 임의의 조합이 본 개시내용의 발명적 범위 내에 포함된다.

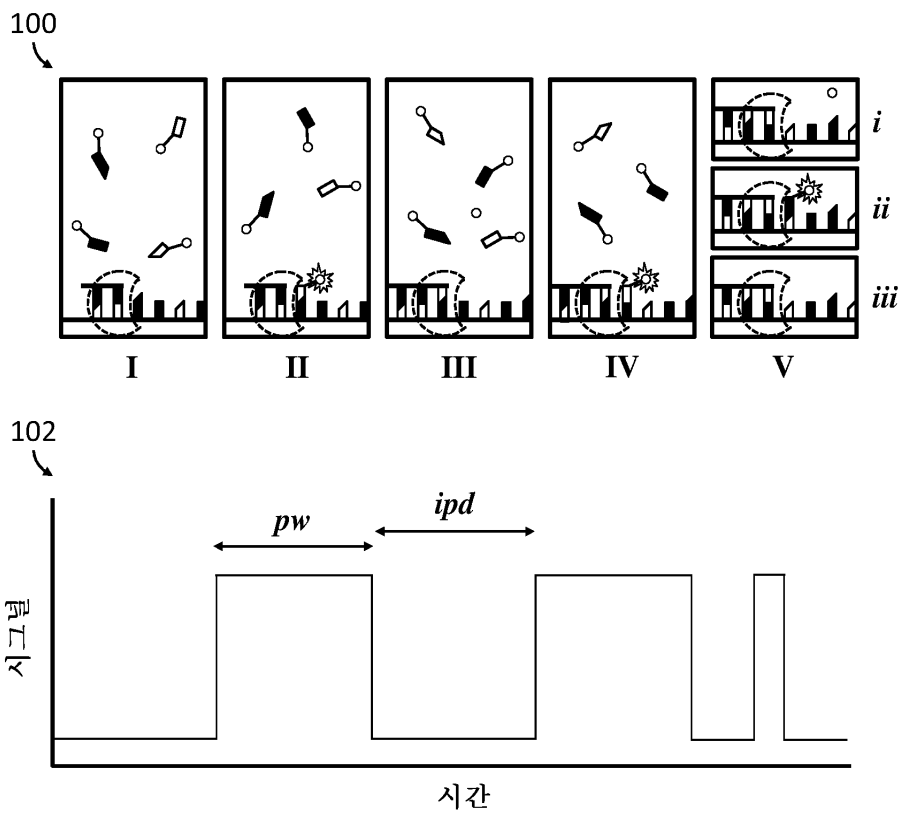
[0217] 본원에 정의되고 사용된 바와 같은 모든 정의가, 사전적 정의, 참조로 포함된 문헌에서의 정의, 및/또는 정의된

용어의 통상적인 의미에 비해 우선하는 것으로 이해되어야 한다.

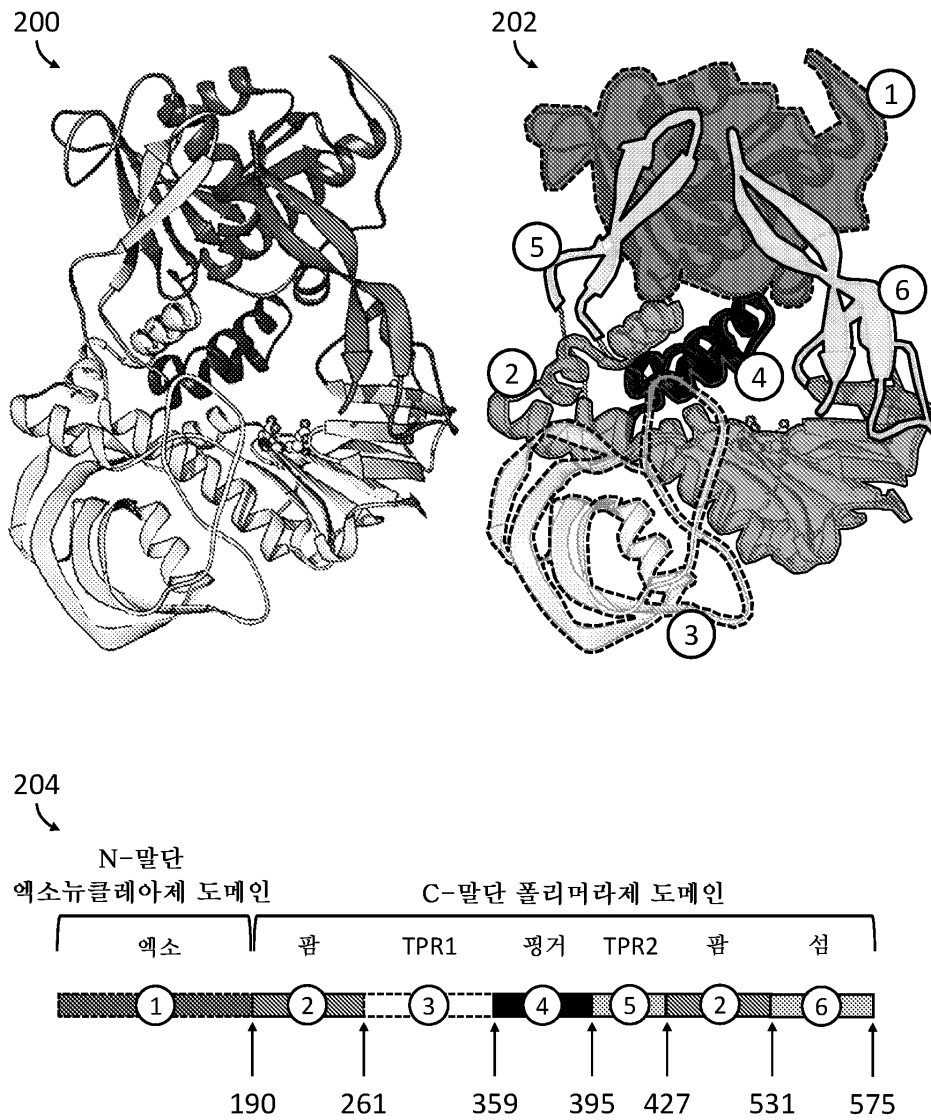
- [0218] 본원에 개시된 모든 참고 문헌, 특허 및 특허 출원은 각각이 인용되는 주제에 관해서 참조로 포함되며, 일부 경우에는 그 문서의 전체를 포괄할 수 있다.
- [0219] 본 명세서 및 청구범위에 사용된 바와 같은 단수 형태는 달리 명백하게 표시되지 않는 한, "적어도 하나"를 의미하는 것으로 이해되어야 한다.
- [0220] 본 명세서 및 청구범위에 사용된 바와 같은 문구 "및/또는"은, 이와 같이 결합된 요소 중 "어느 하나 또는 양쪽", 즉 일부 경우에는 결합적으로 존재하고 다른 경우에는 분리적으로 존재하는 요소를 의미하는 것으로 이해되어야 한다. "및/또는"으로 열거된 다수의 요소는 동일한 방식으로, 즉 결합된 요소 중 "하나 이상"으로 해석되어야 한다. 구체적으로 확인된 요소와 관련이 있거나 관련이 없든지 간에, "및/또는" 구절에 의해 구체적으로 확인된 요소 이외에 다른 요소가 임의로 존재할 수 있다. 따라서, 비-제한적 예로서, "포함하는" 것과 같이 제한을 두지 않은 언어와 연계해서 사용될 때, "A 및/또는 B"에 대한 언급은 한 실시양태에서 A 만을 지칭할 수 있고 (B 이외의 요소를 임의로 포함함); 또 다른 실시 양태에서, B 만을 지칭할 수 있으며 (A 이외의 요소를 임의로 포함함); 또한 또 다른 실시양태에서, A와 B 둘 다를 지칭할 수 있다 (다른 요소를 임의로 포함함).
- [0221] 본 명세서 및 청구범위에 사용된 바와 같은 "또는"은 상기 정의된 바와 같은 "및/또는"과 동일한 의미를 갖는 것으로 이해되어야 한다. 예를 들어, 목록에서 항목을 분리할 때, "또는" 또는 "및/또는"은 포괄적인 것으로 해석되어야 하는데, 즉 수많은 요소 또는 요소 목록, 및 임의로 부가의 목록에 없는 항목 중 적어도 하나뿐만 아니라 2개 이상을 포함한다. 그 반대로 명백하게 표시된 용어, 예컨대 "오직 하나" 또는 "정확히 하나", 또는 청구범위에서 사용되는 경우 "~로 이루어진"이란 용어만이 수많은 요소 또는 요소 목록 중 정확히 하나의 요소를 포함하는 것을 지칭할 것이다. 일반적으로, 본원에 사용된 바와 같은 용어 "또는"은 "어느 하나", "하나", "오직 하나" 또는 "정확히 하나"와 같이 배타적인 용어가 선행될 때, 배타적인 대안 (즉, "하나 또는 다른 것이지만, 둘 다가 아닌")을 표시하는 것으로 해석되어야 한다. 청구범위에서 사용될 때 "본질적으로 이루어지는"은 특허법 분야에서 사용된 바와 같은 그의 통상적인 의미를 지닐 것이다.
- [0222] 본 명세서 및 청구범위에 사용된 바와 같이, 하나 이상의 요소의 목록과 관련하여 "적어도 하나"라는 문구는 상기 요소의 목록 내의 임의의 하나 이상의 요소로부터 선택된 적어도 하나의 요소를 의미하는 것으로 이해되어야 하지만, 요소의 목록 내에 구체적으로 열거된 각각의 및 모든 요소 중 적어도 하나를 반드시 포함하지 않고, 요소의 목록 내의 요소의 임의의 조합을 배제하지 않는다. 이러한 정의는 또한, 구체적으로 확인된 요소와 관련이 있는지의 여부와 상관없이, "적어도 하나"라는 문구가 지칭된 요소 목록 내에서 구체적으로 확인된 요소 이외에 요소가 임의로 존재할 수 있게 해준다. 따라서, 비-제한적 예로서, "A와 B 중 적어도 하나" (또는 동등하게, "A 또는 B 중 적어도 하나" 또는 동등하게는 "A 및/또는 B 중 적어도 하나")는 한 실시양태에서, 적어도 하나, 임의로 2개 이상의 A를 포함하고, B가 존재하지 않은 것 (및 임의로 B 이외의 요소를 포함함)을 지칭할 수 있고; 또 다른 실시 양태에서, 적어도 하나, 임의로 2개 이상의 B를 포함하고, A가 존재하지 않은 것 (및 임의로 A 이외의 요소를 포함함)을 지칭할 수 있으며; 또한 또 다른 실시양태에서, 적어도 하나, 임의로 2개 이상의 A를 포함하고, 적어도 하나, 임의로 2개 이상의 B를 포함하는 것 (및 임의로 다른 원소를 포함함)을 지칭할 수 있다.
- [0223] 반대로 명확하게 표시되지 않는 한, 둘 이상의 단계 또는 동작을 포함하는 본원에 청구된 임의의 방법에서는, 그러한 방법의 단계 또는 동작의 순서가 반드시, 그 방법의 단계 또는 동작이 나열되는 순서로 제한되지 않는다는 것을 이해해야 한다.
- [0224] 청구범위뿐만 아니라 상기 명세서에서, "포함하는", "포함하는", "수반하는", "갖는", "함유하는", "포함하는", "보유하다", "구성된" 등과 같은 모든 이행 어구는 제한을 두지 않는 것으로, 즉 포함하나 이에 제한되지는 않는 것을 의미하는 것으로 이해되어야 한다. 이행 어구 "~로 이루어지는" 및 "본질적으로 ~로 이루어지는" 것만이 미국 특허청 특허 심사 절차 매뉴얼, 섹션 2111.03에 명시된 바와 같이, 각각 폐쇄 또는 반-폐쇄 이행 어구일 것이다. 제한을 두지 않은 이행 어구 (예를 들어, "포함하는")를 사용하여 본 명세서에 기재된 실시양태는 또한, 대안 실시양태에서 제한을 두지 않은 이행 어구에 의해 기재된 특색으로 "이루어진" 및 "본질적으로 이루어진" 것으로 고려된다. 예를 들어, 본 개시내용이 "A 및 B를 포함하는 조성물"을 기재하는 경우, 본 개시내용은 또한, 대안 실시양태에서 "A 및 B로 이루어진 조성물" 및 "본질적으로 A 및 B로 이루어진 조성물"을 고려한다.

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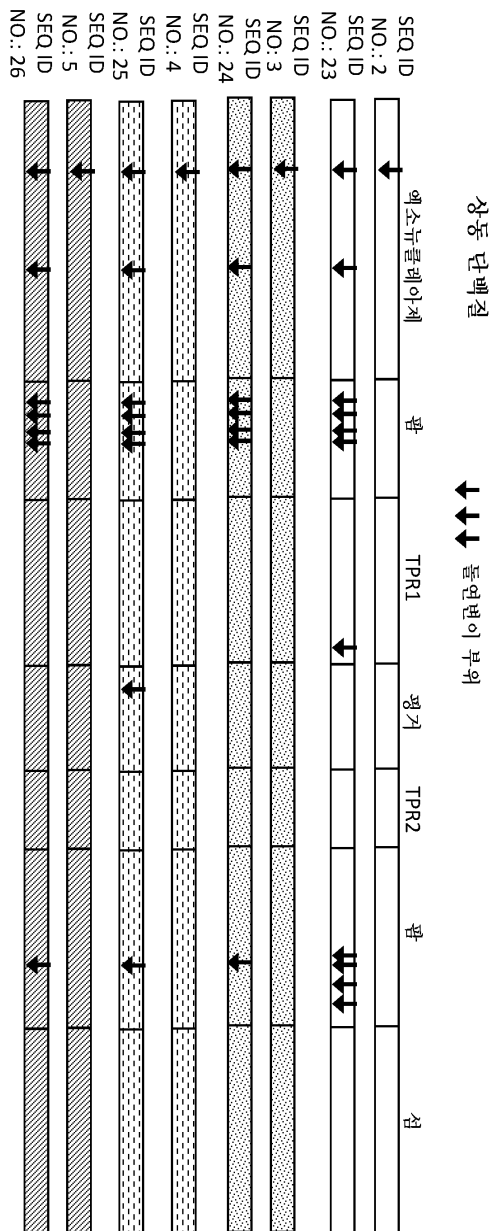
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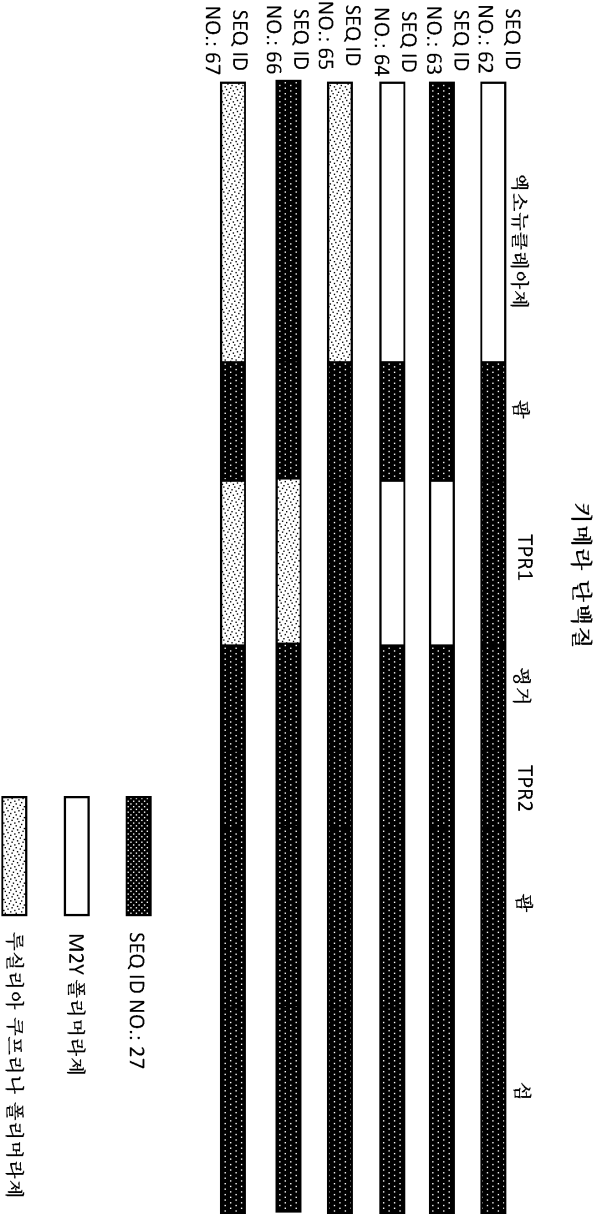
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도면3



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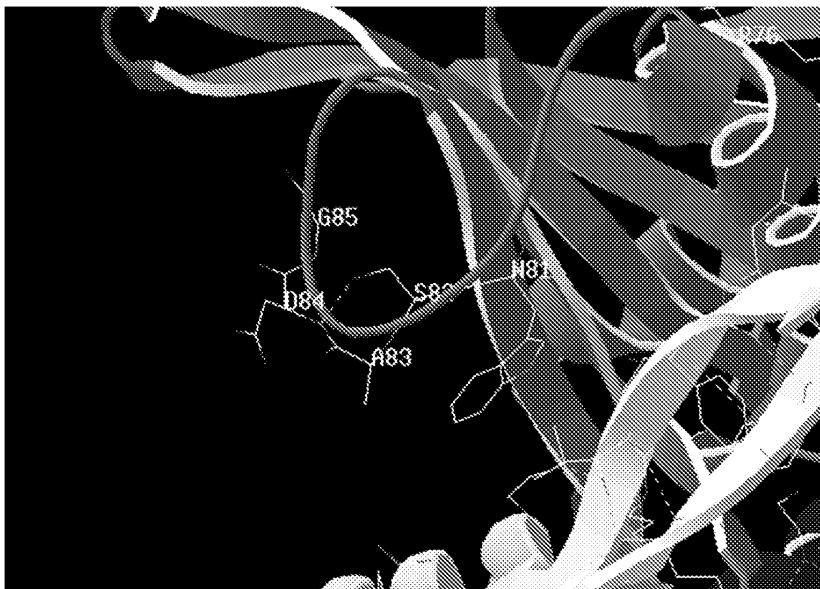


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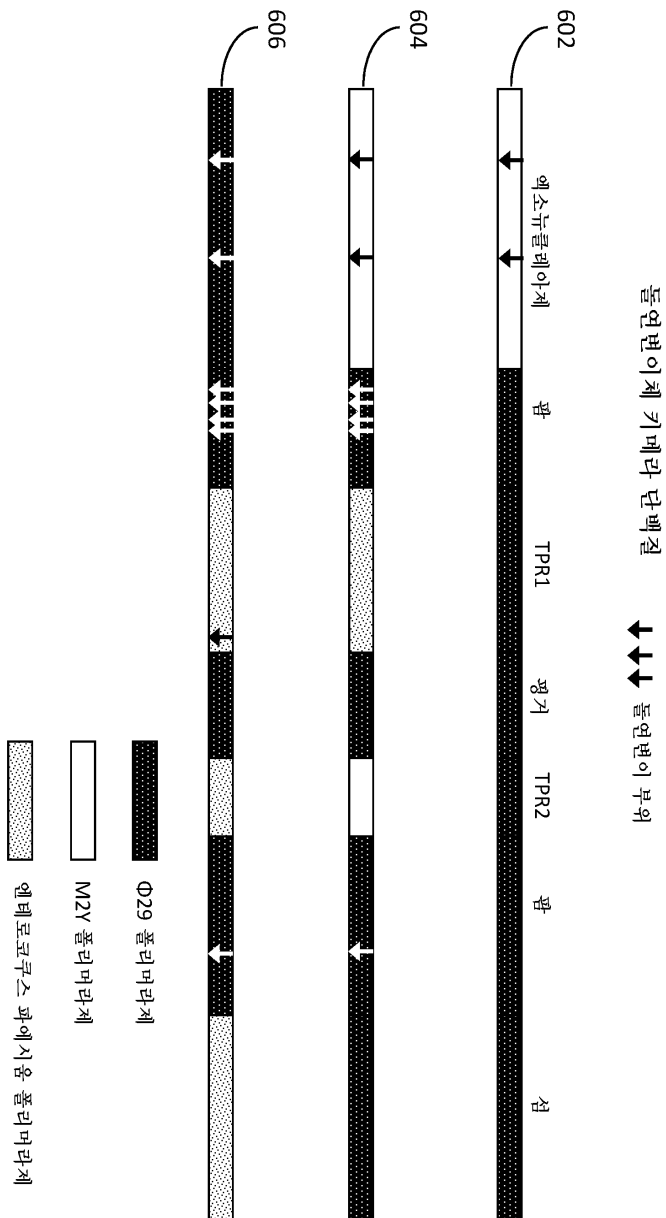
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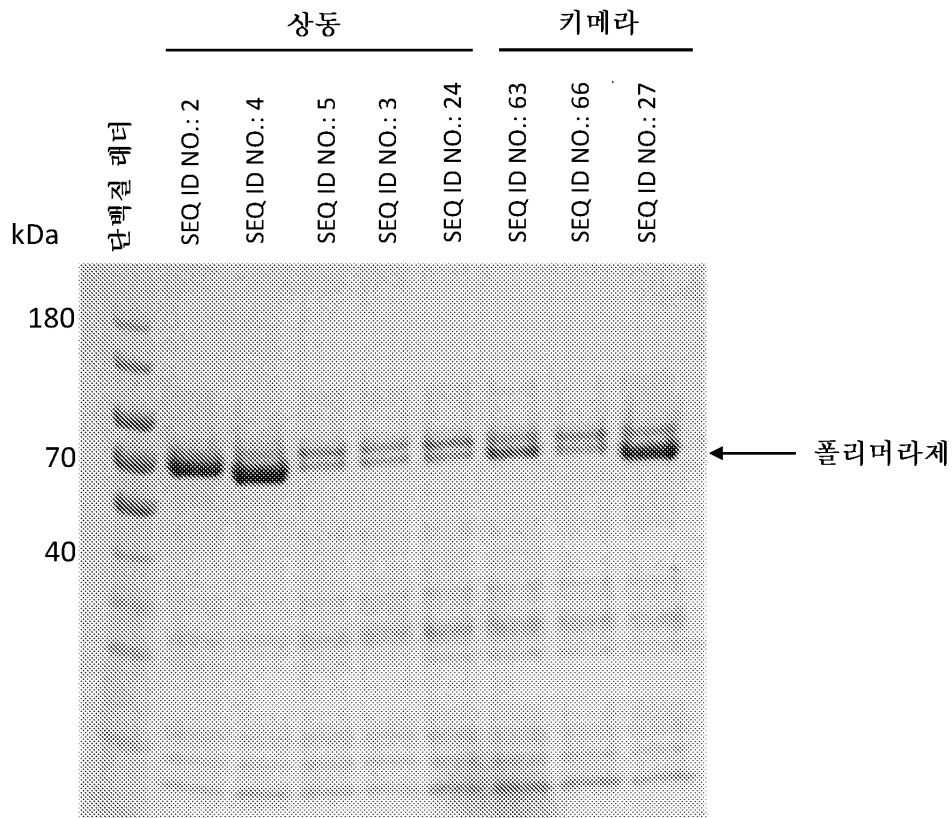
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도면6



도면7



서열 목록

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<151> 2016-12-19

<160> 539

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 Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
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 Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
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Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

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

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

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

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Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr

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

260 265 270

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu

275 280 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn

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

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 Ser Asp Phe Lys Thr Arg Lys Glu Phe Asn Asp Trp Lys Gln Lys Ile
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 Phe Arg Asn Tyr Gly Ser Lys Asn Glu Gly Gly Ile Asn Asp Glu Asp
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 Lys Leu Glu Glu Leu Asn Asn Thr Leu Asn Asp Tyr Phe Asn Glu Thr
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Thr Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Trp Met Glu

260 265 270

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

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Met Glu Trp Met Ile His Ser Ser Ser Arg Leu Tyr Phe His Asn Leu

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Lys Phe Asp Gly Ser Phe Ile Val Asn Trp Leu Leu His Asn Gly Tyr

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

325 330 335

Ser Lys Met Gly Gln Trp Tyr Gly Ile Thr Ile Cys Ser Gly Arg Asp

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

355 360 365

Pro Phe Pro Val Arg Lys Ile Gly Lys Asp Phe Lys Leu Asn Val Leu

370 375 380

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

385 390 395 400

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

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

420 425 430

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

435 440 445

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

450 455 460

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Pro Val Tyr Gly Thr

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

485 490 495

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Cys Ala Gly Met Pro Asp Asn Ile Lys Lys His Val Thr Phe Asp Asn
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Glu Trp Met Ile His Ser Ser Ser Arg Leu Tyr Phe His Asp Leu Lys
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Phe Asp Gly Ser Phe Ile Val Asn Trp Leu Leu His Asn Gly Tyr Thr
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Trp Thr Lys Arg Pro Ser Lys Glu Gly Gln Phe Ser Thr Leu Ile Ser
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Lys Met Gly Gln Trp Tyr Gly Ile Thr Ile Cys Ser Gly Arg Asp Gly
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Arg Lys Lys Lys Leu Thr Thr Ile His Asp Ser Leu Lys Lys Leu Pro
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 Lys Asp Ala Leu Asp Glu Phe Val Asn Met Ser Gly Lys Leu Tyr Glu
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 Lys Leu Phe Pro Val Phe Ser Leu Glu Leu Asn Glu Glu Ile Arg Lys
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 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Pro Val Tyr Gly Thr Lys
 225 230 235 240
 Lys Tyr Val Lys Asp Gly Ile Val Phe Asp Val Asn Ser Leu Tyr Pro
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 Ser Gln Met Tyr Asp Arg Asp Leu Pro Cys Gly Val Pro Ile Pro Phe
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 Glu Gly Glu Tyr Val Tyr Asp Lys Ser His Pro Leu Tyr Ile Gln Lys
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 Leu Thr Phe Glu Phe Glu Leu Lys Glu Asn Tyr Ile Pro Thr Ile Gln
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 Leu Lys Asn Ser Arg Phe Gly Phe Lys Gly Asn Glu Tyr Leu Ser Ser
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 Ser Asn Gly Glu Arg Ile Thr Ile Ser Val Ser Ser Val Asp Trp Glu
 325 330 335
 Leu Ile Arg Glu His Tyr His Val Tyr Asp Val Glu Phe Glu Lys Gly
 340 345 350
 Trp Lys Phe Arg Ser Thr Lys Gln Ala Phe Arg Gln Tyr Ile Asp Lys
 355 360 365
 Trp Met Leu Val Lys Asn Met Ser Ala Gly Ala Lys Lys Ala Ile Ala

370

375

380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Thr Asn Pro Asp

385 390 395 400

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

405 410 415

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

420 425 430

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

435 440 445

Lys Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Met His Leu

450 455 460

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

465 470 475 480

Val Leu Gly Tyr Trp Lys Lys Glu Gly Gln Phe Lys Gln Gly Lys Phe

485 490 495

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

500 505 510

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

515 520 525

Ile Cys Asp Lys Glu Glu Ser Asp Thr Thr Ile Ile Glu Ile Lys Cys

530 535 540

Ala Gly Met Pro Asp Asn Ile Lys Lys His Val Thr Phe Asp Asn Phe

545 550 555 560

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

565 570 575

Gly Gly Val Val Leu Val Glu Glu Thr Tyr Thr Met Lys

580 585

<210> 5

<211> 573

<212> PRT

<213> Enterococcus faecium

<400> 5

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

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
 245 250 255
 Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
 260 265 270
 Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
 275 280 285
 Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
 290 295 300
 Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
 305 310 315 320
 Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
 325 330 335
 Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
 340 345 350
 Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
 355 360 365
 Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
 370 375 380
 Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
 385 390 395 400
 Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
 405 410 415
 Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
 420 425 430
 Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
 435 440 445
 Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
 450 455 460
 Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
 465 470 475 480
 Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu

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

545 550 555 560
 Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
 565 570

<210> 6

<211> 592

<212> PRT

<213> Bacillus phage VMY22

<400> 6

Met Ala Thr Lys Lys Arg Lys Ala Tyr Ser Cys Asp Phe Glu Ala Thr
 1 5 10 15
 Thr Ser Thr Tyr Ser Glu Thr Glu Thr Arg Val Trp Ala Tyr Gly Trp
 20 25 30

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

Ile Ser Lys Gly Gly Gln Trp Tyr Lys Ile Ala Ile His His Glu Gly
 100 105 110
 Lys Gly Thr Thr Gln Ile Phe Asp Ser Leu Lys Lys Leu Pro Phe Pro
 115 120 125

Val Lys Thr Ile Ala Lys Ala Phe Lys Leu Pro Val Leu Lys Gly Asp
130 135 140

Ile Asp Tyr Asn Leu His Arg Asp Glu Asn His Val Ile Thr Ser Glu
145 150 155 160

Glu Phe Thr Tyr Ile Lys His Asp Ile Glu Ile Val Ala Arg Ala Leu
165 170 175

Asp Ile Gln Ile Asn Gln Gln Gly Leu Val Lys Met Thr Asn Gly Ala
180 185 190

Asp Ser Met Asp His Phe Ile Lys Ser Leu Asp Lys Lys Lys Lys Val
195 200 205

Ala Glu Arg Ile Tyr Asn Gln Tyr Phe Pro Lys Met Ser Ile Ala Met
210 215 220

Asp Ser Ile Phe Arg Lys Ala Tyr Arg Gly Gly Phe Thr Trp Val Asn
225 230 235 240

Pro Lys Phe Lys Gly Gln Glu Val Gly Glu Gly Met Val Phe Asp Val
245 250 255

Asn Ser Leu Tyr Pro Ser Val Met Tyr Tyr Lys Pro Leu Pro Trp Gly
260 265 270

Lys Pro Val Pro Phe Val Gly Lys Tyr Glu Glu Asp Pro Asp Phe Pro
275 280 285

Leu Tyr Ile Cys His Ile Lys Thr Gly Phe Val Leu Lys Glu Gly His
290 295 300

Ile Pro Thr Ile Gln Ile Lys Lys Asn Pro Ile Phe Gln Glu Asn Glu
305 310 315 320

Tyr Leu Glu Thr Ser Gly Gly Ala Pro Val Asp Leu His Val Thr Asn
325 330 335

Val Asp Leu Glu Leu Ile Lys Glu His Tyr Glu Leu Tyr Asp Thr Glu
340 345 350

Tyr Val Gly Gly Trp Lys Phe Arg Gln Gln Thr Gly Ile Phe Asn Asn
355 360 365

Phe Ile Asp Tyr Trp Met Lys Ile Lys Thr Asp Pro Lys Ser Thr Pro

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

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

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

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

 <210> 7
 <211> 578
 <212> PRT
 <213> Bacillus phage GA-1
 <400> 7

Met Ala Arg Ser Val Tyr Val Cys Asp Phe Glu Thr Thr Thr Asp Pro

1 5 10 15

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

20 25 30

Asp Lys Trp Ser Tyr Gly Glu Asp Ile Asp Ser Phe Met Glu Trp Ala

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

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

115 120 125

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

130 135 140

Asp Ile Asp Tyr Lys Lys Tyr Arg Pro Val Gly Tyr Val Met Asp Asp

145 150 155 160

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

165 170 175

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

180 185 190

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

195 200 205

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

210 215 220

Ala Tyr Lys Gly Gly Phe Thr Trp Val Asn Pro Lys Tyr Gln Gly Glu

225 230 235 240

Thr Val Tyr Gly Gly Met Val Phe Asp Val Asn Ser Met Tyr Pro Ala

245 250 255
 Met Met Lys Asn Lys Leu Leu Pro Tyr Gly Glu Pro Val Met Phe Lys

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

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

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

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

Val Arg Gln Lys Thr Tyr Phe Ile Glu Thr Thr Trp Lys Glu Asn Asp
500 505 510
Lys Gly Lys Leu Val Val Cys Glu Pro Gln Asp Ala Thr Lys Val Lys
515 520 525
Pro Lys Ile Ala Cys Ala Gly Met Ser Asp Ala Ile Lys Glu Arg Ile
530 535 540
Arg Phe Asn Glu Phe Lys Ile Gly Tyr Ser Thr His Gly Ser Leu Lys
545 550 555 560
Pro Lys Asn Val Leu Gly Gly Val Val Leu Met Asp Tyr Pro Phe Ala
565 570 575
Ile Lys

<210> 8

<211> 566

<212>

> PRT

<213> Actinomyces phage AV-1

<400> 8

Met Val Arg Gln Ser Thr Ile Ala Ser Pro Ala Arg Gly Gly Val Arg
1 5 10 15
Arg Ser His Lys Lys Val Pro Ser Phe Cys Ala Asp Phe Glu Thr Thr
20 25 30
Thr Asp Glu Asp Asp Cys Arg Val Trp Ser Trp Gly Ile Ile Gln Val
35 40 45
Gly Lys Leu Gln Asn Tyr Val Asp Gly Ile Ser Leu Asp Gly Phe Met
50 55 60
Ser His Ile Ser Glu Arg Ala Ser His Ile Tyr Phe His Asn Leu Ala
65 70 75 80
Phe Asp Gly Thr Phe Ile Leu Asp Trp Leu Leu Lys His Gly Tyr Arg
85 90 95
Trp Thr Lys Glu Asn Pro Gly Val Lys Glu Phe Thr Ser Leu Ile Ser
100 105 110

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

115 120 125

Arg Val Glu Phe Arg Asp Ser Phe Lys Lys Leu Pro Met Ser Val Ser

130 135 140

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

145 150 155 160

Tyr Glu Lys Pro Arg Pro Ile Gly Tyr Ile Pro Thr Glu Gln Glu Lys

165 170 175

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

180 185 190

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

195 200 205

Ala Thr Tyr Lys Lys Met Thr Gly Lys Leu Phe Ile Arg Arg Phe Pro

210 215 220

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

225 230 235 240

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

245 250 255

Gly Ser Val Tyr Asp Val Asn Ser Leu Tyr Pro Ser Val Met Arg Thr

260 265 270

Ala Leu Leu Pro Tyr Gly Glu Pro Ile Tyr Ser Glu Gly Ala Pro Arg

275 280 285

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

290 295 300

Lys Pro Asn His Ile Pro Cys Ile Gln Ile Lys Lys Asn Leu Ser Phe

305 310 315 320

Asn Pro Thr Gln Tyr Leu Glu Glu Val Lys Glu Pro Thr Thr Val Val

325 330 335

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

340 345 350

Ile Tyr Ser Trp Asn Gly Thr Phe Glu Phe Arg Gly Ser His Gly Phe

355 360 365
Phe Asp Thr Tyr Val Asp His Phe Met Glu Ile Lys Lys Asn Ser Thr

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

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

500 505 510
Gly Lys Leu Asp Val His Ile Ala Gly Met Pro Arg Asn Val Ala Ala
515 520 525
Thr Leu Thr Leu Glu Asp Met Leu His Gly Gly Thr Trp Asn Gly Lys
530 535 540
Leu Ile Pro Val Arg Val Pro Gly Gly Thr Val Leu Lys Asp Thr Thr
545 550 555 560
Phe Thr Leu Lys Ile Asp
565

<210> 9

<211> 593

<212> PRT

<213> Candidatus Moranbacteria

<400> 9

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Met Lys Leu Lys Ser Lys Tyr Val Ala Asp Phe Glu Ala Thr Gly Glu
1           5           10          15
Glu Gln Tyr Lys Ile Asp Gly Ser Thr His Val Trp Ala Val Gly Val
          20          25          30
Ile Asp Ile Glu Thr Glu Glu Thr Val Leu Ile Ser Asn Asp Ile Ala
          35          40          45
Asp Phe Met Asn Trp Leu Ser Lys Asp Asn His Asn His Lys Asn Lys

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

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

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

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

245 250 255

Ser Tyr Asp Lys Asn Ser Met His Pro Ser Gln Met Lys Asn Met Pro

260 265 270

Met Pro Tyr Gly Ile Pro Val Tyr Tyr Glu Gly Glu Tyr Lys Asn Asp

275 280 285

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

290 295 300

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

305 310 315 320

Ala Thr Thr Glu Phe Leu Glu Asp Thr Lys Gly Glu Pro Ile Gln Leu

325 330 335

Phe Val Thr Ser Ile Asp Leu Met Leu Ile Leu Glu His Tyr Asp Ile

340 345 350

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

355 360 365

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

370 375 380

Thr Gly Pro Leu Arg Glu Ile Ala Lys Leu Met Leu Asn Asn Leu Tyr

385 390 395 400

Gly Lys Phe Gly Thr Asn Pro Ile Arg Ala Arg Lys Glu Pro Ile Tyr

405 410 415

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

420 425 430

Asp Ala Val Tyr Ile Pro Met Ala Cys Phe Ile Thr Ala Tyr Ser Arg

435 440 445

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

450 455 460

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

465 470 475 480

Glu Ala Gln Ile Glu Val His Asp Thr Lys Ile Gly Ala Trp Lys Tyr

485 490 495
Glu Gly Thr Ala Lys Met Phe Lys Ala Leu Arg Pro Lys Thr Tyr Ala

500 505 510
Tyr Ile Asp Glu Asn Asp Glu Leu Asp Val Lys Cys Ala Gly Leu Pro

515 520 525
Lys Lys Ala Lys Lys Asp Ile Thr Phe Asp Thr Phe Gln Tyr Gly Phe

530 535 540
Val Ser Lys Glu Lys Leu Glu Ile Lys Arg Val Lys Gly Gly Thr Ile

545 550 555 560
Leu Leu Lys Thr Lys Phe Glu Ile Lys Lys Gln Val Asp Asn Lys His

565 570 575
Ile Asp Thr Glu Tyr Phe Glu Asp Glu Asp Ile Asp Ile Phe Asn Gln

580 585 590
Leu

<210> 10

<211> 669

<212> PRT

<213> Bacillus phage MG-B1

<400> 10

Met Lys Lys Lys Arg Thr Lys Thr Lys Ile Lys Thr Tyr Ala Cys Asp

1 5 10 15

Phe Glu Thr Asn Thr Glu Ala Trp Leu His Glu Asp Lys Leu Arg Asp

20 25 30

Glu Leu Lys Thr Lys Glu Glu Asn Pro Glu Leu Trp Arg Lys Arg Glu

35 40 45

Ala Trp Lys Leu His Thr Gly Gly Asp Lys Ala Phe Val Trp Ser Trp

50 55 60

Gly Gly Thr Glu Ile Arg Glu Asp Met Ser Phe Lys Gly Glu Leu Asp

65 70 75 80

Asn Phe Val Val Gly Lys Gly Ile Ser Glu Tyr Val Asp Trp Met Leu

85	90	95
Asp Gly Ser Lys Asn Val Trp Phe His Asn Leu Lys Phe Asp Gly Ser		
100	105	110
Phe Ile Ala Val Glu Leu Leu Arg Arg Gly Phe Lys Phe Thr Phe Asp		
115	120	125
Arg Asn Pro Ala Ile Gly Glu Phe Thr Gly Leu Ile Asp Gly Lys Lys		
130	135	140
Met Trp Phe Glu Leu Ile Ile Cys Lys Glu Gly Lys Arg Gly Gly Arg		
145	150	155
Gln Phe Ile Thr Ile Lys Asp Ser Leu Lys Lys Val Pro Phe Gly Leu		
165	170	175
Arg Val Ala Ala Met Ala Phe Gly Leu Asp Val Phe Lys Asp Asp Met		
180	185	190
Asp Tyr Asp Val Ile Arg Glu Pro Phe Glu Pro Ile Gly Glu Ala Asp		
195	200	205
Tyr Lys Tyr Leu Lys Lys Asp Val Glu Ile Thr Ala Lys Ile Ile His		
210	215	220
Tyr Gln Val Phe Gln Ser Gly Leu Lys Lys Thr Thr Ile Gly Ser Asp		
225	230	235
Ala Leu Asn Glu Phe Lys Ser Thr Val Gly Gly Asp Lys Gly Phe Lys		
245	250	255
Glu Ile Phe Pro Val Met Asp Phe Asp Thr Asp Ser Phe Ile Arg Lys		
260	265	270
Ser Tyr Phe Gly Gly Val Thr Gln Val Lys Pro Gly Met Glu Gly Lys		
275	280	285
Leu Ile Gly Glu Gly Ser Val Phe Asp Ile Val Ser Met Tyr Pro Trp		
290	295	300
Val Gln Tyr Thr Lys Leu Leu Pro Tyr Gly Leu Pro Ile Glu Tyr Asn		
305	310	315
Gly Glu Tyr Thr Tyr Asp Glu Glu Tyr Pro Leu Tyr Val Gln Gln Val		
325	330	335

Ser Phe Ser Phe Val Val Lys Asp Asn Met Leu Pro Thr Ile Gln Leu
340 345 350

Lys Lys Gln Asn Val Glu Phe Asn Tyr Asn Glu Ala Asp Asp Val Arg
355 360 365

Lys Phe Asn Gly Arg Glu Phe Gln Lys Thr Ser Tyr Gly Glu Ile Val
370 375 380

Thr Met Tyr Val Thr Asn Val Gln Trp Glu Gln Ile Gln Lys His Tyr
385 390 395 400

Trp Leu Asp Asp Leu His Phe His Lys Gly Met Met Phe Lys Gly Lys
405 410 415

Ile Gly Leu Phe Lys Glu His Ile Asp Lys Trp Leu Lys Val Lys Lys
420 425 430

Gln Ala Asn Asp Asp Gly Asn Asp Ala Leu Lys Ser Leu Ala Lys Leu
435 440 445

Met Leu Asn Ser Pro Tyr Gly Lys Phe Gly Thr Asn Thr Ile Arg Leu
450 455 460

Asn Val Glu Pro Phe Leu Trp Glu Asp Asp Glu Ser Leu Gly Phe Arg
465 470 475 480

Val Glu Asp Asp Asp Pro Pro Pro Ala Asp Pro Ile Tyr Thr Ala Tyr
485 490 495

Ala Ser Phe Val Thr Ala Tyr Ala Arg Glu Glu Leu Val Ser Thr Ile
500 505 510

Met Met Cys Tyr Asp Arg Phe Val Tyr Cys Asp Thr Asp Ser Ile His
515 520 525

Leu Ile Gly Thr Glu Ile Pro Glu Gly Ile Lys His Lys Ile Gly Gly
530 535 540

Asp Leu Gly Asp Trp Glu Pro Glu Ser Glu Phe Lys Leu Ala Lys Phe
545 550 555 560

His Arg Ala Lys Thr Tyr Cys Glu Met Val Tyr Ala Lys Lys Val Met
565 570 575

Lys Lys Asp Arg Trp Gly Asp Val Val Glu Ser Leu Lys His Cys Ser

580 585 590
Lys Glu Glu Trp Gly Thr Leu Pro Gln Asp Gln Lys Thr Leu Asp Lys
595 600 605

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

<210> 11

<211> 572

<212> PRT

<213> Eggerthella sp.

<400> 11

Met Asn Glu Tyr Ile Ser Asp Phe Glu Thr Gln Lys Asp Pro Asp Thr
1 5 10 15
Gly Val Met Ser Val Trp Ala Trp Ser Ile Val Asp Val Asn Asp Leu
20 25 30
Ser Asn Ile Gln Tyr Gly Asn Asn Ile Glu Ser Trp Leu Ser Ala Ile
35 40 45
Gln Gly Leu Pro Asn Gly Ser Leu Ile Gly Phe His Asn Leu Lys Phe

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

115	120	125	
Val Ser Gln Ile Ala Lys Ser Phe Gly Ile Lys Glu Gln Lys Gly Ser			
130	135	140	
Ile Asp Tyr Ala Ile Phe Arg Gly Tyr Asn Tyr Thr Met Thr Pro Lys			
145	150	155	160
Glu Val Glu Tyr Ile Thr Asn Asp Val Lys Ile Val Ala Lys Ala Ile			
165	170	175	
Lys Gln Phe Arg Asn Glu Gly His Glu Arg Asn Thr Ile Ala Ser Asn			
180	185	190	
Ala Met Arg Tyr Tyr Lys Lys Asn Ser Tyr Tyr Ser Asn Tyr Glu Phe			
195	200	205	
Leu Thr Tyr Phe Pro His Leu Asp Asp Asp Leu Tyr His Leu Leu Lys			
210	215	220	
Arg Ala Tyr Lys Gly Gly Tyr Cys Tyr Val Asn Pro Lys Phe Lys Gly			
225	230	235	240
Lys Pro Val Gly His Gly Arg Val Tyr Asp Val Asn Ser Leu Tyr Pro			
245	250	255	
Ser Val Met Ser Asp Pro Gln Asn Lys Tyr Pro Ile Gly Thr Pro Val			
260	265	270	
Phe Phe Glu Gly Lys Tyr Lys Asp Asp Pro Ile Tyr Pro Leu Tyr Ile			
275	280	285	
Gln Phe Ile Thr Ala Gln Phe Glu Leu Lys Lys Gly Lys Ile Pro Thr			
290	295	300	
Ile Gln Ile Lys Asn Asp Lys Arg Phe Asn Pro Arg Glu Tyr Val Thr			
305	310	315	320
Ser Thr Gly Cys Leu Met Val Asn Leu Tyr Leu Thr Asn Val Asp Leu			
325	330	335	
Glu Met Phe Tyr Glu Cys Tyr Asn Ile Lys Glu Ile Gln Tyr Ile Gly			
340	345	350	
Gly Tyr Lys Phe Ile Gly Arg Ser Gly Ile Phe Ile Asp Tyr Val Asn			
355	360	365	

His Phe Lys Glu Met Lys Met Gln Ala Thr Ile Glu Lys Asn Ala Gly

370 375 380

Lys Arg Ser Ile Ala Lys Leu Phe Leu Asn Ser Leu Tyr Gly Lys Phe

385 390 395 400

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

405 410 415

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

420 425 430

Val Tyr Val Pro Val Ala Ala Phe Val Thr Ala Tyr Ala Arg Arg Phe

435 440 445

Ile Gln Thr Leu Phe Ile Lys Asn Val Asp Arg Cys Cys Tyr Cys Asp

450 455 460

Thr Asp Ser Leu His Leu Ile Gly Asp Asp Pro Pro Glu Gly Val Lys

465 470 475 480

Ile Ser Asp Thr Glu Phe Asn Cys Met Ala His Glu Ser Ser Phe Ser

485 490 495

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

500 505 510

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

515 520 525

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

530 535 540

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

545 550 555 560

Ser Thr Phe Lys Ile Arg Glu Arg Gly Thr Arg Phe

565 570

<210> 12

<211> 568

<212> PRT

<213> Streptococcus phage CP-7

<400> 12

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

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

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

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

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

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

Ile Arg Glu Thr Asp Tyr Leu Val
565

<210> 13

<211> 616

<212> PRT

<213> Bacteroides sp.

<400> 13

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

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

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

130	135	140	
Thr Lys His Arg Lys Leu Glu Met Glu Tyr Ile Gly Met Arg His Ala			
145	150	155	160
Asn Cys Glu Ile Thr Pro Glu Glu Tyr Ala Tyr Ile Ile Asn Asp Ile			
	165	170	175
Tyr Val Leu Lys Glu Ala Leu Glu Val Met Ile Lys Ser Gly His Asp			
	180	185	190
Lys Leu Thr Ile Gly Ser Cys Cys Met Asp Glu Phe Lys Asn Lys Phe			
	195	200	205
Asp Ala Met Asp Phe Lys Ala Ala Phe Pro Asn Leu Lys Glu Ile Ala			
	210	215	220
Leu Ile Lys Tyr Glu Leu Gly Ser Asp Asn Val Asp Gln Tyr Ile Arg			
225	230	235	240
Lys Ala Tyr Lys Gly Gly Tyr Cys Tyr Tyr Lys Tyr Lys Gln Arg Lys			
	245	250	255
His Ile Thr Gln Asn Gly Met Thr Phe Asp Val Asn Ser Leu Tyr Pro			
	260	265	270
Ser Val Met His Ser Lys Ser Gly Asn Tyr Tyr Pro Thr Gly Lys Pro			
	275	280	285
Ile Phe Phe Glu Lys Ala Ile Pro Tyr Lys Cys Leu Glu Ala Arg Val			
	290	295	300
Tyr Pro Phe Tyr Val Arg Leu Arg Cys Arg Phe Lys Leu Lys Asp Gly			
305	310	315	320
Phe Leu Pro Thr Val Gln Ile Lys Gly Asp Tyr Lys Tyr Asn Ser Thr			
	325	330	335
Gln Trp Leu Glu Thr Ser Asp Ile Tyr Tyr Arg Gly Lys Tyr Tyr Arg			
	340	345	350
Tyr Phe Thr Asn Lys Glu Gly Gln Lys Glu Glu Ala Arg Pro Glu Leu			
	355	360	365
Thr Leu Phe Met Thr Asp Tyr Leu Leu Leu Leu Glu His Tyr Asp Val			
	370	375	380

Tyr Asp Leu Glu Ile Leu Asp Gly Cys Tyr Phe His Gly Ala Ile Gly
 385 390 395 400
 Leu Phe Asp Thr Tyr Ile Asp His Tyr Met Lys Ile Lys Met Thr Thr
 405 410 415
 Lys Asp Lys Gly Glu Arg Thr Glu Ala Lys Leu Phe Leu Asn Asn Leu
 420 425 430

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

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

 Ile Lys Cys Ala Gly Met Pro Glu Lys Ser Lys Lys Leu Phe Leu Ala
 565 570 575
 Ser His Pro Ile Thr Asp Phe Lys Ile Gly Leu Lys Val Gly Gly Lys
 580 585 590
 Leu Lys Pro Lys Tyr Ile Ser Gly Gly Met Val Leu Val Glu Asp Phe
 595 600 605
 Tyr Thr Leu Arg Ala Lys Arg Cys
 610 615

<210> 14

<211> 641

<212> PRT

<213> Chlamydia trachomatis

<400> 14

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

1 5 10 15

Val Phe Lys Gly Gln Thr Phe Thr Glu Val Trp Ser Ala Cys Phe Cys

20 25 30

Glu Leu Tyr Lys Lys Asp Ala Lys Ile Met His Ser Ile Gln Asp Phe

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Val Arg Trp Leu Glu Thr Lys Asp Met Lys Asn Asn Ser Ile Lys Tyr

100 105 110

Ser Ile Ser Glu Met Gly Gln Trp Tyr Tyr Ile Ile Ile Lys Lys Asn

115 120 125

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

130 135 140

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

145 150 155 160

Met Lys Tyr Glu Gly Tyr Arg Tyr Ala Gly Cys Glu Ile Thr Pro Glu

165 170 175

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

180 185 190

Glu Ile Met Phe Asn Glu Lys His Glu Ser Leu Thr Ile Gly Ser Cys

195 200 205

Cys Leu Asn Glu Tyr Lys Thr Ile Met Thr Lys Phe Leu Ile Glu Arg

210 215 220

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

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

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

 Leu Ile Lys Glu His Tyr Asn Leu Val Asp Phe Glu Ile Leu Asp Gly
 385 390 395 400
 Cys Tyr Phe Asp Lys Glu Ile Gly Leu Phe Asp Glu Tyr Ile Asn Lys
 405 410 415
 Tyr Lys Lys Ile Lys Leu Asn Ser Lys Gly Ala Lys Lys Thr Leu Ala
 420 425 430
 Lys Leu Tyr Leu Asn Asn Leu Tyr Gly Lys Thr Ala Thr Asn Thr Asp
 435 440 445

 Ser Ser Phe Lys Val Ala Tyr Ile Lys Asp Asp Leu Ser Leu Gly Phe
 450 455 460
 Tyr Gly Val Tyr Ala Cys Asp Lys Lys Pro Phe Tyr Ile Pro Val Gly

465 470 475 480
 Ser Ala Ile Thr Ser Tyr Ala Arg Asn Phe Thr Ile Arg Ala Ala Gln
 485 490 495
 Lys Asn Tyr Lys Asn Phe Ile Tyr Ala Asp Thr Asp Ser Ile His Cys
 500 505 510

 Lys Cys Asn Pro Ala Glu Ile Lys Gly Ile Thr Ile Asp Asp Lys Lys
 515 520 525
 Phe Leu Cys Trp Lys Leu Glu Ser Cys Trp Asp Lys Gly Leu Phe Val
 530 535 540
 Arg Gln Lys Thr Tyr Ile Glu His Ile Thr Ala Glu Asn Leu Lys Pro
 545 550 555 560
 Ile Asp Lys Pro Phe Tyr Asn Val Lys Cys Ala Gly Met Pro Glu Gln
 565 570 575

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

Met

<210> 15

<211> 574

<212> PRT

<213> Globodera pallida

<400> 15

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

Val Trp Ser Trp Gly Leu Cys Ser Val Glu Asn Thr Glu Asn Val Glu
35 40 45
Phe Gly Gly Asp Leu Asp Ser Phe Ile Glu Arg Ile Ser Glu Glu Asn
50 55 60
Ser Ile Thr Phe Phe His Asn Leu Lys Phe Asp Gly Ala Phe Ile Leu
65 70 75 80
Asp Arg Leu Phe Arg Leu Gly Tyr Glu Phe Thr Asp Glu Lys Ala Pro
85 90 95
Gln Val Lys Glu Phe Ser Thr Leu Ile Ser Lys Met Gly Gln Phe Tyr
100 105 110
Ser Ile Lys Val Arg Trp Glu Asn Gly Met Phe Thr Glu Phe Arg Asp
115 120 125
Ser Leu Lys Lys Leu Pro Met Ser Val Lys Gln Val Ala Lys Thr Phe
130 135 140
Lys Leu Asp Gln Ala Lys Gly Glu Ile Asp Tyr His Tyr Leu Arg Pro
145 150 155 160
Val Gly Trp Val Met Thr Pro Glu Glu Arg Glu Tyr Val Lys Asn Asp
165 170 175
Val Gln Ile Val Ala Arg Ala Leu Lys Val Gln Leu Gln Glu Gly Met
180 185 190
Thr Arg Leu Thr Val Gly Ala Asp Ser Leu Ala Gln Tyr Lys Ser Met
195 200 205
Met Gly Lys Asp Phe Glu Arg His Phe Pro Val Leu Thr Arg Thr Ile
210 215 220
Asp Ala Glu Ile Arg Arg Ala Tyr Arg Gly Gly Trp Ala Tyr Ala Asp
225 230 235 240
Glu Arg His Arg Gly Lys Val Val Gly Ala Gly Gln Thr Phe Asp Val
245 250 255
Asn Ser Leu Tyr Pro Ser Val Met Tyr Ser Lys Val Leu Pro Tyr Gly
260 265 270
Glu Pro Val Phe Tyr Pro Asn Gly Leu Pro Glu Val Thr Glu Asp His

275 280 285
 Pro Leu Phe Ile Thr Cys Ile Thr Phe Thr Ala Lys Ile Arg Asp Gly
 290 295 300
 His Leu Pro Cys Ile Gln Ile Lys Asn Ser Ser Leu Phe Thr Pro Thr

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

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

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

 500 505 510
 Glu Leu Met Thr Gly Glu Phe His Val Lys Ser Lys Cys Glu Cys Asp
 515 520 525

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

565 570

<210> 16

<211> 584

<212> PRT

<213> Globodera sp.

<400> 16

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

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

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

165 170 175
 Val Gln Ile Val Ala Arg Ala Leu Lys Val Gln Leu Gln Glu Gly Met
 180 185 190
 Thr Arg Leu Thr Val Gly Ala Asp Ser Leu Ala Gln Tyr Lys Ser Met
 195 200 205
 Met Gly Lys Asp Phe Glu Arg His Phe Pro Val Leu Thr Arg Thr Ile
 210 215 220
 Asp Ala Glu Ile Arg Arg Ala Tyr Arg Gly Gly Trp Ala Tyr Ala Asp
 225 230 235 240

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

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

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

Asp Ile Val Arg Leu Ile Glu Gly Pro Pro Asp Glu Arg Asn Pro Val
420 425 430

Tyr Thr Ala Met Gly Val Phe Ile Thr Ser Tyr Ala Arg Asp Leu Thr
435 440 445

Ile Arg Thr Ala Gln Asp His Tyr Asp Arg Phe Leu Tyr Ala Asp Thr
450 455 460

Asp Ser Leu His Leu Leu Thr Ser Asp Gly Thr Asn Asn Gly Arg Lys
465 470 475 480

Ser Lys Ala Leu Glu Val His Pro Ser Lys Leu Gly Tyr Trp Lys His
485 490 495

Glu Tyr Asp Phe Asp Ala Gly Leu Phe Val Arg Ala Lys Ala Tyr Thr
500 505 510

Glu Leu Met Thr Gly Glu Phe His Val Lys Ser Lys Cys Glu Cys Asp
515 520 525

Thr Pro Asn Asp Leu His Tyr Gln Thr His Ile Ala Gly Met Pro Glu
530 535 540

Ala Ile Ala Gln His Ile Thr Phe Glu Ser Tyr Arg Asp Gly Ala Thr
545 550 555 560

Phe Glu Gly Lys Leu Ala Pro Gln Arg Val Pro Gly Gly Ile Val Leu
565 570 575

Val Asp Asp Thr Phe Thr Ile Lys
580

<210> 17

<211> 548

<212> PRT

<213> *Lynx pardinus*

<220><221> misc_feature

<222> (339)..(374)

<223> Xaa can be any naturally occurring amino acid

<400> 17

Met Pro Ser Tyr Thr Ala Asp Phe Glu Thr Thr Thr Val Ala Asp Asp
1 5 10 15

Cys Arg Val Trp Ala Trp Ala Thr Ser Arg Ile Gly Asn Pro Asp Asp
 20 25 30
 Val Gln Leu Gly Asn Ser Ile Asp Thr Phe Leu Glu Trp Cys Arg Val
 35 40 45
 His Ser Gly Ser Arg Val Tyr Phe His Asn Leu Lys Phe Asp Gly Lys
 50 55 60
 Phe Ile Leu His Lys Ile Leu Thr Asp Gly Trp Lys Trp Ile Pro Asp
 65 70 75 80
 Lys Asn Asp Cys Ala Asn Arg Thr Phe Thr Thr Leu Ile Ser Asp Met
 85 90 95
 Ser Gln Phe Tyr Ser Ile Lys Leu Trp Phe Asp Glu Ser Lys Ser Ile
 100 105 110
 Glu Phe Leu Asp Ser Leu Lys Val Ile Pro Leu Pro Ile Ala Ala Ile
 115 120 125
 Pro Lys Ala Phe Gly Leu Glu Ile Glu Lys Leu Asp Leu Asp Tyr Gln
 130 135 140
 Ala Ser Arg Glu Val Gly His Glu Leu Thr Glu Asp Glu Lys Glu Tyr
 145 150 155 160
 Ile Ala His Asp Val Lys Ile Ala Ala Met Ala Met Asp Thr Met Phe
 165 170 175
 Ser Gln Gly Met Lys Lys Ile Thr Ala Gly Ser Asn Ala Phe Ala Asp
 180 185 190
 Tyr Lys Lys Thr Ile Gly Gly Lys Lys Arg Phe Arg Asp Trp Phe Pro
 195 200 205
 Glu Pro Glu Tyr Asp Glu Asp Leu Arg Lys Gly Gly Cys Tyr Lys Gly
 210 215 220
 Gly Phe Thr Ala Val Asn Pro Lys Ile Ala Gly Lys Lys Leu Gly Lys
 225 230 235 240
 Gly Val Ser Phe Asp Val Asn Ser Leu Tyr Pro Ser Val Met Ala Ser
 245 250 255
 Ser His Gly Glu Val Leu Pro Tyr Gly Glu Pro Ile Pro Tyr Asp Gly

260 265 270
 Gly Tyr Glu Gln Asp Glu Asp His Pro Leu Tyr Ile Gln Phe Ile Glu

 275 280 285
 Ala Asp Phe Ala Val Lys Glu Asn Arg Ile Pro Cys Leu Gln Leu Lys
 290 295 300
 Gly Asn Val Met Phe Gly Glu Thr Glu Tyr Ile Arg Asp Ser Lys Gly
 305 310 315 320
 Met Gln Thr Leu Cys Leu Thr Ser Val Asp Met Glu Met Leu Phe Glu
 325 330 335
 His Tyr 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 Arg Thr Ile Ala Lys Leu Gln Leu Asn Ser
 370 375 380
 Leu Phe Ala Ala Asn Pro Val Lys Gln Ser Arg Met Pro Tyr Leu Asp
 385 390 395 400
 Glu Gly Ile Val Lys Tyr Ala Leu Leu Glu Pro Glu His Ala Glu Ala

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

 465 470 475 480
 Cys Phe Lys Ala Ile Arg Ala Lys Thr Tyr Cys Phe Glu Glu Asp Gly
 485 490 495
 Glu Leu Thr Val His Cys Ala Gly Met Pro Ala Arg Cys His Glu His
 500 505 510

Val Thr Met Asp Asn Phe Glu Val Gly Ala Ser Phe Pro Gly Lys Leu
515 520 525
Lys Pro Lys Asp Val Asn Gly Gly Thr Ile Leu Val Glu Asp Val Phe
530 535 540
Thr Ile Arg Pro
545
<210> 18
<211> 611
<212> PRT
<213> Enterococcus faecium (SK)
<400> 18
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30
Asn Ile Thr Phe Gly Leu Asp Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Ser Lys
65 70 75 80
Glu Thr Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95
Gln Trp Tyr Ala Leu Glu Ile Cys Trp Glu Val Asn Tyr Thr Thr Thr
100 105 110
Lys Ser Gly Lys Thr Lys Lys Glu Lys Val Arg Thr Ile Ile Tyr Asp
115 120 125
Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Gln Ile Ala Glu Ala Phe
130 135 140
Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145 150 155 160

Val Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp

165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu

180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Lys Asp Trp

195 200 205

Leu Lys Ala Thr His Gly Lys Ser Thr Phe Lys Gln Trp Phe Pro Ile

210 215 220

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

225 230 235 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Asp Gly

245 250 255

Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg

260 265 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Pro

275 280 285

Asn Asn Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg

290 295 300

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

305 310 315 320

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

325 330 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Glu Leu Phe

340 345 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met

355 360 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile

370 375 380

Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly

385 390 395 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr

405 410 415
Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu

420 425 430
Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe

435 440 445
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys

450 455 460
Phe Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Val Gly

465 470 475 480
Thr Asp Val Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys Leu

485 490 495
Gly Tyr Trp Gly His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg

500 505 510
Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys

515 520 525
Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe

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

545 550 555 560
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His

565 570 575
His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser

580 585 590
Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu

595 600 605
Trp His Glu

610

<210> 19

<211> 646

<212> PRT

<213> Bacillus phage Harambe

<400> 19

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Met Gly Asn Lys Lys Arg Lys Ile Tyr Ser Cys Asp Phe Glu Thr Thr
1           5           10           15
Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Leu Met Glu Ile
           20           25           30
Asp Gly Lys Phe Glu Asn Tyr Lys Glu Gly Asn Asn Ile Asp Glu Phe
           35           40           45
Met Glu Trp Thr Glu Gln Glu Gln Gly Asp Leu Tyr Phe His Asn Leu

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

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

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

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

245 250 255

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

260 265 270

Tyr Gly Leu Pro Val Pro Phe Ser Gly Glu Tyr Glu Tyr Asp Glu Thr

275 280 285

His Pro Leu Phe Ile Gln His Ile Lys Cys Gly Phe Glu Leu Lys Asp

290 295 300

Gly His Ile Pro Thr Ile Gln Ile Lys Lys Asn Phe Arg Phe Ala Asp

305 310 315 320

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

325 330 335

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

340 345 350

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

355 360 365

Lys Asn Tyr Ile Asp Tyr Trp Ser Asp Lys Lys Ile Asn Ala Glu Asp

370 375 380

Pro Ala Ile Arg Gln Met Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly

385 390 395 400

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

405 410 415

Glu Asp Gly Ser Thr Gly Phe Arg Lys Gly Gln Lys Glu Glu Arg Asp

420 425 430

Pro Val Tyr Met Pro Met Gly Ala Phe Ile Thr Ala Tyr Ala Arg Asp

435 440 445

Val Thr Ile Arg Thr Ala Gln Lys Cys Tyr Asp Arg Ile Leu Tyr Cys

450 455 460

Asp Thr Asp Ser Ile His Leu Val Gly Thr Glu Ile Pro Glu Ala Ile

465 470 475 480

Lys Asp Arg Ile His Asp Lys Lys Leu Gly Tyr Trp Ala His Glu Ser

485 490 495
Thr Phe Trp Arg Ala Lys Phe Ile Arg Gln Lys Thr Tyr Ile Glu Asp

500 505 510
Leu Cys Met Arg Phe Glu Gly Glu Lys Val Asn Gly Glu Trp Lys Phe

515 520 525
Lys Met Val Glu Glu Lys Asp Ile Thr Lys Ala Thr Ala Arg Glu Leu

530 535 540
Ser Val Lys Cys Ala Gly Met Pro Ala Gln Val Lys Gln Tyr Val Thr

545 550 555 560
Phe Asp Asn Phe Gly Val Asp Phe Lys His Asp Pro Asn Asp Tyr Thr

565 570 575
Asp Glu Glu Ile Lys Arg Lys Asn Ile Lys Phe Lys Leu Lys Pro Thr

580 585 590
His Arg Lys Gly Gly Gln Val Leu Val Pro Thr Pro Phe Thr Ile Lys

595 600 605
Gly His His His His His His His His His His Gly Gly Gly Ser Gly

610 615 620
Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln

625 630 635 640
Lys Ile Glu Trp His Glu

645

<210> 20

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 20

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

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

130 135 140

Ile His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

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

165 170 175

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

180 185 190

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

195 200 205

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

210 215 220

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

225 230 235 240

Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr

245 250 255

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

260 265 270

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu

275 280 285
Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn

290 295 300
Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
305 310 315 320

Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
325 330 335

Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
340 345 350

Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Val Lys

355 360 365
Thr His Glu Glu Gly Ala Lys Lys Gln Leu Ala Lys Leu Met Leu Asn

370 375 380
Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val

385 390 395 400
Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly Phe Arg Val Gly Asp Glu

405 410 415
Glu Tyr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala

420 425 430
Trp Ala Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg

435 440 445
Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val

450 455 460
Pro Glu Ile Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp

465 470 475 480
Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr

485 490 495
Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp Gly Lys Leu Lys Glu

500 505 510
Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala

515 520 525

Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Ala
530 535 540
Val Gly Phe Ser Ser Met Gly Lys Pro Lys Pro Val Gln Val Asn Gly
545 550 555 560
Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570
<210> 21
<211> 572
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 21
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125
Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140
Ile His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

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

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

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

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

Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly Phe Arg Val Gly Asp Glu
405 410 415

Glu Tyr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
420 425 430

Trp Ala Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
435 440 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
450 455 460

Pro Glu Ile Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465 470 475 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
485 490 495

Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp Gly Lys Leu Lys Glu
500 505 510

Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
515 520 525

Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Ala
530 535 540

Val Gly Phe Ser Ser Met Gly Lys Pro Lys Pro Val Gln Val Asn Gly
545 550 555 560

Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 22

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 22

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

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

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

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

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

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

Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu

275 280 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn

290 295 300

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

305 310 315 320

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

325 330 335

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

340 345 350

Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Val Lys

355 360 365

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

370 375 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val

385 390 395 400

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

405 410 415

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

420 425 430

Trp Ala Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg

435 440 445

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

450 455 460

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

465 470 475 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr

485 490 495

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

500 505 510

Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala

515 520 525
Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Ala

530 535 540
Val Gly Phe Ser Ser Met Gly Lys Pro Lys Pro Val Gln Val Asn Gly
545 550 555 560
Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 23

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 23

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

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140

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

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

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

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

385 390 395 400

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

405 410 415

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

420 425 430

Trp Ala Arg Phe Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg

435 440 445

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

450 455 460

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

465 470 475 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr

485 490 495

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

500 505 510

Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala

515 520 525

Gly Met Thr Asp Thr Ile Lys Lys Lys Val Thr Phe Asp Asn Phe Ala

530 535 540

Val Gly Phe Ser Ser Met Gly Lys Pro Lys Pro Val Gln Val Asn Gly

545 550 555 560

Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 24

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 24

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

1 5 10 15

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

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

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

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

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

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

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

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

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

515 520 525
Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
530 535 540
Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 25

<211> 573

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic polypeptide

<400> 25

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

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

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

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

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

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

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

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

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

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
 515 520 525
 Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
 530 535 540
 Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
 545 550 555 560
 Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
 565 570

<210> 26

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 26

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
 1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
 20 25 30
 Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
 35 40 45
 Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
 50 55 60
 Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
 85 90 95
 Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
 100 105 110
 Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
 115 120 125
 Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
 130 135 140
 Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Ile Thr Lys Glu Arg Pro
 145 150 155 160
 Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
 165 170 175
 Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
 180 185 190
 Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
 195 200 205
 Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
 210 215 220
 Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
 225 230 235 240
 Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
 245 250 255
 Ile Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg

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

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

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

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

 500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
 515 520 525
 Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
 530 535 540
 Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
 545 550 555 560
 Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys

565 570

<210> 27

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 27

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45

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

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
 115 120 125
 Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
 130 135 140

Ile His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
 165 170 175

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

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

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

Thr His Glu Tyr Gly Ala Lys Lys Gln Leu Ala Lys Leu Met Leu Asn
 370 375 380
 Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val

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

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

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

Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
 565 570

<210> 28

<211> 589

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 28

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

20 25 30
 Gly Lys Thr Ser Asn Tyr Lys Ile Gly Thr Asp Phe Asn Glu Phe Met

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

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

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

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

Glu Gly Glu Tyr Val Tyr Asp Lys Ser His Pro Leu Tyr Ile Gln Lys
 275 280 285
 Leu Thr Phe Glu Phe Glu Leu Lys Glu Asn Tyr Ile Pro Thr Ile Gln
 290 295 300
 Leu Lys Asn Ser Arg Phe Gly Phe Lys Gly Asn Glu Tyr Leu Ser Ser
 305 310 315 320
 Ser Asn Gly Glu Arg Ile Thr Ile Ser Val Ser Ser Val Asp Trp Glu
 325 330 335
 Leu Ile Arg Glu His Tyr His Val Tyr Asp Val Glu Phe Glu Lys Gly
 340 345 350
 Trp Lys Phe Arg Ser Thr Lys Gln Ala Phe Arg Gln Tyr Ile Asp Lys
 355 360 365
 Trp Met Leu Val Lys Asn Met Ser Tyr Gly Ala Lys Lys Ala Ile Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Thr Asn Pro Asp
 385 390 395 400
 Ile Thr Gly Lys Arg Pro Tyr Leu Arg Glu Asp Gly Ser Asn Gly Phe
 405 410 415
 Glu Leu Met Glu Glu Glu Phe Arg Asp Pro Val Tyr Thr Pro Val Gly
 420 425 430
 Ile Phe Ile Thr Ser Trp Ala Arg Tyr Thr Thr Ile Thr Ser Ala Gln
 435 440 445
 Lys Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Met His Leu
 450 455 460
 Glu Gly Leu Asp Val Pro Glu Ser Ile Lys Asp Ile Val Ala Asp Asp
 465 470 475 480
 Val Leu Gly Tyr Trp Glu Lys Glu Gly Gln Phe Lys Gln Gly Lys Phe
 485 490 495
 Ile Arg Gln Lys Thr Tyr Met Glu Glu Tyr Tyr Ala Lys Tyr Val Arg
 500 505 510
 Asp Glu Asn Gly Glu Ile Lys Tyr Asp Asp Glu Lys Pro Tyr Lys Thr

515 520 525
Ile Cys Asp Lys Glu Glu Ser Asp Thr Thr Ile Ile Glu Ile Lys Cys

530 535 540
Ala Gly Met Pro Asp Asn Ile Lys Lys His Val Thr Phe Asp Asn Phe

545 550 555 560
Asp Ile Gly Phe Thr Met Glu Gly Lys Leu Lys Pro Lys Gln Val Tyr

565 570 575
Gly Gly Val Val Leu Val Glu Glu Thr Tyr Thr Met Lys

580 585

<210> 29

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 29

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

1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp

20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu

35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly

50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

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

85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr

100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp

115 120 125

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

130 135 140
 Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Ile Thr Lys Glu Arg Pro
 145 150 155 160
 Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
 165 170 175
 Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
 180 185 190
 Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
 195 200 205

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

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

 Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
 340 345 350
 Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
 355 360 365
 Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
 370 375 380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly
385 390 395 400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
405 410 415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
420 425 430

Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
435 440 445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
450 455 460

Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
465 470 475 480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
515 520 525

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

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 30

<211> 592

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 30

Met Ala Thr Lys Lys Arg Lys Ala Tyr Ser Cys Asp Phe Glu Ala Thr

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

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

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

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

Asn Ser Ala Tyr Pro Ser Val Met Tyr Tyr Lys Pro Leu Pro Trp Gly

260 265 270

Lys Pro Val Pro Phe Val Gly Lys Tyr Glu Glu Asp Pro Asp Phe Pro

275 280 285

Leu Tyr Ile Cys His Ile Lys Thr Gly Phe Val Leu Lys Glu Gly His

290 295 300

Ile Pro Thr Ile Gln Ile Lys Lys Asn Pro Ile Phe Gln Glu Asn Glu

305 310 315 320

Tyr Leu Glu Thr Ser Gly Gly Ala Pro Val Asp Leu His Val Thr Asn

325 330 335

Val Asp Leu Glu Leu Ile Lys Glu His Tyr Glu Leu Tyr Asp Thr Glu

340 345 350

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

355 360 365

Phe Ile Asp Tyr Trp Met Lys Ile Lys Thr Asp Pro Lys Ser Thr Pro

370 375 380

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

385 390 395 400

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

405 410 415

Asp Gly Ser Thr Ala Phe Lys Lys Gly Leu Pro Lys Ser Lys Asp Pro

420 425 430

Val Tyr Thr Pro Ala Gly Ala Phe Ile Thr Ala Trp Ala Arg His Met

435 440 445

Thr Ile Thr Thr Ala Gln Lys Val Tyr Asp Arg Ile Leu Tyr Cys Asp

450 455 460

Thr Asp Ser Ile His Ile Leu Gly Ile Asp Ile Pro Glu Ala Ile Lys

465 470 475 480

Asn Asp Ile His Gln Lys Glu Leu Gly Lys Trp Glu Phe Glu Cys Met

485 490 495

Phe Lys Arg Ala Lys Phe Val Arg Gln Lys Thr Tyr Val Glu Asp Met

500 505 510
Tyr Ala Lys Phe Met Lys Tyr Trp Glu Asp Gly Glu Leu Asn Tyr Tyr

515 520 525
Leu Lys Glu Cys Val Lys Glu Glu Ala Thr Ala Arg Leu Leu Asn Val

530 535 540
Lys Cys Ala Gly Met Pro Gln Ala Val Lys Lys Phe Val Thr Phe Arg

545 550 555 560
Thr Phe Ala Val Gly Phe Thr Ser Asp Thr Gly Lys Leu Lys Pro Lys

565 570 575
His Val Lys Gly Gly Gln Ile Leu Val Asp Val Pro Phe Thr Ile Lys

580 585 590
<210> 31

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 31

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

1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp

20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu

35 40 45
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly

50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

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

85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr

100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
 115 120 125
 Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
 130 135 140
 Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
 145 150 155 160
 Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
 165 170 175
 Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
 180 185 190
 Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
 195 200 205
 Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
 210 215 220
 Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
 225 230 235 240
 Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
 245 250 255
 Ile Val Phe Asp Val Asn Ser Leu Tyr Pro Ser Gln Met Tyr Val Arg
 260 265 270
 Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
 275 280 285
 Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
 290 295 300
 Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
 305 310 315 320
 Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
 325 330 335
 Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
 340 345 350
 Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met

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

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

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

545 550 555 560
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 32

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 32

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Ile Thr Lys Glu Arg Pro
145 150 155 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225 230 235 240

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

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

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

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

 Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu

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

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
 545 550 555 560
 Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
 565 570

<210> 33

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 33

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
 1 5 10 15
 Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp

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

85 90 95
 Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
 100 105 110
 Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp

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

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

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

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

 340 345 350
 Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
 355 360 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
 370 375 380
 Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly
 385 390 395 400
 Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr
 405 410 415
 Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu
 420 425 430
 Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Val Pro Leu Ala Ser Phe
 435 440 445
 Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys
 450 455 460
 Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
 465 470 475 480
 Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
 485 490 495
 Gly Tyr Trp Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
 500 505 510
 Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
 515 520 525
 Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
 530 535 540
 Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
 545 550 555 560
 Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
 565 570
 <210> 34
 <211> 573
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 34

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Ile Thr Lys Glu Arg Pro
145 150 155 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225 230 235 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly

245 250 255
 Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ser Gln Met Tyr Val Arg
 260 265 270

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

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

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

 Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
 465 470 475 480
 Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu
 485 490 495

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510
Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
515 520 525

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

<210> 35

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 35

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

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

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

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

130 135 140

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

145 150 155 160

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

165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu

180 185 190

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

195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val

210 215 220

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

225 230 235 240

Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly

245 250 255

Ile Val Phe Asp Ala Asn Ser Ala Tyr Pro Ser Gln Met Tyr Val Arg

260 265 270

Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu

275 280 285

Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg

290 295 300

Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu

305 310 315 320

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

325 330 335

Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe

340 345 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met

355 360 365

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile

370 375 380
 Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly

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

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

 515 520 525
 Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
 530 535 540
 Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
 545 550 555 560
 Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
 565 570

 <210> 36
 <211> 573
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Synthetic polypeptide

 <400> 36

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

245										250					255				
Ile	Val	Phe	Asp	Ala	Asn	Ser	His	Tyr	Pro	Ser	Gln	Met	Tyr	Val	Arg				
260					265					270									
Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	Tyr	Lys	Glu				
275					280					285									
Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val	Arg	Phe	Arg				
290					295					300									
Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln	Ser	Ser	Leu				
305					310					315					320				
Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	Leu	Gly	Val				
325					330					335									
Asp	Glu	Leu	Ile	Asp	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	Asp	Leu	Phe				
340					345					350									
Phe	Glu	His	Tyr	Asp	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	Gly	Tyr	Met				
355					360					365									
Phe	Lys	Ala	Ser	Cys	Asp	Met	Phe	Lys	Gly	Trp	Ile	Asp	Lys	Trp	Ile				
370					375					380									
Glu	Val	Lys	Asn	Thr	Thr	Tyr	Gly	Ala	Arg	Lys	Ala	Asn	Ala	Lys	Gly				
385					390					395					400				
Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Gly	Thr	Asn	Pro	Asp	Ile	Thr				
405					410					415									
Gly	Lys	Val	Pro	Tyr	Met	Gly	Glu	Asp	Gly	Ile	Val	Arg	Leu	Thr	Leu				
420					425					430									
Gly	Glu	Glu	Glu	Leu	Arg	Asp	Pro	Val	Tyr	Val	Pro	Leu	Ala	Ser	Phe				
435					440					445									
Val	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala	Gln	Arg	Cys				
450					455					460									
Phe	Asp	Asn	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu	Thr	Gly				
465					470					475					480				
Thr	Glu	Val	Pro	Glu	Ala	Ile	Glu	His	Leu	Val	Asp	Ser	Lys	Lys	Leu				
485					490					495									

Gly Tyr Trp Lys His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg
500 505 510

Gln Lys Thr Tyr Val Glu Glu Ile Asp Gly Glu Leu Asn Val Lys Cys
515 520 525

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

Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
545 550 555 560

Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys
565 570

<210> 37

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 37

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly

50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp

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

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

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

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

Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile

370

375

380

Glu Val Lys Asn Thr Thr Tyr Gly Ala Arg Lys Ala Asn Ala Lys Gly

385

390

395

400

Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp Ile Thr

405

410

415

Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu Thr Leu

420

425

430

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

435

440

445

Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Arg Cys

450

455

460

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

465

470

475

480

Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu

485

490

495

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

500

505

510

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

515

520

525

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

530

535

540

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

545

550

555

560

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

565

570

<210> 38

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 38

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Ile Thr Lys Glu Arg Pro
145 150 155 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225 230 235 240

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

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

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

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

485 490 495

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Phe Ile Arg

500 505 510

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

515 520 525

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

530 535 540

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

545 550 555 560

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

565 570

<210> 39

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 39

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

1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp

20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu

35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly

50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

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

85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr

100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
 115 120 125
 Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
 130 135 140
 Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Ile Thr Lys Glu Arg Pro
 145 150 155 160
 Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
 165 170 175
 Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
 180 185 190
 Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
 195 200 205
 Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
 210 215 220
 Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
 225 230 235 240
 Phe Thr Trp Val Asn Lys Val Phe Gln Gly Lys Glu Ile Gly Glu Gly
 245 250 255
 Ile Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Val Arg
 260 265 270
 Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr Lys Glu
 275 280 285
 Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg Phe Arg
 290 295 300
 Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser Ser Leu
 305 310 315 320
 Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val
 325 330 335
 Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe
 340 345 350
 Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met

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

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

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

545 550 555 560
Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys

565 570

<210> 40

<211> 591

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 40

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Ile Thr Lys Glu Arg Pro
145 150 155 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Tyr Gln Asp Trp
195 200 205

Val Lys Thr Thr Tyr Gly Lys Ser Arg Phe Lys Gln Trp Phe Pro Val
210 215 220

Leu Ser Leu Gly Phe Asp Lys Asp Leu Arg Lys Ala Tyr Lys Gly Gly
225 230 235 240

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

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

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

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

 Thr Glu Val Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu

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

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

<210> 41

<211> 611

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 41

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

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

65 70 75 80
 Glu Thr Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
 85 90 95
 Gln Trp Tyr Ala Leu Glu Ile Cys Trp Glu Val Asn Tyr Thr Thr Thr

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

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

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

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

 325 330 335
 Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Glu Leu Phe
 340 345 350

Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met
 355 360 365
 Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp Ile Asp Lys Trp Ile
 370 375 380
 Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys Ala Asn Ala Lys Gly

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

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

 515 520 525
 Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr Phe Asp Asn Phe
 530 535 540
 Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro Lys Arg Thr Gln
 545 550 555 560
 Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile Lys Gly His His
 565 570 575
 His His His His His His His His Gly Gly Gly Ser Gly Gly Gly Ser

 580 585 590
 Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys Ile Glu

595 600 605

Trp His Glu

610

<210> 42

<211> 613

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 42

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

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

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

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

 405 410 415
 Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
 420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480
Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys Gly
565 570 575
His His His His His His His His His His Gly Gly Gly Ser Gly Gly
580 585 590
Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys
595 600 605
Ile Glu Trp His Glu
610
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<211> 575
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
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Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
 130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270
 Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
 275 280 285
 Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

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

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

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

 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
 500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 44

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 44

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

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

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

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

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
355 360 365

Tyr Ile Lys Thr Thr Ser Lys Gly Ala Ile Lys Gln Leu Ala Lys Leu
370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415

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

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

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

 <210> 45
 <211> 575
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 45
 Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly

305 310 315 320
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys

340 345 350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr

355 360 365
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu

405 410 415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly

450 455 460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480
Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Lys

500 505 510

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

515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560

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

565 570 575

<210> 46

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 46

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130					135					140									
Asp	Ile	Asp	Ile	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro				
145					150					155					160				
Glu	Glu	Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala				
165					170					175									
Leu	Leu	Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser				
180					185					190									
Asp	Ser	Leu	Lys	Gly	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys				
195					200					205									
Lys	Val	Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys				
210					215					220									
Ala	Tyr	Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys				
225					230					235					240				
Glu	Ile	Gly	Glu	Gly	Met	Val	Phe	Asp	Ala	Asn	Ser	His	Tyr	Pro	Ala				
245					250					255									
Gln	Met	Tyr	Ser	Arg	Leu	Leu	Pro	Tyr	Gly	Glu	Pro	Ile	Val	Phe	Glu				
260					265					270									
Gly	Lys	Tyr	Val	Trp	Asp	Glu	Asp	Tyr	Pro	Leu	His	Ile	Gln	His	Ile				
275					280					285									
Arg	Cys	Glu	Phe	Glu	Leu	Lys	Glu	Gly	Tyr	Ile	Pro	Thr	Ile	Gln	Ile				
290					295					300									
Lys	Arg	Ser	Arg	Phe	Tyr	Lys	Gly	Asn	Glu	Tyr	Leu	Lys	Ser	Ser	Gly				
305					310					315					320				
Gly	Glu	Ile	Ala	Asp	Leu	Trp	Leu	Ser	Asn	Val	Asp	Leu	Glu	Leu	Met				
325					330					335									
Lys	Glu	His	Tyr	Asp	Leu	Tyr	Asn	Val	Glu	Tyr	Ile	Ser	Gly	Leu	Lys				
340					345					350									
Phe	Lys	Ala	Thr	Thr	Gly	Leu	Phe	Lys	Asp	Phe	Ile	Asp	Lys	Trp	Thr				
355					360					365									
Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala	Lys	Leu				
370					375					380									

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Cys His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 47

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 47

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

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

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

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

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

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300

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

305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335

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

340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr

355 360 365

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

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400

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

405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

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

450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr

500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val

515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys

565 570 575

<210> 48

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 48

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240
Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
245 250 255
Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
325 330 335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
355 360 365
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Arg Leu Ala Lys Leu

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

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

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

565 570 575

<210> 49

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 49

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

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Thr	Lys	Val	Glu	Asp	Cys	Arg	Val	Trp	Ala	Tyr	Gly	Tyr	Met	Asn	Ile
	20	25	30												
Glu	Asp	His	Ser	Glu	Tyr	Lys	Ile	Gly	Asn	Ser	Leu	Asp	Glu	Phe	Met
	35	40	45												
Ala	Trp	Val	Leu	Lys	Val	Gln	Ala	Asp	Leu	Tyr	Phe	His	Asn	Leu	Lys
	50	55	60												
Phe	Asp	Gly	Ala	Phe	Ile	Ile	Asn	Trp	Leu	Glu	Arg	Asn	Gly	Phe	Lys
65	70	75	80												
Trp	Ser	Ala	Asp	Gly	Leu	Pro	Asn	Thr	Tyr	Asn	Thr	Ile	Ile	Ser	Arg
	85	90	95												
Met	Gly	Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Leu	Gly	Tyr	Lys	Gly	Lys
	100	105	110												
Arg	Lys	Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe
	115	120	125												
Pro	Val	Glu	Lys	Ile	Ala	Lys	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly
	130	135	140												
Asp	Ile	Asp	Ile	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro
145	150	155	160												
Glu	Glu	Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala
	165	170	175												
Leu	Leu	Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser
	180	185	190												
Asp	Ser	Leu	Lys	Gly	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys
	195	200	205												
Lys	Val	Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys
	210	215	220												
Ala	Tyr	Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys
225	230	235	240												
Glu	Ile	Gly	Glu	Gly	Met	Val	Phe	Asp	Ala	Arg	Ser	His	Tyr	Pro	Ala
	245	250	255												

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

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

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr

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

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570 575

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<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 50

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 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
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 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

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

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

130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

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

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

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

 355 360 365
 Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Asp Lys Lys Leu
465 470 475 480
Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575
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Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

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

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260	265	270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile		
275	280	285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile		
290	295	300
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly		
305	310	315
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met		
325	330	335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys		
340	345	350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe		
355	360	365
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu		
370	375	380
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr		
385	390	395
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu		
405	410	415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe		
420	425	430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys		
435	440	445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly		
450	455	460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu		
465	470	475
Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg		
485	490	495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr		
500	505	510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
 515 520 525
 Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
 530 535 540

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

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

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

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

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300

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

305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335

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

340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr

355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385	390								395								400							
Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe	Arg	Leu									
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Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	Gly	Val	Phe									
					420				425				430											
Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	Gln	Ala	Cys									
					435				440				445											
Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu	Thr	Gly									
					450				455				460											
Thr	Glu	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	Asp	Pro	Asp	Lys	Leu									
465					470				475				480											
Gly	Tyr	Trp	Ala	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	Tyr	Leu	Arg									
					485				490				495											
Gln	Lys	Thr	Tyr	Ile	Gln	Asp	Ile	Tyr	Met	Lys	Arg	Val	Lys	Gly	Tyr									
					500				505				510											
Leu	Val	Gln	Gly	Ser	Pro	Asp	Asp	Tyr	Thr	Asp	Ile	Lys	Phe	Ser	Val									
					515				520				525											
Lys	Cys	Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Lys	Glu	Val	Thr	Phe	Glu									
530					535				540															
Asn	Phe	Lys	Val	Gly	Phe	Ser	Arg	Lys	Met	Lys	Pro	Lys	Pro	Val	Gln									
545					550				555											560				
Val	Pro	Gly	Gly	Val	Val	Leu	Val	Asp	Glu	Thr	Phe	Thr	Ile	Lys										
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1	5				10										15									

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

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

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

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

260	265	270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile		
275	280	285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile		
290	295	300
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly		
305	310	315
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met		
325	330	335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys		
340	345	350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr		
355	360	365
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu		
370	375	380
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr		
385	390	395
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu		
405	410	415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe		
420	425	430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys		
435	440	445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly		
450	455	460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu		
465	470	475
Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg		
485	490	495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr		
500	505	510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 54

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 54

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly

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

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

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

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

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400

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

405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

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

450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys

500 505 510

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

515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys

565 570 575

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<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 55

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 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

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

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

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

 245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

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

305 310 315 320

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

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
355 360 365

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

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Cys His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys

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

565 570 575

<210> 56

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 56

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly

130 135 140
 Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175

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

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

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

 Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380

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

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

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

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
 565 570 575

<210> 57
 <211> 575
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
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Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
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Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
 130 135 140
 Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
 245 250 255
 Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270
 Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
 275 280 285
 Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

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

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

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

 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
 500 505 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
 515 520 525
 Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
 530 535 540
 Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

 545 550 555 560
 Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
 565 570 575
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 <400> 58
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 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30

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

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

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

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

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
355 360 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415

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

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

 Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
 545 550 555 560
 Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
 565 570 575

 <210> 59
 <211> 575
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 59
 Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

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

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly

305 310 315 320
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys

340 345 350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr

355 360 365
Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu

405 410 415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430
Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly

450 455 460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480
Gly Tyr Trp Gln His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys

500 505 510

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

515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys

565 570 575

<210> 60

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 60

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly

130					135					140									
Asp	Ile	Asp	Tyr	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro				
145					150					155					160				
Glu	Glu	Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala				
165					170					175									
Leu	Leu	Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser				
180					185					190									
Asp	Ser	Leu	Lys	Gly	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys				
195					200					205									
Lys	Val	Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Tyr				
210					215					220									
Ala	Tyr	Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Glu	Lys				
225					230					235					240				
Glu	Ile	Gly	Glu	Gly	Met	Val	Phe	Asp	Val	Asn	Ser	Leu	Tyr	Pro	Ala				
245					250					255									
Gln	Met	Tyr	Ser	Arg	Leu	Leu	Pro	Tyr	Gly	Glu	Pro	Ile	Val	Phe	Glu				
260					265					270									
Gly	Lys	Tyr	Val	Trp	Asp	Glu	Asp	Tyr	Pro	Leu	His	Ile	Gln	His	Ile				
275					280					285									
Arg	Cys	Glu	Phe	Glu	Leu	Lys	Glu	Gly	Tyr	Ile	Pro	Thr	Ile	Gln	Ile				
290					295					300									
Lys	Arg	Ser	Arg	Phe	Tyr	Lys	Gly	Asn	Glu	Tyr	Leu	Lys	Ser	Ser	Gly				
305					310					315					320				
Gly	Glu	Ile	Ala	Asp	Leu	Trp	Leu	Ser	Asn	Val	Asp	Leu	Glu	Leu	Met				
325					330					335									
Lys	Glu	His	Tyr	Asp	Leu	Tyr	Asn	Val	Glu	Tyr	Ile	Ser	Gly	Leu	Lys				
340					345					350									
Phe	Lys	Ala	Thr	Thr	Gly	Leu	Phe	Lys	Asp	Phe	Ile	Asp	Lys	Trp	Thr				
355					360					365									
Tyr	Ile	Lys	Thr	Thr	Ser	Glu	Gly	Ala	Ile	Lys	Gln	Leu	Ala	Lys	Leu				
370					375					380									

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
500 505 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
565 570 575

<210> 61

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 61

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

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

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

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

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

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300

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

305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335

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

340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe

355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400

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

405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

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

450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Lys

500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val

515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys

565 570 575

<210> 62

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 62

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240
Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
245 250 255
Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
325 330 335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
355 360 365
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

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

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

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

 565 570 575

<210> 63

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 63

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

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

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

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

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

 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

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

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Gln His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr

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

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570 575

<210> 64

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 64

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

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

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

130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

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

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

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

 355 360 365
 Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
 385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415
 Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
 420 425 430
 Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
 435 440 445
 Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
 450 455 460
 Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Phe
 465 470 475 480
 Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
 500 505 510
 Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
 515 520 525
 Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
 530 535 540
 Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
 545 550 555 560
 Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570 575
 <210> 65
 <211> 575
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 65
 Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

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

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
245 250 255

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

260 265 270
 Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
 275 280 285

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

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

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

 Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
 500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

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

<210> 66

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 66

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

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

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

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

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ser

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300

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

305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335

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

340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe

355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu

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

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

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

 <210> 67
 <211> 575
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 67
 Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15

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

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

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

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

260	265	270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile		
275	280	285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile		
290	295	300
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly		
305	310	315
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met		
325	330	335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys		
340	345	350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe		
355	360	365
Tyr Ile Lys Asp Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu		
370	375	380
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr		
385	390	395
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu		
405	410	415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe		
420	425	430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys		
435	440	445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly		
450	455	460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu		
465	470	475
Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg		
485	490	495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr		
500	505	510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 68

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 68

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

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

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

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

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

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400

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

405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

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

450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr

500 505 510

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

515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560

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

565 570 575

<210> 69

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 69

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

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

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

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

 245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

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

305 310 315 320

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

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
355 360 365

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

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr

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

565 570 575

<210> 70

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 70

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175

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

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

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

 Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380

Phe Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480
Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575
<210> 71
<211> 575
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 71
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45
Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125
Pro Val Glu Lys Ile Ala Lys Ala Phe Lys Leu Thr Val Lys Lys Gly
130 135 140
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240
Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
245 250 255
Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270
 Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
 275 280 285
 Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

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

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

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

 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
 500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 72

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 72

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
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Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

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

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

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

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
355 360 365

Tyr Ile Lys Thr Arg Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415

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

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

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

 <210> 73
 <211> 575
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 73
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 1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly

305 310 315 320
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys

340 345 350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Asp

355 360 365
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu

405 410 415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly

450 455 460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Lys

465 470 475 480
Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr

500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 74
<211> 575
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 74

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
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Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130	135	140	
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro			
145	150	155	160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala			
	165	170	175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser			
	180	185	190
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys			
195	200	205	
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys			
210	215	220	
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys			
225	230	235	240
Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala			
	245	250	255
Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu			
260	265	270	
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile			
275	280	285	
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile			
290	295	300	
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly			
305	310	315	320
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met			
	325	330	335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys			
340	345	350	
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Glu			
355	360	365	
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu			
370	375	380	

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Lys
465 470 475 480

Gly Tyr Trp Ala His Ala Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 75

<211> 613

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 75

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

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

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

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

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

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300

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

305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335

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

340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr

355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400

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

405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

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

450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr

500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val

515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys Gly

565 570 575
His His His His His His His His His His Gly Gly Gly Ser Gly Gly

580 585 590
Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys

595 600 605
Ile Glu Trp His Glu

610

<210> 76

<211> 613

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 76

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

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

20 25 30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

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

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300

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

305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys

340 345 350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr

355 360 365
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu

405 410 415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly

450 455 460
Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu

465 470 475 480
Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr

500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val

515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu

530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys Gly

565 570 575

His His His His His His His His His His Gly Gly Gly Ser Gly Gly
580 585 590
Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys
595 600 605
Ile Glu Trp His Glu
610
<210> 77
<211> 613
<212> PRT
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<220><223> Synthetic polypeptide
<400> 77
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
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Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45
Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125
Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300

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

305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335

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

340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe

355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400

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

405 410 415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly

450 455 460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480
Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr

500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val

515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys Gly

565 570 575
His His His His His His His His His His Gly Gly Gly Ser Gly Gly

580 585 590
Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala Gln Lys

595 600 605
Ile Glu Trp His Glu

610

<210

> 78

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 78

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

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

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

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

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Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300

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

305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335

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

340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe

355 360 365

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

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400

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

405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

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

450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Lys

500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val

515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys

565 570 575

<210> 79

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 79

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

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

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

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

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

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

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

 Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570 575

 <210> 80
 <211> 575
 <212> PRT
 <213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 80

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

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

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

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

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

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys

500 505 510

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

515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560

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

565 570 575

<210> 81

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 81

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100	105	110	
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe			
115	120	125	
Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly			
130	135	140	
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro			
145	150	155	160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala			
165	170	175	
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser			
180	185	190	
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys			
195	200	205	
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr			
210	215	220	
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys			
225	230	235	240
Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala			
245	250	255	
Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu			
260	265	270	
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile			
275	280	285	
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile			
290	295	300	
Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly			
305	310	315	320
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met			
325	330	335	
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys			
340	345	350	

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe

355

360

365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370

375

380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385

390

395

400

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

405

410

415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420

425

430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435

440

445

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

450

455

460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465

470

475

480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485

490

495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys

500

505

510

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

515

520

525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530

535

540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545

550

555

560

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

565

570

575

<210> 82

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 82

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

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

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

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

           210          215          220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys

```

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

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

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

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

 465 470 475 480

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

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

<210> 83

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 83

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

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

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

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

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe

355	360	365
Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu		
370	375	380
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr		
385	390	395
		400
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu		
405	410	415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe		
420	425	430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys		
435	440	445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly		
450	455	460
Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu		
465	470	475
		480
Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg		
485	490	495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys		
500	505	510
Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val		
515	520	525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu		
530	535	540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln		
545	550	555
		560
Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys		
565	570	575
<210> 84		
<211> 575		
<212> PRT		
<213> Artificial sequence		
<220><223> Synthetic polypeptide		

<400> 84

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

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

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

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

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
355 360 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val Asp Gly Lys
500 505 510
Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Phe Ser Val

515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
565 570 575

<210> 85

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 85

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45
Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

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

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

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

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300

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

305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335

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

340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe

355 360 365
Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu

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

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

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

565 570 575

<210> 86

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 86

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

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

225	230								235								240							
Glu	Ile	Gly	Glu	Gly	Met	Val	Phe	Asp	Val	Asn	Ser	His	Tyr	Pro	Ala									
245					250					255														
Gln	Met	Tyr	Ser	Arg	Leu	Leu	Pro	Tyr	Gly	Glu	Pro	Ile	Val	Phe	Glu									
260					265					270														
Gly	Lys	Tyr	Val	Trp	Asp	Glu	Asp	Tyr	Pro	Leu	His	Ile	Gln	His	Ile									
275					280					285														
Arg	Cys	Glu	Phe	Glu	Leu	Lys	Glu	Gly	Tyr	Ile	Pro	Thr	Ile	Gln	Ile									
290					295					300														
Lys	Arg	Ser	Arg	Phe	Tyr	Lys	Gly	Asn	Glu	Tyr	Leu	Lys	Ser	Ser	Gly									
305					310					315					320									
Gly	Glu	Ile	Ala	Asp	Leu	Trp	Leu	Ser	Asn	Val	Asp	Leu	Glu	Leu	Met									
325					330					335														
Lys	Glu	His	Tyr	Asp	Leu	Tyr	Asn	Val	Glu	Tyr	Ile	Ser	Gly	Leu	Lys									
340					345					350														
Phe	Lys	Ala	Thr	Thr	Gly	Leu	Phe	Lys	Asp	Phe	Ile	Asp	Lys	Trp	Phe									
355					360					365														
Tyr	Ile	Lys	Thr	Thr	Ser	Glu	Gly	Ala	Ile	Lys	Gln	Leu	Ala	Lys	Leu									
370					375					380														
Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp	Val	Thr									
385					390					395					400									
Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe	Arg	Leu									
405					410					415														
Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	Gly	Val	Phe									
420					425					430														
Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	Gln	Ala	Cys									
435					440					445														
Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu	Thr	Gly									
450					455					460														
Thr	Glu	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	Asp	Pro	Lys	Lys	Leu									
465					470					475					480									

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
500 505 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Leu Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
565 570 575

<210> 87

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 87

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

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

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

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

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

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

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

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe

355

360

365

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

370

375

380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385

390

395

400

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

405

410

415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420

425

430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435

440

445

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

450

455

460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465

470

475

480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485

490

495

Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val Asp Gly Lys

500

505

510

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

515

520

525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530

535

540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545

550

555

560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys

565

570

575

<210> 88

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 88

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

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

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

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

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

				465				470				475				480			
Gly	Tyr	Trp	Ala	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	Tyr	Leu	Arg				
				485				490				495							
Pro	Lys	Thr	Tyr	Ile	Gln	Asp	Ile	Tyr	Met	Lys	His	Val	His	Gly	Lys				
				500				505				510							
Leu	Val	Glu	Gly	Ser	Pro	Asp	Asp	Tyr	Thr	Lys	Ile	Lys	Leu	Ser	Val				
				515				520				525							
Lys	Cys	Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Lys	Glu	Val	Thr	Phe	Glu				
				530				535				540							
Asn	Phe	Lys	Val	Gly	Phe	Ser	Arg	Lys	Met	Lys	Pro	Lys	Pro	Val	Gln				
545				550				555				560							
Val	Pro	Gly	Gly	Val	Val	Leu	Val	Asp	Asp	Thr	Phe	Thr	Ile	Lys					
				565				570				575							
<210> 89																			
<211> 575																			
<212> PRT																			
<213> Artificial sequence																			
<220><223> Synthetic polypeptide																			
<400> 89																			
Met	Lys	His	Met	Pro	Arg	Lys	Arg	Tyr	Ser	Cys	Asp	Phe	Glu	Thr	Thr				
1				5				10				15							
Thr	Lys	Val	Glu	Asp	Cys	Arg	Val	Trp	Ala	Tyr	Gly	Tyr	Met	Asn	Ile				
				20				25				30							
Glu	Asp	His	Ser	Glu	Tyr	Lys	Ile	Gly	Asn	Ser	Leu	Asp	Glu	Phe	Met				
				35				40				45							
Ala	Trp	Ala	Leu	Lys	Val	Gln	Ala	Asp	Leu	Tyr	Phe	His	Asn	Leu	Lys				
				50				55				60							
Phe	Asp	Gly	Ala	Phe	Ile	Ile	Asn	Trp	Leu	Glu	Arg	Asn	Gly	Phe	Lys				
65				70				75				80							
Trp	Ser	Ala	Asp	Gly	Leu	Pro	Asn	Thr	Tyr	Asn	Thr	Ile	Ile	Ser	Arg				

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125
Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
130 135 140
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
210 215 220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225 230 235 240
Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
245 250 255
Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300
Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
325 330 335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys

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

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

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

530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
565 570 575

<210> 90

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 90

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

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

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

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

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

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

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

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

<210> 91

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 91

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

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

65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly

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

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

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

 325 330 335
 Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
 340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
 355 360 365
 Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380
 Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

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

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

 515 520 525
 Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
 530 535 540
 Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
 545 550 555 560
 Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
 565 570 575
 <210> 92
 <211> 575
 <212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 92

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
 260 265 270
 Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
 275 280 285
 Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
 290 295 300
 Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
 305 310 315 320
 Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
 325 330 335
 Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
 340 345 350
 Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
 355 360 365
 Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380
 Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
 385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415
 Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
 420 425 430
 Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
 435 440 445
 Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
 450 455 460
 Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480
 Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
 485 490 495
 Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val Asp Gly Lys

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

 565 570 575

<210> 93

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 93

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45

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

100	105	110	
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe			
115	120	125	
Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly			
130	135	140	
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro			
145	150	155	160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala			
165	170	175	
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser			
180	185	190	
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys			
195	200	205	
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr			
210	215	220	
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys			
225	230	235	240
Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala			
245	250	255	
Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu			
260	265	270	
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile			
275	280	285	
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile			
290	295	300	
Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly			
305	310	315	320
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met			
325	330	335	
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys			
340	345	350	

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe
355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val His Gly Lys
500 505 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Lys Ile Lys Leu Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
565 570 575

<210> 94

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 94

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210 215 220

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

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

290 295 300

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

305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335

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

340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Phe

355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400

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

405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

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

450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480
Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

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

545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys

565 570 575

<210> 95

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 95

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

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

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

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly
130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser His Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

Lys Asn Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

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

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

340				345				350							
Phe	Lys	Ala	Thr	Thr	Gly	Leu	Phe	Lys	Asp	Phe	Ile	Asp	Lys	Trp	Phe
355				360				365							
Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala	Lys	Leu
370				375				380							
Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp	Val	Thr
385				390				395				400			
Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe	Arg	Leu
405				410				415							
Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	Gly	Val	Phe
420				425				430							
Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	Gln	Ala	Cys
435				440				445							
Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu	Thr	Gly
450				455				460							
Thr	Glu	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	Asp	Pro	Lys	Lys	Leu
465				470				475				480			
Gly	Tyr	Trp	Ala	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	Tyr	Leu	Arg
485				490				495							
Pro	Lys	Thr	Tyr	Ile	Gln	Asp	Ile	Tyr	Met	Lys	His	Val	His	Gly	Lys
500				505				510							
Leu	Val	Asn	Gly	Ser	Pro	Asp	Asp	Tyr	Thr	Lys	Ile	Lys	Leu	Ser	Val
515				520				525							
Lys	Cys	Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Lys	Glu	Val	Thr	Phe	Glu
530				535				540							
Asn	Phe	Lys	Val	Gly	Phe	Ser	Arg	Lys	Met	Lys	Pro	Lys	Pro	Val	Gln
545				550				555				560			
Val	Pro	Gly	Gly	Val	Val	Leu	Val	Asp	Asp	Thr	Phe	Thr	Ile	Lys	
565				570				575							
<210>		96													
<211>		575													

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 96

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Lys Leu Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

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

210				215				220							
Ala	Tyr	Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Glu	Lys
225				230				235				240			
Glu	Ile	Gly	Glu	Gly	Met	Val	Phe	Asp	Val	Asn	Ser	His	Tyr	Pro	Ala
				245				250				255			
Gln	Met	Tyr	Ser	Arg	Leu	Leu	Pro	Tyr	Gly	Glu	Pro	Ile	Val	Phe	Glu
				260				265				270			
Gly	Lys	Tyr	Val	Trp	Asp	Glu	Asp	Tyr	Pro	Leu	His	Ile	Gln	His	Ile
275				280				285							
Arg	Cys	Glu	Phe	Glu	Leu	Lys	Glu	Gly	Tyr	Ile	Pro	Thr	Ile	Gln	Ile
290				295				300							
Lys	Asn	Ser	Arg	Phe	Tyr	Lys	Gly	Asn	Glu	Tyr	Leu	Lys	Ser	Ser	Gly
305				310				315				320			
Gly	Glu	Ile	Ala	Asp	Leu	Trp	Leu	Ser	Asn	Val	Asp	Leu	Glu	Leu	Met
				325				330				335			
Lys	Glu	His	Tyr	Asp	Leu	Tyr	Asn	Val	Glu	Tyr	Ile	Ser	Gly	Leu	Lys
340				345				350							
Phe	Lys	Ala	Thr	Thr	Gly	Leu	Phe	Lys	Asp	Phe	Ile	Asp	Lys	Trp	Phe
355				360				365							
Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala	Lys	Leu
370				375				380							
Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp	Val	Thr
385				390				395				400			
Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe	Arg	Leu
405				410				415							
Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	Gly	Val	Phe
420				425				430							
Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	Gln	Ala	Cys
435				440				445							
Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu	Thr	Gly
450				455				460							

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495

Pro Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys His Val Asp Gly Lys

500 505 510

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

515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys

565 570 575

<210> 97

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 97

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

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

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

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

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

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

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

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

 Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
 530 535 540
 Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
 545 550 555 560
 Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570

<210> 98

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 98

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125
Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140
Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160
Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

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

180 185 190
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

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

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

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

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

 450 455 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465 470 475 480
Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
485 490 495
Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
500 505 510
Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
515 520 525
Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
530 535 540
Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545 550 555 560
Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570
<210> 99
<211> 572
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 99
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
 115 120 125

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

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

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

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

340 345 350
 Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
 355 360 365
 Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
 370 375 380

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

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

 Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
 515 520 525
 Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
 530 535 540
 Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
 545 550 555 560
 Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570

<210> 100

<

211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 100

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

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

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

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

165 170 175

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

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

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

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Ser Arg Ile Leu Pro Tyr Gly Asp Pro Ile Val Phe Asp Gly Lys Tyr
 260 265 270
 Val Trp Asp Asp Glu Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
 275 280 285
 Phe Glu Leu Lys Asp Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
 290 295 300
 Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
 305 310 315 320
 Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
 325 330 335
 Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
 340 345 350
 Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
 355 360 365
 Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
 370 375 380
 Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
 385 390 395 400
 Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
 405 410 415
 Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
 420 425 430
 Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
 435 440 445
 Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
 450 455 460
 Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp

465 470 475 480
 Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
 485 490 495
 Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln

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

 565 570

<210> 101

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 101

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45

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

100	105	110	
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys			
115	120	125	
Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp			
130	135	140	
Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr			
145	150	155	160
Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile			
165	170	175	
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu			
180	185	190	
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe			
195	200	205	
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg			
210	215	220	
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly			
225	230	235	240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr			
245	250	255	
Ser Arg Ile Leu Pro Tyr Gly Asp Pro Ile Val Phe Asp Gly Lys Tyr			
260	265	270	
Val Trp Asp Asp Glu Tyr Pro Leu His Ile Gln His Ile Arg Cys Asp			
275	280	285	
Phe Glu Leu Lys Asp Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser			
290	295	300	
Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Asp Leu			
305	310	315	320
Val Glu Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His			
325	330	335	
Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala			
340	345	350	

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

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
370 375 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385 390 395 400

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

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
420 425 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
435 440 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
450 455 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465 470 475 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
485 490 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
515 520 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545 550 555 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570

<210> 102

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 102

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

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

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

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

165 170 175

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

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

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

210 215 220

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

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

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

260 265 270

Val Trp Asp Asp Glu Tyr Pro Leu His Ile Gln His Ile Arg Cys Asp

275 280 285

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

290 295 300

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

305 310 315 320

Val Glu Leu Trp Ile Ser Gln Val Asp Ile Asp Leu Met Lys Glu His

325 330 335

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

340 345 350

Thr Thr Gly Ile Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys

355 360 365

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

370 375 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val

385 390 395 400

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

405 410 415

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

420 425 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg

435 440 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile

450 455 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp

465 470 475 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr

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

500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala

515 520 525

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

530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly

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

565 570

<210> 103

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 103

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Arg Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Leu Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Asn Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Leu Val Asn Trp Leu Glu Gln His Gly Phe Arg Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
245 250 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
260 265 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
275 280 285

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

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305 310 315 320

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

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

[illegible]

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 104

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Arg Leu

1 5 10 15

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

20 25 30

Asp Asn Tyr Lys Leu Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Asn Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Leu Val Asn Trp Leu Glu Gln His Gly Phe Arg Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

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

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

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

165 170 175

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

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

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

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

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

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

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

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp

465 470 475 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr

485 490 495

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

500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala

515 520 525

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

530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly

545 550 555 560

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

565 570

<210> 105

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 105

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

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

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

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

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

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

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

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

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
530 535 540
Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545 550 555 560
Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570

<210> 106

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 106

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

1 5 10 15
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp

20 25 30
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu

35 40 45
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly

50 55 60
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

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

180 185 190
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

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

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

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

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

 450 455 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465 470 475 480
Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
485 490 495
Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
500 505 510
Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
515 520 525
Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
530 535 540
Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545 550 555 560
Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570
<210> 107
<211> 582
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 107
Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30
Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45
Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60
Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro
145 150 155 160

Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
165 170 175

Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
180 185 190

Asp Arg Met Thr Ala Gly Ser Asp Ser Leu Lys Gly Phe Lys Asp Ile
195 200 205

Ile Thr Thr Lys Lys Phe Lys Lys Val Phe Pro Thr Leu Ser Leu Gly
210 215 220

Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu
225 230 235 240

Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly Glu Gly Met Val Phe Asp
245 250 255

Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Ser Arg Leu Leu Pro Tyr
260 265 270

Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr Val Trp Asp Glu Asp Tyr
275 280 285

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

Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser Arg Phe Tyr Lys Gly Asn
305 310 315 320

Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile Ala Asp Leu Trp Leu Ser
325 330 335

Asn Val Asp Leu Glu Leu Met Lys Glu His Tyr Asp Leu Tyr Asn Val

340 345 350
 Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala Thr Thr Gly Leu Phe Lys
 355 360 365
 Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala
 370 375 380

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

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

 Met Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr
 515 520 525
 Thr Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile
 530 535 540
 Lys Lys Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys
 545 550 555 560
 Met Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp
 565 570 575

 Glu Thr Phe Thr Ile Lys
 580

<210> 108

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 108

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

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

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

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

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240

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

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

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

 Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
 435 440 445
 Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly

450 455 460
 Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
 465 470 475 480
 Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
 500 505 510
 Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
 515 520 525
 Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
 530 535 540
 Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
 545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570 575

<210> 109

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 109

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

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

85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

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

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

 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
 325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 450 455 460
 Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
 465 470 475 480
 Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
 500 505 510
 Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
 515 520 525
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
 530 535 540
 Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
 545 550 555 560
 Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr
 565 570 575
 Phe Thr Ile Lys

580

<210> 110

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 110

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn

1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp

20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu

35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly

50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Ile Lys Arg Ser
 290 295 300
 Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
 305 310 315 320
 Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
 325 330 335
 Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala

 340 345 350
 Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
 355 360 365
 Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
 370 375 380
 Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
 385 390 395 400
 Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu

 405 410 415
 Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
 420 425 430
 Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
 435 440 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
450 455 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp

465 470 475 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
485 490 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
515 520 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys

530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545 550 555 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570

<210> 111

<211> 587

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 111

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65			70					75					80				
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Leu	Ile	Ser	Asn	Met	Gly		
			85					90					95				
Gln	Trp	Tyr	Ala	Leu	Glu	Ile	Cys	Trp	Asn	Val	Lys	Cys	Thr	Thr	Thr		
			100					105					110				
Lys	Thr	Gly	Lys	Thr	Lys	Lys	Glu	Lys	Gln	Arg	Thr	Ile	Ile	Tyr	Asp		
			115					120					125				
Ser	Leu	Lys	Lys	Tyr	Pro	Phe	Pro	Val	Lys	Glu	Ile	Ala	Glu	Ala	Phe		
130								135					140				
Asn	Phe	Pro	Ile	Lys	Lys	Gly	Glu	Ile	Asp	Tyr	Thr	Lys	Glu	Arg	Pro		
145			150					155					160				
Ile	Gly	Tyr	Asn	Pro	Thr	Asp	Asp	Glu	Trp	Asp	Tyr	Leu	Lys	Asn	Asp		
			165					170					175				
Ile	Gln	Ile	Met	Ala	Met	Ala	Leu	Lys	Ile	Gln	Phe	Asp	Gln	Gly	Leu		
			180					185					190				
Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser	Leu	Lys	Gly	Phe	Lys	Asp	Ile		
195								200					205				
Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val	Phe	Pro	Thr	Leu	Ser	Leu	Gly		
210								215					220				
Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr	Arg	Gly	Gly	Phe	Thr	Trp	Leu		
225			230					235					240				
Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile	Gly	Glu	Gly	Met	Val	Phe	Asp		
			245					250					255				
Ala	Asn	Ser	His	Tyr	Pro	Ala	Gln	Met	Tyr	Val	Arg	Pro	Leu	Pro	Tyr		
			260					265					270				
Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	Tyr	Lys	Glu	Asn	Ile	Asp	Tyr		
			275					280					285				
Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val	Arg	Phe	Arg	Leu	Lys	Glu	Arg		
290								295					300				
His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln	Ser	Ser	Leu	Phe	Ile	Gln	Asn		
305			310					315					320				

Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu Gly Val Asp Glu Leu Ile
325 330 335

Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu His Tyr
340 345 350

Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser
355 360 365

Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr
370 375 380

Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn Ser
385 390 395 400

Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val Pro
405 410 415

Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu
420 425 430

Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala Trp
435 440 445

Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg Ile
450 455 460

Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile Pro
465 470 475 480

Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp Glu
485 490 495

His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr
500 505 510

Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln Gly
515 520 525

Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala Gly
530 535 540

Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys Val
545 550 555 560

Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly Gly

565 570 575
Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
580 585
<210> 112
<211> 572
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 112
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125
Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140
Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145 150 155 160
Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr

260 265 270
Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu

275 280 285
Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser

290 295 300
Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile

305 310 315 320
Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His

325 330 335
Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala

340 345 350
Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys

355 360 365
Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn

370 375 380
Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val

385 390 395 400
Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu

405 410 415
Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala

420 425 430
Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg

435 440 445
Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile

450 455 460
Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp

465 470 475 480
Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr

485 490 495
Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln

500 505 510
Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala

515 520 525
Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys

530 535 540
Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly

545 550 555 560
Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys

565 570

<210> 113

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 113

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
245 250 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
260 265 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
275 280 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser

290	295	300	
Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile			
305	310	315	320
Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His			
	325	330	335
Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala			
	340	345	350
Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys			
	355	360	365
Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn			
	370	375	380
Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val			
385	390	395	400
Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu			
	405	410	415
Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala			
	420	425	430
Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg			
	435	440	445
Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile			
	450	455	460
Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp			
465	470	475	480
Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr			
	485	490	495
Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln			
	500	505	510
Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala			
	515	520	525
Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys			
	530	535	540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545 550 555 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570

<210> 114

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 114

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asp Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln
 260 265 270
 Gly Lys Tyr Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile
 275 280 285
 Arg Phe Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

 290 295 300
 Lys Lys Asn Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly
 305 310 315 320
 Val Glu Pro Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile
 325 330 335
 Gln Glu His Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys
 340 345 350
 Phe Arg Glu Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr

 355 360 365
 Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380
 Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
 385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly

450 455 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu

465 470 475 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr

500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val

515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu

530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys

565 570 575

<210> 115

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 115

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
 65 70 75 80
 Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
 85 90 95

 Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
 115 120 125
 Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
 130 135 140
 Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
 145 150 155 160

 Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220

 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln Gly Lys Tyr
 260 265 270
 Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe Glu
 275 280 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys Asn
 290 295 300
 Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu Pro
 305 310 315 320
 Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu His
 325 330 335
 Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg Glu
 340 345 350

 Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
 355 360 365
 Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
 370 375 380
 Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
 385 390 395 400
 Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
 405 410 415

 Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
 420 425 430
 Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
 435 440 445
 Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
 450 455 460
 Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
 465 470 475 480

 Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
 485 490 495
 Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
 500 505 510
 Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
 515 520 525
 Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys

530	535										540										
Val	Gly	Phe	Ser	Arg	Lys	Met	Lys	Pro	Lys	Pro	Val	Gln	Val	Pro	Gly						
545	550										555										560
Gly	Val	Val	Leu	Val	Asp	Glu	Thr	Phe	Thr	Ile	Lys										
	565										570										
<210>	116																				
<211>	576																				
<212>	PRT																				
<213>	Artificial sequence																				
<220><223>	Synthetic polypeptide																				
<400>	116																				
Met	Lys	His	Met	Pro	Arg	Lys	Met	Tyr	Ser	Cys	Asp	Phe	Glu	Thr	Thr						
1	5				10						15										
Thr	Asp	Val	Asn	Asp	Cys	Arg	Val	Trp	Ala	Tyr	Gly	Trp	Met	Glu	Ile						
	20				25						30										
Gly	Lys	Thr	Ser	Asn	Tyr	Lys	Ile	Gly	Thr	Asp	Phe	Asn	Glu	Phe	Met						
	35				40						45										
Glu	Trp	Met	Ile	His	Ser	Ser	Ser	Arg	Leu	Tyr	Phe	His	Asp	Leu	Lys						
	50				55						60										
Phe	Asp	Gly	Ser	Phe	Ile	Val	Asn	Trp	Leu	Leu	His	Asn	Gly	Tyr	Thr						
65	70				75						80										
Trp	Thr	Lys	Arg	Pro	Ser	Lys	Glu	Gly	Gln	Phe	Ser	Thr	Leu	Ile	Ser						
	85				90						95										
Lys	Met	Gly	Gln	Trp	Tyr	Gly	Ile	Thr	Ile	Cys	Ser	Gly	Arg	Asp	Gly						
	100				105						110										
Arg	Lys	Lys	Lys	Leu	Thr	Thr	Ile	His	Asp	Ser	Leu	Lys	Lys	Leu	Pro						
	115				120						125										
Phe	Pro	Val	Arg	Lys	Ile	Gly	Lys	Asp	Phe	Lys	Leu	Asn	Val	Leu	Lys						
	130				135						140										
Gly	Asp	Ile	Asp	Tyr	His	Lys	Pro	Arg	Pro	Ile	Gly	Tyr	Glu	Ile	Asp						
145	150				155						160										

Asp Glu Glu Tyr Gln Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu
 165 170 175
 Ala Leu Glu Val Gln Thr Val Gln Gly Leu Thr Gly Met Thr Asn Gly
 180 185 190
 Ser Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe
 195 200 205
 Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg
 210 215 220
 Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly
 225 230 235 240
 Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro
 245 250 255
 Ala Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe
 260 265 270
 Glu Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His
 275 280 285
 Ile Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln
 290 295 300
 Ile Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser
 305 310 315 320
 Gly Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu
 325 330 335
 Met Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu
 340 345 350
 Lys Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp
 355 360 365
 Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys
 370 375 380
 Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val
 385 390 395 400
 Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg

405 410 415
 Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val
 420 425 430
 Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala
 435 440 445
 Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr
 450 455 460
 Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys

465 470 475 480
 Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu
 485 490 495
 Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly
 500 505 510
 Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser
 515 520 525
 Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe

530 535 540
 Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val
 545 550 555 560
 Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570 575

<210> 117

<211> 576

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 117

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asp Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

 130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Asp Arg Asp Leu Pro Cys Gly Val Pro Ile Pro Phe Glu

 260 265 270
 Gly Glu Tyr Val Tyr Asp Lys Ser His Pro Leu Tyr Ile Gln Lys Leu
 275 280 285

Thr Phe Glu Phe Glu Leu Lys Glu Asn Tyr Ile Pro Thr Ile Gln Leu
290 295 300

Lys Asn Ser Arg Phe Gly Phe Lys Gly Asn Glu Tyr Leu Ser Ser Ser
305 310 315 320

Asn Gly Glu Arg Ile Thr Ile Ser Val Ser Ser Val Asp Trp Glu Leu
325 330 335

Ile Arg Glu His Tyr His Val Tyr Asp Val Glu Phe Glu Lys Gly Trp
340 345 350

Lys Phe Arg Ser Thr Lys Gln Ala Phe Lys Asp Phe Ile Asp Lys Trp
355 360 365

Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys
370 375 380

Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val
385 390 395 400

Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg
405 410 415

Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val
420 425 430

Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala
435 440 445

Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr
450 455 460

Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys
465 470 475 480

Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu
485 490 495

Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly
500 505 510

Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser
515 520 525

Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe

530 535 540
 Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val
 545 550 555 560
 Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570 575
 <210> 118
 <211> 577
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 118
 Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15
 Thr Asp Val Asn Asp Cys Arg Val Trp Ala Tyr Gly Trp Met Glu Ile
 20 25 30
 Gly Lys Thr Ser Asn Tyr Lys Ile Gly Thr Asp Phe Asn Glu Phe Met
 35 40 45
 Glu Trp Met Ile His Ser Ser Ser Arg Leu Tyr Phe His Asp Leu Lys
 50 55 60
 Phe Asp Gly Ser Phe Ile Val Asn Trp Leu Leu His Asn Gly Tyr Thr
 65 70 75 80
 Trp Thr Lys Arg Pro Ser Lys Glu Gly Gln Phe Ser Thr Leu Ile Ser
 85 90 95
 Lys Met Gly Gln Trp Tyr Gly Ile Thr Ile Cys Ser Gly Arg Asp Gly
 100 105 110
 Arg Lys Lys Lys Leu Thr Thr Ile His Asp Ser Leu Lys Lys Leu Pro
 115 120 125
 Phe Pro Val Arg Lys Ile Gly Lys Asp Phe Lys Leu Asn Val Leu Lys
 130 135 140
 Gly Asp Ile Asp Tyr His Lys Pro Arg Pro Ile Gly Tyr Glu Ile Asp
 145 150 155 160
 Asp Glu Glu Tyr Gln Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175
Ala Leu Glu Val Gln Thr Val Gln Gly Leu Thr Gly Met Thr Asn Gly

180 185 190
Ser Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205
Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220
Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240
Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro

245 250 255
Ala Gln Met Tyr Asp Arg Asp Leu Pro Cys Gly Val Pro Ile Pro Phe

260 265 270
Glu Gly Glu Tyr Val Tyr Asp Lys Ser His Pro Leu Tyr Ile Gln Lys

275 280 285
Leu Thr Phe Glu Phe Glu Leu Lys Glu Asn Tyr Ile Pro Thr Ile Gln

290 295 300
Leu Lys Asn Ser Arg Phe Gly Phe Lys Gly Asn Glu Tyr Leu Ser Ser

305 310 315 320
Ser Asn Gly Glu Arg Ile Thr Ile Ser Val Ser Ser Val Asp Trp Glu

325 330 335
Leu Ile Arg Glu His Tyr His Val Tyr Asp Val Glu Phe Glu Lys Gly

340 345 350
Trp Lys Phe Arg Ser Thr Lys Gln Ala Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys

<210> 119

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 119

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Phe Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile

275 280 285
 Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

 290 295 300
 Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
 305 310 315 320
 Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
 325 330 335
 Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
 340 345 350
 Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr

 355 360 365
 Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380
 Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
 385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415
 Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

 420 425 430
 Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
 435 440 445
 Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
 450 455 460
 Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
 465 470 475 480
 Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
 500 505 510
 Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
 515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570 575

<210> 120
<211> 582
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 120

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15
Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asn Glu Lys Phe Asp Gly
50 55 60

Glu Phe Met Leu Ser Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly
85 90 95

Gln Trp Tyr Ala Leu Glu Ile Cys Trp Asn Val Lys Cys Thr Thr Thr
100 105 110

Lys Thr Gly Lys Thr Lys Lys Glu Lys Gln Arg Thr Ile Ile Tyr Asp
115 120 125

Ser Leu Lys Lys Tyr Pro Phe Pro Val Lys Glu Ile Ala Glu Ala Phe
130 135 140

Asn Phe Pro Ile Lys Lys Gly Glu Ile Asp Tyr Thr Lys Glu Arg Pro

145 150 155 160
 Ile Gly Tyr Asn Pro Thr Asp Asp Glu Trp Asp Tyr Leu Lys Asn Asp
 165 170 175
 Ile Gln Ile Met Ala Met Ala Leu Lys Ile Gln Phe Asp Gln Gly Leu
 180 185 190
 Thr Arg Met Thr Arg Gly Ser Asp Ala Leu Gly Asp Phe Lys Asp Ile
 195 200 205
 Ile Thr Thr Lys Lys Phe Lys Lys Val Phe Pro Thr Leu Ser Leu Gly
 210 215 220

 Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu
 225 230 235 240
 Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly Glu Gly Met Val Phe Asp
 245 250 255
 Ala Asn Ser His Tyr Pro Ala Gln Met Tyr Ser Arg Leu Leu Pro Tyr
 260 265 270
 Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr Val Trp Asp Glu Asp Tyr
 275 280 285

 Pro Leu His Ile Gln His Ile Arg Cys Glu Phe Glu Leu Lys Glu Gly
 290 295 300
 Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser Arg Phe Tyr Lys Gly Asn
 305 310 315 320
 Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile Ala Asp Leu Trp Leu Ser
 325 330 335
 Asn Val Asp Leu Glu Leu Met Lys Glu His Tyr Asp Leu Tyr Asn Val
 340 345 350

 Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala Thr Thr Gly Leu Phe Lys
 355 360 365
 Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala
 370 375 380
 Ile Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe
 385 390 395 400

Ala Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn

405 410 415

Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val

420 425 430

Tyr Thr Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr

435 440 445

Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr

450 455 460

Asp Ser Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp

465 470 475 480

Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe

485 490 495

Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr

500 505 510

Met Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr

515 520 525

Thr Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile

530 535 540

Lys Lys Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys

545 550 555 560

Met Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp

565 570 575

Glu Thr Phe Thr Ile Lys

580

<210> 121

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 121

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
 65 70 75 80

 Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
 115 120 125
 Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
 130 135 140

 Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205

 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
260 265 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
275 280 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
290 295 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305 310 315 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
325 330 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
340 345 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
355 360 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
370 375 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385 390 395 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
405 410 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
420 425 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
435 440 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val
450 455 460

Pro Glu Ala Ile Glu His Leu Val Asp Ser Lys Lys Leu Gly Tyr Trp
465 470 475 480

Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr
485 490 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln

500 505 510
 Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
 515 520 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
 530 535 540
 Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
 545 550 555 560
 Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570

<210> 122

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 122

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80
 Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
 115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130

135

140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145

150

155

160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr

260

265

270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu

275

280

285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser

290

295

300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile

305

310

315

320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His

325

330

335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala

340

345

350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys

355

360

365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn

370 375 380
Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val

385 390 395 400
Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu

405 410 415
Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala

420 425 430
Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg

435 440 445
Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val

450 455 460
Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys Leu Gly Tyr Trp

465 470 475 480
Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr

485 490 495
Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln

500 505 510
Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala

515 520 525
Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys

530 535 540
Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly

545 550 555 560
Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys

565 570

<210> 123

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 123

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140
Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145 150 155 160
Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
165 170 175
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
210 215 220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225 230 235 240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

				245				250				255			
Ser	Arg	Leu	Leu	Pro	Tyr	Gly	Glu	Pro	Ile	Val	Phe	Glu	Gly	Lys	Tyr
260				265				270							
Val	Trp	Asp	Glu	Asp	Tyr	Pro	Leu	His	Ile	Gln	His	Ile	Arg	Cys	Glu
275				280				285							
Phe	Glu	Leu	Lys	Glu	Gly	Tyr	Ile	Pro	Thr	Ile	Gln	Ile	Lys	Arg	Ser
290				295				300							
Arg	Phe	Tyr	Lys	Gly	Asn	Glu	Tyr	Leu	Lys	Ser	Ser	Gly	Gly	Glu	Ile
305				310				315				320			
Ala	Asp	Leu	Trp	Leu	Ser	Asn	Val	Asp	Leu	Glu	Leu	Met	Lys	Glu	His
325				330				335							
Tyr	Asp	Leu	Tyr	Asn	Val	Glu	Tyr	Ile	Ser	Gly	Leu	Lys	Phe	Lys	Ala
340				345				350							
Thr	Thr	Gly	Leu	Phe	Lys	Asp	Phe	Ile	Asp	Lys	Trp	Thr	Tyr	Ile	Lys
355				360				365							
Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala	Lys	Leu	Met	Leu	Asn
370				375				380							
Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp	Val	Thr	Gly	Lys	Val
385				390				395				400			
Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe	Arg	Leu	Gly	Glu	Glu
405				410				415							
Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	Gly	Val	Phe	Ile	Thr	Ala
420				425				430							
Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	Gln	Ala	Cys	Tyr	Asp	Arg
435				440				445							
Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu	Thr	Gly	Thr	Glu	Ile
450				455				460							
Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	Asp	Pro	Lys	Lys	Leu	Gly	Tyr	Trp
465				470				475				480			
Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	Tyr	Leu	Arg	Gln	Lys	Thr
485				490				495							

Tyr Ile Gln Asp Ile Tyr Val Lys Lys Val Arg Gly Tyr Leu Val Gln
500 505 510

Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala
515 520 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545 550 555 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
565 570

<210> 124

<

211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 124

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125
 Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
 130 135 140
 Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

 245 250 255
 Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
 260 265 270
 Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
 275 280 285
 Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
 290 295 300
 Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile

 305 310 315 320
 Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
 325 330 335
 Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
 340 345 350
 Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
 355 360 365

Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn

370 375 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val

385 390 395 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu

405 410 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala

420 425 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg

435 440 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Val

450 455 460

Pro Glu Ala Ile Glu His Leu Val Asp Pro Lys Lys Leu Gly Tyr Trp

465 470 475 480

Glu His Glu Ser Thr Phe Gln Arg Ala Lys Phe Ile Arg Gln Lys Thr

485 490 495

Tyr Ile Gln Asp Ile Tyr Val Lys Lys Val Arg Gly Tyr Leu Val Gln

500 505 510

Cys Ser Pro Asp Glu Ala Thr Thr Thr Lys Phe Ser Val Lys Cys Ala

515 520 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys

530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly

545 550 555 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys

565 570

<210> 125

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 125

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn
1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp
20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu
35 40 45

Met Gln Gly Ser Thr Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
 260 265 270
 Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
 275 280 285
 Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
 290 295 300

 Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
 305 310 315 320
 Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
 325 330 335
 Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
 340 345 350
 Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
 355 360 365

 Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
 370 375 380
 Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
 385 390 395 400
 Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
 405 410 415
 Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
 420 425 430

 Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
 435 440 445
 Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
 450 455 460
 Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
 465 470 475 480
 Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr

485 490 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln

500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala

515 520 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys

530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly

545 550 555 560

Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys

565 570

<210> 126

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 126

Met Ile Lys Lys Tyr Thr Gly Asp Phe Glu Thr Thr Thr Asp Leu Asn

1 5 10 15

Asp Cys Arg Val Trp Ser Trp Gly Val Cys Asp Ile Asp Asn Val Asp

20 25 30

Asn Ile Thr Phe Gly Leu Glu Ile Asp Ser Phe Phe Glu Trp Cys Glu

35 40 45

Met Gln Gly Ser Thr Asp Ile Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys

<210> 127

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 127

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys

<210> 128

<211> 596

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 128

Met Val Arg Gln Ser Thr Ile Ala Ser Pro Ala Arg Gly Gly Val Arg

1 5 10 15
 Arg Ser His Lys Lys Val Pro Ser Phe Cys Ala Asp Phe Glu Thr Thr
 20 25 30
 Thr Asp Glu Asp Asp Cys Arg Val Trp Ser Trp Gly Ile Ile Gln Val
 35 40 45
 Gly Lys Leu Gln Asn Tyr Val Asp Gly Ile Ser Leu Asp Gly Phe Met
 50 55 60
 Ser His Ile Ser Glu Arg Ala Ser His Ile Tyr Phe His Asp Leu Lys

65 70 75 80
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

85 90 95
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 100 105 110
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 115 120 125
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

 130 135 140
 Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
 145 150 155 160
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 165 170 175
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 180 185 190
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

 195 200 205
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 210 215 220
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 225 230 235 240
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 245 250 255
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

 260 265 270
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 275 280 285
 Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
 290 295 300
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 305 310 315 320
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

 325 330 335

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
 340 345 350
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
 355 360 365
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 370 375 380
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

 385 390 395 400
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 405 410 415
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
 420 425 430
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
 435 440 445
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

 450 455 460
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 465 470 475 480
 Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
 485 490 495
 Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
 500 505 510
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

 515 520 525
 Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
 530 535 540
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
 545 550 555 560
 Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
 565 570 575
 Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

580 585 590

Phe Thr Ile Lys

595

<210> 129

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 129

Met Asn Glu Tyr Ile Ser Asp Phe Glu Thr Gln Lys Asp Pro Asp Thr

1 5 10 15

Gly Val Met Ser Val Trp Ala Trp Ser Ile Val Asp Val Asn Asp Leu

20 25 30

Ser Asn Ile Gln Tyr Gly Asn Asn Ile Glu Ser Trp Leu Ser Ala Ile

35 40 45

Gln Gly Leu Pro Asn Gly Ser Leu Ile Gly Phe His Asp Leu Lys Phe

50 55 60

Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp

65 70 75 80

Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met

85 90 95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg

100 105 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190
 Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys
 195 200 205
 Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala
 210 215 220
 Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

 225 230 235 240
 Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln
 245 250 255
 Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly
 260 265 270
 Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys
 275 280 285
 Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys

 290 295 300
 Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn
 305 310 315 320
 Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp
 325 330 335
 Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr
 340 345 350
 Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile

 355 360 365
 Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln
 370 375 380
 Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn
 385 390 395 400
 Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu
 405 410 415
 Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro

 420 425 430

Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala
435 440 445
Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile
450 455 460
His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp
465 470 475 480
Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala
485 490 495
Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg
500 505 510
Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile
515 520 525
Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu
530 535 540
Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro
545 550 555 560
Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe
565 570 575
Thr Ile Lys

<210> 130

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 130

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125
Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp
130 135 140
Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
145 150 155 160
Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
165 170 175
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
210 215 220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225 230 235 240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys

<210> 131

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 131

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Gly Trp
 355 360 365
 Ile Asp Lys Trp Ile Glu Val Lys Asn Thr Thr Glu Gly Ala Arg Lys
 370 375 380
 Ala Asn Ala Lys Gly Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460
 Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
 465 470 475 480
 Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
 500 505 510
 Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu
 530 535 540
 Leu Val Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys
 545 550 555 560
 Leu Leu Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met
 565 570 575
 Phe Thr Ile Lys

580

<210> 132

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 132

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

 115 120 125
 Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
 130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr
 385 390 395 400
 Asn Pro Asp Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile
 405 410 415
 Val Arg Leu Thr Leu Gly Glu Glu Glu Leu Arg Asp Pro Val Tyr Thr
 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 450 455 460
 Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
 465 470 475 480
 Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

 500 505 510
 Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu
 530 535 540
 Leu Val Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys
 545 550 555 560
 Leu Leu Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met

565 570 575
 Phe Thr Ile Lys
 580

<210> 133

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 133

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Tyr Ser Glu
 260 265 270
 Gly Ala Pro Arg Thr Asn Arg Pro Leu Tyr Ile Ala Ser Ile Thr Phe
 275 280 285
 Thr Ala Lys Leu Lys Pro Asn His Ile Pro Cys Ile Gln Ile Lys Lys

 290 295 300
 Asn Leu Ser Phe Asn Pro Thr Gln Tyr Leu Glu Glu Val Lys Glu Pro
 305 310 315 320
 Thr Thr Val Val Ala Thr Asn Ile Asp Ile Glu Leu Trp Lys Lys His
 325 330 335
 Tyr Asp Phe Lys Ile Tyr Ser Trp Asn Gly Thr Phe Glu Phe Arg Gly
 340 345 350
 Ser His Gly Phe Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys

 355 360 365
 Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
 370 375 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
385 390 395 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
405 410 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala

420 425 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
435 440 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
450 455 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
465 470 475 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr

485 490 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
515 520 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly

545 550 555 560
Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys

565 570

<210> 134

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 134

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Ile Gly Thr Pro Val Phe Phe Glu

260 265 270
 Gly Lys Tyr Lys Asp Asp Pro Ile Tyr Pro Leu Tyr Ile Gln Phe Ile
 275 280 285

 Thr Ala Gln Phe Glu Leu Lys Lys Gly Lys Ile Pro Thr Ile Gln Ile
 290 295 300
 Lys Asn Asp Lys Arg Phe Asn Pro Arg Glu Tyr Val Thr Ser Thr Gly
 305 310 315 320
 Cys Leu Met Val Asn Leu Tyr Leu Thr Asn Val Asp Leu Glu Met Phe
 325 330 335
 Tyr Glu Cys Tyr Asn Ile Lys Glu Ile Gln Tyr Ile Gly Gly Tyr Lys
 340 345 350

 Phe Ile Gly Arg Ser Gly Ile Phe Lys Asp Phe Ile Asp Lys Trp Thr
 355 360 365
 Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380
 Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
 385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415

 Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
 420 425 430
 Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
 435 440 445
 Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
 450 455 460
 Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
 465 470 475 480

 Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
 500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
 515 520 525
 Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
 530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
 545 550 555 560
 Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile Lys
 565 570 575

<210> 135

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 135

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
 65 70 75 80
 Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

 420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

 435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

 500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

 565 570 575
Lys

<210> 136

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 136

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575
Lys

<210> 137

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 137

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Asn
65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 138

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 138

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Thr Leu Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys

 <210> 139
 <211> 577
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 139
 Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp
 500 505 510
 Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575

Lys

<210> 140

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 140

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp

500 505 510
Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 141

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 141

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

 420 425 430
 Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

 435 440 445
 Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
 Lys

<210> 142

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 142

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 143

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 143

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp

500 505 510

Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys

<210> 144

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 144

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130

135

140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145

150

155

160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290

295

300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305

310

315

320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325

330

335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340

345

350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355

360

365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

 420 425 430
 Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp

 500 505 510
 Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

 565 570 575
 Lys

<210> 145

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 145

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

420 425 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445

Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp

500 505 510
Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 146

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 146

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln
435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp
500 505 510

Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys

<210> 147

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 147

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290

295

300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305

310

315

320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325

330

335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340

345

350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355

360

365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370

375

380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385

390

395

400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405

410

415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420

425

430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435

440

445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp

500 505 510
Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 148

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 148

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80
 Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
 115 120 125
 Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140
 Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp
 500 505 510
 Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys

<210> 149

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 149

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
210 215 220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225 230 235 240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 150

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 150

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln
435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys

<210> 151

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 151

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

420 425 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445

Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp

500 505 510

Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

Lys

<210> 152

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 152

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp
500 505 510
Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575
Lys

<210> 153

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 153

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala
420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp

500 505 510
Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 154

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 154

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp

 500 505 510
Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe

 515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

 565 570 575
Lys

<210> 155

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 155

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

 35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

 50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp

385 390 395 400
Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu

405 410 415
Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp

500 505 510
Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr

530 535 540
Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro

545 550 555 560
Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile

565 570 575

Lys

<210> 156

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 156

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125
Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140
Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160
Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp

385 390 395 400

Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu

405 410 415

Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

420 425 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp

500 505 510
Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 157

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 157

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

 420 425 430
 Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

 435 440 445
 Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp

 500 505 510
 Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr

 530 535 540

Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro
 545 550 555 560
 Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile

565 570 575
 Lys

<210> 158

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 158

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80
 Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95
 Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125
 Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140
 Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp

385 390 395 400

Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu

405 410 415
Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp

500 505 510
Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr

530 535 540
Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro

545 550 555 560
Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile

565 570 575
Lys

<210> 159

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 159

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp

385 390 395 400
Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu

405 410 415
Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp

500 505 510

Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575
Lys

<210> 160

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 160

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130

135

140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145

150

155

160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290

295

300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305

310

315

320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325

330

335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340

345

350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355

360

365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

 420 425 430
 Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

 435 440 445
 Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp

 500 505 510
 Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr

 530 535 540
 Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro

 545 550 555 560
 Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile

 565 570 575
 Lys

<210> 161

<211> 618

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 161

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Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1           5           10           15
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
           20           25           30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
           35           40           45
Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

           50           55           60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65           70           75           80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
           85           90           95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
           100          105          110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

           115          120          125
Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
           130          135          140
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145          150          155          160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
           165          170          175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

           180          185          190
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
           195          200          205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
           210          215          220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225          230          235          240

```

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Phe

340 345 350

Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460

Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480

Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565 570 575
Phe Thr Ile Lys Gly His His His His His His His His His Gly

580 585 590
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe

595 600 605
Phe Glu Ala Gln Lys Ile Glu Trp His Glu

610 615

<210> 162

<211> 618

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 162

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe	Asp	Gly	Ala	Phe	Ile	Ile	Asn	Trp	Leu	Glu	Arg	Asn	Gly	Phe	Lys				
65					70					75					80				
Trp	Ser	Ala	Asp	Gly	Leu	Pro	Asn	Thr	Tyr	Asn	Thr	Ile	Ile	Ser	Arg				
85					90					95									
Met	Gly	Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Leu	Gly	Tyr	Lys	Gly	Lys				
100					105					110									
Arg	Lys	Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe				
115					120					125									
Pro	Val	Glu	Lys	Ile	Ala	Lys	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly				
130					135					140									
Asp	Ile	Asp	Ile	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro				
145					150					155					160				
Glu	Glu	Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala				
165					170					175									
Leu	Leu	Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser				
180					185					190									
Asp	Ser	Leu	Lys	Gly	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys				
195					200					205									
Lys	Val	Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys				
210					215					220									
Ala	Tyr	Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys				
225					230					235					240				
Glu	Ile	Gly	Glu	Gly	Met	Val	Phe	Asp	Ala	Asn	Ser	His	Tyr	Pro	Ala				
245					250					255									
Gln	Met	Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu				
260					265					270									
Gly	Glu	Tyr	Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile				
275					280					285									
Lys	Val	Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val				
290					295					300									
Lys	Gln	Ser	Ser	Leu	Phe	Ile	Gln	Thr	Glu	Tyr	Leu	Glu	Ser	Ser	Val				

305						310						315						320
Asn	Lys	Leu	Gly	Val	Asp	Glu	Leu	Ile	Glu	Leu	Thr	Leu	Thr	Asn	Val			
325					330					335								
Asp	Leu	Asp	Leu	Phe	Phe	Glu	His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Phe			
340					345					350								
Thr	Tyr	Gly	Tyr	Met	Phe	Arg	Gly	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe			
355					360					365								
Ile	Asp	Lys	Phe	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys			
370					375					380								
Gln	Leu	Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser			
385					390					395					400			
Asn	Pro	Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala			
405					410					415								
Leu	Gly	Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr			
420					425					430								
Pro	Met	Gly	Val	Phe	Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr			
435					440					445								
Ala	Ala	Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser			
450					455					460								
Ile	His	Leu	Thr	Gly	Thr	Glu	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val			
465					470					475					480			
Asp	Pro	Lys	Lys	Leu	Gly	Tyr	Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg			
485					490					495								
Ala	Lys	Tyr	Leu	Arg	Gln	Lys	Thr	Tyr	Ile	Gln	Asp	Ile	Tyr	Met	Lys			
500					505					510								
Arg	Val	Lys	Gly	Tyr	Leu	Val	Gln	Gly	Ser	Pro	Asp	Asp	Tyr	Thr	Asp			
515					520					525								
Ile	Lys	Phe	Ser	Val	Lys	Cys	Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Lys			
530					535					540								
Glu	Val	Thr	Phe	Glu	Asn	Phe	Lys	Val	Gly	Phe	Ser	Arg	Lys	Met	Lys			
545					550					555					560			

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr
565 570 575

Phe Thr Ile Lys Gly His His His His His His His His His Gly
580 585 590

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe
595 600 605

Phe Glu Ala Gln Lys Ile Glu Trp His Glu
610 615

<210> 163

<211> 618

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 163

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln

 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Ile
 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 290 295 300
 Lys Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val

 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460

Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480

Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510

Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys

530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565 570 575

Phe Thr Ile Lys Gly His His His His His His His His His Gly

580 585 590

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe

595 600 605

Phe Glu Ala Gln Lys Ile Glu Trp His Glu

610 615

<210> 164

<211> 618

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 164

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270

 Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu
 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Thr Glu Tyr Leu Glu Ser Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val
 325 330 335

 Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400

 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460

Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480

Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510

Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525

Ile	Lys	Phe	Ser	Val	Lys	Cys	Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Lys		
530					535					540							
Glu	Val	Thr	Phe	Glu	Asn	Phe	Lys	Val	Gly	Phe	Ser	Arg	Lys	Met	Lys		
545					550					555						560	
Pro	Lys	Pro	Val	Gln	Val	Pro	Gly	Gly	Val	Val	Leu	Val	Asp	Glu	Thr		
565					570					575							
Phe	Thr	Ile	Lys	Gly	His	His	His	His	His	His	His	His	His	His	Gly		
580					585					590							

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe
595 600 605
Phe Glu Ala Gln Lys Ile Glu Trp His Glu
610 615

<210> 165

<211> 618

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 165

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
 130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 290 295 300
 Lys Gln Asn Ser Leu Phe Ile Gln Thr Glu Tyr Leu Glu Asn Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Val Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Phe

 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Phe Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 450 455 460
 Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val

 465 470 475 480
 Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
 500 505 510
 Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
 515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys

530

535

540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545

550

555

560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565

570

575

Phe Thr Ile Lys Gly His His His His His His His His His Gly

580

585

590

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe

595

600

605

Phe Glu Ala Gln Lys Ile Glu Trp His Glu

610

615

<210> 166

<211> 618

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 166

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1

5

10

15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20

25

30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35

40

45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50

55

60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65

70

75

80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85

90

95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
 130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu
 275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Thr Glu Tyr Leu Glu Ser Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Val Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Phe
 340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
355 360 365

Ile Asp Lys Phe Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
420 425 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
435 440 445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460

Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480

Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
500 505 510

Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr
565 570 575

Phe Thr Ile Lys Gly His His His His His His His His His Gly
580 585 590

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe

595	600	605
Phe Glu Ala Gln Lys Ile Glu Trp His Glu		
610	615	
<210>	167	
<211>	618	
<212>	PRT	
<213>	Artificial sequence	
<220><223>	Synthetic polypeptide	
<400>	167	
Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr		
1	5	10
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile		
	20	25
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met		
	35	40
Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys		
50	55	60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys		
65	70	75
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg		
	85	90
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys		
	100	105
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe		
	115	120
Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly		
130	135	140
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro		
145	150	155
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala		

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu
 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val

 290 295 300
 Lys Gln Asn Ser Leu Phe Ile Gln Thr Glu Tyr Leu Glu Asn Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Phe
 340 345 350
 Thr Tyr Gly Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe

 355 360 365
 Ile Asp Lys Phe Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430
Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
435 440 445
Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460
Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480
Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
500 505 510
Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr
565 570 575
Phe Thr Ile Lys Gly His His His His His His His His His Gly
580 585 590
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe
595 600 605
Phe Glu Ala Gln Lys Ile Glu Trp His Glu

610 615

<210> 168

<211> 618

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 168

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45

 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110

 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
 130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175

 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240

 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln
260 265 270

Gly Glu Tyr Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Leu
275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
290 295 300

Lys Gln Asn Ser Leu Phe Ile Gln Thr Glu Tyr Leu Glu Asn Ser Val
305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val
325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Phe
340 345 350

Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe
355 360 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
420 425 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
435 440 445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460

Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480

Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
 Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
 515 520 525
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
 530 535 540
 Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
 545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr
 565 570 575
 Phe Thr Ile Lys Gly His His His His His His His His His Gly
 580 585 590
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe
 595 600 605
 Phe Glu Ala Gln Lys Ile Glu Trp His Glu
 610 615

<210> 169

<211> 577

<212>

> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 169

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

 305 310 315 320
 Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp
 325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys

<210> 170

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 170

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu
 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Val Thr Asn Val Asp Leu Asp
 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575
Lys

<210> 171

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 171

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

 85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
 115 120 125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225 230 235 240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr
 260 265 270
Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn
290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320
 Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp
 325 330 335
 Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys

<210> 172

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 172

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
115 120 125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
145 150 155 160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
210 215 220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225 230 235 240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
260 265 270
Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg
275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser
290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305 310 315 320
Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp
325 330 335
Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly
340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 173

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 173

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg
 275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Val Thr Asn Val Asp Leu Asp
 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Phe Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Phe Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 174

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 174

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
115 120 125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
130 135 140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu
 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
 325 330 335
 Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys

<210> 175

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 175

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys

<210> 176

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 176

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Asn

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

 565 570 575
 Lys

<210> 177

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 177

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 178

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 178

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Asn

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys

<210> 179

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 179

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Asn

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 180

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 180

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270
 Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Asn
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320
 Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Phe Thr Tyr Gly
 340 345 350
 Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Phe Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys

<210> 181

<211> 618

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 181

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255
Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln

260 265 270
Gly Glu Tyr Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu
275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val
290 295 300

Lys Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val

305 310 315 320
Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val

325 330 335
Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr
340 345 350

Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe
355 360 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380
Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400
Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430
Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460
Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480
Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565 570 575
Phe Thr Ile Lys Gly His His His His His His His His His Gly

580 585 590
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe

595 600 605
Phe Glu Ala Gln Lys Ile Glu Trp His Glu

610 615

<210> 182

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 182

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45
Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125
Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240
Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

				245				250				255			
Gln	Met	Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Gln
260								265				270			
Gly	Glu	Tyr	Lys	Glu	Asn	Ile	Gln	His	Pro	Leu	Tyr	Ile	Gln	Asn	Leu
275								280				285			
Lys	Val	Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val
290								295				300			
Lys	Gln	Asn	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Asn	Ser	Val
305				310				315				320			
Asn	Lys	Leu	Gly	Val	Asp	Glu	Leu	Ile	Glu	Leu	Thr	Val	Thr	Asn	Val
325								330				335			
Asp	Leu	Asp	Leu	Phe	Phe	Glu	His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Tyr
340								345				350			
Thr	Tyr	Gly	Tyr	Met	Phe	Arg	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe
355								360				365			
Ile	Asp	Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys
370				375				380							
Gln	Leu	Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser
385				390				395				400			
Asn	Pro	Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala
405								410				415			
Leu	Gly	Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr
420								425				430			
Pro	Met	Gly	Val	Phe	Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr
435				440				445							
Ala	Ala	Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser
450				455				460							
Ile	His	Leu	Thr	Gly	Thr	Glu	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val
465				470				475				480			
Asp	Pro	Lys	Lys	Leu	Gly	Tyr	Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg
485				490				495							

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
500 505 510

Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr
565 570 575

Phe Thr Ile Lys
580

<210> 183

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 183

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Asn
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Leu

100	105	110	
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu			
115	120	125	
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp			
130	135	140	
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr			
145	150	155	160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile			
165	170	175	
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu			
180	185	190	
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe			
195	200	205	
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg			
210	215	220	
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly			
225	230	235	240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr			
245	250	255	
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr			
260	265	270	
Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg			
275	280	285	
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn			
290	295	300	
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu			
305	310	315	320
Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp			
325	330	335	
Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly			
340	345	350	

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys Gly His His His His His His His His His Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605

Gln Lys Ile Glu Trp His Glu

610 615

<210> 184

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 184

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Glu Val Asp

500 505 510
Gly Lys Leu Lys Glu Cys Ser Pro Asp Glu Ala Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys Gly His His His His His His His His His His Gly Gly Gly Ser

580 585 590
Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu

610 615

<210> 185

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 185

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Val Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Arg Cys Phe Asp Asn Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp
500 505 510

Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
595 600 605

Gln Lys Ile Glu Trp His Glu
610 615

<210> 186
<211> 615
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 186

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Lys Asp Phe Gln Leu Pro Leu Leu Lys Gly Asp Ile Asp

130 135 140

Tyr His Thr Glu Arg Pro Val Gly His Glu Ile Thr Pro Glu Glu Tyr

145 150 155 160

Glu Tyr Ile Lys Asn Asp Ile Glu Ile Ile Ala Arg Ala Leu Asp Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Val Lys Arg Val Asp

500 505 510
Gly Tyr Leu Val Glu Cys Ser Pro Asp Glu Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605

Gln Lys Ile Glu Trp His Glu
610 615

<210> 187
<211> 615
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 187

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Phe Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys Gly His His His His His His His His His His Gly Gly Gly Ser

580 585 590
Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu

610 615

<210> 188

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 188

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225				230				235				240			
Glu	Gly	Met	Val	Phe	Asp	Ala	Asn	Ser	His	Tyr	Pro	Ala	Gln	Met	Tyr
				245				250				255			
Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	Tyr
				260				265				270			
Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val	Arg
				275				280				285			
Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val	Lys	Gln	Ser
290				295				300							
Ser	Leu	Phe	Ile	Gln	Thr	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	Leu
305				310				315				320			
Gly	Val	Asp	Glu	Leu	Ile	Glu	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	Asp
				325				330				335			
Leu	Phe	Phe	Glu	His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Phe	Thr	Tyr	Gly
				340				345				350			
Tyr	Met	Phe	Arg	Gly	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	Lys
355				360				365							
Phe	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala
370				375				380							
Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp
385				390				395				400			
Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe
				405				410				415			
Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	Gly
420				425				430							
Val	Phe	Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	Gln
435				440				445							
Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu
450				455				460							
Thr	Gly	Thr	Glu	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	Asp	Pro	Lys
465				470				475				480			

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
595 600 605

Gln Lys Ile Glu Trp His Glu
610 615

<210> 189

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 189

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn
 290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys Gly His His His His His His His His His Gly Gly Gly Ser

580 585 590
Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu

610 615

<210> 190

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 190

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Thr Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys Gly His His His His His His His His His His Gly Gly Gly Ser

 580 585 590
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
 595 600 605
 Gln Lys Ile Glu Trp His Glu
 610 615

<210> 191

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 191

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

290 295 300

Ser Leu Phe Ile Gln Thr Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Val Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Phe Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Phe Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys Gly His His His His His His His His His His Gly Gly Gly Ser

580 585 590
Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu

610 615

<210> 192

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 192

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Thr Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Val Thr Asn Val Asp Leu Asp
325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Phe Thr Tyr Gly
340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Phe Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys Gly His His His His His His His His His Gly Gly Gly Ser

580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605

Gln Lys Ile Glu Trp His Glu

610 615

<210> 193

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 193

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100	105	110	
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu			
115	120	125	
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp			
130	135	140	
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr			
145	150	155	160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile			
165	170	175	
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu			
180	185	190	
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe			
195	200	205	
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg			
210	215	220	
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly			
225	230	235	240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr			
245	250	255	
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr			
260	265	270	
Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg			
275	280	285	
Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Asn			
290	295	300	
Ser Leu Phe Ile Gln Thr Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu			
305	310	315	320
Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp Leu Asp			
325	330	335	
Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Phe Thr Tyr Gly			
340	345	350	

Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365

 Phe Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430

 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495

 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560

 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys Gly His His His His His His His His His Gly Gly Gly Ser
 580 585 590
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu
610 615
<210> 194
<211> 615
<212> PRT
<213> Artificial sequence

<220><223> Synthetic polypeptide
<400> 194
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
130 135 140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
145 150 155 160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

290 295 300
Ser Leu Phe Ile Gln Thr Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Phe Thr Tyr Gly

340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys Gly His His His His His His His His His His Gly Gly Gly Ser

580 585 590
Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu

610 615

<210> 195

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 195

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
595 600 605

Gln Lys Ile Glu Trp His Glu
610 615

<210> 196
<211> 615
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 196

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys Trp Ser Ala
65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85

90

95

Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Ile

100

105

110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115

120

125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130

135

140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145

150

155

160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290

295

300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305

310

315

320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser
580 585 590
Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
595 600 605
Gln Lys Ile Glu Trp His Glu
610 615
<210> 197
<211> 615
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 197
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
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Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Leu
100 105 110
His Thr Ile Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
115 120 125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Leu Lys Lys Gly Asp Ile Asp
130 135 140
Ile His Lys Glu Arg Pro Ile Gly Tyr Lys Ile Thr Pro Asp Glu Tyr
145 150 155 160

Ala Tyr Leu Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys Gly His His His His His His His His His His Gly Gly Gly Ser

580 585 590
Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu

610 615

<210> 198

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 198

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu

100 105 110

His Thr Ile Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Leu Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Ile Gly Tyr Lys Ile Thr Pro Asp Glu Tyr

145 150 155 160

Ala Tyr Leu Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225				230				235				240			
Glu	Gly	Met	Val	Phe	Asp	Ala	Asn	Ser	His	Tyr	Pro	Ala	Gln	Met	Tyr
245				250				255							
Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	Tyr
260				265				270							
Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val	Arg
275				280				285							
Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln	Ser
290				295				300							
Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	Leu
305				310				315				320			
Gly	Val	Asp	Glu	Leu	Ile	Asp	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	Asp
325				330				335							
Leu	Phe	Phe	Glu	His	Tyr	Asp	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	Gly
340				345				350							
Tyr	Met	Phe	Lys	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	Lys
355				360				365							
Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala
370				375				380							
Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp
385				390				395				400			
Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe
405				410				415							
Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	Gly
420				425				430							
Val	Phe	Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	Gln
435				440				445							
Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu
450				455				460							
Thr	Gly	Thr	Glu	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	Asp	Pro	Lys
465				470				475				480			

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
595 600 605

Gln Lys Ile Glu Trp His Glu
610 615

<210> 199

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 199

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80
 Glu Gly Ile Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Phe Gly Tyr Lys Gly Lys Arg Lys Leu
 100 105 110
 His Thr Ile Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Leu Lys Lys Gly Asp Ile Asp
 130 135 140
 Ile His Lys Glu Arg Pro Ile Gly Tyr Lys Ile Thr Pro Asp Glu Tyr
 145 150 155 160
 Ala Tyr Leu Lys Asn Asp Ile Gln Ile Leu Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys Gly His His His His His His His His His Gly Gly Gly Ser

580 585 590
Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu

610 615

<210> 200

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 200

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn

65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys Gly His His His His His His His His His His Gly Gly Gly Ser

 580 585 590
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
 595 600 605
 Gln Lys Ile Glu Trp His Glu
 610 615

<210> 201

<211> 616

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 201

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

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Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430

Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
 Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro

 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val

 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr
 565 570 575
 Ile Lys Gly His His His His His His His His His His Gly Gly Gly
 580 585 590
 Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu

 595 600 605
 Ala Gln Lys Ile Glu Trp His Glu
 610 615
 <210> 202
 <211> 616
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 202
 Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Leu His Asn Gly Tyr Thr Trp Thr Lys
 65 70 75 80
 Arg Pro Ser Lys Glu Gly Gln Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95

 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160

 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220

 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415

 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met
 420 425 430
 Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro
 465 470 475 480

 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr
565 570 575

Ile Lys Gly His His His His His His His His His Gly Gly Gly
580 585 590

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu
595 600 605

Ala Gln Lys Ile Glu Trp His Glu
610 615

<210> 203

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 203

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
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Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Leu His Lys Gly Tyr Glu Cys Asn Glu
65 70 75 80

Ser Gly Arg Pro Lys Thr Phe Asp Thr Ile Ile Ser Arg Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys Gly His His His His His His His His His Gly Gly Gly Ser

580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu
610 615

<210> 204
<211> 616
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 204

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
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20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Leu Lys His Gly Tyr Arg Trp Thr Lys
65 70 75 80
Glu Asn Pro Gly Val Lys Glu Phe Thr Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr
 565 570 575
 Ile Lys Gly His His His His His His His His His Gly Gly Gly
 580 585 590
 Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu
 595 600 605
 Ala Gln Lys Ile Glu Trp His Glu
 610 615
 <210> 205
 <211> 616
 <212> PRT
 <213> Artificial sequence

 <220><223> Synthetic polypeptide
 <400> 205

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190
Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240
Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met
 420 425 430
 Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val

530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr

565 570 575

Ile Lys Gly His His His His His His His His His His Gly Gly Gly

580 585 590

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu

595 600 605

Ala Gln Lys Ile Glu Trp His Glu

610 615

<210> 206

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 206

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

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Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Lys Asn Gly Phe Lys Trp Thr Ala

65 70 75 80
 Glu Gly Glu Pro Asn Thr Tyr Ser Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
 115 120 125

 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190

 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255

 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
 305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565

570

575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser

580

585

590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595

600

605

Gln Lys Ile Glu Trp His Glu

610

615

<210> 207

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 207

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

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15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20

25

30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35

40

45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Leu Lys Asn Gly Phe Lys Trp Thr Ala

65

70

75

80

Glu Gly Leu Pro Arg Thr Tyr Ser Thr Ile Ile Ser Arg Met Gly Gln

85

90

95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100

105

110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115

120

125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130

135

140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205

 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
 260 265 270

 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
 325 330 335

 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser

580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605

Gln Lys Ile Glu Trp His Glu

610 615

<210> 208

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 208

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Tyr Lys Trp Thr Ala

65 70 75 80

Glu Gly Leu Pro Asn Thr Phe Ser Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210					215					220						
Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile	Gly	
225					230					235					240	
Glu	Gly	Met	Val	Phe	Asp	Ala	Asn	Ser	His	Tyr	Pro	Ala	Gln	Met	Tyr	
245					250					255						
Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	Tyr	
260					265					270						
Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val	Arg	
275					280					285						
Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln	Ser	
290					295					300						
Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	Leu	
305					310					315					320	
Gly	Val	Asp	Glu	Leu	Ile	Asp	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	Asp	
325					330					335						
Leu	Phe	Phe	Glu	His	Tyr	Asp	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	Gly	
340					345					350						
Tyr	Met	Phe	Lys	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	Lys	
355					360					365						
Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala	
370					375					380						
Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp	
385					390					395					400	
Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe	
405					410					415						
Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	Gly	
420					425					430						
Val	Phe	Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	Gln	
435					440					445						
Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu	
450					455					460						

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
595 600 605

Gln Lys Ile Glu Trp His Glu
610 615

<210> 209

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 209

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
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Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Lys Asn Gly Tyr Lys Trp Thr Ala
 65 70 75 80
 Glu Gly Leu Pro Lys Thr Phe Ser Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110

 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175

 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240

 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560

 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys Gly His His His His His His His His His His Gly Gly Gly Ser
 580 585 590
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
 595 600 605
 Gln Lys Ile Glu Trp His Glu
 610 615
 <210> 210
 <211> 618
 <212> PRT
 <213> Artificial sequence

 <220><223> Synthetic polypeptide
 <400> 210
 Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
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 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Leu Arg Asn Gly Tyr Val His Thr Glu
 65 70 75 80
 Glu Asp Arg Thr Asn Thr Pro Lys Glu Phe Thr Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365
Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380
Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
420 425 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460

Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480

Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565 570 575
Phe Thr Ile Lys Gly His His His His His His His His His Gly
580 585 590

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe
595 600 605

Phe Glu Ala Gln Lys Ile Glu Trp His Glu

610

615

<210> 211

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 211

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1

5

10

15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20

25

30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35

40

45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Phe Arg Leu Gly Tyr Glu Phe Thr Asp

65

70

75

80

Glu Lys Ala Pro Gln Val Lys Glu Phe Ser Thr Ile Ile Ser Arg Met

85

90

95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg

100

105

110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115

120

125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130

135

140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145

150

155

160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165

170

175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180	185	190
Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys		
195	200	205
Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala		
210	215	220
Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu		
225	230	235
Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln		
245	250	255
Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly		
260	265	270
Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys		
275	280	285
Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys		
290	295	300
Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn		
305	310	315
Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp		
325	330	335
Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr		
340	345	350
Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile		
355	360	365
Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln		
370	375	380
Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn		
385	390	395
Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu		
405	410	415
Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro		
420	425	430

Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala
435 440 445

Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile
450 455 460

His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp
465 470 475 480

Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala
485 490 495

Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg
500 505 510

Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile
515 520 525

Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu
530 535 540

Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro
545 550 555 560

Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe
565 570 575

Thr Ile Lys

<210> 212

<211> 618

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 212

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Leu Thr Asp Gly Trp Lys Trp Ile Pro
 65 70 75 80
 Asp Lys Asn Asp Cys Ala Asn Arg Thr Phe Thr Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110

 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
 130 135 140
 Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175

 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240

 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala
 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
 275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
355 360 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
420 425 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
435 440 445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460

Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480

Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
500 505 510

Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys

530 535 540
 Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
 545 550 555 560

 Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr
 565 570 575
 Phe Thr Ile Lys Gly His His His His His His His His His His Gly
 580 585 590
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe
 595 600 605
 Phe Glu Ala Gln Lys Ile Glu Trp His Glu
 610 615
 <210> 213
 <211> 617
 <212>
 > PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 213
 Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Leu Glu Asn Gly Phe Lys His Ser Arg
 65 70 75 80
 Glu Arg Ala Leu Tyr Ser Asn Glu Phe Ser Thr Ile Ile Ser Arg Met
 85 90 95
 Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg
 100 105 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly

260 265 270

Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys

275 280 285

Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys

290 295 300

Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn

305 310 315 320

Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp

325 330 335

Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr

340 345 350

Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365

Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln

370 375 380
Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn
385 390 395 400
Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu
405 410 415
Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro
420 425 430
Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala

435 440 445
 Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile
 450 455 460
 His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp
 465 470 475 480
 Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala
 485 490 495
 Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg

500					505					510					
Val	Lys	Gly	Tyr	Leu	Val	Gln	Gly	Ser	Pro	Asp	Asp	Tyr	Thr	Asp	Ile
515					520					525					
Lys	Phe	Ser	Val	Lys	Cys	Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Lys	Glu
530					535					540					
Val	Thr	Phe	Glu	Asn	Phe	Lys	Val	Gly	Phe	Ser	Arg	Lys	Met	Lys	Pro
545					550					555					560
Lys	Pro	Val	Gln	Val	Pro	Gly	Gly	Val	Val	Leu	Val	Asp	Glu	Thr	Phe

565 570 575

Thr Ile Lys Gly His His His His His His His His His His Gly Gly

580 585 590

Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe

595 600 605

Glu Ala Gln Lys Ile Glu Trp His Glu

610

615

<210> 214

<211> 619

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 214

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1

5

10

15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20

25

30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35

40

45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Leu Gly Val Ala Lys Trp Glu Tyr Asn

65

70

75

80

Asp Lys Pro Lys Ala Arg Lys Ala Lys Thr Val Glu Thr Ile Ile Ser

85

90

95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly

100

105

110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115

120

125

Phe Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys

130

135

140

Gly Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145

150

155

160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165

170

175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180	185	190	
Ser Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe			
195	200	205	
Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg			
210	215	220	
Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly			
225	230	235	240
Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro			
245	250	255	
Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr			
260	265	270	
Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn			
275	280	285	
Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln			
290	295	300	
Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser			
305	310	315	320
Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn			
325	330	335	
Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His			
340	345	350	
Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp			
355	360	365	
Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile			
370	375	380	
Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala			
385	390	395	400
Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly			
405	410	415	
Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr			
420	425	430	

Thr Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile
435 440 445

Thr Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp
450 455 460

Ser Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile
465 470 475 480

Val Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys
485 490 495

Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met
500 505 510

Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr
515 520 525

Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys
530 535 540

Lys Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met
545 550 555 560

Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu
565 570 575

Thr Phe Thr Ile Lys Gly His His His His His His His His His
580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp
595 600 605

Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu
610 615

<210> 215

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 215

Met Ser Arg Lys Met Tyr Ser Ala Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
 Asp Asp Cys Arg Val Trp Ser Tyr Gly Trp Met Glu Val Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Asp Ile Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ser Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

 65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

 130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys Gly His His His His His His His His His His Gly Gly Gly Ser

580 585 590
Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu

610 615
<210> 216

<211> 615
<212> PRT

<213> Artificial sequence
<220><223> Synthetic polypeptide

<400> 216

Met Ser Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Val Met Glu Val Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Asp Ile Asp Glu Phe Met Gln Trp Ile

35 40 45
Met Glu Ile Gln Ser Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605

Gln Lys Ile Glu Trp His Glu
610 615

<210> 217
<211> 615
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 217

Met Ser Arg Lys Val Phe Thr Ala Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Trp Met Glu Val Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Ile Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys Gly His His His His His His His His His His Gly Gly Gly Ser

580 585 590
Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala

595 600 605
Gln Lys Ile Glu Trp His Glu

610 615

<210> 218

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 218

Met Ser Arg Lys Val Tyr Thr Ala Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Trp Met Glu Val Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Ile Asp Glu Phe Met Gln Trp Ile

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225				230				235				240			
Glu	Gly	Met	Val	Phe	Asp	Ala	Asn	Ser	His	Tyr	Pro	Ala	Gln	Met	Tyr
				245				250				255			
Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	Tyr
				260				265				270			
Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val	Arg
				275				280				285			
Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln	Ser
290				295				300							
Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	Leu
305				310				315				320			
Gly	Val	Asp	Glu	Leu	Ile	Asp	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	Asp
				325				330				335			
Leu	Phe	Phe	Glu	His	Tyr	Asp	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	Gly
				340				345				350			
Tyr	Met	Phe	Lys	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	Lys
355				360				365							
Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala
370				375				380							
Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp
385				390				395				400			
Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe
				405				410				415			
Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	Gly
420				425				430							
Val	Phe	Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	Gln
435				440				445							
Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu
450				455				460							
Thr	Gly	Thr	Glu	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	Asp	Pro	Lys
465				470				475				480			

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys Gly His His His His His His His His His His Gly Gly Gly Ser
580 585 590

Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
595 600 605

Gln Lys Ile Glu Trp His Glu
610 615

<210> 219

<211> 615

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 219

Met Ser Arg Lys Met Tyr Thr Ala Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Asp Ile Asp Glu Phe Met Gln Trp Ile
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545	550										555					560							
Val	Gln	Val	Pro	Gly	Gly	Val	Val	Leu	Val	Asp	Glu	Thr	Phe	Thr	Ile								
				565					570					575									
Lys	Gly	His	His	His	His	His	His	His	His	His	His	Gly	Gly	Gly	Ser								
				580					585					590									
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Leu	Asn	Asp	Phe	Phe	Glu	Ala								
				595					600					605									
Gln	Lys	Ile	Glu	Trp	His	Glu																	
				610					615														
<210>	220																						
<211>	615																						
<212>	PRT																						
<213>	Artificial sequence																						
<220><223>	Synthetic polypeptide																						
<400>	220																						
Met	Ser	Arg	Lys	Met	Tyr	Ser	Ala	Asp	Phe	Glu	Thr	Thr	Thr	Lys	Leu								
				5					10					15									
Asp	Asp	Cys	Arg	Val	Trp	Ala	Tyr	Gly	Tyr	Met	Glu	Val	Gly	Asn	Leu								
				20					25					30									
Asp	Asn	Tyr	Lys	Ile	Gly	Asn	Ser	Ile	Asp	Glu	Phe	Met	Gln	Trp	Ile								
				35					40					45									
Met	Glu	Ile	Gln	Ser	Asp	Leu	Tyr	Phe	His	Asp	Leu	Lys	Phe	Asp	Gly								
				50					55					60									
Ala	Phe	Ile	Ile	Asn	Trp	Leu	Glu	Arg	Asn	Gly	Phe	Lys	Trp	Ser	Ala								
				65					70					75					80				
Asp	Gly	Leu	Pro	Asn	Thr	Tyr	Asn	Thr	Ile	Ile	Ser	Arg	Met	Gly	Gln								
				85					90					95									
Trp	Tyr	Met	Ile	Asp	Ile	Cys	Leu	Gly	Tyr	Lys	Gly	Lys	Arg	Lys	Ile								
				100					105					110									
His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val	Glu								
				115					120					125									

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys Gly His His His His His His His His His His Gly Gly Gly Ser

 580 585 590
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp Phe Phe Glu Ala
 595 600 605
 Gln Lys Ile Glu Trp His Glu
 610 615

<210> 221

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 221

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210

215

220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225

230

235

240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245

250

255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260

265

270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275

280

285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290

295

300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305

310

315

320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325

330

335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340

345

350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355

360

365

Ile Asp Lys Trp Phe Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys

370

375

380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385

390

395

400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405

410

415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420

425

430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435

440

445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460
Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480
Asp Pro Lys Lys Leu Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565 570 575
Phe Thr Ile Lys

580

<210> 222

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 222

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45
Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Phe Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

 450 455 460
 Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
 465 470 475 480
 Asp Pro Lys Lys Leu Gly Tyr Trp Asn His Glu Ser Thr Phe Lys Arg
 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
 500 505 510
 Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

 515 520 525
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
 530 535 540
 Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
 545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565 570 575

Phe Thr Ile Lys

580

<210> 223

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 223

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Phe Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys

370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430
Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460
Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480
Asp Pro Lys Lys Leu Gly Tyr Trp Gln His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565 570 575
Phe Thr Ile Lys

580

<210> 224

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 224

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

 355 360 365
 Ile Asp Lys Trp Phe Tyr Ile Lys Thr Arg Ser Glu Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 450 455 460
 Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
 465 470 475 480
 Asp Pro Lys Lys Leu Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg

 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
 500 505 510
 Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
 515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565 570 575

Phe Thr Ile Lys

580

<210> 225

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 225

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

Lys

<210> 226

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 226

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile
565 570 575
Lys

<210> 227

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 227

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr
530 535 540
Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 228

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 228

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys

 <210> 229
 <211> 577
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 229
 Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575

Lys

<210> 230

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 230

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125
Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr
530 535 540
Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile
565 570 575
Lys

<210> 231

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 231

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65

70

75

80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85

90

95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100

105

110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115

120

125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130

135

140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145

150

155

160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

 530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
 Lys

<210> 232

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 232

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 233

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 233

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Gln Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540

Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575

Lys

<210> 234

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 234

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130

135

140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145

150

155

160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290

295

300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305

310

315

320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325

330

335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340

345

350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355

360

365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 235

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 235

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 236

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 236

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln
435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460

Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys
465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile
565 570 575

Lys

<210> 237

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 237

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr

565 570 575
Ile Lys

<210> 238

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 238

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met
 420 425 430
 Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
 Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr
565 570 575

Ile Lys

<210> 239

<211> 577

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 239

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 240

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 240

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr

565 570 575

Ile Lys

<210> 241

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 241

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

 420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

 435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

 500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

 515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

 530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

 565 570 575
Ile Lys

<210> 242

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 242

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270
Tyr Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 243

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 243

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 244

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 244

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Thr Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

 <210> 245
 <211> 578
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 245
 Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575

Ile Lys

<210> 246

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 246

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Ile Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Gln His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Phe Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 247

<211> 580

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 247

Met His Lys Met Ser Lys Lys Met Phe Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val

20 25 30

Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met

35 40 45

Gln Trp Ile Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

 450 455 460
 Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
 465 470 475 480
 Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

 500 505 510
 Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

 515 520 525
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys

 530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr
565 570 575
Phe Thr Ile Lys
580
<210> 248
<211> 580
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 248
Met His Lys Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr
1 5 10 15
Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val
20 25 30
Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Ser Ile Asp Glu Phe Met
35 40 45
Gln Trp Val Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys
50 55 60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125
Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140
Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415
Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430
Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460
Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480
Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565 570 575
Phe Thr Ile Lys

580

<210> 249

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 249

Met Ser Lys Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met Gln Trp Ile

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys

<210> 250

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 250

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met Gln Trp Ile

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130

135

140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145

150

155

160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290

295

300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305

310

315

320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325

330

335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340

345

350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355

360

365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 251

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 251

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Leu Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met Gln Trp Ile

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 252

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 252

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Leu Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Thr Ile Asp Glu Phe Met Gln Trp Ile

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 253

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 253

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Thr Ile Asp Glu Phe Met Gln Trp Ile

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 254

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 254

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met Gln Trp Ile

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu
 115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys

<210> 255

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 255

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Thr Ile Asp Glu Phe Met Gln Trp Ile

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 256

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 256

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Thr Leu Asp Glu Phe Met Gln Trp Ile

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575

Lys

<210> 257

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 257

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Ile Asp Glu Phe Met Gln Trp Ile

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

Lys

<210> 258

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 258

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Leu Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Ile Asp Glu Phe Met Gln Trp Ile

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575
Lys

<210> 259

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 259

Met His Lys Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr
1 5 10 15
Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val
20 25 30
Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met
35 40 45
Gln Trp Ala Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys
50 55 60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365
Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380
Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
385 390 395 400
Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
405 410 415
Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
420 425 430
Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460
Ile His Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480
Asp Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys
530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr

565 570 575
Phe Thr Ile Lys
580

<210> 260

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 260

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
 565 570 575
 Lys

 <210> 261
 <211> 577
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 261
 Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met Gln Trp Ile
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys

<210> 262

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 262

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Thr Ile Asp Glu Phe Met Gln Trp Ile

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575
Lys

<210> 263

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 263

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65

70

75

80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85

90

95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100

105

110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115

120

125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130

135

140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145

150

155

160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
 Lys

<210> 264

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 264

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 265

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 265

Met His Lys Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val

20 25 30

Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met

35 40 45

Gln Trp Ala Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro

245 250 255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260 265 270
Glu Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn

275 280 285
Leu Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln

290 295 300
Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser
305 310 315 320
Val Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn

325 330 335
Val Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His

340 345 350
Tyr Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp

355 360 365
Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile
370 375 380
Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

385 390 395 400
Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly

405 410 415
Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

420 425 430
Thr Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile
435 440 445
Thr Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

450 455 460
Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile

465 470 475 480
Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

485 490 495
Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met

500 505 510

Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr
515 520 525

Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys

530 535 540

Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

545 550 555 560

Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser

565 570 575

Val Phe Thr Ile Lys

580

<210> 266

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 266

Met His Lys Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val

20 25 30

Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met

35 40 45

Gln Trp Ala Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys

130

135

140

Gly Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145

150

155

160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165

170

175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180

185

190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195

200

205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210

215

220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225

230

235

240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro

245

250

255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260

265

270

Glu Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn

275

280

285

Leu Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln

290

295

300

Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305

310

315

320

Val Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn

325

330

335

Val Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His

340

345

350

Tyr Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp

355

360

365

Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile

370 375 380
 Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

 385 390 395 400
 Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly

 405 410 415
 Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

 420 425 430
 Thr Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile

 435 440 445
 Thr Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

 450 455 460
 Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile

 465 470 475 480
 Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

 485 490 495
 Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met

 500 505 510
 Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

 515 520 525
 Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys

 530 535 540
 Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

 545 550 555 560
 Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser

 565 570 575
 Val Phe Thr Ile Lys

 580

 <210
 > 267
 <211> 581
 <212> PRT
 <213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 267

Met His Lys Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val

20 25 30

Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met

35 40 45

Gln Trp Ala Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro

245 250 255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260 265 270

Gln Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn

275 280 285

Leu Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln

290 295 300

Val Lys Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305 310 315 320

Val Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn

325 330 335

Val Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His

340 345 350

Tyr Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp

355 360 365

Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile

370 375 380

Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

385 390 395 400

Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly

405 410 415

Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

420 425 430

Thr Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile

435 440 445

Thr Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

450 455 460

Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile

465 470 475 480

Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

485 490 495
Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met

500 505 510
Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

515 520 525
Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys

530 535 540
Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

545 550 555 560
Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser

565 570 575
Val Phe Thr Ile Lys

580

<210> 268

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 268

Met His Lys Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val

20 25 30

Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met

35 40 45

Gln Trp Ala Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro

245 250 255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260 265 270

Gln Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn

275 280 285

Leu Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln

290 295 300

Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305 310 315 320

Val Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn

325 330 335

Val Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His

340 345 350
 Tyr Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp

 355 360 365
 Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile
 370 375 380
 Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala
 385 390 395 400
 Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly
 405 410 415
 Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

 420 425 430
 Thr Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile
 435 440 445
 Thr Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp
 450 455 460
 Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile
 465 470 475 480
 Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

 485 490 495
 Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met
 500 505 510
 Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr
 515 520 525
 Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys
 530 535 540
 Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

 545 550 555 560
 Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser
 565 570 575
 Val Phe Thr Ile Lys
 580

<210> 269

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 269

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 270

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 270

Met His Lys Met Ser Lys Lys Met Phe Ser Cys Asp Phe Glu Thr Thr

1 5 10 15
Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Val

20 25 30
Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Asn Ile Asp Glu Phe Met

35 40 45
Gln Trp Ile Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro

245 250 255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260 265 270

Glu Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn

275 280 285

Leu Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln

290 295 300

Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305 310 315 320
 Val Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn

 325 330 335
 Val Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His
 340 345 350
 Tyr Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp
 355 360 365
 Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile
 370 375 380
 Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

 385 390 395 400
 Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly
 405 410 415
 Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr
 420 425 430
 Thr Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile
 435 440 445
 Thr Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

 450 455 460
 Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile
 465 470 475 480
 Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys
 485 490 495
 Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met
 500 505 510
 Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

 515 520 525
 Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys
 530 535 540
 Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met
 545 550 555 560

Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser
565 570 575

Val Phe Thr Ile Lys
580

<210

> 271

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 271

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp

50 55 60

Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys

65 70 75 80

Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met

85 90 95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg

100 105 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190
Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205
Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220
Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240
Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255
Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270
Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys

275 280 285
Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290 295 300
Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn

305 310 315 320
Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp

325 330 335
Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr

340 345 350
Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365
Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln

370 375 380
Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn

385 390 395 400
Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu

405 410 415
Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro

420 425 430
Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr

435 440 445
Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile

450 455 460
His Leu Thr Gly Thr Lys Val Pro Asp Ile Ile Lys Asp Leu Val His

465 470 475 480
Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala

485 490 495
Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg

500 505 510
Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile

515 520 525
Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu

530 535 540
Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro

545 550 555 560
Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe

565 570 575
Thr Ile Lys

<210> 272

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 272

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp

50 55 60

Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys

65 70 75 80

Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met

85 90 95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg

100 105 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270

Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys

275 280 285
Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290 295 300
Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn
305 310 315 320
Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp
325 330 335
Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr
340 345 350
Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365
Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln
370 375 380
Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn
385 390 395 400
Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu
405 410 415
Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro

420 425 430
Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr
435 440 445
Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile
450 455 460
His Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His
465 470 475 480
Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala

485 490 495
Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg
500 505 510
Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile
515 520 525

Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu
530 535 540

Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro

545 550 555 560

Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe

565 570 575

Thr Ile Lys

<210> 273

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 273

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp

50 55 60

Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys

65 70 75 80

Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met

85 90 95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg

100 105 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270

Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys

275 280 285

Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290 295 300

Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn

305 310 315 320

Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp

325 330 335

Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr

340 345 350

Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365

Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln

370 375 380

Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn

385 390 395 400
Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu

 405 410 415
Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro

 420 425 430
Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr

 435 440 445
Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile

 450 455 460
His Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His

465 470 475 480
Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala

 485 490 495
Lys Tyr Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys Arg

 500 505 510
Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile

 515 520 525
Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu

 530 535 540
Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro

545 550 555 560
Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe

 565 570 575
Thr Ile Lys

<210> 274

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 274

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp

50 55 60

Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys

65 70 75 80

Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met

85 90 95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg

100 105 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255
Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270
Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys

275 280 285
Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290 295 300
Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn

305 310 315 320
Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp

325 330 335
Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr

340 345 350
Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365
Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln

370 375 380
Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn

385 390 395 400
Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu

405 410 415
Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro

420 425 430
Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr

435 440 445
Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile

450 455 460
His Leu Thr Gly Thr Lys Val Pro Asp Ile Ile Lys Asp Ile Val His

465 470 475 480
Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala

485 490 495

Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg
500 505 510
Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Thr
515 520 525
Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu
530 535 540
Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro
545 550 555 560
Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe
565 570 575
Thr Ile Lys

<210> 275

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 275

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp
50 55 60
Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys
65 70 75 80
Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met
85 90 95
Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg
100 105 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270

Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys

275 280 285

Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290 295 300

Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn

305 310 315 320

Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp

325 330 335

Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr

340 345 350

Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365
Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln

370 375 380
Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn
385 390 395 400

Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu
405 410 415

Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro
420 425 430

Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr

435 440 445
Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile
450 455 460

His Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Ile Val His
465 470 475 480

Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala
485 490 495

Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg

500 505 510
Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Gly
515 520 525

Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu
530 535 540

Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro
545 550 555 560

Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe

565 570 575
Thr Ile Lys

<210> 276

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 276

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp

50 55 60

Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys

65 70 75 80

Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met

85 90 95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg

100 105 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270

Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys

275 280 285

Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290 295 300

Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn

305 310 315 320

Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp

325 330 335

Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr

340 345 350

Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365

Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln

370 375 380

Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn

385 390 395 400

Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu

405 410 415

Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro

420 425 430

Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr

435 440 445

Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile

450 455 460

His Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His

Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala

Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg

500 505 510

Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Gly

515 520 525

Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu

Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro

Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe

565 570 575

Thr Ile Lys

<210> 277

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 277

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp

Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys

65 70 75 80

Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met

85 90 95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg

100 105 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270

Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Val Gln Asn Leu Lys

275 280 285

Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290 295 300

Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn

305 310 315 320

Lys Leu Gly Val Asp Glu Leu Ile Glu Ile Thr Leu Thr Asn Val Asp

325 330 335
Val Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr

340 345 350
Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365
Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln

370 375 380
Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn

385 390 395 400
Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu

405 410 415
Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro

420 425 430
Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr

435 440 445
Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile

450 455 460
His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His

465 470 475 480
Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala

485 490 495
Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg

500 505 510
Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile

515 520 525
Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu

530 535 540
Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro

545 550 555 560
Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe

565 570 575

Thr Ile Lys

<210> 278

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 278

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp

50 55 60
Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys

65 70 75 80
Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met

85 90 95
Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg

100 105 110
Lys Leu His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125
Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140
Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160
Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175
Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270

Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Val Gln Asn Leu Lys

275 280 285

Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290 295 300

Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn

305 310 315 320

Lys Leu Gly Val Asp Glu Leu Ile Glu Ile Thr Leu Thr Asn Val Asp

325 330 335

Val Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr

340 345 350

Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365

Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln

370 375 380

Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn

385 390 395 400

Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu

405 410 415

Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro

420 425 430

Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr

435 440 445
Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile

450 455 460
His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His
465 470 475 480

Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala
485 490 495

Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg
500 505 510

Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile

515 520 525
Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu

530 535 540
Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro

545 550 555 560
Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe

565 570 575
Thr Ile Lys

<210> 279

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 279

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp

50 55 60

Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys

65 70 75 80

Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met

85 90 95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg

100 105 110

Lys Gln His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270

Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Val Gln Asn Leu Lys

275 280 285

Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290				295				300							
Gln	Asn	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn
305				310				315				320			
Lys	Leu	Gly	Val	Asp	Glu	Leu	Ile	Glu	Ile	Thr	Leu	Thr	Asn	Val	Asp
325				330				335							
Val	Asp	Leu	Phe	Phe	Glu	His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Tyr	Thr
340				345				350							
Tyr	Gly	Tyr	Met	Phe	Arg	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile
355				360				365							
Asp	Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln
370				375				380							
Leu	Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn
385				390				395				400			
Pro	Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu
405				410				415							
Gly	Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro
420				425				430							
Leu	Ala	Ser	Phe	Val	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr
435				440				445							
Ala	Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile
450				455				460							
His	Leu	Thr	Gly	Thr	Lys	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	His
465				470				475				480			
Pro	Lys	Lys	Leu	Gly	Tyr	Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala
485				490				495							
Lys	Tyr	Leu	Arg	Gln	Lys	Thr	Tyr	Ile	Gln	Asp	Ile	Tyr	Met	Lys	Arg
500				505				510							
Val	Lys	Gly	Tyr	Leu	Val	Gln	Gly	Ser	Pro	Asp	Asp	Tyr	Thr	Asp	Ile
515				520				525							
Lys	Phe	Ser	Val	Lys	Cys	Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Glu	Glu
530				535				540							

Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro
 545 550 555 560
 Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe

565 570 575
 Thr Ile Lys

<210> 280

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 280

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp

50 55 60
 Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys

65 70 75 80
 Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met

85 90 95
 Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg

100 105 110
 Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125
 Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140
 Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270

Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys

275 280 285

Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290 295 300

Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn

305 310 315 320

Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp

325 330 335

Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr

340 345 350

Tyr Gly Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365

Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln

370 375 380

Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn

385 390 395 400

Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu

405 410 415
Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro

420 425 430
Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr

435 440 445
Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile

450 455 460
His Leu Thr Gly Thr Lys Val Pro Asp Val Ile Lys Asp Ile Val His

465 470 475 480
Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala

485 490 495
Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg

500 505 510
Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile

515 520 525
Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu

530 535 540
Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro

545 550 555 560
Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe

565 570 575
Thr Ile Lys

<210> 281

<211> 579

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 281

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe Phe His Asp Leu Lys Phe Asp

50 55 60

Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys

65 70 75 80

Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met

85 90 95

Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg

100 105 110

Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro

115 120 125

Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp

130 135 140

Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu

145 150 155 160

Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu

165 170 175

Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp

180 185 190

Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys

195 200 205

Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala

210 215 220

Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu

225 230 235 240

Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln

245 250 255

Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly

260 265 270
Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys

275 280 285
Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys

290 295 300

Gln Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn

305 310 315 320

Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp

325 330 335

Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr

340 345 350

Tyr Gly Tyr Met Phe Arg Ser Ser Cys Asp Met Phe Lys Asp Phe Ile

355 360 365

Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln

370 375 380

Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn

385 390 395 400

Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu

405 410 415

Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro

420 425 430

Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr

435 440 445

Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile

450 455 460

His Leu Thr Gly Thr Lys Val Pro Asp Val Ile Lys Asp Ile Val His

465 470 475 480

Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala

485 490 495

Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg

500 505 510

Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile
515 520 525

Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu

530 535 540

Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro

545 550 555 560

Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe

565 570 575

Thr Ile Lys

<210> 282

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 282

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 283

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 283

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Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
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Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
           20           25           30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
           35           40           45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

           50           55           60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65           70           75           80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
           85           90           95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
           100          105          110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

           115          120          125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
           130          135          140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145          150          155          160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
           165          170          175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

           180          185          190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
           195          200          205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
           210          215          220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225          230          235          240

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Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 284

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 284

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 285

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 285

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 286

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 286

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 287

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 287

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240
Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
260 265 270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
290 295 300
Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Val Pro Asp Ile Ile Lys Asp Leu Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 288

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 288

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35

40

45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65

70

75

80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85

90

95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100

105

110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115

120

125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130

135

140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145

150

155

160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165

170

175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180

185

190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195

200

205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210

215

220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225

230

235

240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245

250

255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260

265

270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460
Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro
465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575

Ile Lys

<210> 289

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 289

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

 420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

 435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys Arg Val

 500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

 515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

 530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

 565 570 575
Ile Lys

<210> 290

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 290

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Val Pro Asp Ile Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Thr Lys
515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 291

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 291

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460
Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Ile Val His Pro
465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Gly Lys
515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 292

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 292

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro

465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Gly Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

 <210> 293
 <211> 578
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 293
 Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Val Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Ile Thr Leu Thr Asn Val Asp Val

325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575

Ile Lys

<210> 294

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 294

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110
Leu His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Val Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Ile Thr Leu Thr Asn Val Asp Val

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 295

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 295

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Gln His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Val Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
 Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Ile Thr Leu Thr Asn Val Asp Val

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

 530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
 Ile Lys

<210> 296

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 296

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Val Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 297

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 297

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300
 Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

 340 345 350
 Gly Tyr Met Phe Arg Ser Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Val Pro Asp Val Ile Lys Asp Ile Val His Pro

 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575

Ile Lys

<210> 298

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 298

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130

135

140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145

150

155

160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165

170

175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180

185

190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195

200

205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210

215

220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225

230

235

240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245

250

255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260

265

270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275

280

285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290

295

300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305

310

315

320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325

330

335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340

345

350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355

360

365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Val Pro Asp Ile Ile Lys Asp Leu Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 299

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 299

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Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1           5           10           15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
           20           25           30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
           35           40           45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

           50           55           60
Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65           70           75           80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
           85           90           95
Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
           100          105          110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

           115          120          125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
           130          135          140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145          150          155          160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
           165          170          175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

           180          185          190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
           195          200          205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
           210          215          220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225          230          235          240

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Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro

465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 300

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 300

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys

260 265 270

Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys

275 280 285

Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg

290 295 300

Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu

305 310 315 320

Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu

325 330 335

His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys

340 345 350
Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile

355 360 365
Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu

370 375 380
Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys

385 390 395 400
Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

405 410 415
Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr

420 425 430
Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp

435 440 445
Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460
Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480
Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys

485 490 495
Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val

500 505 510
Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

515 520 525
Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

530 535 540
Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560
Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 301

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 301

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210	215	220	
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile			
225	230	235	240
Gly Glu Gly Met Val Phe Asp Val Asn Ser Met Tyr Pro Ala Met Met			
	245	250	255
Lys Asn Lys Leu Leu Pro Tyr Gly Glu Pro Val Met Phe Lys Gly Glu			
	260	265	270
Tyr Lys Lys Asn Val Glu Tyr Pro Leu Tyr Ile Gln Gln Val Arg Cys			
275	280	285	
Phe Phe Glu Leu Lys Lys Asp Lys Ile Pro Cys Ile Gln Ile Lys Gly			
290	295	300	
Asn Ala Arg Phe Gly Gln Asn Glu Tyr Leu Ser Thr Ser Gly Asp Glu			
305	310	315	320
Tyr Val Asp Leu Tyr Val Thr Asn Val Asp Trp Glu Leu Ile Lys Lys			
	325	330	335
His Tyr Asp Ile Phe Glu Glu Glu Phe Ile Gly Gly Phe Met Phe Lys			
340	345	350	
Gly Phe Ile Gly Phe Phe Asp Glu Tyr Ile Asp Arg Phe Met Glu Ile			
355	360	365	
Lys Asn Ser Pro Asp Ser Ser Ala Glu Gln Ser Leu Gln Ala Lys Leu			
370	375	380	
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr			
385	390	395	400
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu			
	405	410	415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe			
420	425	430	
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys			
435	440	445	
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly			
450	455	460	

Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr
500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570 575

<210> 302

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 302

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Lys Asn Val Glu Tyr Pro Leu Tyr Ile Gln Gln Val Arg Cys

 275 280 285
 Phe Phe Glu Leu Lys Lys Asp Lys Ile Pro Cys Ile Gln Ile Lys Gly
 290 295 300
 Asn Ala Arg Phe Gly Gln Asn Glu Tyr Leu Ser Thr Ser Gly Asp Glu
 305 310 315 320
 Tyr Val Asp Leu Tyr Val Thr Asn Val Asp Trp Glu Leu Ile Lys Lys
 325 330 335

His Tyr Asp Ile Phe Glu Glu Glu Phe Ile Gly Gly Phe Met Phe Lys

340 345 350

Gly Phe Ile Gly Phe Phe Asp Asp Phe Ile Asp Lys Trp Thr Tyr Ile

355 360 365

Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu

370 375 380

Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys

385 390 395 400

Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

405 410 415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr

420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp

435 440 445

Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys

485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val

500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 303

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 303

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Ser Arg Pro Leu Pro Tyr Gly Ala Pro Ile Val Phe Gln Gly Lys
 260 265 270

 Tyr Glu Lys Asp Glu Gln Tyr Pro Leu Tyr Ile Gln Arg Ile Arg Phe
 275 280 285
 Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Lys
 290 295 300
 Asn Pro Phe Phe Lys Gly Asn Glu Tyr Leu Lys Asn Ser Gly Val Glu
 305 310 315 320
 Pro Val Glu Leu Tyr Leu Thr Asn Val Asp Leu Glu Leu Ile Gln Glu
 325 330 335

 His Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Asp Gly Phe Lys Phe Arg
 340 345 350
 Glu Lys Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400

 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
 405 410 415
 Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
 420 425 430
 Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
 435 440 445
 Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys

 485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val

 500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

 515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

 530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

 565 570

<210> 304

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 304

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

 35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

 50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

<210> 305

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 305

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Pro Asn Asn Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Asp Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Glu Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
 Ile Lys

<210> 306

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 306

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg

 290 295 300

Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

<210> 307

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 307

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

 275 280 285
 Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg
 290 295 300
 Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu
 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu
 325 330 335
 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg

 340 345 350
 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400
 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

 405 410 415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
435 440 445

Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys
450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 308

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 308

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met
245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
275 280 285

Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg

290 295 300
 Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu
 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Glu Leu Met Lys Glu
 325 330 335

 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg
 340 345 350
 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400

 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
 405 410 415
 Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
 420 425 430
 Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
 435 440 445
 Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys
 450 455 460

 Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
 465 470 475 480
 Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
 485 490 495
 Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
 500 505 510
 Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
 515 520 525

 Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
 530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 309

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 309

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met
245 250 255

Tyr Val Arg Leu Leu Pro Tyr Gly Glu Pro Leu Phe Tyr Glu Gly Glu
260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
275 280 285

Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg
290 295 300

Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu
305 310 315 320

Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Glu Leu Met Lys Glu
325 330 335

His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Lys
340 345 350

Ala Thr Thr Gly Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
355 360 365

Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
370 375 380

Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
385 390 395 400

Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
405 410 415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr

420 425 430
Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
435 440 445
Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460
Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
465 470 475 480
Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
485 490 495
Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
500 505 510
Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

515 520 525
Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
530 535 540
Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
545 550 555 560
Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 310

<211> 578

<212> PRT

<213> Artificial sequence

<220

><223> Synthetic polypeptide

<400> 310

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125

 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190

 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Leu Leu Pro Tyr Gly Glu Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Thr Thr Gly Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575

Ile Lys

<210> 311

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 311

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165	170	175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser		
180	185	190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val		
195	200	205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr		
210	215	220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile		
225	230	235
		240
Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met		
245	250	255
Tyr Val Arg Leu Leu Pro Tyr Gly Glu Pro Leu Phe Tyr Glu Gly Glu		
260	265	270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val		
275	280	285
Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg		
290	295	300
Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu		
305	310	315
Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu		
325	330	335
His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Lys		
340	345	350
Ala Thr Thr Gly Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile		
355	360	365
Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu		
370	375	380
Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys		
385	390	395
Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu		
405	410	415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
435 440 445

Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys
450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 312

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 312

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Arg

290 295 300

Ser Arg Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Glu

305 310 315 320

Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu

325 330 335

His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg

340 345 350

Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile

355 360 365

Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu

370 375 380

Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys

385 390 395 400

Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

405 410 415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr

420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp

435 440 445

Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys

485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val

500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

530 535 540
Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560
Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 313

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 313

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220

 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285

 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Arg
 290 295 300
 Ser Arg Leu Phe Lys Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Glu
 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu
 325 330 335
 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg
 340 345 350

 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400
 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

405 410 415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr

420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp

435 440 445

Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480

Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	Tyr	Leu	Arg	Gln	Lys
485							490				495				
Thr	Tyr	Ile	Gln	Asp	Ile	Tyr	Met	Lys	Arg	Val	Lys	Gly	Tyr	Leu	Val
500							505				510				
Gln	Gly	Ser	Pro	Asp	Asp	Tyr	Thr	Asp	Ile	Lys	Phe	Ser	Val	Lys	Cys
515							520				525				
Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Glu	Glu	Val	Thr	Phe	Glu	Asn	Phe
530							535				540				

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
545 550 555 560
Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 314

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 314

Met	Ser	Arg	Lys	Arg	Phe	Ser	Cys	Asp	Phe	Glu	Thr	Thr	Thr	Lys	Leu
1				5					10					15	
Asp	Asp	Cys	Arg	Val	Trp	Ala	Tyr	Gly	Tyr	Met	Glu	Ile	Gly	Asn	Leu

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Arg
 290 295 300
 Ser Arg Leu Tyr Lys Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Glu
 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu
 325 330 335
 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg

 340 345 350
 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400
 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

 405 410 415
 Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
 420 425 430
 Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
 435 440 445
 Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys
 450 455 460
 Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

 465 470 475 480
 Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
 485 490 495
 Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
 500 505 510
 Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
 515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

530

535

540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545

550

555

560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565

570

<210> 315

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 315

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1

5

10

15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20

25

30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35

40

45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65

70

75

80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85

90

95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100

105

110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115

120

125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130

135

140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205

 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Arg
 290 295 300
 Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Glu Ser Ser Val Asn Glu
 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu
 325 330 335

 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg
 340 345 350
 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400

Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
 405 410 415
 Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
 420 425 430
 Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
 435 440 445
 Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys
 450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
 465 470 475 480
 Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
 485 490 495
 Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
 500 505 510
 Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
 515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
 530 535 540
 Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
 545 550 555 560
 Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
 565 570

<210> 316

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 316

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Arg
 290 295 300
 Ser Arg Leu Phe Lys Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Glu
 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu

 325 330 335
 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg
 340 345 350
 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys

 385 390 395 400
 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
 405 410 415
 Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
 420 425 430
 Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
 435 440 445
 Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

 450 455 460
 Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
 465 470 475 480
 Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
 485 490 495
 Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
 500 505 510
 Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

 515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 317
<211> 574
<212> PRT
<213> Artificial sequence
<220>
><223> Synthetic polypeptide
<400> 317

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190

 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Leu Pro Val Pro Phe Ser Gly Glu
 260 265 270
 Tyr Glu Tyr Asp Glu Thr His Pro Leu Phe Ile Gln His Ile Lys Cys
 275 280 285
 Gly Phe Glu Leu Lys Asp Gly His Ile Pro Thr Ile Gln Ile Lys Lys
 290 295 300
 Asn Phe Arg Phe Ala Asp Asn Glu Tyr Leu His Ser Ser Glu Gly Asn
 305 310 315 320

 Ile Leu Asp Leu His Val Thr Asn Val Asp Leu Ala Leu Ile Lys Glu
 325 330 335
 His Tyr Thr Leu Tyr Glu Glu Glu Tyr Leu Gln Gly Tyr Lys Phe Lys
 340 345 350
 Gln Val Thr Gly Leu Phe Lys Asn Tyr Ile Asp Tyr Trp Ser Asp Lys
 355 360 365
 Lys Ile Asn Ala Glu Asp Pro Ala Ile Arg Gln Met Ala Lys Leu Met
 370 375 380

 Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly
 385 390 395 400
 Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly

405 410 415
 Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val
 420 425 430
 Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr
 435 440 445

 Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr
 450 455 460
 Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly
 465 470 475 480
 Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln
 485 490 495
 Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu
 500 505 510

 Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys
 515 520 525
 Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn
 530 535 540
 Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val
 545 550 555 560
 Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
 565 570

<210> 318

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 318

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175

 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240

 Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

<210> 319

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 319

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220

 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285

 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300
 Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 320

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 320

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80

 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140

 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205

 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Glu
305 310 315 320

Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu
325 330 335

His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg
340 345 350

Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
355 360 365

Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
370 375 380

Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
385 390 395 400

Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
405 410 415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
435 440 445

Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys
450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val

500 505 510
Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
530 535 540
Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
545 550 555 560
Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 321

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 321

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130

135

140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145

150

155

160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165

170

175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180

185

190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195

200

205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210

215

220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225

230

235

240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser His Tyr Pro Ala Gln Met

245

250

255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260

265

270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275

280

285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290

295

300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305

310

315

320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325

330

335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340

345

350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355

360

365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 322

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 322

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 323

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 323

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Val Asn Ser Met Tyr Pro Ala Met Met

245 250 255

Lys Asn Lys Leu Leu Pro Tyr Gly Glu Pro Val Met Phe Lys Gly Glu

260 265 270

Tyr Lys Lys Asn Val Glu Tyr Pro Leu Tyr Ile Gln Gln Val Arg Cys

275 280 285

Phe Phe Glu Leu Lys Lys Asp Lys Ile Pro Cys Ile Gln Ile Lys Gly

290 295 300

Asn Ala Arg Phe Gly Gln Asn Glu Tyr Leu Ser Thr Ser Gly Asp Glu

305 310 315 320

Tyr Val Asp Leu Tyr Val Thr Asn Val Asp Trp Glu Leu Ile Lys Lys

325 330 335

His Tyr Asp Ile Phe Glu Glu Glu Phe Ile Gly Gly Phe Met Phe Lys

340 345 350
Gly Phe Ile Gly Phe Phe Asp Glu Tyr Ile Asp Arg Phe Met Glu Ile

355 360 365
Lys Asn Ser Pro Asp Ser Ser Ala Glu Gln Ser Leu Gln Ala Lys Leu

370 375 380
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu

405 410 415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe

420 425 430
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys

435 440 445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly

450 455 460
Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu

465 470 475 480
Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

485 490 495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr

500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val

515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu

530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570 575

<210> 324

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 324

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210					215					220									
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile				
225					230					235					240				
Gly	Glu	Gly	Met	Val	Phe	Asp	Ala	Asn	Ser	His	Tyr	Pro	Ala	Gln	Met				
245					250					255									
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Gln	Gly	Glu				
260					265					270									
Tyr	Lys	Glu	Asn	Ile	Asp	His	Pro	Leu	Tyr	Ile	Gln	Asn	Leu	Lys	Val				
275					280					285									
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val	Lys	Arg				
290					295					300									
Ser	Arg	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Glu				
305					310					315					320				
Leu	Ile	Glu	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	Asp	Leu	Phe	Phe	Glu				
325					330					335									
His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	Gly	Tyr	Met	Phe	Arg				
340					345					350									
Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	Lys	Trp	Thr	Tyr	Ile				
355					360					365									
Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala	Lys	Leu	Met	Leu				
370					375					380									
Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp	Val	Thr	Gly	Lys				
385					390					395					400				
Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe	Arg	Leu	Gly	Glu				
405					410					415									
Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Leu	Ala	Ser	Phe	Val	Thr				
420					425					430									
Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala	Gln	Ala	Cys	Tyr	Asp				
435					440					445									
Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu	Thr	Gly	Thr	Lys				
450					455					460									

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 325

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 325

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Arg
 290 295 300
 Ser Arg Leu Phe Lys Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Glu
 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu
 325 330 335

His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg

340 345 350

Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile

355 360 365

Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu

370 375 380

Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys

385 390 395 400

Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

405 410 415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr

420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp

435 440 445

Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys

485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val

500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 326

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 326

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Arg
 290 295 300
 Ser Arg Leu Tyr Lys Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Glu
 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu
 325 330 335

 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg
 340 345 350
 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400

 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
 405 410 415
 Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
 420 425 430
 Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
 435 440 445
 Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys

 485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val

 500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

 515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

 530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

 565 570

<210> 327

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 327

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

 35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

 50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Arg
 290 295 300
 Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Glu Ser Ser Val Asn Glu
 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu

325 330 335
 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg
 340 345 350
 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys

 385 390 395 400
 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
 405 410 415
 Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
 420 425 430
 Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
 435 440 445
 Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

 450 455 460
 Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
 465 470 475 480
 Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
 485 490 495
 Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
 500 505 510
 Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

 515 520 525
 Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
 530 535 540
 Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
 545 550 555 560
 Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
 565 570
 <210> 328

<211> 578

<212> PRT

<213> Artificial sequence

<220

><223> Synthetic polypeptide

<400> 328

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Arg
 290 295 300
 Ser Arg Leu Phe Lys Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510

 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575

Ile Lys

<210> 329

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 329

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45

 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175

 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240

 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg
 290 295 300

 Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575

Ile Lys

<210> 330

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 330

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220

 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285

 Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg
 290 295 300
 Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu
 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu
 325 330 335
 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg
 340 345 350

 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400
 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
 405 410 415

 Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
 420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
435 440 445

Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys
450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 331

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 331

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240
Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
245 250 255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
260 265 270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
275 280 285
Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg
290 295 300
Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu

305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Glu Leu Met Lys Glu
 325 330 335
 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg

 340 345 350
 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380
 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400
 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

 405 410 415
 Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr
 420 425 430
 Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp
 435 440 445
 Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys
 450 455 460
 Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

 465 470 475 480
 Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
 485 490 495
 Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
 500 505 510
 Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
 515 520 525
 Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

 530 535 540
 Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
 545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565

570

<210> 332

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 332

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1

5

10

15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20

25

30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35

40

45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65

70

75

80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85

90

95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100

105

110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115

120

125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130

135

140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145

150

155

160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165

170

175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180

185

190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser His Tyr Pro Ala Gln Met
245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525

 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

<210> 333

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 333

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125

 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190

 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575

Ile Lys

<210> 334

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 334

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165	170	175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser		
180	185	190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val		
195	200	205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr		
210	215	220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile		
225	230	235
		240
Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met		
245	250	255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu		
260	265	270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val		
275	280	285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln		
290	295	300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys		
305	310	315
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu		
325	330	335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr		
340	345	350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp		
355	360	365
Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu		
370	375	380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro		
385	390	395
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly		
405	410	415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 335

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 335

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

				20				25				30			
Asp	Asn	Tyr	Lys	Ile	Gly	Asn	Ser	Leu	Asp	Glu	Phe	Met	Gln	Trp	Ala
35				40				45							
Met	Glu	Ile	Gln	Ala	Asp	Leu	Tyr	Phe	His	Asn	Leu	Lys	Phe	Asp	Gly
50				55				60							
Ala	Phe	Ile	Ile	Asn	Trp	Leu	Phe	Lys	Asn	Gly	Phe	Lys	Trp	Cys	Lys
65				70				75				80			
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Ile	Ile	Ser	Arg	Met	Gly
85				90				95							
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Leu	Gly	Tyr	Lys	Gly	Lys	Arg	Lys
100				105				110							
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val
115				120				125							
Glu	Lys	Ile	Ala	Lys	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile
130				135				140							
Asp	Ile	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu
145				150				155				160			
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu
165				170				175							
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser
180				185				190							
Leu	Lys	Asp	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val
195				200				205							
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr
210				215				220							
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile
225				230				235				240			
Gly	Glu	Gly	Met	Val	Phe	Asp	Ala	Asn	Ser	His	Tyr	Pro	Ala	Gln	Met
245				250				255							
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu
260				265				270							

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 336

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 336

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205

 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg
 290 295 300
 Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 337

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 337

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245					250					255									
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu				
260					265					270									
Tyr	Lys	Glu	Asn	Ile	Asp	His	Pro	Leu	Tyr	Ile	Gln	Asn	Leu	Lys	Val				
275					280					285									
Arg	Phe	Arg	Leu	Lys	Glu	Gly	Tyr	Ile	Pro	Thr	Ile	Gln	Ile	Lys	Arg				
290					295					300									
Ser	Arg	Phe	Tyr	Lys	Gly	Asn	Glu	Tyr	Leu	Lys	Ser	Ser	Gly	Gly	Glu				
305					310					315					320				
Leu	Ile	Glu	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	Asp	Leu	Phe	Phe	Glu				
325					330					335									
His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	Gly	Tyr	Met	Phe	Arg				
340					345					350									
Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	Lys	Trp	Phe	Tyr	Ile				
355					360					365									
Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala	Lys	Leu	Met	Leu				
370					375					380									
Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp	Val	Thr	Gly	Lys				
385					390					395					400				
Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe	Arg	Leu	Gly	Glu				
405					410					415									
Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Leu	Ala	Ser	Phe	Val	Thr				
420					425					430									
Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala	Gln	Ala	Cys	Tyr	Asp				
435					440					445									
Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu	Thr	Gly	Thr	Lys				
450					455					460									
Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	His	Pro	Lys	Lys	Leu	Gly	Tyr				
465					470					475					480				
Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	Tyr	Leu	Arg	Gln	Lys				
485					490					495									

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val
500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 338

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 338

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg
 290 295 300
 Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu

 305 310 315 320
 Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Glu Leu Met Lys Glu
 325 330 335
 His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg
 340 345 350
 Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Phe Tyr Ile
 355 360 365

Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu

370 375 380

Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys

385 390 395 400

Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

405 410 415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr

420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp

435 440 445

Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys

485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val

500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 339

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 339

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300

 Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Val Pro Asp Ile Ile Lys Asp Leu Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575

Ile Lys

<210> 340

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 340

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340				345				350							
Gly	Tyr	Met	Phe	Arg	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp
355				360				365							
Lys	Trp	Phe	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu
370				375				380							
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro
385				390				395				400			
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly
405				410				415							
Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Leu
420				425				430							
Ala	Ser	Phe	Val	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala
435				440				445							
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His
450				455				460							
Leu	Thr	Gly	Thr	Lys	Val	Pro	Asp	Ala	Ile	Lys	Asp	Leu	Val	His	Pro
465				470				475				480			
Lys	Lys	Leu	Gly	Tyr	Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys
485				490				495							
Tyr	Leu	Arg	Gln	Lys	Thr	Tyr	Ile	Gln	Asp	Ile	Tyr	Met	Lys	Arg	Val
500				505				510							
Lys	Gly	Tyr	Leu	Val	Gln	Gly	Ser	Pro	Asp	Asp	Tyr	Thr	Asp	Ile	Lys
515				520				525							
Phe	Ser	Val	Lys	Cys	Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Glu	Glu	Val
530				535				540							
Thr	Phe	Glu	Asn	Phe	Lys	Val	Gly	Phe	Ser	Arg	Lys	Met	Lys	Pro	Lys
545				550				555				560			
Pro	Val	Gln	Val	Pro	Gly	Gly	Val	Val	Leu	Val	Asp	Ser	Val	Phe	Thr
565				570				575							
Ile Lys															

<210> 341

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 341

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300
 Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 342

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 342

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125

 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190

 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

Leu Thr Gly Thr Lys Val Pro Asp Ile Ile Lys Asp Ile Val His Pro
 465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Thr Lys
 515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575

Ile Lys

<210> 343

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 343

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165	170	175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser		
180	185	190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val		
195	200	205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr		
210	215	220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile		
225	230	235
		240
Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met		
245	250	255
Tyr Val Lys Asn Lys Leu Leu Pro Tyr Gly Glu Pro Val Met Phe Lys		
260	265	270
Gly Glu Tyr Lys Lys Asn Val Glu Tyr Pro Leu Tyr Ile Gln Gln Val		
275	280	285
Arg Cys Phe Phe Glu Leu Lys Lys Asp Lys Ile Pro Cys Ile Gln Ile		
290	295	300
Lys Gly Asn Ala Arg Phe Gly Gln Asn Glu Tyr Leu Ser Thr Ser Gly		
305	310	315
Asp Glu Tyr Val Asp Leu Tyr Val Thr Asn Val Asp Trp Glu Leu Ile		
325	330	335
Lys Lys His Tyr Asp Ile Phe Glu Glu Glu Phe Ile Gly Gly Phe Met		
340	345	350
Phe Lys Gly Met Phe Lys Asp Phe Ile Asp Lys Trp Phe Tyr Ile Lys		
355	360	365
Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn		
370	375	380
Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val		
385	390	395
Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu		
405	410	415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe Val Thr Ala
420 425 430

Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys Tyr Asp Arg
435 440 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys Ile
450 455 460

Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr Trp
465 470 475 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr
485 490 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly Tyr Leu Val Gln
500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
515 520 525

Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe Lys
530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
545 550 555 560

Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 344

<211> 576

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 344

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys
 65 70 75 80
 Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser
 85 90 95
 Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly

 100 105 110
 Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro
 115 120 125
 Phe Pro Val Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys
 130 135 140
 Gly Asp Ile Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr
 145 150 155 160
 Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

 165 170 175
 Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly
 180 185 190
 Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe
 195 200 205
 Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg
 210 215 220
 Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

 225 230 235 240
 Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro
 245 250 255
 Ala Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe
 260 265 270
 Glu Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His
 275 280 285

Ile Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln

290 295 300

Ile Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser

305 310 315 320

Gly Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu

325 330 335

Met Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu

340 345 350

Lys Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp

355 360 365

Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys

370 375 380

Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val

385 390 395 400

Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg

405 410 415

Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser

420 425 430

Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala

435 440 445

Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr

450 455 460

Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys

465 470 475 480

Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu

485 490 495

Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys Gly

500 505 510

Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser

515 520 525

Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe

530 535 540
Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val

545 550 555 560
Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570 575

<210> 345

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 345

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala
 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 450 455 460
 Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val

 465 470 475 480
 His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
 500 505 510
 Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
 515 520 525
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu

 530 535 540
 Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
 545 550 555 560
 Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val
 565 570 575
 Phe Thr Ile Lys
 580
 <210> 346
 <211> 575
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 346
 Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

 1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

 130 135 140
 Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala
 245 250 255
 Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

 260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp His Pro Leu His Ile Gln His Leu
 275 280 285
 Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Cys Ile Gln Ile
 290 295 300
 Lys Gln Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
 305 310 315 320
 Gly Glu Ile Ala Glu Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
 325 330 335
 Lys Glu His Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
 340 345 350
 Phe Arg Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
 355 360 365
 Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380
 Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
 385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415
 Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
 420 425 430
 Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
 435 440 445
 Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
 450 455 460
 Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu
 465 470 475 480
 Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr
 500 505 510
 Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val

515 520 525
 Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu
 530 535 540
 Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
 545 550 555 560
 Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
 565 570 575
 <210> 347
 <211> 580
 <212> PRT
 <213> Artificial sequence

 <220><223> Synthetic polypeptide
 <400> 347
 Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

 115 120 125
 Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
 130 135 140
 Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu
 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
420 425 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
435 440 445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460

Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480

His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
500 505 510

Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu
530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val
565 570 575

Phe Thr Ile Lys
580

<210> 348
<211> 572
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 348

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
 115 120 125
 Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140
 Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr
 245 250 255
 Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr

260 265 270
 Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
 275 280 285
 Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Gln Ser

 290 295 300
 Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
 305 310 315 320
 Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
 325 330 335
 Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
 340 345 350
 Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys

 355 360 365
 Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
 370 375 380
 Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val
 385 390 395 400
 Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
 405 410 415
 Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala

 420 425 430
 Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
 435 440 445
 Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys Ile
 450 455 460
 Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr Trp
 465 470 475 480
 Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr

 485 490 495
 Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr Leu Val Gln
 500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
515 520 525

Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe Lys
530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly

545 550 555 560

Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570

<210> 349

<211> 576

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 349

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys
65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser
85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly
100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro
115 120 125

Phe Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys
130 135 140

Gly Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr
145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu
165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly
180 185 190

Ser Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe
195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg
210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly
225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro
245 250 255

Ala Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe
260 265 270

Glu Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His
275 280 285

Ile Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln
290 295 300

Ile Lys Gln Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser
305 310 315 320

Gly Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu
325 330 335

Met Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu
340 345 350

Lys Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp
355 360 365

Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys
370 375 380

Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val

385 390 395 400
 Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg
 405 410 415

 Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val
 420 425 430
 Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala
 435 440 445
 Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr
 450 455 460
 Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys
 465 470 475 480

 Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu
 485 490 495
 Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly
 500 505 510
 Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser
 515 520 525
 Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe
 530 535 540

 Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val
 545 550 555 560
 Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
 565 570 575

 <210> 350
 <211> 575
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 350
 Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys
 65 70 75 80

 Trp Ser Ala Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys
 100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
 130 135 140

 Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205

 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala
 245 250 255
 Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260	265	270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile		
275	280	285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile		
290	295	300
Lys Gln Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly		
305	310	315
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met		
325	330	335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys		
340	345	350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr		
355	360	365
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu		
370	375	380
Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr		
385	390	395
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu		
405	410	415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe		
420	425	430
Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys		
435	440	445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly		
450	455	460
Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu		
465	470	475
Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg		
485	490	495
Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr		
500	505	510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu
530 535 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570 575

<210> 351

<211> 572

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 351

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Ile
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
 Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr
 245 250 255
 Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr

 260 265 270
 Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
 275 280 285
 Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Gln Ser
 290 295 300
 Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
 305 310 315 320
 Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His

 325 330 335
 Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
 340 345 350
 Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
 355 360 365
 Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu Asn
 370 375 380

Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys Val

385 390 395 400

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu

405 410 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala

420 425 430

Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg

435 440 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys Ile

450 455 460

Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr Trp

465 470 475 480

Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys Thr

485 490 495

Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr Leu Val Gln

500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala

515 520 525

Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe Lys

530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly

545 550 555 560

Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 352

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 352

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60

 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125

 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190

 Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys
 260 265 270
 Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys
 275 280 285
 Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Gln
 290 295 300
 Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu
 305 310 315 320

 Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu
 325 330 335
 His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys
 340 345 350
 Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365
 Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380

 Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400
 Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
 405 410 415
 Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr
 420 425 430
 Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp
 435 440 445

 Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys
 450 455 460
 Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
 465 470 475 480
 Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
 485 490 495
 Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr Leu Val

500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 353

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 353

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140
Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190
Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240
Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala
245 250 255
Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270
Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285
Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300
Lys Gln Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320
Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
325 330 335
Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350
Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
355 360 365
Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380
 Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
 385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415
 Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe
 420 425 430
 Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys

 435 440 445
 Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
 450 455 460
 Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu
 465 470 475 480
 Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr

 500 505 510
 Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
 515 520 525
 Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu
 530 535 540
 Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
 545 550 555 560
 Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

 565 570 575

<210> 354

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 354

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45

 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
 100 105 110

 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
 130 135 140
 Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
 165 170 175

 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240

 Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala
 245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
290 295 300

Lys Gln Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
325 330 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
340 345 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460

Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro Lys Lys Leu
465 470 475 480

Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495

Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr

500 505 510
 Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
 515 520 525
 Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu
 530 535 540
 Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
 545 550 555 560

Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
 565 570 575

<210> 355

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 355

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15
 Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
 20 25 30
 Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45
 Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
 65 70 75 80
 Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
 85 90 95
 Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110
 Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
 115 120 125
 Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140
 Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
 145 150 155 160
 Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

 165 170 175
 Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
 180 185 190
 Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala
 245 250 255
 Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
 260 265 270
 Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
 275 280 285
 Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile

 290 295 300
 Lys Gln Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
 305 310 315 320
 Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
 325 330 335
 Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
 340 345 350
 Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr

 355 360 365
 Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385 390 395 400
Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
405 410 415
Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala Ser Phe
420 425 430
Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln Ala Cys
435 440 445
Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
450 455 460
Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro Lys Lys Leu
465 470 475 480
Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
485 490 495
Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr
500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu
530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
565 570 575
<210> 356
<211> 575
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 356
Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270
 Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
 275 280 285

 Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
 290 295 300
 Lys Gln Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
 305 310 315 320
 Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
 325 330 335
 Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
 340 345 350

 Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
 355 360 365
 Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu
 370 375 380
 Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
 385 390 395 400
 Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
 405 410 415

 Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
 420 425 430
 Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
 435 440 445
 Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
 450 455 460
 Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu
 465 470 475 480

 Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
 485 490 495
 Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr
 500 505 510

Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
 515 520 525
 Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu
 530 535 540

 Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
 545 550 555 560
 Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys
 565 570 575

 <210> 357
 <211> 577
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 357

 Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
 115 120 125
 Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
 130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

Lys

<210> 358

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 358

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile
 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

 450 455 460
 Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val
 465 470 475 480
 His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
 485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
500 505 510

Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu
530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val
565 570 575

Phe Thr Ile Lys
580

<210> 359

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 359

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 360

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 360

Met Lys His Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu

260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp His Pro Leu His Ile Gln His Leu

275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Cys Ile Gln Ile

290 295 300

Lys Gln Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly

305 310 315 320

Gly Glu Ile Ala Glu Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met

325 330 335

Lys Glu His Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys

340 345 350

Phe Arg Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr

355 360 365

Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu

370 375 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr

385 390 395 400

Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu

405 410 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe

420 425 430

Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys

435 440 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly

450 455 460

Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro Lys Lys Leu

465 470 475 480
Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg

 485 490 495
Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr

 500 505 510
Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val

 515 520 525
Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu

 530 535 540
Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln

545 550 555 560
Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

 565 570 575

<210> 361

<211> 575

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 361

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala
245 250 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
260 265 270

Gly Lys Tyr Val Trp Asp Glu Asp His Pro Leu His Ile Gln His Leu
275 280 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Cys Ile Gln Ile
290 295 300

Lys Gln Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305 310 315 320

Gly Glu Ile Ala Glu Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
325 330 335

Lys Glu His Tyr Glu Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys

				340				345				350			
Phe	Arg	Ala	Thr	Thr	Gly	Leu	Phe	Lys	Asp	Phe	Ile	Asp	Lys	Trp	Thr
355				360				365							
Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	Ala	Lys	Leu
370				375				380							
Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	Asp	Val	Thr
385				390				395				400			
Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	Phe	Arg	Leu
405				410				415							
Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	Gly	Val	Phe
420				425				430							
Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	Gln	Ala	Cys
435				440				445							
Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	Leu	Thr	Gly
450				455				460							
Thr	Lys	Val	Pro	Asp	Ala	Ile	Lys	Asp	Leu	Val	His	Pro	Lys	Lys	Leu
465				470				475				480			
Gly	Tyr	Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	Tyr	Leu	Arg
485				490				495							
Gln	Lys	Thr	Tyr	Val	Gln	Asp	Ile	Tyr	Met	Lys	Arg	Val	Arg	Gly	Tyr
500				505				510							
Leu	Val	Gln	Gly	Ser	Pro	Asp	Asp	Tyr	Thr	Asp	Ile	Lys	Phe	Ser	Val
515				520				525							
Lys	Cys	Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Glu	Glu	Val	Thr	Phe	Glu
530				535				540							
Asn	Phe	Lys	Val	Gly	Phe	Ser	Arg	Lys	Met	Lys	Pro	Lys	Pro	Val	Gln
545				550				555				560			
Val	Pro	Gly	Gly	Val	Val	Leu	Val	Asp	Ser	Val	Phe	Thr	Ile	Lys	
565				570				575							
<210>	362														
<211>	580														

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 362

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala
 245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
 420 425 430
 Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 450 455 460

Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480

His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510

Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu

530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val

565 570 575

Phe Thr Ile Lys

580

<210> 363

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 363

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
 115 120 125
 Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

 130 135 140
 Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

 195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

 260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
 305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

	565	570	575
Lys			
<210>	364		
<211>	580		
<212>	PRT		
<213>	Artificial sequence		
<220><223>	Synthetic polypeptide		
<400>	364		
Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr			
1	5	10	15
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile			
	20	25	30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met			
	35	40	45
Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys			
	50	55	60
Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys			
65	70	75	80
Trp Ser Ala Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg			
	85	90	95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys			
	100	105	110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe			
	115	120	125
Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly			
	130	135	140
Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro			
145	150	155	160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala			
	165	170	175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190
 Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
 195 200 205
 Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
 210 215 220
 Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
 225 230 235 240
 Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255
 Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu
 260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu
 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr
 340 345 350
 Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430
Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460
Ile His Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val
465 470 475 480

His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val

565 570 575
Phe Thr Ile Lys

580

<210> 365

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 365

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys
305 310 315 320
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575

Ile Lys

<210> 366

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 366

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

 420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

 435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

 500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

 515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

 530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

 565 570 575
Ile Lys

<210> 367

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 367

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 368

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 368

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 369

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 369

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

 <210> 370
 <211> 578
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 370
 Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575

Ile Lys

<210> 371

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 371

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Val Gly Tyr Lys Gly Lys Arg Lys

100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 372

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 372

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
 Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

 530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
 Ile Lys

<210> 373

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 373

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110
 Gln His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
 Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Val Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 374

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 374

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Ile Thr Leu Thr Asn Val Asp Val
325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 375

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 375

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Val Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Ile Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 376

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 376

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Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
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Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
           20           25           30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
           35           40           45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

           50           55           60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65           70           75           80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
           85           90           95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
           100          105          110
Gln His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

           115          120          125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
           130          135          140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145          150          155          160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
           165          170          175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

           180          185          190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
           195          200          205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
           210          215          220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225          230          235          240

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Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Val

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 377

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 377

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 378

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 378

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210

215

220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225

230

235

240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245

250

255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260

265

270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275

280

285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290

295

300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305

310

315

320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp Leu

325

330

335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340

345

350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355

360

365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370

375

380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385

390

395

400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405

410

415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420

425

430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435

440

445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Val Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 379

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 379

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
 Leu Thr Gly Thr Lys Val Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 380

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 380

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240
Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Val Thr Asn Val Asp Leu

325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Arg Gly Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Val Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 381

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 381

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Asp Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575

Ile Lys

<210> 382

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 382

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Leu Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

<210> 383

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 383

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu

 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Val Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300
 Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Ile Thr Leu Thr Asn Val Asp Val

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 384

<211> 577

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 384

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala
420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 385

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 385

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430

Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

 <210> 386
 <211> 577
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 386
 Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
 65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85

90

95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100

105

110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115

120

125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130

135

140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145

150

155

160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290

295

300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305

310

315

320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575

Lys

<210> 387

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 387

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575
Lys

<210> 388

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 388

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65

70

75

80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85

90

95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100

105

110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115

120

125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130

135

140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145

150

155

160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

 305 310 315 320
 Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
 Lys

<210> 389

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 389

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
 Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
 Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125
 Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
 Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 390

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 390

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys

<210> 391

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 391

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

 420 425 430
 Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

 565 570 575
 Lys

<210> 392

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 392

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Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1           5           10           15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
           20           25           30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
           35           40           45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

           50           55           60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65           70           75           80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
           85           90           95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
           100          105          110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

           115          120          125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp
           130          135          140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
145          150          155          160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
           165          170          175
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

           180          185          190
Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
           195          200          205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
           210          215          220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225          230          235          240

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Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 393

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 393

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 394

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 394

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 395

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 395

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met
 420 425 430
 Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
 Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr
565 570 575

Ile Lys

<210> 396

<211> 577

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 396

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190
Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
210 215 220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
225 230 235 240
Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr
260 265 270
Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg
275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser
290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp
325 330 335
Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly
340 345 350
Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
355 360 365
Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
Lys

<210> 397

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 397

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575

Lys

<210> 398

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 398

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

 420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

 435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

 500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

 565 570 575
Lys

<210> 399

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 399

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270
Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320
Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335
Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 400

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 400

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr

565 570 575
Ile Lys

<210> 401

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 401

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

 <210> 402
 <211> 578
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 402
 Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Arg Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80

Asp Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575

Ile Lys

<210> 403

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 403

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115 120 125
Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160
Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175
Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr
530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile
565 570 575
Lys

<210> 404

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 404

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65

70

75

80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85

90

95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100

105

110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Glu

115

120

125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130

135

140

Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145

150

155

160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165

170

175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180

185

190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195

200

205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Asn

290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Asn Ser Val Asn Lys Leu

 305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly

 340 345 350
 Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

 420 425 430
 Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Lys

 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr

 530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560
 Val Gln Val Pro Gly Gly Val Val Leu Val Asp Glu Thr Phe Thr Ile

565 570 575
 Lys

<210> 405

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 405

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125
 Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
 Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 406

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 406

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575

Lys

<210> 407

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 407

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys

130

135

140

Gly Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145

150

155

160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165

170

175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180

185

190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195

200

205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210

215

220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225

230

235

240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro

245

250

255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260

265

270

Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn

275

280

285

Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln

290

295

300

Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305

310

315

320

Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn

325

330

335

Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His

340

345

350

Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp

355

360

365

Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile

370 375 380
Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

385 390 395 400
Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly

405 410 415
Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

420 425 430
Thr Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile

435 440 445
Thr Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

450 455 460
Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile

465 470 475 480
Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

485 490 495
Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met

500 505 510
Lys Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

515 520 525
Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys

530 535 540
Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

545 550 555 560
Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser

565 570 575
Val Phe Thr Ile Lys

580

<210

> 408

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 408

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Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1           5           10           15
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
           20           25           30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
           35           40           45
Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

           50           55           60
Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys
65           70           75           80
Trp Ser Ala Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
           85           90           95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys
           100          105          110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

           115          120          125
Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
           130          135          140
Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145          150          155          160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
           165          170          175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

           180          185          190
Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
           195          200          205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
           210          215          220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225          230          235          240

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Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430

Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445

Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460

Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480

His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val

565 570 575
Phe Thr Ile Lys

580

<210> 409

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 409

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

 420 425 430
 Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 450 455 460
 Ile His Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val
 465 470 475 480
 His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys
 500 505 510
 Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
 515 520 525
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu
 530 535 540
 Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

 545 550 555 560
 Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val
 565 570 575
 Phe Thr Ile Lys
 580

<210> 410

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 410

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210

215

220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225

230

235

240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245

250

255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260

265

270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275

280

285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290

295

300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305

310

315

320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325

330

335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340

345

350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355

360

365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370

375

380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385

390

395

400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405

410

415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420

425

430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435

440

445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 411

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 411

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
 85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
 100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
 115 120 125
 Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
 Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
 145 150 155 160
 Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile
 165 170 175
 Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
 180 185 190
 Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
 Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg
 210 215 220
 Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly
 225 230 235 240
 Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr
 245 250 255
 Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
 Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg
 275 280 285
 Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser
 290 295 300
 Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala
 420 425 430
 Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys Arg Val Arg
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile
565 570 575

Lys

<210> 412

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 412

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190
Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe
195 200 205
Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg
210 215 220
Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly
225 230 235 240
Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro

245 250 255
Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr
260 265 270
Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn
275 280 285
Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln
290 295 300
Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305 310 315 320
Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn
325 330 335
Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His
340 345 350
Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp
355 360 365
Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile

370 375 380
Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala
385 390 395 400
Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly
405 410 415
Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

420 425 430
Thr Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile

435 440 445
Thr Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

450 455 460
Ser Ile His Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu

465 470 475 480
Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

485 490 495
Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met

500 505 510
Lys Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

515 520 525
Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys

530 535 540
Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

545 550 555 560
Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser

565 570 575
Val Phe Thr Ile Lys

580

<210> 413

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 413

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35

40

45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50

55

60

Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Glu Lys Asn Gly Phe Lys

65

70

75

80

Trp Ser Ala Glu Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85

90

95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys

100

105

110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115

120

125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130

135

140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145

150

155

160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165

170

175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180

185

190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195

200

205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210

215

220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225

230

235

240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245

250

255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260

265

270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285
Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300
Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
305 310 315 320
Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
325 330 335
Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr
340 345 350
Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365
Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
370 375 380
Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
385 390 395 400
Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
405 410 415
Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430
Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
435 440 445
Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460
Ile His Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val
465 470 475 480
His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys
500 505 510
Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu
530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val
565 570 575
Phe Thr Ile Lys
580
<210> 414
<211> 578
<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 414
Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125
Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

 420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

 435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

 450 455 460
Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met Lys Arg Val

 500 505 510
Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

 515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

 530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

 565 570 575
Ile Lys

<210> 415

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 415

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro

245 250 255
 Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

 260 265 270
 Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn
 275 280 285
 Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln
 290 295 300
 Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser
 305 310 315 320
 Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn

 325 330 335
 Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His
 340 345 350
 Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp
 355 360 365
 Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile
 370 375 380
 Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

 385 390 395 400
 Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly
 405 410 415
 Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr
 420 425 430
 Thr Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile
 435 440 445
 Thr Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

 450 455 460
 Ser Ile His Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu
 465 470 475 480
 Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys
 485 490 495

Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met
500 505 510

Lys Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

515 520 525
Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys
530 535 540

Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met
545 550 555 560

Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser
565 570 575

Val Phe Thr Ile Lys
580

<210

> 416

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 416

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430
Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 417

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 417

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro

245 250 255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260 265 270

Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn

275 280 285

Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln

290 295 300

Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305 310 315 320

Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn

325 330 335

Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His

340 345 350

Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp

355 360 365

Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile

370 375 380

Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

385 390 395 400

Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly

405 410 415

Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

420 425 430

Thr Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile

435 440 445

Thr Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

450 455 460

Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile

Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

485 490 495

Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met

Lys Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

515 520 525

Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys

Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser

565 570 575

Val Phe Thr Ile Lys

580

<210> 418

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 418

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met
 420 425 430
 Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575

Ile Lys

<210> 419

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 419

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430

Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 420

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 420

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65

70

75

80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85

90

95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100

105

110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115

120

125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130

135

140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145

150

155

160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165

170

175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180

185

190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195

200

205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210

215

220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225

230

235

240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245

250

255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260

265

270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275

280

285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

 420 425 430
 Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

 530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
 Ile Lys

<210> 421

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 421

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430
Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 422

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 422

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430
Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 423

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 423

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430
Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 424

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 424

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Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1           5           10           15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
           20           25           30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
           35           40           45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

           50           55           60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65           70           75           80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
           85           90           95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
           100          105          110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

           115          120          125
Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
           130          135          140
Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145          150          155          160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
           165          170          175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

           180          185          190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
           195          200          205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
           210          215          220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225          230          235          240

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Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430

Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 425

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 425

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430
Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 426

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 426

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro

245 250 255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260 265 270

Glu Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn

275 280 285

Leu Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln

290 295 300

Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305 310 315 320

Val Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn

325 330 335

Val Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His

340 345 350

Tyr Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp

355 360 365

Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile

370 375 380

Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

385 390 395 400

Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly

405 410 415

Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

420 425 430

Thr Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile

435 440 445

Thr Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

450 455 460
Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile

465 470 475 480
Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

485 490 495
Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met

500 505 510
Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

515 520 525
Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys

530 535 540
Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

545 550 555 560
Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser

565 570 575
Val Phe Thr Ile Lys

580

<210> 427

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 427

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45
Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro

245 250 255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260 265 270

Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn

275 280 285

Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln

290 295 300

Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305 310 315 320
 Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn

 325 330 335
 Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His
 340 345 350
 Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp
 355 360 365
 Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile
 370 375 380
 Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

 385 390 395 400
 Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly
 405 410 415
 Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr
 420 425 430
 Thr Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile
 435 440 445
 Thr Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

 450 455 460
 Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile
 465 470 475 480
 Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys
 485 490 495
 Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met
 500 505 510
 Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

 515 520 525
 Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys
 530 535 540
 Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met
 545 550 555 560

Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser
565 570 575

Val Phe Thr Ile Lys
580

<210

> 428

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 428

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys
65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser
85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly
100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys
130 135 140

Gly Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr
145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu
165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190
Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205
Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220
Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240
Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro

245 250 255
Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260 265 270
Glu Gly Glu Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn

275 280 285
Leu Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln

290 295 300
Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305 310 315 320
Val Asn Lys Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn

325 330 335
Val Asp Leu Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His

340 345 350
Tyr Thr Tyr Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp

355 360 365
Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile

370 375 380
Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

385 390 395 400
Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly

405 410 415
Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

420 425 430
Thr Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile

435 440 445
Thr Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

450 455 460

Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile

465 470 475 480

Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

485 490 495

Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met

500 505 510

Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

515 520 525

Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys

530 535 540

Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

545 550 555 560

Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser

565 570 575

Val Phe Thr Ile Lys

580

<210> 429

<211> 581

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 429

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys

65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro

245 250 255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260 265 270

Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn

275 280 285
Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln

290 295 300
Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser
305 310 315 320
Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn
325 330 335
Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His
340 345 350
Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp

355 360 365
Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile
370 375 380
Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala
385 390 395 400
Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly
405 410 415
Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

420 425 430
Thr Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile
435 440 445
Thr Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp
450 455 460
Ser Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile
465 470 475 480
Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

485 490 495
Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met
500 505 510
Lys Arg Val Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr
515 520 525

Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys
530 535 540

Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

545 550 555 560

Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser

565 570 575

Val Phe Thr Ile Lys

580

<210> 430

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 430

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

 405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

 420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

 435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

 485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

 500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

 530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

 565 570 575
Lys

<210> 431

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 431

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270
Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290 295 300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320
Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325 330 335
Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350
Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415
Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430
Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 432

<211> 580

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 432

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile
20 25 30

Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365
Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380
Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
385 390 395 400
Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
405 410 415
Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
420 425 430
Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460
Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480
His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu
530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val

565 570 575
Phe Thr Ile Lys

580

<210> 433

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 433

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Met Lys His Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr
1           5           10           15
Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile
           20           25           30
Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

           35           40           45
Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
           50           55           60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65           70           75           80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
           85           90           95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

           100          105          110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
           115          120          125
Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
           130          135          140
Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145          150          155          160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

           165          170          175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
           180          185          190
Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
           195          200          205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
210          215          220

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Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460

Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480
 His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
 500 505 510
 Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
 515 520 525
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu
 530 535 540
 Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

 545 550 555 560
 Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val
 565 570 575
 Phe Thr Ile Lys
 580

 <210> 434
 <211> 581
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 434
 Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
 1 5 10 15
 Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile

 20 25 30
 Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
 35 40 45
 Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
 50 55 60
 Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys
 65 70 75 80

Trp Cys Lys Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser

85 90 95

Arg Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly

100 105 110

Lys Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro

115 120 125

Phe Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys

130 135 140

Gly Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr

145 150 155 160

Pro Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu

165 170 175

Ala Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly

180 185 190

Ser Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe

195 200 205

Lys Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg

210 215 220

Lys Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly

225 230 235 240

Lys Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro

245 250 255

Ala Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr

260 265 270

Glu Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn

275 280 285

Ile Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln

290 295 300

Val Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser

305 310 315 320

Val Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn

325 330 335
Val Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His

340 345 350
Tyr Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp

355 360 365
Phe Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile

370 375 380
Lys Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala

385 390 395 400
Ser Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly

405 410 415
Ala Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr

420 425 430
Thr Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile

435 440 445
Thr Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp

450 455 460
Ser Ile His Leu Thr Gly Thr Lys Val Pro Asp Ala Ile Lys Asp Leu

465 470 475 480
Val His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys

485 490 495
Arg Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Val Gln Asp Ile Tyr Met

500 505 510
Lys Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr

515 520 525
Asp Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys

530 535 540
Glu Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met

545 550 555 560
Lys Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser

565 570 575

Val Phe Thr Ile Lys

580

<210> 435

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 435

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15
Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45
Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125
Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140
Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430

Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460
Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480

His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val

565 570 575
Phe Thr Ile Lys

580

<210> 436

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 436

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser His Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

 420 425 430
 Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 450 455 460
 Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val
 465 470 475 480
 His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

 500 505 510
 Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
 515 520 525
 Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu
 530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val
565 570 575
Phe Thr Ile Lys
580
<210> 437
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<212> PRT
<213> Artificial sequence
<220><223> Synthetic polypeptide
<400> 437
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Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
20 25 30
Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45
Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125
Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
130 135 140
Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415
Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430
Pro Leu Ala Val Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460
Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480
His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val

565 570 575
Phe Thr Ile Lys

580

<210> 438

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 438

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1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
 385 390 395 400
 Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

 405 410 415
 Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
 420 425 430
 Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 450 455 460
 Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val

 465 470 475 480
 His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
 500 505 510

Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu

530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val

565 570 575

Phe Thr Ile Lys

580

<210> 439

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 439

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

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Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130

135

140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145

150

155

160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165

170

175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180

185

190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195

200

205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210

215

220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225

230

235

240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245

250

255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260

265

270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275

280

285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290

295

300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305

310

315

320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325

330

335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340

345

350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355

360

365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380
Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400
Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415
Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430
Pro Leu Ala Val Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460
Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480
His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val

565 570 575
Phe Thr Ile Lys

580

<210> 440

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 440

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Met Lys His Met Ser Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
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Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile
           20           25           30
Gly Asn Leu Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
           35           40           45
Gln Trp Ala Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

           50           55           60
Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65           70           75           80
Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
           85           90           95
Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
           100          105          110
Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

           115          120          125
Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly
           130          135          140
Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro
145          150          155          160
Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
           165          170          175
Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

           180          185          190
Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
           195          200          205
Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys
           210          215          220
Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys
225          230          235          240

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Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365

Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380

Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400

Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415

Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430

Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445

Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460

Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480

His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp

515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu

530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys

545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val

565 570 575
Phe Thr Ile Lys

580

<210> 441

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 441

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Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 442

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 442

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Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile Glu Asp His

20 25 30

Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 443

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 443

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

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Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Ala Trp Ala

35 40 45
Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
 Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

 325 330 335
 Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
 340 345 350
 Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys
 355 360 365
 Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
 370 375 380
 Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

 385 390 395 400
 Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
 405 410 415
 Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly
 420 425 430
 Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
 435 440 445
 Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

 450 455 460
 Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys
 465 470 475 480
 Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr
 485 490 495
 Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg
 500 505 510
 Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

 515 520 525
 Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr
 530 535 540
 Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro
 545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile
565 570 575

Lys

<210> 444

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 444

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile Glu Asp His

20 25 30

Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Ala Trp Ala

35 40 45

Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190
Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205
Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220
Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240
Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255
Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270
Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 445

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 445

Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr Thr Lys Val

1 5 10 15

Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Ala Trp Ala

35 40 45

Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285
Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300
Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu
305 310 315 320
Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp
325 330 335
Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly
340 345 350
Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365
Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala
370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp
385 390 395 400
Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe
405 410 415
Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln
435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu
450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys
465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg
500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe
515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr
530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575

Lys

<210> 446

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 446

Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr Thr Lys Val

1 5 10 15

Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile Glu Asp His

20 25 30

Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp

Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe

Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510

Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525

Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540

Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

Lys

<210> 447

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 447

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile

20 25 30

Gly Asn Leu Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Gln Trp Ala Met Lys Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255
Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270
Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285
Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300
Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320
Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335
Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350
Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365
Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380
Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser

385 390 395 400
Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala

405 410 415
Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr

420 425 430
Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser

450 455 460
Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val

465 470 475 480
His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg

485 490 495

Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
500 505 510

Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu
530 535 540

Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560

Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val
565 570 575

Phe Thr Ile Lys
580

<210> 448

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 448

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr
1 5 10 15

Thr Lys Leu Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile
20 25 30

Gly Asn His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Gln Trp Ala Met Lys Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270

Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

275 280 285

Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val

290 295 300

Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val

305 310 315 320

Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val

325 330 335

Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

340 345 350

Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe

355 360 365
Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys

370 375 380
Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser
385 390 395 400
Asn Pro Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala
405 410 415
Leu Gly Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr
420 425 430
Pro Met Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr

435 440 445
Ala Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
450 455 460
Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val
465 470 475 480
His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
485 490 495
Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys

500 505 510
Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525
Ile Lys Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu
530 535 540
Glu Val Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys
545 550 555 560
Pro Lys Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val

565 570 575
Phe Thr Ile Lys

580

<210> 449

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 449

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro

385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly

405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430

Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

 545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

 <210> 450
 <211> 578
 <212> PRT
 <213> Artificial sequence
 <220><223> Synthetic polypeptide
 <400> 450
 Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro
 385 390 395 400
 Asp Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg

 405 410 415
 Leu Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met
 420 425 430
 Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val

 530 535 540
 Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu
 545 550 555 560
 Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr
 565 570 575

Ile Lys

<210> 451

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 451

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro

385 390 395 400

Asp Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg

405 410 415

Leu Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met

420 425 430

Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala

435 440 445
Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His

450 455 460
Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro

465 470 475 480
Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

485 490 495
Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565 570 575
Ile Lys

<210> 452

<211> 578

<

212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 452

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50

55

60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65

70

75

80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85

90

95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100

105

110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115

120

125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130

135

140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145

150

155

160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165

170

175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180

185

190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195

200

205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210

215

220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225

230

235

240

Gly Glu Gly Met Val Phe Asp Ala Asn Ser His Tyr Pro Ala Gln Met

245

250

255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260

265

270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275

280

285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln

290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu

 325 330 335
 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr

 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp

 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu

 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro
 385 390 395 400
 Asp Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg

 405 410 415
 Leu Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu

 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala

 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys

 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

 500 505 510
 Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525
 Phe Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val

 530 535 540

Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu
 545 550 555 560
 Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr

565 570 575
 Ile Lys

<210> 453

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 453

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
 Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
 Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
 His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125
 Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140
 Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp

385 390 395 400

Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu

405 410 415
Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly

420 425 430
Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr

530 535 540
Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro

545 550 555 560
Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile

565 570 575
Lys

<210> 454

<211> 580

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 454

Met Lys His Met Pro Arg Lys Arg Tyr Ser Cys Asp Phe Glu Thr Thr

1 5 10 15

Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile

20 25 30

Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met

35 40 45

Ala Trp Ala Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys

50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys

65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg

85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys

100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe

115 120 125

Pro Val Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly

130 135 140

Asp Ile Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro

145 150 155 160

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala

165 170 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser

180 185 190

Asp Ser Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys

195 200 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys

210 215 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys

225 230 235 240

Glu Ile Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala

245 250 255

Gln Met Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu

260 265 270
 Gly Glu Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile

 275 280 285
 Lys Val Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val
 290 295 300
 Lys Gln Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val
 305 310 315 320
 Asn Lys Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val
 325 330 335
 Asp Leu Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr

 340 345 350
 Thr Tyr Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe
 355 360 365
 Ile Asp Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys
 370 375 380
 Gln Leu Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr
 385 390 395 400
 Asn Pro Asp Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile

 405 410 415
 Val Arg Leu Thr Leu Gly Glu Glu Thr Lys Asp Pro Val Tyr Thr
 420 425 430
 Pro Leu Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr
 435 440 445
 Thr Ala Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser
 450 455 460
 Ile His Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val

 465 470 475 480
 His Pro Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg
 485 490 495
 Ala Lys Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys
 500 505 510

Arg Val Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp
515 520 525

Ile Lys Phe Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu

530 535 540
Leu Val Thr Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys
545 550 555 560

Leu Leu Pro Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met
565 570 575

Phe Thr Ile Lys
580

<210> 455

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 455

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80
Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95
Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110
His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380
Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp

385 390 395 400
Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu

405 410 415
Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430
Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445
Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460
Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480
Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr

530 535 540
Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro

545 550 555 560
Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile

565 570 575
Lys

<210> 456

<211> 577

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 456

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala

65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln

85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile

100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys

115 120 125

Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile Asp

130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr

145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu Ile

165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu

180 185 190

Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe

195 200 205

Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr Arg

210 215 220

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile Gly

225 230 235 240

Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met Tyr

245 250 255

Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu Tyr

260 265 270

Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val Arg

275 280 285

Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln Ser

290 295 300

Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys Leu

305 310 315 320

Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp

325 330 335

Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly

340 345 350

Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys

355 360 365

Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala

370 375 380

Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Gly Thr Asn Pro Asp

385 390 395 400

Ile Thr Gly Lys Val Pro Tyr Met Gly Glu Asp Gly Ile Val Arg Leu

405 410 415

Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu Ala

420 425 430

Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala Gln

435 440 445

Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu

450 455 460

Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys

465 470 475 480

Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr

485 490 495
Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg

500 505 510
Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe

515 520 525
Ser Val Lys Cys Ala Gly Met Pro Asp Arg Ile Lys Glu Leu Val Thr

530 535 540
Phe Asp Asn Phe Glu Val Gly Phe Ser Ser Tyr Gly Lys Leu Leu Pro

545 550 555 560
Lys Arg Thr Gln Gly Gly Val Val Leu Val Asp Thr Met Phe Thr Ile

565 570 575
Lys

<210> 457

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 457

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Gln

290 295 300

Ser Leu Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu

305 310 315 320

Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu

325 330 335

His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Lys

340 345 350
Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile

355 360 365
Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu

370 375 380
Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys

385 390 395 400
Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

405 410 415
Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr

420 425 430
Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp

435 440 445
Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460
Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480
Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys

485 490 495
Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr Leu Val

500 505 510
Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

515 520 525
Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

530 535 540
Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560
Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 458

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 458

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210					215					220									
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile				
225					230					235					240				
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met				
245					250					255									
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu				
260					265					270									
Tyr	Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val				
275					280					285									
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln				
290					295					300									
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys				
305					310					315					320				
Leu	Gly	Val	Asp	Glu	Leu	Ile	Asp	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu				
325					330					335									
Asp	Leu	Phe	Phe	Glu	His	Tyr	Asp	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr				
340					345					350									
Gly	Tyr	Met	Phe	Lys	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp				
355					360					365									
Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu				
370					375					380									
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro				
385					390					395					400				
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly				
405					410					415									
Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met				
420					425					430									
Gly	Val	Phe	Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala				
435					440					445									
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His				
450					455					460									

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 459

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 459

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65				70				75				80			
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Ile	Ile	Ser	Arg	Met	Gly
85				90				95							
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Leu	Gly	Tyr	Lys	Gly	Lys	Arg	Lys
100				105				110							
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val
115				120				125							
Lys	Lys	Ile	Ala	Gln	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile
130				135				140							
Asp	Tyr	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu
145				150				155				160			
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu
165				170				175							
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser
180				185				190							
Leu	Lys	Gly	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val
195				200				205							
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr
210				215				220							
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile
225				230				235				240			
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met
245				250				255							
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu
260				265				270							
Tyr	Lys	Glu	Asn	Ile	Asp	His	Pro	Leu	Tyr	Ile	Gln	Asn	Leu	Lys	Val
275				280				285							
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val	Lys	Arg
290				295				300							
Ser	Arg	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Glu
305				310				315				320			

Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Asp Leu Phe Phe Glu
 325 330 335

His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg
 340 345 350

Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile
 355 360 365

Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu
 370 375 380

Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys
 385 390 395 400

Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu
 405 410 415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr
 420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp
 435 440 445

Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys
 450 455 460

Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr
 465 470 475 480

Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys
 485 490 495

Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr Leu Val
 500 505 510

Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys
 515 520 525

Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe
 530 535 540

Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro
 545 550 555 560

Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565

570

<210> 460

<211> 573

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 460

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260 265 270

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val

275 280 285

Arg Phe Arg Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg

290 295 300

Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu

305 310 315 320

Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu Glu Leu Met Lys Glu

325 330 335

His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr Gly Tyr Met Phe Arg

340 345 350

Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile

355 360 365

Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu Ala Lys Leu Met Leu

370 375 380

Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr Gly Lys

385 390 395 400

Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu

405 410 415

Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr

420 425 430

Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp

435 440 445
Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Lys

450 455 460
Ile Pro Asp Val Ile Lys Asp Ile Val His Pro Lys Lys Leu Gly Tyr

465 470 475 480
Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg Gln Lys

485 490 495
Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val Arg Gly Tyr Leu Val

500 505 510
Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys

515 520 525
Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val Thr Phe Glu Asn Phe

530 535 540
Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro

545 550 555 560
Gly Gly Val Val Leu Val Asp Ser Val Phe Thr Ile Lys

565 570

<210> 461

<211> 578

<212> PRT

<213> Artificial sequence

<220

><223> Synthetic polypeptide

<400> 461

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240
Gly Glu Gly Met Val Phe Asp Ala Asn Ser Ala Tyr Pro Ala Gln Met
245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
260 265 270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
275 280 285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
290 295 300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305	310							315							320						
Leu	Gly	Val	Asp	Glu	Leu	Ile	Glu	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu						
				325				330				335									
Asp	Leu	Phe	Phe	Glu	His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr						
				340				345				350									
Gly	Tyr	Met	Phe	Arg	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp						
				355				360				365									
Lys	Trp	Phe	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu						
370								375								380					
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro						
385				390				395				400									
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly						
				405				410				415									
Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met						
				420				425				430									
Gly	Val	Phe	Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala						
435								440				445									
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His						
450				455				460													
Leu	Thr	Gly	Thr	Lys	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	His	Pro						
465				470				475				480									
Lys	Lys	Leu	Gly	Tyr	Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys						
				485				490				495									
Tyr	Leu	Arg	Gln	Lys	Thr	Tyr	Ile	Gln	Asp	Ile	Tyr	Met	Lys	Arg	Val						
				500				505				510									
Lys	Gly	Tyr	Leu	Val	Gln	Gly	Ser	Pro	Asp	Asp	Tyr	Thr	Asp	Ile	Lys						
515				520				525													
Phe	Ser	Val	Lys	Cys	Ala	Gly	Met	Thr	Asp	Lys	Ile	Lys	Glu	Glu	Val						
530				535				540													
Thr	Phe	Glu	Asn	Phe	Lys	Val	Gly	Phe	Ser	Arg	Lys	Met	Lys	Pro	Lys						
545				550				555				560									

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 462

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 462

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165	170	175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser		
180	185	190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val		
195	200	205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr		
210	215	220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile		
225	230	235
		240
Gly Glu Gly Met Val Phe Asp Ile Asn Ser His Tyr Pro Ala Gln Met		
245	250	255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu		
260	265	270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val		
275	280	285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln		
290	295	300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys		
305	310	315
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu		
325	330	335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr		
340	345	350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp		
355	360	365
Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu		
370	375	380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro		
385	390	395
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly		
405	410	415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met
420 425 430

Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 463

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 463

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

	20					25					30					
Asp	Asn	Tyr	Lys	Ile	Gly	Asn	Ser	Leu	Asp	Glu	Phe	Met	Gln	Trp	Ala	
35						40						45				
Met	Glu	Ile	Gln	Ala	Asp	Leu	Tyr	Phe	His	Asn	Leu	Lys	Phe	Asp	Gly	
50						55						60				
Ala	Phe	Ile	Ile	Asn	Trp	Leu	Phe	Lys	Asn	Gly	Phe	Lys	Trp	Cys	Lys	
65						70						75			80	
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Ile	Ile	Ser	Arg	Met	Gly	
			85						90						95	
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Leu	Gly	Tyr	Lys	Gly	Lys	Arg	Lys	
100						105						110				
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val	
115						120						125				
Glu	Lys	Ile	Ala	Lys	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile	
130						135						140				
Asp	Ile	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu	
145						150						155			160	
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu	
			165						170						175	
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser	
180						185						190				
Leu	Lys	Asp	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val	
195						200						205				
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr	
210						215						220				
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile	
225						230						235			240	
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met	
			245						250						255	
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	
260						265						270				

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met
 420 425 430

Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 464

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 464

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
 Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205

 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Val Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Phe Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met
420 425 430

Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 465

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 465

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Val Asn Ser Ala Tyr Pro Ala Gln Met

245					250					255						
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	
260					265					270						
Tyr	Lys	Glu	Asn	Ile	Asp	His	Pro	Leu	Tyr	Ile	Gln	Asn	Leu	Lys	Val	
275					280					285						
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val	Lys	Gln	
290					295					300						
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	
305					310					315					320	
Leu	Gly	Val	Asp	Glu	Leu	Ile	Glu	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	
325					330					335						
Asp	Leu	Phe	Phe	Glu	His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	
340					345					350						
Gly	Tyr	Met	Phe	Arg	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	
355					360					365						
Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	
370					375					380						
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	
385					390					395					400	
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	
405					410					415						
Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	
420					425					430						
Gly	Val	Phe	Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	
435					440					445						
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	
450					455					460						
Leu	Thr	Gly	Thr	Lys	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	His	Pro	
465					470					475					480	
Lys	Lys	Leu	Gly	Tyr	Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	
485					490					495						

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 466

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 466

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100	105	110	
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val			
115	120	125	
Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile			
130	135	140	
Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu			
145	150	155	160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu			
165	170	175	
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser			
180	185	190	
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val			
195	200	205	
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr			
210	215	220	
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile			
225	230	235	240
Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met			
245	250	255	
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu			
260	265	270	
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val			
275	280	285	
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln			
290	295	300	
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys			
305	310	315	320
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu			
325	330	335	
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr			
340	345	350	

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met
420 425 430

Gly Val Phe Ile Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Ala Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 467

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 467

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Ile Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Glu Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Ile His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210					215					220						
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile	
225					230					235					240	
Gly	Glu	Gly	Met	Val	Phe	Asp	Ala	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met	
245					250					255						
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	
260					265					270						
Tyr	Lys	Glu	Asn	Ile	Asp	His	Pro	Leu	Tyr	Ile	Gln	Asn	Leu	Lys	Val	
275					280					285						
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val	Lys	Gln	
290					295					300						
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	
305					310					315					320	
Leu	Gly	Val	Asp	Glu	Leu	Ile	Glu	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	
325					330					335						
Asp	Leu	Phe	Phe	Glu	His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	
340					345					350						
Gly	Tyr	Met	Phe	Arg	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	
355					360					365						
Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	
370					375					380						
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	
385					390					395					400	
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	
405					410					415						
Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Met	
420					425					430						
Gly	Val	Phe	Ile	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Ala	Ala	
435					440					445						
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	
450					455					460						

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Lys Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 468

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 468

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65				70				75				80			
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Ile	Ile	Ser	Arg	Met	Gly
85				90				95							
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Ile	Gly	Tyr	Lys	Gly	Lys	Arg	Lys
100				105				110							
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val
115				120				125							
Lys	Lys	Ile	Ala	Gln	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile
130				135				140							
Asp	Tyr	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu
145				150				155				160			
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu
165				170				175							
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser
180				185				190							
Leu	Lys	Asp	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val
195				200				205							
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr
210				215				220							
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile
225				230				235				240			
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met
245				250				255							
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu
260				265				270							
Tyr	Lys	Glu	Asn	Ile	Asp	His	Pro	Leu	Tyr	Ile	Gln	Asn	Leu	Lys	Val
275				280				285							
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val	Lys	Gln
290				295				300							
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys
305				310				315				320			

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565

570

575

Ile Lys

<210> 469

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 469

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 470

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 470

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175

 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240

 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

<210> 471

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 471

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220

 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285

 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 472

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 472

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80

 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140

 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205

 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly
 405 410 415
 Phe Arg Val Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 473

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 473

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190

 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp Asp Gly Ile Leu Gly
405 410 415

Phe Arg Val Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 474

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 474

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300

 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp Asp Gly Ala Leu Gly
 405 410 415
 Phe Arg Val Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460
 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 475

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 475

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85

90

95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100

105

110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115

120

125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130

135

140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145

150

155

160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165

170

175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180

185

190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195

200

205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210

215

220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225

230

235

240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245

250

255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260

265

270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275

280

285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290

295

300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305

310

315

320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325

330

335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asp Gly Ala Leu Gly
405 410 415

Phe Arg Val Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 476

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 476

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asp Gly Ile Val Arg
 405 410 415
 Leu Thr Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 477

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 477

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125

 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190

 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asp Gly Ile Val Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575

Ile Lys

<210> 478

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 478

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165	170	175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser		
180	185	190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val		
195	200	205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr		
210	215	220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile		
225	230	235
		240
Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met		
245	250	255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu		
260	265	270
Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val		
275	280	285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln		
290	295	300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys		
305	310	315
Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu		
325	330	335
Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr		
340	345	350
Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp		
355	360	365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu		
370	375	380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro		
385	390	395
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp Asp Gly Ile Val Gly		
405	410	415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 479

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 479

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

				20				25				30			
Asp	Asn	Tyr	Lys	Ile	Gly	Asn	Ser	Leu	Asp	Glu	Phe	Met	Gln	Trp	Val
35				40				45							
Met	Glu	Ile	Gln	Ala	Asp	Leu	Tyr	Phe	His	Asn	Leu	Lys	Phe	Asp	Gly
50				55				60							
Ala	Phe	Ile	Val	Asn	Trp	Leu	Phe	Lys	Asn	Gly	Phe	Lys	Trp	Cys	Lys
65				70				75				80			
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Ile	Ile	Ser	Arg	Met	Gly
85				90				95							
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Ile	Gly	Tyr	Lys	Gly	Lys	Arg	Lys
100				105				110							
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val
115				120				125							
Lys	Lys	Ile	Ala	Gln	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile
130				135				140							
Asp	Tyr	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu
145				150				155				160			
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu
165				170				175							
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser
180				185				190							
Leu	Lys	Asp	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val
195				200				205							
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr
210				215				220							
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile
225				230				235				240			
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met
245				250				255							
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu
260				265				270							

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp Asp Gly Ile Val Gly
 405 410 415

Phe Arg Val Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 480

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 480

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205

 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp Asp Gly Ala Val Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 481

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 481

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245					250					255						
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	
260					265					270						
Tyr	Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val	
275					280					285						
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln	
290					295					300						
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	
305					310					315					320	
Leu	Gly	Val	Asp	Glu	Leu	Ile	Asp	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	
325					330					335						
Asp	Leu	Phe	Phe	Glu	His	Tyr	Asp	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	
340					345					350						
Gly	Tyr	Met	Phe	Lys	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	
355					360					365						
Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	
370					375					380						
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	
385					390					395					400	
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ile	Val	Gly	
405					410					415						
Phe	Arg	Val	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Leu	
420					425					430						
Ala	Ser	Phe	Val	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala	
435					440					445						
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	
450					455					460						
Leu	Thr	Gly	Thr	Lys	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	His	Pro	
465					470					475					480	
Lys	Lys	Leu	Gly	Tyr	Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	
485					490					495						

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 482

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 482

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100	105	110	
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val			
115	120	125	
Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile			
130	135	140	
Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu			
145	150	155	160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu			
165	170	175	
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser			
180	185	190	
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val			
195	200	205	
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr			
210	215	220	
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile			
225	230	235	240
Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met			
245	250	255	
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu			
260	265	270	
Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val			
275	280	285	
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln			
290	295	300	
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys			
305	310	315	320
Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu			
325	330	335	
Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr			
340	345	350	

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Arg Ile Lys Glu Glu Val
530 535 540

Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Lys Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 483

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 483

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285

 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415

 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Arg Ile Lys Glu Glu Val
530 535 540

Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 484

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 484

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65				70				75				80			
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Ile	Ile	Ser	Arg	Met	Gly
85				90				95							
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Ile	Gly	Tyr	Lys	Gly	Lys	Arg	Lys
100				105				110							
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val
115				120				125							
Lys	Lys	Ile	Ala	Gln	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile
130				135				140							
Asp	Tyr	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu
145				150				155				160			
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu
165				170				175							
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser
180				185				190							
Leu	Lys	Asp	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val
195				200				205							
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr
210				215				220							
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile
225				230				235				240			
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met
245				250				255							
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu
260				265				270							
Tyr	Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val
275				280				285							
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln
290				295				300							
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys
305				310				315				320			

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Arg Ile Lys Glu Glu Val
 530 535 540

Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Thr Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565

570

575

Ile Lys

<210> 485

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 485

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Arg Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Thr Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 486

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 486

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175

 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240

 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Thr Ile Lys Glu Glu Val

530 535 540
 Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Lys Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

<210> 487

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 487

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220

 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285

 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Thr Ile Lys Glu Glu Val
530 535 540

Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 488

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 488

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80

 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140

 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205

 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
260 265 270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Thr Ile Lys Glu Glu Val
530 535 540
Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Thr Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 489

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 489

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Ile Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190

 Leu Lys Asp Phe Lys Asp Ile Leu Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Ile Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Val Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 490

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 490

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Leu Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Ile Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225				230				235				240			
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met
				245				250				255			
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu
				260				265				270			
Tyr	Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val
				275				280				285			
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln
290				295				300							
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys
305				310				315				320			
Leu	Gly	Val	Asp	Glu	Leu	Ile	Asp	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu
				325				330				335			
Asp	Leu	Phe	Phe	Glu	His	Tyr	Asp	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr
				340				345				350			
Gly	Tyr	Met	Phe	Lys	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp
355				360				365							
Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu
370				375				380							
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro
385				390				395				400			
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly
				405				410				415			
Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Leu
420				425				430							
Ala	Ser	Phe	Val	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala
435				440				445							
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His
450				455				460							
Leu	Thr	Gly	Thr	Lys	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	His	Pro
465				470				475				480			

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 491

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 491

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Arg Met Gly

85

90

95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100

105

110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115

120

125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130

135

140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145

150

155

160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165

170

175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180

185

190

Leu Lys Asp Phe Lys Asp Ile Leu Thr Thr Lys Lys Phe Lys Lys Val

195

200

205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Ile Arg Lys Ala Tyr

210

215

220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225

230

235

240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245

250

255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260

265

270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275

280

285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290

295

300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305

310

315

320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325

330

335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 492

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 492

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Gln Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300
 Asn Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 493

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 493

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50					55					60									
Ala	Phe	Ile	Val	Asn	Trp	Leu	Phe	Lys	Asn	Gly	Phe	Lys	Trp	Cys	Lys				
65					70					75					80				
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Leu	Ile	Ser	Arg	Met	Gly				
85					90					95									
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Ile	Gly	Tyr	Lys	Gly	Lys	Arg	Lys				
100					105					110									
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val				
115					120					125									
Lys	Lys	Ile	Ala	Gln	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile				
130					135					140									
Asp	Tyr	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu				
145					150					155					160				
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu				
165					170					175									
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser				
180					185					190									
Leu	Lys	Asp	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val				
195					200					205									
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr				
210					215					220									
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile				
225					230					235					240				
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met				
245					250					255									
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu				
260					265					270									
Tyr	Lys	Glu	Asn	Ile	Asp	His	Pro	Leu	Tyr	Ile	Gln	Asn	Leu	Lys	Val				
275					280					285									
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val	Lys	Gln				
290					295					300									

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp Asp Gly Ala Leu Gly
405 410 415

Phe Arg Val Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575

Ile Lys

<210> 494

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 494

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165	170	175
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser		
180	185	190
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val		
195	200	205
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr		
210	215	220
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile		
225	230	235
		240
Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met		
245	250	255
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu		
260	265	270
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val		
275	280	285
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln		
290	295	300
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys		
305	310	315
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu		
325	330	335
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr		
340	345	350
Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp		
355	360	365
Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu		
370	375	380
Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro		
385	390	395
Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ile Val Gly		
405	410	415

Phe Arg Val Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 495

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 495

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

	20				25				30							
Asp	Asn	Tyr	Lys	Ile	Gly	Asn	Ser	Leu	Asp	Glu	Phe	Met	Gln	Trp	Val	
	35					40					45					
Met	Glu	Ile	Gln	Ala	Asp	Leu	Tyr	Phe	His	Asn	Leu	Lys	Phe	Asp	Gly	
	50					55					60					
Ala	Phe	Ile	Val	Asn	Trp	Leu	Phe	Lys	Asn	Gly	Phe	Lys	Trp	Cys	Lys	
65					70					75					80	
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Leu	Ile	Ser	Arg	Met	Gly	
			85					90					95			
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Ile	Gly	Tyr	Lys	Gly	Lys	Arg	Lys	
	100					105					110					
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val	
	115					120					125					
Lys	Lys	Ile	Ala	Gln	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile	
	130					135					140					
Asp	Tyr	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu	
145					150					155					160	
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu	
	165					170					175					
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser	
	180					185					190					
Leu	Lys	Asp	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val	
	195					200					205					
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr	
	210					215					220					
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile	
225					230					235					240	
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met	
	245					250					255					
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	
	260					265					270					

Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ile Val Gly
405 410 415

Phe Arg Val Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Arg Ile Lys Glu Glu Val
530 535 540

Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Lys Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 496

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 496

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205

 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ile Val Gly
405 410 415

Phe Arg Val Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Arg Ile Lys Glu Glu Val
530 535 540

Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Thr Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 497

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 497

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Leu Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Ile Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245					250					255						
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	
260					265					270						
Tyr	Lys	Glu	Asn	Ile	Asp	His	Pro	Leu	Tyr	Ile	Gln	Asn	Leu	Lys	Val	
275					280					285						
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val	Lys	Gln	
290					295					300						
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	
305					310					315					320	
Leu	Gly	Val	Asp	Glu	Leu	Ile	Glu	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	
325					330					335						
Asp	Leu	Phe	Phe	Glu	His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	
340					345					350						
Gly	Tyr	Met	Phe	Arg	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	
355					360					365						
Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	
370					375					380						
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	
385					390					395					400	
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ile	Val	Gly	
405					410					415						
Phe	Arg	Val	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Leu	
420					425					430						
Ala	Ser	Phe	Val	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala	
435					440					445						
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	
450					455					460						
Leu	Thr	Gly	Thr	Lys	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	His	Pro	
465					470					475					480	
Lys	Lys	Leu	Gly	Tyr	Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	
485					490					495						

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Arg Ile Lys Glu Glu Val
530 535 540

Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Thr Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 498

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 498

Met Ser Arg Lys Arg Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Ala
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60
Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100	105	110	
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val			
115	120	125	
Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile			
130	135	140	
Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu			
145	150	155	160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu			
165	170	175	
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser			
180	185	190	
Leu Lys Asp Phe Lys Asp Ile Leu Thr Thr Lys Lys Phe Lys Lys Val			
195	200	205	
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Ile Arg Lys Ala Tyr			
210	215	220	
Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile			
225	230	235	240
Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met			
245	250	255	
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu			
260	265	270	
Tyr Lys Glu Asn Ile Asp His Pro Leu Tyr Ile Gln Asn Leu Lys Val			
275	280	285	
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Cys Ile Gln Val Lys Gln			
290	295	300	
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys			
305	310	315	320
Leu Gly Val Asp Glu Leu Ile Glu Leu Thr Leu Thr Asn Val Asp Leu			
325	330	335	
Asp Leu Phe Phe Glu His Tyr Glu Ile Leu Glu Ile His Tyr Thr Tyr			
340	345	350	

Gly Tyr Met Phe Arg Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ile Val Gly
405 410 415

Phe Arg Val Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Arg Ile Lys Glu Glu Val
530 535 540

Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Thr Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 499

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 499

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Leu Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Ile Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Leu Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Ile Arg Lys Ala Tyr

210					215					220						
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile	
225					230					235					240	
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met	
245					250					255						
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	
260					265					270						
Tyr	Lys	Glu	Asn	Ile	Asp	His	Pro	Leu	Tyr	Ile	Gln	Asn	Leu	Lys	Val	
275					280					285						
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Cys	Ile	Gln	Val	Lys	Gln	
290					295					300						
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	
305					310					315					320	
Leu	Gly	Val	Asp	Glu	Leu	Ile	Glu	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	
325					330					335						
Asp	Leu	Phe	Phe	Glu	His	Tyr	Glu	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	
340					345					350						
Gly	Tyr	Met	Phe	Arg	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	
355					360					365						
Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	
370					375					380						
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	
385					390					395					400	
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ile	Val	Gly	
405					410					415						
Phe	Arg	Val	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Leu	
420					425					430						
Ala	Ser	Phe	Val	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala	
435					440					445						
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	
450					455					460						

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Arg Ile Lys Glu Glu Val
530 535 540

Thr Phe Asp Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Thr Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 500

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 500

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65				70				75				80			
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Ile	Ile	Ser	Arg	Met	Gly
85				90				95							
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Ile	Gly	Tyr	Lys	Gly	Lys	Arg	Lys
100				105				110							
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val
115				120				125							
Lys	Lys	Ile	Ala	Gln	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile
130				135				140							
Asp	Tyr	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu
145				150				155				160			
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu
165				170				175							
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser
180				185				190							
Leu	Lys	Asp	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val
195				200				205							
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr
210				215				220							
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Arg	Phe	Lys	Gly	Lys	Glu	Ile
225				230				235				240			
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met
245				250				255							
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu
260				265				270							
Tyr	Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val
275				280				285							
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln
290				295				300							
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys
305				310				315				320			

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly
 405 410 415

Phe Arg Val Gly Asp Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565

570

575

Ile Lys

<210> 501

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 501

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Asp Asp Gly Ser Leu Gly
 405 410 415
 Phe Arg Val Gly Asp Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Thr Ile Lys Glu Glu Val
530 535 540

Thr Phe Asp Asn Phe Ala Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 502

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 502

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

 Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175

 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240

 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Val Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val

530 535 540
 Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575
 Ile Lys

<210> 503

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 503

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Lys Leu Thr Thr Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220

 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285

 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 504

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 504

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45
 Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80

 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Gln Arg Thr Ile Phe Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140

 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205

 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445
 Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

 Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480
 Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495
 Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val

500 505 510
Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540
Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 505

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 505

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15
Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30
Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45
Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80
Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95
Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110
Gln Arg Thr Ile Phe Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190

 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320

 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 506

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 506

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Asn His Val Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225				230				235				240			
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met
				245				250				255			
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu
				260				265				270			
Tyr	Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val
				275				280				285			
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln
290				295				300							
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys
305				310				315				320			
Leu	Gly	Val	Asp	Glu	Leu	Ile	Asp	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu
				325				330				335			
Asp	Leu	Phe	Phe	Glu	His	Tyr	Asp	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr
				340				345				350			
Gly	Tyr	Met	Phe	Lys	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp
355				360				365							
Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu
370				375				380							
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro
385				390				395				400			
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly
				405				410				415			
Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Leu
420				425				430							
Ala	Ser	Phe	Val	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala
435				440				445							
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His
450				455				460							
Leu	Thr	Gly	Thr	Lys	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	His	Pro
465				470				475				480			

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 507

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 507

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85

90

95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100

105

110

Asn His Val Val Phe Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115

120

125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130

135

140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145

150

155

160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165

170

175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180

185

190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195

200

205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210

215

220

Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile

225

230

235

240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245

250

255

Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu

260

265

270

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val

275

280

285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln

290

295

300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys

305

310

315

320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu

325

330

335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 508

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 508

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Gly Thr Thr Gln Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415
 Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430
 Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 509

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 509

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110
 Phe Arg Val Glu Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125

 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190

 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255

 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys

545 550 555 560
 Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
 565 570 575

Ile Lys

<210> 510

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 510

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
 1 5 10 15
 Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
 20 25 30
 Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
 35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
 50 55 60
 Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
 65 70 75 80
 Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
 85 90 95
 Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
 100 105 110

Phe Arg Val Glu Phe Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
 115 120 125
 Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
 130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205
 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Gly Lys Glu Ile
 225 230 235 240

 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270
 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300

 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335
 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380
 Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400
 Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 511

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 511

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

	20				25				30							
Asp	Asn	Tyr	Lys	Ile	Gly	Asn	Ser	Leu	Asp	Glu	Phe	Met	Gln	Trp	Val	
	35					40					45					
Met	Glu	Ile	Gln	Ala	Asp	Leu	Tyr	Phe	His	Asn	Leu	Lys	Phe	Asp	Gly	
	50					55					60					
Ala	Phe	Ile	Val	Asn	Trp	Leu	Phe	Lys	Asn	Gly	Phe	Lys	Trp	Cys	Lys	
65					70					75					80	
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Ile	Ile	Ser	Arg	Met	Gly	
			85					90					95			
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Ile	Gly	Tyr	Lys	Gly	Lys	Arg	Lys	
	100					105					110					
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val	
	115					120					125					
Lys	Lys	Ile	Ala	Gln	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile	
	130					135					140					
Asp	Tyr	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu	
145					150					155					160	
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu	
	165					170					175					
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser	
	180					185					190					
Leu	Lys	Asp	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val	
	195					200					205					
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr	
	210					215					220					
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asn	Asp	Lys	Tyr	Lys	Gly	Lys	Glu	Ile	
225					230					235					240	
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met	
	245					250					255					
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	
	260					265					270					

Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
275 280 285

Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
290 295 300

Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
305 310 315 320

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys

515 520 525
Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560
Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575
Ile Lys

<210> 512

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 512

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140
 Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
 145 150 155 160
 Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
 165 170 175
 Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
 180 185 190
 Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
 195 200 205

 Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
 210 215 220
 Arg Gly Gly Phe Thr Trp Leu Asn Pro Lys Tyr Lys Gly Lys Glu Ile
 225 230 235 240
 Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met
 245 250 255
 Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu
 260 265 270

 Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val
 275 280 285
 Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln
 290 295 300
 Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys
 305 310 315 320
 Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

 Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350
 Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365
 Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 513

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 513

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys
100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val
115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile
130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu
145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu
165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser
180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val
195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr
210 215 220

Arg Gly Gly Phe Thr Trp Leu Asn Pro Lys Phe Lys Gly Lys Glu Ile
225 230 235 240

Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met

245					250					255						
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	
260					265					270						
Tyr	Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val	
275					280					285						
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln	
290					295					300						
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	
305					310					315					320	
Leu	Gly	Val	Asp	Glu	Leu	Ile	Asp	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	
325					330					335						
Asp	Leu	Phe	Phe	Glu	His	Tyr	Asp	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	
340					345					350						
Gly	Tyr	Met	Phe	Lys	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	
355					360					365						
Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	
370					375					380						
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	
385					390					395					400	
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	
405					410					415						
Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Leu	
420					425					430						
Ala	Ser	Phe	Val	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala	
435					440					445						
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	
450					455					460						
Leu	Thr	Gly	Thr	Lys	Ile	Pro	Asp	Val	Ile	Lys	Asp	Ile	Val	His	Pro	
465					470					475					480	
Lys	Lys	Leu	Gly	Tyr	Trp	Glu	His	Glu	Ser	Thr	Phe	Lys	Arg	Ala	Lys	
485					490					495						

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 514

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 514

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys
65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly
85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100	105	110	
Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val			
115	120	125	
Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile			
130	135	140	
Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu			
145	150	155	160
Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu			
165	170	175	
Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser			
180	185	190	
Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val			
195	200	205	
Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr			
210	215	220	
Arg Gly Gly Phe Thr Trp Leu Asn Pro Arg Tyr Lys Gly Lys Glu Ile			
225	230	235	240
Gly Glu Gly Met Val Phe Asp Ile Asn Ser Ala Tyr Pro Ala Gln Met			
245	250	255	
Tyr Val Arg Pro Leu Pro Tyr Gly Thr Pro Leu Phe Tyr Glu Gly Glu			
260	265	270	
Tyr Lys Glu Asn Ile Asp Tyr Pro Leu Tyr Ile Gln Asn Ile Lys Val			
275	280	285	
Arg Phe Arg Leu Lys Glu Arg His Ile Pro Thr Ile Gln Val Lys Gln			
290	295	300	
Ser Ser Leu Phe Ile Gln Asn Glu Tyr Leu Glu Ser Ser Val Asn Lys			
305	310	315	320
Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu			
325	330	335	
Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr			
340	345	350	

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 515

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 515

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu

1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu

20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val

35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly

50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65 70 75 80

Glu Ala Lys Glu Glu Arg Thr Phe Ser Thr Ile Ile Ser Arg Met Gly

85 90 95

Gln Trp Tyr Met Ile Asp Ile Cys Ile Gly Tyr Lys Gly Lys Arg Lys

100 105 110

Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val

115 120 125

Lys Lys Ile Ala Gln Asp Phe Lys Leu Thr Val Lys Lys Gly Asp Ile

130 135 140

Asp Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu

145 150 155 160

Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala Leu Leu

165 170 175

Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser

180 185 190

Leu Lys Asp Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val

195 200 205

Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Lys Ala Tyr

210					215					220						
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asp	Pro	Lys	Tyr	Lys	Gly	Lys	Glu	Ile	
225					230					235					240	
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met	
245					250					255						
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu	
260					265					270						
Tyr	Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val	
275					280					285						
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln	
290					295					300						
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys	
305					310					315					320	
Leu	Gly	Val	Asp	Glu	Leu	Ile	Asp	Leu	Thr	Leu	Thr	Asn	Val	Asp	Leu	
325					330					335						
Asp	Leu	Phe	Phe	Glu	His	Tyr	Asp	Ile	Leu	Glu	Ile	His	Tyr	Thr	Tyr	
340					345					350						
Gly	Tyr	Met	Phe	Lys	Ala	Ser	Cys	Asp	Met	Phe	Lys	Asp	Phe	Ile	Asp	
355					360					365						
Lys	Trp	Thr	Tyr	Ile	Lys	Thr	Thr	Ser	Tyr	Gly	Ala	Ile	Lys	Gln	Leu	
370					375					380						
Ala	Lys	Leu	Met	Leu	Asn	Ser	Leu	Tyr	Gly	Lys	Phe	Ala	Ser	Asn	Pro	
385					390					395					400	
Asp	Val	Thr	Gly	Lys	Val	Pro	Tyr	Leu	Lys	Glu	Asn	Gly	Ala	Leu	Gly	
405					410					415						
Phe	Arg	Leu	Gly	Glu	Glu	Glu	Thr	Lys	Asp	Pro	Val	Tyr	Thr	Pro	Leu	
420					425					430						
Ala	Ser	Phe	Val	Thr	Ala	Trp	Gly	Arg	Tyr	Thr	Thr	Ile	Thr	Thr	Ala	
435					440					445						
Gln	Ala	Cys	Tyr	Asp	Arg	Ile	Ile	Tyr	Cys	Asp	Thr	Asp	Ser	Ile	His	
450					455					460						

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr
565 570 575

Ile Lys

<210> 516

<211> 578

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 516

Met Ser Arg Lys Met Phe Ser Cys Asp Phe Glu Thr Thr Thr Lys Leu
1 5 10 15

Asp Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Glu Ile Gly Asn Leu
20 25 30

Asp Asn Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Gln Trp Val
35 40 45

Met Glu Ile Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Val Asn Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys

65				70				75				80			
Glu	Ala	Lys	Glu	Glu	Arg	Thr	Phe	Ser	Thr	Ile	Ile	Ser	Arg	Met	Gly
85				90				95							
Gln	Trp	Tyr	Met	Ile	Asp	Ile	Cys	Ile	Gly	Tyr	Lys	Gly	Lys	Arg	Lys
100				105				110							
Ile	His	Thr	Val	Ile	Tyr	Asp	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Pro	Val
115				120				125							
Lys	Lys	Ile	Ala	Gln	Asp	Phe	Lys	Leu	Thr	Val	Lys	Lys	Gly	Asp	Ile
130				135				140							
Asp	Tyr	His	Lys	Glu	Arg	Pro	Val	Gly	Tyr	Lys	Ile	Thr	Pro	Glu	Glu
145				150				155				160			
Tyr	Ala	Tyr	Ile	Lys	Asn	Asp	Ile	Gln	Ile	Ile	Ala	Glu	Ala	Leu	Leu
165				170				175							
Ile	Gln	Phe	Lys	Gln	Gly	Leu	Asp	Arg	Met	Thr	Ala	Gly	Ser	Asp	Ser
180				185				190							
Leu	Lys	Asp	Phe	Lys	Asp	Ile	Ile	Thr	Thr	Lys	Lys	Phe	Lys	Lys	Val
195				200				205							
Phe	Pro	Thr	Leu	Ser	Leu	Gly	Leu	Asp	Lys	Glu	Val	Arg	Lys	Ala	Tyr
210				215				220							
Arg	Gly	Gly	Phe	Thr	Trp	Leu	Asp	Pro	Arg	Tyr	Lys	Gly	Lys	Glu	Ile
225				230				235				240			
Gly	Glu	Gly	Met	Val	Phe	Asp	Ile	Asn	Ser	Ala	Tyr	Pro	Ala	Gln	Met
245				250				255							
Tyr	Val	Arg	Pro	Leu	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Tyr	Glu	Gly	Glu
260				265				270							
Tyr	Lys	Glu	Asn	Ile	Asp	Tyr	Pro	Leu	Tyr	Ile	Gln	Asn	Ile	Lys	Val
275				280				285							
Arg	Phe	Arg	Leu	Lys	Glu	Arg	His	Ile	Pro	Thr	Ile	Gln	Val	Lys	Gln
290				295				300							
Ser	Ser	Leu	Phe	Ile	Gln	Asn	Glu	Tyr	Leu	Glu	Ser	Ser	Val	Asn	Lys
305				310				315				320			

Leu Gly Val Asp Glu Leu Ile Asp Leu Thr Leu Thr Asn Val Asp Leu
 325 330 335

Asp Leu Phe Phe Glu His Tyr Asp Ile Leu Glu Ile His Tyr Thr Tyr
 340 345 350

Gly Tyr Met Phe Lys Ala Ser Cys Asp Met Phe Lys Asp Phe Ile Asp
 355 360 365

Lys Trp Thr Tyr Ile Lys Thr Thr Ser Tyr Gly Ala Ile Lys Gln Leu
 370 375 380

Ala Lys Leu Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro
 385 390 395 400

Asp Val Thr Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly
 405 410 415

Phe Arg Leu Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Leu
 420 425 430

Ala Ser Phe Val Thr Ala Trp Gly Arg Tyr Thr Thr Ile Thr Thr Ala
 435 440 445

Gln Ala Cys Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His
 450 455 460

Leu Thr Gly Thr Lys Ile Pro Asp Val Ile Lys Asp Ile Val His Pro
 465 470 475 480

Lys Lys Leu Gly Tyr Trp Glu His Glu Ser Thr Phe Lys Arg Ala Lys
 485 490 495

Tyr Leu Arg Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Arg Val
 500 505 510

Arg Gly Tyr Leu Val Gln Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys
 515 520 525

Phe Ser Val Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Glu Glu Val
 530 535 540

Thr Phe Glu Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys
 545 550 555 560

Pro Val Gln Val Pro Gly Gly Val Val Leu Val Asp Ser Val Phe Thr

565

570

575

Ile Lys

<210> 517

<211> 27

<212> PRT

<213> Artificial sequence

<220><223> Synthetic polypeptide

<400> 517

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Leu Asn Asp

1 5 10 15

Phe Phe Glu Ala Gln Lys Ile Glu Trp His Glu

20 25

<210> 518

<211> 53

<212> PRT

<213> Bacillus phage phi29

<400> 518

Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly Ala Phe Ile Ile Asn

1 5 10 15

Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala Asp Gly Leu Pro Asn

20 25 30

Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln Trp Tyr Met Ile Asp

35 40 45

Ile Cys Leu Gly Tyr

50

<210> 519

<211> 53

<212> PRT

<213> Bacteriophage M2Y

<400> 519

Asp Leu Tyr Phe His Asp Leu Lys Phe Asp Gly Ala Phe Ile Val Asn

1 5 10 15

Trp Leu Glu Gln His Gly Phe Lys Trp Ser Asn Glu Gly Leu Pro Asn

20 25 30
Thr Tyr Asn Thr Ile Ile Ser Lys Met Gly Gln Trp Tyr Met Ile Asp

35 40 45

Ile Cys Phe Gly Tyr

50

<210> 520

<211> 54

<212> PRT

<213> *Lucilia cuprina*

<400> 520

Arg Leu Tyr Phe His Asp Leu Lys Phe Asp Gly Ser Phe Ile Val Asn

1 5 10 15

Trp Leu Leu His Asn Gly Tyr Thr Trp Thr Lys Arg Pro Ser Lys Glu

20 25 30
Gly Gln Phe Ser Thr Leu Ile Ser Lys Met Gly Gln Trp Tyr Gly Ile

35 40 45

Thr Ile Cys Ser Gly Arg

50

<210> 521

<211> 54

<212> PRT

<213> *Enterococcus faecium*

<400> 521

Asp Ile Tyr Phe His Asp Glu Lys Phe Asp Gly Glu Phe Met Leu Ser

1 5 10 15

Trp Leu Phe Lys Asn Gly Phe Lys Trp Cys Lys Glu Ala Lys Glu Glu

20 25 30
Arg Thr Phe Ser Thr Leu Ile Ser Asn Met Gly Gln Trp Tyr Ala Leu

35 40 45

Glu Ile Cys Trp Asn Val

50

<210> 522

<211> 56

<212> PRT

<213> Bacillus phage GA-1

<400> 522

Asp Ile Tyr Phe His Asn Leu Lys Phe Asp Gly Ser Phe Ile Leu Pro

1 5 10 15

Trp Trp Leu Arg Asn Gly Tyr Val His Thr Glu Glu Asp Arg Thr Asn

20 25 30

Thr Pro Lys Glu Phe Thr Thr Thr Ile Ser Gly Met Gly Gln Trp Tyr

35 40 45

Ala Val Asp Val Cys Ile Asn Thr

50 55

<210> 523

<211> 53

<212> PRT

<213> Bacillus phage VMY22

<400> 523

Asp Leu Tyr Phe His Asp Leu Arg Tyr Asp Gly Glu Phe Ile Val Asn

1 5 10 15

Trp Leu Leu His Lys Gly Tyr Glu Cys Asn Glu Ser Gly Arg Pro Lys

20 25 30

Thr Phe Asp Thr Val Ile Ser Lys Gly Gly Gln Trp Tyr Lys Ile Ala

35 40 45

Ile His His Glu Gly

50

<210> 524

<211> 54

<212> PRT

<213> Actinomyces phage AV-1

<400> 524

His Ile Tyr Phe His Asn Leu Ala Phe Asp Gly Thr Phe Ile Leu Asp

1 5 10 15

Trp Leu Leu Lys His Gly Tyr Arg Trp Thr Lys Glu Asn Pro Gly Val

20 25 30
Lys Glu Phe Thr Ser Leu Ile Ser Arg Met Gly Lys Tyr Tyr Ser Ile
35 40 45
Thr Val Val Phe Glu Thr

50

<210> 525

<211> 55

<212> PRT

<213> Globodera sp.

<400> 525

Ile Thr Phe Phe His Asn Leu Lys Phe Asp Gly Ala Phe Ile Leu Asp
1 5 10 15
Arg Leu Phe Arg Leu Gly Tyr Glu Phe Thr Asp Glu Lys Ala Pro Gln

20 25 30
Val Lys Glu Phe Ser Thr Leu Ile Ser Lys Met Gly Gln Phe Tyr Ser
35 40 45
Ile Lys Val Arg Trp Glu Asn

50

55

<210> 526

<211> 56

<212> PRT

<213> Lynx pardinus

<400> 526

Arg Val Tyr Phe His Asn Leu Lys Phe Asp Gly Lys Phe Ile Leu His
1 5 10 15
Lys Ile Leu Thr Asp Gly Trp Lys Trp Ile Pro Asp Lys Asn Asp Cys

20 25 30
Ala Asn Arg Thr Phe Thr Thr Leu Ile Ser Asp Met Ser Gln Phe Tyr
35 40 45
Ser Ile Lys Leu Trp Phe Asp Glu

50

55

<210> 527

<211> 55

<212> PRT

<213> Candidatus Moranbacteria

<400> 527

Glu Val Phe Phe His Asn Leu Lys Tyr Asp Gly Asp Phe Ile Val Lys

1 5 10 15

Phe Leu Leu Glu Asn Gly Phe Lys His Ser Arg Glu Arg Ala Leu Tyr

20 25 30

Ser Asn Glu Phe Ser Thr Leu Ile Ser Asp Thr Gly Thr Trp Tyr Glu

35 40 45

Ile Lys Ile Cys Phe His Ala

50 55

<210> 528

<211> 57

<212> PRT

<213> Eggerthella sp.

<400> 528

Leu Ile Gly Phe His Asn Leu Lys Phe Asp Gly Ser Tyr Ile Leu Ser

1 5 10 15

Tyr Leu Leu Gly Val Ala Lys Trp Glu Tyr Asn Asp Lys Pro Lys Ala

20 25 30

Arg Lys Ala Lys Thr Val Glu Cys Leu Ile Ser Ser Ile Gly Val His

35 40 45

Tyr Asn Tyr Arg Ile Asn Phe Thr Lys

50 55

<210> 529

<211> 12

<212> PRT

<213> Bacillus phage phi29

<400> 529

Asn Gly Phe Lys Trp Ser Ala Asp Gly Leu Pro Asn

1 5 10

<210> 530

<211> 12

<212> PRT

<213> Bacteriophage M2Y

<400> 530

His Gly Phe Lys Trp Ser Asn Glu Gly Leu Pro Asn

1 5 10

<210> 531

<211> 13

<212> PRT

<213> Lucilia cuprina

<400> 531

Asn Gly Tyr Thr Trp Thr Lys Arg Pro Ser Lys Glu Gly

1 5 10

<210> 532

<211> 13

<212> PRT

<213> Enterococcus faecium

<400> 532

Asn Gly Phe Lys Trp Cys Lys Glu Ala Lys Glu Glu Arg

1 5 10

<210> 533

<211> 15

<212> PRT

<213> Bacillus phage GA-1

<400> 533

Asn Gly Tyr Val His Thr Glu Glu Asp Arg Thr Asn Thr Pro Lys

1 5 10 15

<210> 534

<211> 12

<212> PRT

<213> Bacillus phage VMY22

<400> 534

Lys Gly Tyr Glu Cys Asn Glu Ser Gly Arg Pro Lys

1 5 10

<210> 535

<211> 13

<212> PRT

<213> Actinomyces phage AV-1

<400> 535

His Gly Tyr Arg Trp Thr Lys Glu Asn Pro Gly Val Lys

1 5 10

<210> 536

<211> 14

<212> PRT

<213> Globodera sp.

<400> 536

Leu Gly Tyr Glu Phe Thr Asp Glu Lys Ala Pro Gln Val Lys

1 5 10

<210> 537

<211> 15

<212> PRT

<213> Lynx pardinus

<400> 537

Asp Gly Trp Lys Trp Ile Pro Asp Lys Asn Asp Cys Ala Asn Arg

1 5 10 15

<210> 538

<211> 14

<212> PRT

<213> Eggerthella sp.

<400> 538

Asn Gly Phe Lys His Ser Arg Glu Arg Ala Leu Tyr Ser Asn

1 5 10

<210> 539

<211> 16

<212> PRT

<213> Eggerthella sp.

<400> 539

Val Ala Lys Trp Glu Tyr Asn Asp Lys Pro Lys Ala Arg Lys Ala Lys

1 5 10 15