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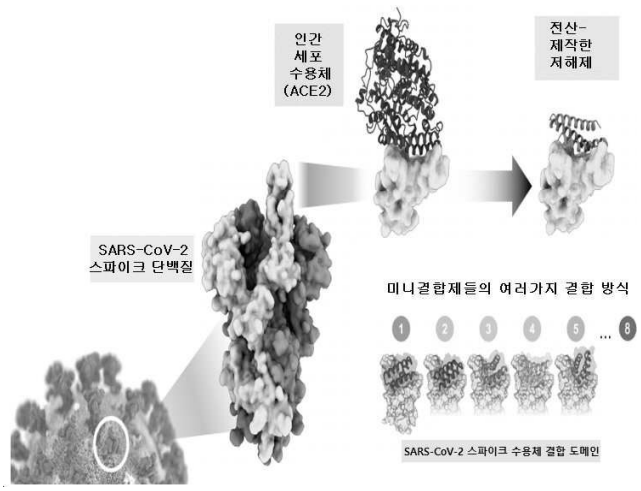
(54) 발명의 명칭 **SARS-COV-2 저해제**

(57) 요 약

서열번호 1-17, 19-21, 23-34 및 100-101로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는 폴리펩타이드 저해제, 및 SARS-CoV-2 감염을 치료 및 진행을 제한하기 위한 이의 용도가 개시된다.

대 표 도 - 도1

설계된 미니결합제는 SARS-CoV-2 스파이크를 표적으로 한다



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명 세 서

청구범위

청구항 1

서열번호 1-17, 19-21, 23-34 및 100-101로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고; SARS-CoV-2 스파이크 당단백질 수용체 결합 도메인 (RBD)에 결합하는, 폴리펩타이드.

청구항 2

제1항에 있어서, 참조 폴리펩타이드의 아미노산 서열을 기준으로 아미노산 치환이 표 1에 제공된 아미노산 치환 예들로부터 선택되는, 폴리펩타이드.

청구항 3

제1항 또는 제2항에 있어서, 인터페이스 잔기가 참조 폴리펩타이드의 인터페이스 잔기와 동일하거나, 또는 참조 폴리펩타이드의 인터페이스 잔기에 대해 보존적으로 치환된, 폴리펩타이드.

청구항 4

제1항 내지 제3항 중 어느 한 항에 있어서, 서열번호 1-10, 13-17, 19-21, 33-34 및 100-101로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 5

제1항 내지 제4항 중 어느 한 항에 있어서, 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 6

제5항에 있어서, 상기 폴리펩타이드가 서열번호 1의 아미노산 서열에 대해 2, 4, 5, 14, 15, 17, 18, 27, 28, 32, 37, 38, 39, 41, 42, 49, 52, 및 55로 이루어진 군으로부터 선택되는 잔기들 중 1개, 2개, 3개, 4개, 5개, 6개, 7개, 8개, 9개, 10개, 11개, 12개, 13개, 14개, 15개, 16개, 17개 또는 전체 18개에서 아미노산 치환을 포함하는, 폴리펩타이드.

청구항 7

제6항에 있어서, 상기 치환이 표 4에 열거된 치환들로부터 개별적으로 또는 해당 열의 조합으로 선택되는, 폴리펩타이드.

청구항 8

제1항 내지 제4항 중 어느 한 항에 있어서, 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 9

제8항에 있어서, 상기 폴리펩타이드가 서열번호 13의 아미노산 서열에 대해 2, 6, 8, 9, 13, 14, 19, 22, 25, 26, 28, 29, 34, 35, 37, 40, 43, 45, 49 및 62로 이루어진 군으로부터 선택되는 잔기들 중 1개, 2개, 3개, 4개, 5개, 6개, 7개, 8개, 9개, 10개, 11개, 12개, 13개, 14개, 15개, 16개, 17개, 18개, 19개 또는 전체 20개에서 아미노산 치환을 포함하는, 폴리펩타이드.

청구항 10

제6항에 있어서, 상기 치환이 표 6에 열거된 치환들로부터 개별적으로 또는 해당 열의 조합으로 선택되는, 폴리펩타이드.

청구항 11

제1항 내지 제4항 중 어느 한 항에 있어서, 서열번호 33-34 및 100-101 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 12

제11항에 있어서, 상기 폴리펩타이드가 서열번호 101의 아미노산 서열에 대해 63 및 75로 이루어진 군으로부터 선택되는 잔기 또는 양쪽 잔기에서 아미노산 치환을 포함하는, 폴리펩타이드.

청구항 13

제12항에 있어서, 상기 치환이 R63A 및/또는 K75T를 포함하는, 폴리펩타이드.

청구항 14

제1항 내지 제13항 중 어느 한 항에 있어서, N-말단 및/또는 C-말단에 하나 이상의 첨가된 시스테인 잔기를 더 포함하는, 폴리펩타이드.

청구항 15

제1항 내지 제14항 중 어느 한 항에 있어서, N-연결된 당화 부위 (즉, NX(S/T), X는 임의의 아미노산임)를 포함하는, 폴리펩타이드.

청구항 16

제1항 내지 제15항 중 어느 한 항에 있어서, 서열번호 1-17, 19-21, 23-34 및 100-101로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 2 카피 이상 포함하는, 폴리펩타이드.

청구항 17

제16항에 있어서, 상기 폴리펩타이드 2 카피 이상이 모두 동일한, 폴리펩타이드.

청구항 18

제16항에 있어서, 상기 폴리펩타이드 2 카피 이상이 모두 동일하지 않은, 폴리펩타이드.

청구항 19

제16항 내지 제18항 중 어느 한 항에 있어서, 상기 폴리펩타이드 2 카피 이상이 아미노산 링커 서열에 의해 분리된, 폴리펩타이드.

청구항 20

제9항에 있어서, 상기 아미노산 링커 서열이 Gly-Ser 풍부 (Gly-Ser 잔기가 적어도 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100%임) 아미노산 링커를 포함하는, 폴리펩타이드.

청구항 21

제20항에 있어서, 상기 Gly-Ser 풍부 링커가 GG 및 서열번호 35-46 및 165-171로 이루어진 군으로부터 선택되는 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 22

제19항에 있어서, 상기 아미노산 링커 서열이 Pro-풍부 (Pro 잔기가 적어도 15%, 20%, 25% 또는 그 이상임) 아미노산 링커를 포함하는, 폴리펩타이드.

청구항 23

제22항에 있어서, 상기 Pro-풍부 아미노산 링커가 서열번호 97-98 및 172-176으로 이루어진 군으로부터 선택되는 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 24

제19항에 있어서, 상기 아미노산 링커가 서열번호 99 및 177-178로 이루어진 군으로부터 선택되는 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 25

제19항 내지 제24항 중 어느 한 항에 있어서, 상기 아미노산 링커가 독립적으로 아미노산 2-100개 길이인, 폴리펩타이드.

청구항 26

제16항 내지 제25항 중 어느 한 항에 있어서, 상기 폴리펩타이드가 식 Z1-Z2-Z3를 포함하고, 식에서

Z1은 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

Z2는 선택적인 아미노산 링커를 포함하고; 및

Z3는 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하며;

Z1과 Z3가 서로 동일하거나 또는 상이할 수 있는, 폴리펩타이드.

청구항 27

제26항에 있어서, Z1과 Z3가 서로 동일한, 폴리펩타이드.

청구항 28

제26항에 있어서, Z1과 Z3가 서로 상이한, 폴리펩타이드.

청구항 29

제26항 내지 제28항 중 어느 한 항에 있어서,

Z1이 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

Z3가 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 30

제26항 내지 제28항 중 어느 한 항에 있어서,

Z1이 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

Z3가 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 31

제26항 내지 제28항 중 어느 한 항에 있어서,

Z1이 서열번호 33-34, 100-100 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

Z3가 서열번호 33-34, 100-100 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 32

제26항 내지 제28항 중 어느 한 항에 있어서,

Z1 및 Z3 중 하나가 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

Z1 및 Z3 중 다른 하나는 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 33

제26항 내지 제28항 중 어느 한 항에 있어서,

Z1 및 Z3 중 하나가 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

Z1 및 Z3 중 다른 하나는 서열번호 33-34, 100-100 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 34

제26항 내지 제28항 중 어느 한 항에 있어서,

Z1 및 Z3 중 하나가 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

Z1 및 Z3 중 다른 하나는 서열번호 33-34, 100-100 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 35

제26항 내지 제34항 중 어느 한 항에 있어서, 상기 폴리펩타이드가 식 B1-B2-Z1-Z2-Z3-B3-B4를 포함하고, 식에서

Z1, Z2, 및 Z3는 제26항 내지 제34항 중 어느 한 항에 정의된 바와 같이 정의되고;

B2 및 B3는 선택적인 아미노산 링커를 포함하고; 및

B1 및 B4 중 하나 또는 둘다는 독립적으로 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하되, B1 및 B4 중 하나는 생략될 수 있는, 폴리펩타이드.

청구항 36

제35항에 있어서, B1 및 B4 중 하나가 생략된, 폴리펩타이드.

청구항 37

제35항에 있어서, B1 및 B4가 독립적으로 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 38

제37항에 있어서, B1과 B4가 동일한, 폴리펩타이드.

청구항 39

제37항에 있어서, B1과 B4가 동일하지 않은, 폴리펩타이드.

청구항 40

제35항 내지 제39항 중 어느 한 항에 있어서, 존재하는 경우 B1과 존재하는 경우 B4가 Z1 및 Z3 중 하나 또는 둘다와 동일하거나, 또는 존재하는 경우 B1과 존재하는 경우 B4가 Z1 및 Z3 중 어느 하나와 동일하지 않은, 폴리펩타이드.

청구항 41

제35항 내지 제40항 중 어느 한 항에 있어서, 존재하는 경우 B1과 존재하는 경우 B4가 독립적으로 서열번호 1-10, 13-17, 19-21, 33-34, 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 42

제35항 내지 제40항 중 어느 한 항에 있어서, 존재하는 경우 B1과 존재하는 경우 B4가 독립적으로 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 43

제35항 내지 제40항 중 어느 한 항에 있어서, 존재하는 경우 B1과 존재하는 경우 B4가 독립적으로 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 44

제35항 내지 제40항 중 어느 한 항에 있어서, 존재하는 경우 B1과 존재하는 경우 B4가 독립적으로 서열번호 33-34, 100-101 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 45

제35항 내지 제40항 중 어느 한 항에 있어서, B1 및 B4가 둘다 존재하고,

· B1 및 B4 중 하나는 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고, 다른 하나는 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하거나;

· B1 및 B4 중 하나는 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고, 다른 하나는 서열번호 33-34, 100-101 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하거나, 또는

· B1 및 B4 중 하나는 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고, 다른 하나는 서열번호 33-34, 100-101 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 46

제1항 내지 제45항 중 어느 한 항에 있어서, 서열번호 47-60,193-355 및 454-588로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열 및 표 8의 우측 칸에 언급된 것들로부터 선택되는 유형을 포함하되, 이러한 유형에서 위치 X1, X2, X3 및 X4는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 아미노산 1개 이상으로 된 임의 서열일 수 있으며, 폴리펩타이드에서 임의의 N-말단 메티오닌 잔기가 존재하거나 또는 생략될 수 있으며;

바람직하게는, 폴리펩타이드는 서열번호 454-588로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

가장 바람직하게는, 폴리펩타이드는 서열번호 693-701로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하되, 임의의 N-말단 메티오닌 잔기가 생략되거나 또는 존재할 수 있으며, 괄호 안 잔기는 존재하거나 또는 생략될 수 있으며 (바람직하게는 생략되고), 동일성 % 결정에 고려되지 않는, 폴리펩타이드.

청구항 47

제1항 내지 제46항 중 어느 한 항에 있어서, 추가적인 기능성 펩타이드 도메인을 추가로 포함하는, 폴리펩타이드.

청구항 48

제47항에 있어서, 상기 추가적인 기능성 펩타이드 도메인이 표적화 도메인, 검출가능한 도메인, 스캐폴드 도메인, 분비 신호, Fc 도메인 또는 추가의 치료학적 펩타이드 도메인을 포함하는, 폴리펩타이드.

청구항 49

제48항에 있어서, 상기 추가적인 기능성 도메인이 서열번호 64의 아미노산 서열을 포함하는 Fc 도메인을 포함하나 이로 제한되는 것은 아닌 Fc 도메인을 포함하는, 폴리펩타이드.

청구항 50

제47항 내지 제49항 중 어느 한 항에 있어서, 상기 첨가되는 기능성 도메인이 올리고머화 도메인을 포함하는, 폴리펩타이드.

청구항 51

제50항에 있어서, 상기 올리고머화 도메인이 동형삼량체화 도메인을 포함하는, 폴리펩타이드.

청구항 52

제50항 또는 제51항에 있어서, 상기 올리고머화 도메인이 서열번호 179-189 및 589-594로 이루어진 군으로부터 선택되는 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 53

제50항 내지 제52항 중 어느 한 항에 있어서, 서열번호 356-453 및 595-692로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열 및 표 9의 우측 칸에 언급된 것들로부터 선택되는 유형을 포함하되, 이러한 유형에서 위치 X1, X2, X3 및 X4는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 아미노산 1개 이상으로 된 임의 서열일 수 있으며, 폴리펩타이드에서 임의의 N-말단 메티오닌 잔기가 존재하거나 또는 생략될 수 있으며; 바람직하게는 폴리펩타이드는 서열번호 595-692로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하는, 폴리펩타이드.

청구항 54

제1항 내지 제53항 중 어느 한 항에 있어서, 상기 폴리펩타이드가 폴리에틸렌 글리콜 (PEG), 알부민, 하이드록시에틸 전분 (HES), 아미노산 Pro, Ala 및/또는 Ser으로 된 ('PASylation') 입체구조적으로 무질서한 폴리펩타이드 서열, 및/또는 아미노산 Lys 및 Ala으로 구성되고 Glu이 첨가 또는 비-첨가된 뮤신 확산성 (mucin diffusivity) 폴리펩타이드를 포함하지만 이들로 제한되지 않는 안정화 도메인에 연결된, 폴리펩타이드.

청구항 55

제1항 내지 제54항 중 어느 한 항에 있어서, 서열번호 65-96으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고, 분비 신호 (MARAWIFFLLCLAGRALA; 서열번호 63)가 존재하는 경우에는 임의의 다른 분비 신호로 대체될 수 있는, 폴리펩타이드.

청구항 56

제1항 내지 제55항 중 어느 한 항에 있어서, 상기 폴리펩타이드가 첨부된 실시예에 기술된 바와 같이 측정시 적어도 10 nM의 친화성으로 SARS-CoV-2 스파이크 당단백질에 결합하는, 폴리펩타이드.

청구항 57

제1항 내지 제56항 중 어느 한 항에 따른 폴리펩타이드를 암호화하는 핵산.

청구항 58

프로모터에 작동가능하게 연결된 제57항에 따른 핵산을 포함하는 발현 벡터.

청구항 59

임의의 전술한 청구항에 따른 폴리펩타이드, 핵산 및/또는 발현 벡터를 포함하는 숙주 세포.

청구항 60

제1항 내지 제56항 중 어느 한 항에 따른 폴리펩타이드의 올리고머.

청구항 61

제60항에 있어서, 상기 올리고머가 동형삼량체를 포함하나 이로 제한되지 않는 삼량체를 포함하는, 올리고머.

청구항 62

폴리펩타이드 입자 지지체를 포함하나 이로 제한되지 않는 지지체에 부착된 제1항 내지 제56항 중 어느 한 항에 따른 폴리펩타이드를 2, 3 또는 4 카피 이상으로 포함하는, 조성물.

청구항 63

임의 청구항에 따른 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리고머 및/또는 조성물과 약제학적으로 허용 가능한 담체를 포함하는, 약학적 조성물.

청구항 64

필요한 개체에 임의 청구항에 따른 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리고머, 조성물 및/또는 약학적 조성물을 감염을 치료하기에 유효한 함량으로 투여하는 것을 포함하는, 중증 급성 호흡기 증후군 (SARS) 코로나바이러스 감염 (SARS-Co-V 및 SARS-CoV-2 포함)의 치료 방법.

청구항 65

제64항에 있어서, 상기 SARS 코로나바이러스가 SARS-CoV-2를 포함하는, 방법.

청구항 66

필요한 개체에 임의 청구항에 따른 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리고머, 조성물 및/또는 약학적 조성물을 감염을 치료하기에 유효한 함량으로 투여하는 것을 포함하는, 중증 급성 호흡기 증후군 (SARS) 코로나바이러스 감염 (SARS-Co-V 및 SARS-CoV-2 포함)의 진행을 제한하는 방법.

청구항 67

제66항에 있어서, 상기 SARS 코로나바이러스가 SARS-CoV-2를 포함하는, 방법.

청구항 68

제64항 내지 제67항 중 어느 한 항에 있어서, 상기 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리고머, 조성물 및/또는 약학적 조성물이 비강내로 투여되는, 방법.

청구항 69

제64항 내지 제67항 중 어느 한 항에 있어서, 상기 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리고머, 조성물 및/또는 약학적 조성물이 전신으로 투여되는, 방법.

청구항 70

본원에 개시된 임의 구현예 또는 구현예들의 조합으로 기술된 단계들을 포함하는, SARS-Cov-2의 수용체 결합 부위 (RBD)에 결합하는 폴리펩타이드를 설계하는 방법.

청구항 71

제70항에 있어서, 설계한 폴리펩타이드를 무세포 합성하는 단계 및 합성한 폴리펩타이드를 임의의 적절한 기법을 이용해 SARS-Cov-2 RBD 결합성에 대해 평가하는 단계를 추가로 포함하는, 방법.

청구항 72

임의의 청구항에 따른 폴리펩타이드, 핵산, 및/또는 발현 벡터를 포함하는 무세포성 시스템.

발명의 설명

기 술 분 야

[0001] **교차 참조**

[0002] 본 출원은 2020년 7월 14일자 미국 가출원 번호 63/051,474 및 2020년 8월 19일자 미국 가출원 번호 63/067,593에 대해 우선권을 주장하며, 이들 각 문헌은 그 전체가 원용에 의해 본 명세서에 포함된다.

[0003] **연방 지원에 대한 진술**

[0004] 본 발명은 미국 국방부 고등 연구 계획국에 의해 부여된 교부 번호 FA8750-17-C-0219 및 국립 보건원에 의해 부여된 교부 번호 HHSN272201700059C 및 R01 GM120553 하에 정부의 지원을 받아 이루어졌다. 정부가 본 발명에 대해 일부 권리를 가진다.

[0005] **서열목록에 대한 진술:**

[0006] 서열목록의 컴퓨터 판독가능한 형태가 본 출원과 함께 전자 제출을 통해 제출되며, 이는 그 전체가 원용에 의해 본 명세서에 포함된다. 서열목록은 1,112kb의 파일명 "20-1074-WO_SeqList_ST25"으로 2021년 5월 25일자에 생성된 파일에 수록되어 있다.

배 경 기 술

[0007] SARS-CoV-2 감염은 흔히 코에서 시작하고, 여기서 바이러스는 수회 증식한 후 더 넓은 호흡계로 퍼진다. 따라서, 바이러스 저해제를 고 농도로 코 및 호흡계에 전달하여, 잠재적으로 예방학적 보호를, 그리고 감염 초기에 치료학적 효능을 제공할 수 있으며, 의료 종사자 및 감염된 개체와 자주 접촉하는 사람에게 특히 유익할 수 있다.

발명의 내용

[0008] 제1 측면에서, 본 발명은 서열번호 1-17, 19-21, 23-34 및 100-101로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하며; SARS-CoV-2 스파이크 당단백질 수용체 결합 도메인(RBD)에 결합하는, 폴리펩타이드를 제공한다. 일 구현예에서, 참조 폴리펩타이드 아미노산 서열을 기준으로 한 아미노산의 치환은 표 1에 제공된 아미노산 치환 예들로부터 선택된다. 다른 구현예에서, 인터페이스 잔기(interface residue)는 참조 폴리펩타이드와 동일하거나, 또는 참조 폴리펩타이드의 인터페이스 잔기에 대해 보존적으로 치환된다. 추가적인 구현예에서, 폴리펩타이드는 서열번호 1-17, 19-21, 23-34 및 100-101로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 2 카피 이상으로 포함한다. 일 구현예에서, 폴리펩타이드는 식 Z1-Z2-Z3를 포함하며, 여기서:

[0009] Z1은 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

[0010] Z2는 선택적인 아미노산 링커를 포함하고;

[0011] Z3는 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하되;

[0012] 여기서, Z1과 Z3는 서로 동일하거나 또는 서로 다를 수 있다.

[0013] 다른 구현예에서, 폴리펩타이드는 식 B1-B2-Z1-Z2-Z3-B3-B4를 포함하되,

[0014] Z1, Z2 및 Z3는 상기에서 정의된 바와 같이 정의되고;

[0015] B2 및 B3는 선택적인 아미노산 링커를 포함하고;

[0016] B1 및 B4 중 하나 또는 둘다 독립적으로 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하되, B1 및 B4 중 하나는 생략될 수 있다.

[0017] 일 구현예에서, 폴리펩타이드는 서열번호 47-60, 193-355 및 454-588로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열, 및 표 8의 우측 칸에 언급된 것들로부터 선택되는 유형 (genus)을 포함하되, 이러한 유형에서 위치 X1, X2, X3 및 X4는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 아미노산 1개 이상으로 된 임의 서열일 수 있다.

[0018] 다른 구현예에서, 폴리펩타이드는 서열번호 356-453 및 595-692로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열, 및 표 9의 중간 칸에 언급될 것들로부터 선택되는 유형을 포함하되, 이러한 유형에서 위치 X1, X2, X3 및 X4는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 아미노산 1개 이상으로 된 임의 서열일 수 있다.

[0019] 추가적인 구현예에서, 폴리펩타이드는 서열번호 65-96으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하되, 분비 신호 (MARAWIFFLLCLAGRALA; 서열번호 63)가 존재하는 구현예의 경우 임의의 다른 분비 신호로 교체될 수 있다.

[0020] 다른 측면에서, 본 발명은 본 발명의 폴리펩타이드를 암호화하는 핵산, 프로모터에 작동가능하게 연결된 핵산을 포함하는 발현 벡터, 본 발명의 폴리펩타이드, 핵산 및/또는 발현 벡터를 포함하는 숙주 세포, 본 발명의 폴리펩타이드의 올리고머, 폴리펩타이드 입자 지지체를 포함하나 이로 제한되는 것은 아닌 지지체에 부착된 본 발명의 임의 구현예에 따른 폴리펩타이드를 2, 3 또는 4 카피 이상으로 포함하는 조성물, 및 본 발명의 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리고머 및/또는 조성물과 약제학적으로 허용가능한 담체를 포함하는, 약학적 조성물을 제공한다.

[0021] 다른 측면에서, 본 발명은 필요한 개체에 감염을 치료하거나 또는 진행을 제한하는데 유효한 양으로 본 발명의 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리고머, 조성물 및/또는 약학적 조성물을 투여하는 것을 포함하는, 중증 급성 호흡기 증후군 (SARS) 코로나바이러스 감염 (SARS-Co-V 및 SARS-CoV-2 포함)을 치료하거나 또는 진행을 제한하는 방법을 제공한다.

도면의 간단한 설명

[0022] **도 1. SARS-CoV-2 스파이크 수용체 결합 도메인에 대해 설계된 미니결합제 단백질.** 방식 1 및 방식 2에 따른 디자인은 긴 올리고뉴클레오티드에 암호화하고, 효모 세포 표면 상의 형광 태깅된 RBD에의 결합에 대하여 선별하였다. 심층 서열분석을 통해, RBD 결합에 대해 FACS 분류한 다음 명확하게 농화된 드 노보 인터페이스 디자인 (방식 2) 150종과 Ace2 나선 스캐폴드 디자인 (방식 1) 3종이 동정되었다. 이들 디자인은 *E. coli*에서 발현시켜 정제하였으며, 다수가 용해성으로 발현되어 생물층 간섭측정 실험에서 RBD에 결합하였으며, RBD에의 결합에 대해 ACE-2와 효과적으로 경쟁할 수 있었다 (도 2에 나타낸 실시예). BLI 데이터 (예, 도 2 참조)를 기반으로 미니결합제들의 RBD 결합 친화성은 다음과 같다: LCB1 <1nM, LCB3 <1nM. LCB2, LCB4, LCB5, LCB6, LCB7, LCB8의 친화성은 1~20 nM 범위이고, 여러가지 결합제들의 상대적인 강도는 LCB4 > LCB2 > LCB9 = LCB5 > LCB6 > LCB7 이다.

도 2. SARS-CoV-2 스파이크 RBD에 대한 드 노보 설계한 미니결합제의 고 친화성 결합. 바이오틴화된 스파이크 RBD 단백질을 스트렙타비딘 생물층 간섭측정 (BLI) 팁 (ForteBio Octet™)에 로딩하고, 이를 헹군 후 여러가지 농도의 정제된 콤보 1 항-RBD 미니결합제에 팁을 침지하였다. 로딩 후, 팁을 완충제 단독에 넣었다. (좌측 및 중앙) 반응 곡선은 ~Kd 300 pM의 친화성을 보여준다. (우측) ACE-2를 RBD 팁에 로딩한 다음 콤보 1을 첨가하면, 미니결합제는 BLI 팁의 ACE-2를 빠르게 대체한다.

도 3. SARS-CoV-2 스파이크 RBD에 대해 드 노보 설계한 미니결합제는 열 안정적이다. 정제한 콤보 1 미니결합제를 원이색성 분광광도계에서 25℃, 95℃ 및 95℃로 열처리한 후 25℃에서 측정하였다. CD 스펙트럼들은 형태적으로 모두 매우 비슷하였는데, 이는 단백질이 모든 조건들에서 접힌 상태로 유지됨을 의미한다.

도 4. SARS-CoV-2 스파이크 RBD에 대해 드 노보 설계한 미니결합제는 바이러스 중화 분석에서 강력하다. SARS-CoV-2 균주 2019 n-CoV/USA_WA1/2020을 질환 방제 및 예방 센터에서 입수하였다 (Natalie Thornburg로부터 선물 받음). 바이러스 원액을 Vero CCL81 세포 (ATCC)에서 생산하고, Vero E6 세포에서 포커스-형성 분석에 의해 역가를 측정하였다. mAb 또는 미니결합제의 연속 희석물을 SARS-CoV-2 10^2 FFU (focus-forming unit)와 함께 1시간 동안 37℃에서 인큐베이션하였다. 96웰 플레이트에서 Vero E6 세포 단일층에 RBD 미니결합제 (또는 mAb)-바이러스 복합체를 첨가하여, 37℃에서 1시간 동안 인큐베이션하였다. 그 후, 2% FBS가 첨가된 MEM 중의 1% (w/v) 메틸셀룰로스를 세포 위에 적층하였다. 30시간 후 적층을 제거하여 플레이트를 회수하고, PBS 중의 4% PFA로 실온에서 20분간 고정하였다. 플레이트를 헹군 다음, 0.1% 사포닌 및 0.1% BSA 첨가된 PBS 중에서 1 μg/mL CR3022 ([1]) 항-S 항체 및 HRP-접합된 염소 항-인간 IgG와 함께 순차적으로 인큐베이션하였다. SARS-CoV-

2-감염 세포 포커스를 TrueBlue™ 퍼옥시다제 기질 (KPL)을 사용해 가시화하고, ImmunoSpot™ 마이크로분석기 (Cellular Technologies)에서 정량하였다. 데이터는 Prism 소프트웨어로 가공 처리하였다 (GraphPad Prism™ 8.0).

도 5(A-J). LCB1-Fc 예방은 SARS-CoV-2 감염으로부터 보호한다. (**A**) SARS-CoV-2 스파이크 단백질 삼량체의 개개 프로토머에 결합된 LCB1v1.3 미니단백질 3개를 나타낸 분자 표면도 (좌측: 측면도; 우측: 상면도). (**B**) 생물층 간섭측정에 의해 모니터링한, 정제한 LCB1v1.3 및 LCB1-Fc의 SARS-CoV-2 RBD에의 결합 곡선 (한가지 실험은 기술적인 두플리케이트로 수행됨). (**C**) LCB1v1.3, LCB1-Fc 또는 대조군 결합제의 SARS-CoV-2 WA1/2020 분리주에 대한 중화 곡선 (EC_{50} 값: 각각 14.4 pM, 71.8 pM 및 >10,000 nM; 2번의 실험의 평균으로서, 각각 두플리케이트로 수행됨). (**D-J**) SARS-CoV-2 10^3 PFU를 i.n. 접종 하루 전에, LCB1-Fc 또는 대조군 결합제 250 ㎍을 7-8주령의 K18-hACE2 형질전환 마우스 암컷 및 수컷에 i.p. 주사에 의해 투여하였다. 4 및 7 dpi에 조직을 수집하였다. (**D**) LCB1-Fc를 투여한 이후의 체중 변화 (평균 ± SEM; n = 8, 2번의 실험: 이원식 ANOVA 및 시다크의 사후 검정: *** $P < 0.001$, **** $P < 0.0001$). (**E**) 4 또는 7 dpi에 폐에서 플라크 분석에 의해 측정한 감염성 바이러스 (n = 8, 2번의 실험: 만-휘트니 검정; *** $P < 0.001$). (**F-J**) 4 또는 7 dpi에 폐, 심장, 비장, 뇌 또는 코 세척액에서의 바이러스 RNA 수준 (n = 8, 2번의 실험: 만-휘트니 검정: ns, 유의하지 않음, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$).

도 6(A-C). LCB1-Fc 예방은 SARS-CoV-2-매개 폐 질환을 방지한다. (**A**) 호흡 역학 매개변수: 7 dpi7 dpi에 측정한 최대흡기량, 저항, 탄력성 조직 저항 (tissue damping), 준정적 유순도 및 압력-용량 곡선 (n = 3-6, 2번의 실험: 이원식 ANOVA 터키의 사후 검정: ns, 유의하지 않음, 언급된 군들 간의 * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). (**B**) D-1에 처리하고 7 dpi에 수집한 SARS-CoV-2를 가진 마우스의 폐 단편에 대한 헤마톡실린 및 에오신 염색. 사진은 저배율 (좌측) 및 고배율 (우측; 좌측의 박스 영역)로 도시하다. 전체 사진에서 기준자, 100 ㎛. 마우스 n = 3/군으로부터 수득한 대표적인 사진. (**C**) 4 dpi에 SARS-CoV-2 감염 마우스의 폐 조직에서 사이토카인 mRNA 수준에 대한 히트-맵. 각각의 사이토카인은 *Gapdh*에 대해 표준화한 후 나이-매칭된 나이브 대조군 동물에 대한 배수 변화를 계산하였으며, Log_2 (배수 변화)를 그래프로 작성하였다 (마우스 n = 8/군 vs n = 3/나이브 대조군).

도 7(A-J). 항-RBD 결합제의 노출-후 전달은 SARS-CoV-2 부담을 감소시킨다. (**A-G**) SARS-CoV-2 10^3 PFU를 i.n. 접종한 다음날 LCB1-Fc 또는 대조군 결합제 250 ㎍을 7-8주령의 암컷 및 수컷 K18-hACE2 형질전환 마우스에 i.p. 주사에 의해 투여하였다. 4 또는 7 dpi에 조직을 수집하였다. (**A**) LCB1-Fc 투여 후 체중 변화 (평균 ± SEM; n = 6, 2번의 실험: 이원식 ANOVA 및 시다크의 사후 검정: ** $P < 0.01$, **** $P < 0.0001$). (**B**) 4 또는 7 dpi에 폐에서 플라크 분석에 의해 측정한 감염성 바이러스 (n = 6, 2번의 실험: ** $P < 0.01$). (**C-G**) 4 또는 7 dpi에 폐, 심장, 비장, 뇌 또는 코 세척액 내 바이러스 RNA 수준 (n = 6, 2번의 실험: 만-휘트니 검정: ns, 유의하지 않음, * $P < 0.05$, ** $P < 0.01$). (**H**) D+1에 처리하고 7 dpi에 수집한 SARS-CoV-2를 가진 마우스의 폐 단편에 대한 헤마톡실린 및 에오신 염색. 사진은 저배율 (좌측) 및 고배율 (우측; 좌측의 박스 영역)로 도시하다. 전체 사진에서 기준자, 100 ㎛. 마우스 n = 3/군으로부터 수득한 대표적인 사진. (**I-J**) SARS-CoV-2를 10^3 PFU로 접종한 후 1일 또는 2일차에, 7-8주령의 수컷 K18-hACE2 형질전환 마우스에 LCB1v1.3 또는 대조군 결합제를 50 ㎍으로 1회 i.n. 용량으로 투여하였다. 7 dpi에 폐 (**I**) 또는 코 세척액 (**J**) 내 바이러스 RNA 수준 (n = 6, 2번의 실험: 일원식 ANOVA: ns, 유의하지 않음, * $P < 0.05$, **** $P < 0.0001$).

도 8(A-K). LCB1v1.3의 비강내 투여는 SARS-CoV-2 노출 5일 전 제공시에도 바이러스 감염을 감소시킨다. (**A-D**) SARS-CoV-2를 10^3 PFU로 i.n. 접종하기 전 지정된 시점에 7-8주령의 암컷 K18-hACE2 형질전환 마우스에 LCB1v1.3 또는 대조군 결합제를 50 ㎍으로 1회 i.n. 용량으로 투여하였다. 4 또는 7 dpi에 조직을 수집하여, 바이러스 RNA 수준을 측정하였다 (동물 n = 5-6마리/군, 2번의 실험: 이원식 ANOVA 및 시다크의 사후 검정: ns, 유의하지 않음, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$). (**E-J**) SARS-CoV-2를 10^3 PFU로 i.n. 접종하기 하루 전 7-8주령의 암컷 K18-hACE2 형질전환 마우스에 LCB1v1.3 또는 대조군 결합제를 지정된 i.n. 용량으로 투여하였다. (**E**) LCB1v1.3 또는 대조군 결합제를 투여한 이후의 체중 변화 (평균 ± SEM; n = 6, 2번의 실험: 이원식 ANOVA 및 시다크의 사후 검정, 대조군 결합제 처리 군 대비: ** $P < 0.01$, **** $P < 0.0001$). (**F-J**) 7 dpi에 폐, 심장, 비장, 뇌 또는 코 세척액에서의 바이러스 RNA 수준 (n = 6, 2번의 실험: 크루스칼-발리스 ANOVA 및 던의 사후 검정: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). (**K**) D-1에 LCB1v1.3 또는

대조군 결합제를 1회 50 ㎍ i.n. 용량으로 처리하고 7 dpi에 수집한 SARS-CoV-2를 가진 마우스로부터 수득한 폐 단편에 대한 헤마톡실린 및 에오신 염색. 사진은 저배율 (좌측) 및 고배율 (우측; 좌측의 박스 영역)로 도시하다. 전체 사진에서 기준자, 100 ㎛. 마우스 n = 3/군으로부터 수득한 대표적인 사진.

도 9(A-H). LCB1v1.3의 면역원성 및 챌린지로부터 보호. (**A**) 실험 세부 사항에 대한 도표. K18-hACE2 형질전환 마우스 (n = 10-12/군)에 LCB1v1.3 또는 대조군 결합제 50 ㎍을 i.n. 투여에 의해 3일 간격으로 처리하였다. 처리 후 18일차에 동물에서 채혈하여 항-LCB1v1.3 항체를 측정하였다. 다음날, 동물에 SARS-CoV-2를 10^3 PFU로 기회 감염시키고, 7 dpi에 조직을 수집하였다. (**B**) ELISA에 의해 측정한 혈청 항체의 LCB1v1.3에 대한 결합성 (3번의 실험). 점선은 분석의 검출 한계를 표시한다. (**C**) LCB1v1.3 또는 대조군 결합제를 투여한 이후의 체중 변화 (평균 ± SEM; 2번의 실험: 이원식 ANOVA 및 시다크의 사후 검정: **** $P < 0.0001$). (**D-H**) 7 dpi에 폐, 심장, 비장, 뇌 또는 코 세척액에서의 바이러스 RNA 수준 (2번의 실험: 만-휘트니 검정: * $P < 0.05$, ** $P < 0.01$, **** $P < 0.0001$).

도 10(A-M). LCB1v1.3는 B.1.1.7 변종 및 WA1/2020 E484K/N501Y/D614G 균주로부터 보호한다. (**A**) LCB1v1.3의 B.1.1.7 또는 WA1/2020 E484K/N501Y/D614G SARS-CoV-2 중화 (EC_{50} 값: 각각 802 pM 및 667 pM; 2번의 실험의 평균, 각각 두플리케이트로 수행). (**B-G**) B.1.1.7을 10^3 PFU로 i.n. 접종하기 하루 전에 LCB1v1.3 또는 대조군 결합제를 1회 50 ㎍ i.n. 용량으로 7-8주령의 암컷 K18-hACE2 형질전환 마우스에 처리하였다. (**B**) LCB1v1.3 또는 대조군 결합제를 투여한 이후의 체중 변화 (평균 ± SEM; n = 6, 2번의 실험: 이원식 ANOVA 및 시다크의 사후 검정: *** $P < 0.001$, **** $P < 0.0001$). (**C-G**) 6 dpi에 폐, 심장, 비장, 코 세척액 또는 뇌에서의 바이러스 RNA 수준 (n = 6, 2번의 실험: 만-휘트니 검정: * $P < 0.05$, ** $P < 0.01$). (**H-M**) WA1/2020 E484K/N501Y/D614G를 10^3 PFU로 i.n. 접종하기 하루 전에 LCB1v1.3 또는 대조군 결합제를 1회 50 ㎍ i.n. 용량으로 7-8주령의 수컷 K18-hACE2 형질전환 마우스에 처리하였다. (**H**) LCB1v1.3 또는 대조군 결합제를 투여한 이후의 체중 변화 (평균 ± SEM; n = 6, 2번의 실험: 이원식 ANOVA 및 시다크의 사후 검정: * $P < 0.05$, **** $P < 0.0001$). (**I-M**) 6 dpi에 폐, 심장, 비장, 코 세척액 또는 뇌에서의 바이러스 RNA 수준 (n = 6, 2번의 실험: 만-휘트니 검정: * $P < 0.05$, ** $P < 0.01$).

도 11. SARS-CoV-2 감염 후 사이토카인 및 케모카인의 유도. 대조군 또는 LCB1-Fc 결합제를 처리한 후 4 dpi에 SARS-CoV-2 감염 마우스의 폐에서 사이토카인 및 케모카인에 대한 각각의 도표 (n = 8 /그룹, 2번의 실험: 만-휘트니 검정: ns, 유의하지 않음, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). 데이터를 이용해 **도 6C**에서 히트-맵을 작성하였다.

도 12(A-C). SARS-CoV-2 감염 후 1일 또는 2일차에 LCB1v1.3의 비강내 전달은 도 7과 관련하여 바이러스 부담을 낮춘다. (**A-C**) SARS-CoV-2를 10^3 PFU로 접종한 후 1일 또는 2일차에 LCB1v1.3 또는 대조군 결합제를 1회 50 ㎍ i.n. 용량으로 7-8주령의 수컷 K18-hACE2 형질전환 마우스에 투여하였다. 7 dpi에 심장 (**A**), 비장 (**B**) 또는 뇌 (**C**)에서의 바이러스 RNA 수준 (n = 6, 2번의 실험: 일원식 ANOVA: * $P < 0.05$, ** $P < 0.01$).

도 13. LCB1v1.3의 비강내 예방은 도 8과 관련하여 체중 감소를 완화한다. SARS-CoV-2를 10^3 PFU로 i.n. 접종하기 전 지정된 시점에 LCB1v1.3 또는 대조군 결합제를 1회 50 ㎍ i.n. 용량으로 7-8주령의 암컷 K18-hACE2 형질전환 마우스에 투여하였다. 체중 변화를 매일 기록하였다 (평균 ± SEM; n = 6, 2번의 실험: 이원식 ANOVA 및 시다크의 사후 검정: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$).

도 14(A-B). 다가 미니결합제는 융합-전 (pre-fusion) SARS-CoV-2 스파이크 단백질 상의 복수의 에피토프에 동시에 결합하여, 매우 느린 해리 속도를 나타낸다. (**A, B**) 미니결합제 구조체 및 수용체 결합 도메인 (RBD) (**A**) 또는 헥사프로 스파이크 단백질 (S6P) (**B**) 복합체의 해리를 100배 몰 과량의 비-태깅된 M1과의 경쟁을 통해 AlphaLISA™를 이용해 모니터링하였다 (평균 ± SEM, n=3).

도 15(A-F). SARS-CoV-2 S 당단백질과 복합체를 형성한 다가 미니결합제에 대한 Cryo-EM 구조. (**A**) RBD에 결합한 미니결합제 3개를 모두 도시한 리본 도표. (**B**) RBD 2개와 복합체를 형성한 F31-G10에 대한 Cryo-EM 맵. (**C**) RBD 3개와 복합체를 형태한 F231-P24에 대한 Cryo-EM 맵. (**D**) S 당단백질에 결합한 H2-1의 디자인 모형. (**E**) 2가지 오르소고날 배향성으로 S 당단백질과 복합체를 이룬 H2-1의 Cryo-EM 맵. (**F**) H2-1과 S 당단백질 인터페이스의 상호작용 잔기들을 나타낸 Cryo-EM 맵.

도 16(A-F). 다가성 (multivalency)은 미니결합제에 의한 SARS-CoV-2 변종에 대한 중화 범위와 효력을

강화한다. (**A**) 24시간 후 S6P 변이체로부터 미니결합제 구조체의 해리를 비-태깅된 H2-0와의 경쟁을 통해 AlphaLISA를 이용해 측정하였다 (평균, n=3). X 표시된 칸은 결합한 단백질의 분획을 정량하는데 비-경쟁자 조건에서 신호가 충분하지 않음을 표시한다. (**B**) S6P에 대한 미니결합제와 ACE3의 경쟁을 ELISA에 의해 측정하였다 (평균, n=2). (**C**) SARS-CoV-2 슈도바이러스 변종에 대한 미니결합제의 중화 곡선 (평균, n=2) (**D**) SARS-CoV-2 슈도바이러스 변종에 대한 다가 미니결합제 구조체들의 중화 효력을 요약한 표. N/A는 IC_{50} 값이 검사한 농도 범위보다 높다는 것을 의미하며, IC_{50} 값은 > 50,000 pM이다. (**E**) 어센틱 (authentic) SARS-CoV-2 분리주에 대한 미니결합제 구조체들의 중화 곡선 (평균, n=2). (**F**) 오센틱 SARS-CoV-2 분리주에 대한 다가 미니결합제 구조체들의 중화 효력을 요약한 표.

도 17(A-C). 상위 다가 미니결합제 후보물질들은 탈출 내성이며, 노출 전 비강내 투여를 통해 SARS-CoV-2 감염으로부터 마우스를 보호한다. (**A**) 대조군 중화 항체 (2B04)와 F231-P12 및 H2-1 다가 미니결합제에 대한 VSV-SARS-CoV-2 키메라 바이러스 탈출 돌연변이를 단리하기 위해 플라크 분석을 수행하였다. 사진은 다가 미니결합제 당 레플리케이트 35개를 보여준다. 검정 화살표로 강조 표시한 큰 플라크는 탈출을 의미한다. (**B**, **C**) 0일에 SARS-CoV-2 변종 B.1.1.7, B1.351, B.1.1.24를 10^3 플라크 형성 단위로 비강내 감염시키기 24시간 전 (T-24h)에, K18-hACE2-형질전환 마우스 (n=6/시점)에 H2-0 50 ㎍을 비강내 투여하였다 (i.n., 2 x 25 ㎕ 투여/콧구멍, 총 100 ㎕). (**B**) 감염 후 매일 체중 변화 (평균 ± SEM; n = 6, 이원식 ANOVA 및 시다크의 사후 검정: * P < 0.05, *** P < 0.001, **** P < 0.0001). (**C**) 감염 후 수일 경과 후 (6 dpi), 동물 (n=6/시점)을 희생시키고, 폐, 심장, 비장, 뇌 또는 코 세척액에서 정량적인 실시간 RT-PCR에 의해 SARS-CoV-2 바이러스 RNA의 존재를 분석하였다 (n = 6: 만-휘트니 검정: ns, 유의하지 않음, * P < 0.05, ** P < 0.01).

발명을 실시하기 위한 구체적인 내용

[0023] 인용된 모든 참조문헌들은 그 전체가 원용에 의해 본 명세서에 포함된다. 본 출원에서, 달리 언급되지 않은 한, 이용된 기술들은 Molecular Cloning: A Laboratory Manual (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), Gene Expression Technology (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA), "Guide to Protein Purification" in Methods in Enzymology (M.P. Deutshcer, ed., (1990) Academic Press, Inc.); PCR Protocols: A Guide to Methods and Applications (Innis, et al. 1990. Academic Press, San Diego, CA), Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed. (R.I. Freshney. 1987. Liss, Inc. New York, NY), Gene Transfer and Expression Protocols, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.), 및 the Ambion 1998 Catalog (Ambion, Austin, TX)와 같이 잘 알려진 수종의 임의의 참조문헌들에서 확인할 수 있다.

[0024] 본원에서 사용된 바와 같이, 단수 형태 ("a", "an" 및 "the")는 문맥상 명확하게 달리 기술되지 않은 한 복수의 언급을 망라한다.

[0025] 본원에서 사용된 바와 같이, 아미노산 잔기는 다음과 같이 약칭된다: 알라닌 (Ala; A), 아스파라긴 (Asn; N), 아스파르트산 (Asp; D), 아르기닌 (Arg; R), 시스테인 (Cys; C), 글루탐산 (Glu; E), 글루타민 (Gln; Q), 글리신 (Gly; G), 히스티딘 (His; H), 이소루신 (Ile; I), 루신 (Leu; L), 라이신 (Lys; K), 메티오닌 (Met; M), 페닐알라닌 (Phe; F), 프롤린 (Pro; P), 세린 (Ser; S), 트레오닌 (Thr; T), 트립토판 (Trp; W), 티로신 (Tyr; Y), 및 발린 (Val; V).

[0026] 본원에 개시된 폴리펩타이드에 대한 모든 구현예들에서, N-말단 메티오닌 잔기는 선택적이다 (즉, 존재하거나 또는 생략될 수 있음).

[0027] 본원의 임의 측면에 대한 모든 구현예들은 문맥상 명시적으로 달리 기술되지 않은 한 조합하여 이용할 수 있다.

[0028] 문맥상 명확하게 달리 요구되지 않은 한, 명세서 및 청구항 전체에서, 용어 '포함한다', '포함하는' 등은 배타적이거나 또는 모두 망라하는 의미와는 반대되는 광의적인 의미로 해석되어야 하며; 즉, "포함하지만 이로 제한되는 것은 아닌" 의미이다. 단수 또는 복수로 기재된 용어들은 각각 복수 및 단수를 포함한다. 아울러, 용어 "여기서", "상기한" 및 "하기", 및 이와 비슷한 의미의 용어는 본 출원에 사용되는 경우 본 출원의 임의 특정 일부분이 아닌 전체로서 본 발명을 지칭하는 것이다.

[0029] 제1 측면에서, 본 발명은 서열번호 1-17, 19-21, 23-34 및 100-101로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하며; SARS-CoV-2 스파이크 당단백질 수용체 결합 도메인

(RBD)에 결합하는, 폴리펩타이드를 제공한다.

[0030] >LCB1-1: DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER (서열번호 1)

[0031] >LCB1-2: DKEEILNKIYEIMRLLDELGNAEASMRVSDLILEFMKKGDERLLEEAERLLEEVER (서열번호 2)

[0032] >LCB1-3: DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 3)

[0033] >LCB1-4: DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 4)

[0034] >LCB1-5: DKENILQKIYEIMKTLDQLGHAEASMNVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 5)

[0035] LCB1_v1.1_Cys: DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERC (서열번호 6)

[0036] >LCB1_v1.2: DKENILQKIYEIMKTLDQLGHAEASMYVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 7)

[0037] >LCB1_v1.3: DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 8)

[0038] >LCB1_v1.4: DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDENLLEEAEQLLQEVER (서열번호 9)

[0039] >LCB1_v1.5 (LCB1_v1.3 + N-연결된 당화): DKENILQKIYEIMKTLEQLGHAEASMNVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 10)

[0040] >LCB2-1: SDDEDSVRYLLYMAELRYEQGNPEKAKKILEMAEFIAKRNNNEELERLVREVKKRL (서열번호 11)

[0041] >LCB2-2: SDDEDAVRYLLYMAELLYKQGNPEEAKKLLELAEFIAKRNNNEELERLVREVKKRL (서열번호 12)

[0042] >LCB3-1: NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS (서열번호 13)

[0043] >LCB3-2: NDDELLMLVTDLVAEALLFAKDEEIKKRVFTLFELADKAYKNNDRDTLSKVVSELKELLERLQ (서열번호 14)

[0044] >LCB3_v1.2: NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (서열번호 15)

[0045] >LCB3-4: NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFENATKAYKNKDRQKLEKVVEELKELLERLLS (서열번호 16)

[0046] >LCB3_v1.1: NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNNDRQKLEKVVEELKELLERLLS (서열번호 17)

[0047] >LCB3_v1.3: NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (서열번호 19)

[0048] >LCB3_v1.4: NDDELHMQMTDLVYEALHKAKDEEFQKHVFQLFEKATKARKNKDRQKLEKVVEELKELLERLLS (서열번호 20)

[0049] >LCB3_v1.5: NDDELHMQMTDLVYEALHKAKDEEMQKRVFQLFEQADKAYKTKDRQKLEKVVEELKELLERLLS (서열번호 21)

[0050] >LCB4-1: QREKRLKQLEMLLEYAIERNDPYLMFDVAVEMLRLAEENNDERIIERAKRILEEYE (서열번호 23)

[0051] >LCB4-2: DREERLKYLEMLLELAVERNDPYLIFDVAIELLRLAEENNDERIYERAKRILEEVE (서열번호 24)

[0052] >LCB5-1: SLEELKEQVKELKKELSPEMRRLIEEALRFLEEGNPAMAMMVLSDLVYQLGDPRVIDLYMLVTKT (서열번호 25)

[0053] >LCB5-2: SLEEVKEILKELKKELSPEDRRLIEEALRLLEEGNPAMASMVLSDLVFLLGDPRVIELLMLVTKT (서열번호 26)

[0054] >LCB6-1: DREQRLVRFLVRLASKFNLSPEQILQLFEVLEELLERGVSEEEIRKQLEEVAKELG (서열번호 27)

[0055] >LCB6-2: DREQRLVRFLVRLASKFNLSMEQILILFDVLEELLERGVSEEEIRKILEEVAKEL (서열번호 28)

[0056] >LCB7-1: DDDIRYLIYMAKLRLEQGNPEEAEKVLEMARFLAERLGMEELLKEVRELLRKIEELR (서열번호 29)

[0057] >LCB7-2: DDDVRYLIYMAKLLLEQGNPEEAEKVLESARFAAELLGNEELLKEVRELLRKIEELR (서열번호 30)

[0058] >LCB8-1: PIIELLREAKEKNDEFAISDALYLVNELLQRTGDPRLEEVLYLIWRALKEKDPRLLDRAIELFER (서열번호 31)

[0059] >LCB8-2: PVTELLREAKEKNDPMAISDALFLVFELAQRTGDPRLEEVLFLIWRALKEKDPRLLDRAIELFER (서열번호 32)

[0060] >AHB1-1: DEDLEELERLYRKAEEVAKEAKDASRRGDDERAKEQMERAMRLFDQVFELAQELQEKQTDGNRQKATHLDKAVKEAADELYQRVR(서열번호 33)

[0061] >AHB1-2: DEDLEELERLYRKAEEVAKEAEEASRRGDKERAKELLERALHLFDQVFELAQELQEKLTDEKRQKATHLDKAVHEAADELYQRVR (서열번호 34)

[0062] >AHB2-1: ELEERVMHLLDQVSELAHELLHKLTGEELQRATHFDKWANEAILELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 100)

[0063] >AHB2-2_: ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)

[0064] 후술한 실시예에서 상세히 기술되는 바와 같이, 폴리펩타이드는 SARS-CoV-2 스파이크 당단백질 수용체 결합 도메인 (RBD)에 높은 친화성으로 결합한다.

[0065] 본원의 모든 구현예들에서, 동일성 % 요건은 폴리펩타이드에 병합될 수 있는 임의의 추가적인 기능성 도메인은 포함하지 않는다. 일 구현예에서, N 및/또는 C 말단에서 아미노산 1개, 2개 또는 3개가 결손될 수 있다.

[0066] 폴리펩타이드에 대해 후술한 실시예에 기술된 바와 같은 폴리펩타이드의 각 잔기에서 허용가능한 치환의 결정을 허용하는 광범위한 돌연변이 분석을 수행하였다. 치환 예는 **표 1**에 나타낸 바와 같다 (숫자는 잔기 번호이고, 문자는 잔기에 존재할 수 있는 아미노산의 단문자이다). 따라서, 일 구현예에서, 참조 폴리펩타이드 아미노산 서열 (즉, 서열번호 1-17, 19-21, 23-34 및 100-101 중 하나)을 기준으로 아미노산 치환은 표 1에 제공된 아미노산 치환 예들로부터 선택된다.

[0067] **표 1: 치환 예:**

[0068] LCB1 (서열번호 1-10 및 102-136)

[0069] 1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0070] 2 -- A,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0071] 3 -- A,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y

[0072] 4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0073] 5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0074] 6 -- A,C,I,L,M,Q,T,V

[0075] 7 -- A,C,D,E,F,G,H,M,N,P,Q,R,S,V,W,Y

[0076] 8 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0077] 9 -- C,I,L,M,N,Q,T,V

[0078] 10 -- C,F,V,W,Y

[0079] 11 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0080] 12 -- A,C,D,H,I,L,M,N,S,T,V,Y

[0081] 13 -- C,I,M,Q

[0082] 14 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0083] 15 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0084] 16 -- C,F,I,L,M,T,V

[0085] 17 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0086] 18 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0087] 19 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0088] 20 -- A,C,D,E,F,G,H,K,L,M,N,Q,R,S,T,W

[0089] 21 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0090] 22 -- A,C,D,F,G,H,I,L,M,N,P,Q,S,T,V,W,Y

[0091] 23 -- C,E,M,N,P,Q,S,T,V

[0092] 24 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y

[0093] 25 -- A,C,G,M,N,Q,S,T,V

[0094] 26 -- M,N,V

[0095] 27 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0096] 28 -- A,C,G,I,L,S,T,V

[0097] 29 -- A,C,S,V,W

[0098] 30 -- D

[0099] 31 -- A,C,D,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0100] 32 -- C,F,H,I,L,M,N,P,T,V

[0101] 33 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0102] 34 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0103] 35 -- A,C,D,F,H,M,Q,V,W,Y

[0104] 36 -- A,C,D,E,G,H,I,L,M,N,Q,R,S,T,V,W,Y

[0105] 37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0106] 38 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0107] 39 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y

[0108] 40 -- D,E,G,H,N,P,Q

[0109] 41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0110] 42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0111] 43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0112] 44 -- A,C,D,E,F,G,H,I,K,L,M,Q,R,S,V,W,Y

[0113] 45 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0114] 46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0115] 47 -- A,C,G,P,S,T,V

[0116] 48 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0117] 49 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0118] 50 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0119] 51 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0120] 52 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0121] 53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0122] 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0123] 55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0124] 56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0125] LCB2 (서열번호 11-12)

[0126] 1 -- A,C,D,E,G,N,P,S,T

[0127] 2 -- D,M,P,Q,Y

[0128] 3 -- A,D,E,N,Q

[0129] 4 -- C,D,E,V

[0130] 5 -- D

[0131] 6 -- A,C,D,E,G,N,Q,S,T,V

[0132] 7 -- A,C,G,I,L,M,P,S,T,V

[0133] 8 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0134] 9 -- D,N,Y

[0135] 10 -- I,L,T

[0136] 11 -- C,E,G,I,L,M,W

[0137] 12 -- F,H,Y

[0138] 13 -- E,M,Q,R,V

[0139] 14 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0140] 15 -- A,C,D,E,G,H,I,K,L,M,N,Q,R,S,T,V

[0141] 16 -- C,H,L,T

[0142] 17 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0143] 18 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0144] 19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0145] 20 -- A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y

[0146] 21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0147] 22 -- A,C,D,E,G,I,K,L,N,P,Q,R,S,T,V

[0148] 23 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0149] 24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0150] 25 -- A,C,E,G,H,I,K,N,P,Q,R,S,T,Y

[0151] 26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0152] 27 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0153] 28 -- H,K,R,T,Y

[0154] 29 -- C,D,E,H,I,K,L,M,N,P,Q,R,S,T,V,Y

[0155] 30 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,S,T,V,W,Y

[0156] 31 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y

[0157] 32 -- F,H,I,K,L,M,P,Q,R,Y

[0158] 33 -- A,C,G,P,S,T

[0159] 34 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0160] 35 -- F,H,Y

[0161] 36 -- A,C,E,H,I,L,M,S,V

[0162] 37 -- A,C,E,G,H,L,M,Q,R,S,T,V,W

[0163] 38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0164] 39 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V

[0165] 40 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0166] 41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0167] 42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0168] 43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0169] 44 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0170] 45 -- A,C,E,F,I,L,M,P,S,T,V,W,Y

[0171] 46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0172] 47 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0173] 48 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0174] 49 -- A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0175] 50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0176] 51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0177] 52 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0178] 53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0179] 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0180] 55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0181] 56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0182] LCB3 (서열번호 13-17, 19-21 및 137-163)

[0183] 1 -- C,E,F,I,M,N,T,W

[0184] 2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0185] 3 -- D,G,L,M,N,S,Y

[0186] 4 -- A,C,E,F,H,K,Q,T

[0187] 5 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0188] 6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0189] 7 -- A,C,D,F,I,L,M,P,R,S,V,W

[0190] 8 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0191] 9 -- A,C,E,F,G,H,I,L,M,N,Q,R,S,T,V,Y

[0192] 10 -- A,C,F,G,H,K,M,N,Q,R,S,T,Y

[0193] 11 -- D,F,H,L,M,N,Q

[0194] 12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0195] 13 -- A,F,I,L,M,N,Q,S,T,V

[0196] 14 -- A,C,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0197] 15 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0198] 16 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y

[0199] 17 -- A,C,D,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W

[0200] 18 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0201] 19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0202] 20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0203] 21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0204] 22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0205] 23 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0206] 24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0207] 25 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0208] 26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0209] 27 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0210] 28 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0211] 29 -- A,C,D,E,F,G,I,L,M,N,P,S,T,V,W,Y

[0212] 30 -- C,E,F,H,L,N,S,W,Y

[0213] 31 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0214] 32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0215] 33 -- A,C,E,F,I,K,P,Q,S,V,W,Y

[0216] 34 -- A,D,E,F,G,H,M,N,P,Q,R,S,V,W,Y

[0217] 35 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0218] 36 -- A,C,E,G,H,I,M,N,Q,S,T,V

[0219] 37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0220] 38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0221] 39 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0222] 40 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y

[0223] 41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0224] 42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0225] 43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0226] 44 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0227] 45 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0228] 46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0229] 47 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0230] 48 -- A,C,E,F,G,I,K,L,M,N,P,Q,S,T,V,W

[0231] 49 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0232] 50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0233] 51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0234] 52 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0235] 53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0236] 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0237] 55 -- A,C,E,F,G,H,I,K,L,M,N,Q,S,T,V,W,Y

[0238] 56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0239] 57 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0240] 58 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0241] 59 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0242] 60 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0243] 61 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0244] 62 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0245] 63 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0246] 64 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0247] LCB4 (서열번호 23-24)

[0248] 1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0249] 2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0250] 3 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0251] 4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0252] 5 -- C,D,H,K,N,Q,R,Y

[0253] 6 -- A,C,F,G,I,K,L,M,P,Q,R,S,T,V,Y

[0254] 7 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0255] 8 -- A,C,H,I,M,N,Q,R,S,T,V,Y

[0256] 9 -- A,C,D,G,H,I,K,L,M,N,Q,R,S,T,V,Y

[0257] 10 -- A,C,D,E,M,N,P,Q,S,T,V

[0258] 11 -- C,D,G,H,I,K,L,M,N,P,R,S,T,V

[0259] 12 -- F,G,I,L

[0260] 13 -- F,I,L,M,S,V,Y

[0261] 14 -- A,C,D,E,G,L,M,N,Q,R,S,T,V

[0262] 15 -- C,E,F,G,H,I,L,M,S,V,W,Y

[0263] 16 -- A,G,T,Y

[0264] 17 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0265] 18 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0266] 19 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0267] 20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0268] 21 -- C,D,Q,Y

[0269] 22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0270] 23 -- E,F,H,Y

[0271] 24 -- A,F,G,I,L,M,W

[0272] 25 -- A,C,E,G,H,I,K,L,M,N,Q,R,S,T,V,Y

[0273] 26 -- C,F,H,I,L,N,S,T,V,W

[0274] 27 -- D,Q,W,Y

[0275] 28 -- A,C,D,I,L,V,Y

[0276] 29 -- A,C,E,G,K,L,N,Q,R,S,T

[0277] 30 -- C,I,L,M,P,T,V

[0278] 31 -- C,D,E

[0279] 32 -- A,C,E,I,L,M,Q,S,T,V,Y

[0280] 33 -- A,C,E,F,G,H,I,K,L,M,Q,R,S,T,V,Y

[0281] 34 -- C,D,F,G,H,L,M,N,P,R,S,T,W,Y

[0282] 35 -- A,C,E,F,G,H,I,K,L,N,P,R,T,V,W

[0283] 36 -- A,C,G,S,T,V

[0284] 37 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y

[0285] 38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0286] 39 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0287] 40 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,Y

[0288] 41 -- A,C,D,E,G,H,K,N,Q,S,W

[0289] 42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0290] 43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y

[0291] 44 -- A,E,F,G,H,I,K,L,M,N,Q,R,S,T,V

[0292] 45 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0293] 46 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0294] 47 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0295] 48 -- A,C,M,S,T,V

[0296] 49 -- A,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0297] 50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0298] 51 -- A,F,I,K,L,M,R,T,V,W,Y

[0299] 52 -- F,I,K,L,M,V

[0300] 53 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0301] 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0302] 55 -- A,C,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0303] 56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0304] LCB5 (서열번호 25-26)

[0305] 1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0306] 2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0307] 3 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0308] 4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0309] 5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0310] 6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0311] 7 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0312] 8 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0313] 9 -- A,C,E,F,G,H,I,L,M,N,Q,S,T,V,W,Y

[0314] 10 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0315] 11 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0316] 12 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y

[0317] 13 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0318] 14 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0319] 15 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0320] 16 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0321] 17 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0322] 18 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0323] 19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0324] 20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0325] 21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0326] 22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0327] 23 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,W,Y

[0328] 24 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,S,T,V,W,Y

[0329] 25 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0330] 26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0331] 27 -- A,C,G,H,I,S,T,V

[0332] 28 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0333] 29 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0334] 30 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0335] 31 -- A,C,E,F,H,I,K,L,M,N,Q,S,T,V,W,Y

[0336] 32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0337] 33 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0338] 34 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0339] 35 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0340] 36 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0341] 37 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y

[0342] 38 -- A,C,D,E,G,I,L,M,N,P,Q,S,T,V,W

[0343] 39 -- A,C,F,G,L,M,N,S,T,V,W

[0344] 40 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,Y

[0345] 41 -- C,H,I,L,M,P,R

[0346] 42 -- A,C,E,G,H,I,L,M,P,T,V,Y

[0347] 43 -- C,I,L,M,Q,T,V

[0348] 44 -- A,C,D,F,G,H,I,M,S,T

[0349] 45 -- D,Y

[0350] 46 -- A,C,D,F,I,L,R,V

[0351] 47 -- C,E,G,I,V

[0352] 48 -- F,I,V,W,Y

[0353] 49 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0354] 50 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0355] 51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0356] 52 -- C,D,E,H,I,K,N,P,Q,R,S,T,Y

[0357] 53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0358] 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0359] 55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0360] 56 -- F,I,L,M,T,V,W

[0361] 57 -- A,C,D,E,F,G,H,N,P,Q,R,S,T,W,Y

[0362] 58 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0363] 59 -- A,C,F,I,L,M,T,V,Y

[0364] 60 -- C,F,M,N,V,Y

[0365] 61 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0366] 62 -- A,C,F,G,I,L,M,S,T,V,W

[0367] 63 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0368] 64 -- A,C,E,F,G,H,K,L,N,P,R,S,T,W,Y

[0369] 65 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0370] LCB6 (서열번호 27-28)

[0371] 1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0372] 2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0373] 3 -- E,W

[0374] 4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0375] 5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0376] 6 -- F,L,M,R,S

[0377] 7 -- H,T,V

[0378] 8 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0379] 9 -- F,M

[0380] 10 -- A,K,L,W

[0381] 11 -- D,E,G,V,Y

[0382] 12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0383] 13 -- E,L

[0384] 14 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0385] 15 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0386] 16 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0387] 17 -- F,N,P,S

[0388] 18 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0389] 19 -- L,N,Q,V

[0390] 20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0391] 21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0392] 22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0393] 23 -- C,D,P,Q,R,W

[0394] 24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0395] 25 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0396] 26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0397] 27 -- D,H,L,S,W

[0398] 28 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0399] 29 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0400] 30 -- L,Q,V,W

[0401] 31 -- I,K,L,S

[0402] 32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0403] 33 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0404] 34 -- A,F,L,T,V

[0405] 35 -- C,D,G,H,K,L,N,T

[0406] 36 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0407] 37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0408] 38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0409] 39 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0410] 40 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0411] 41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0412] 42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0413] 43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0414] 44 -- F,I

[0415] 45 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0416] 46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0417] 47 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0418] 48 -- L,Q,R,T

[0419] 49 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0420] 50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0421] 51 -- C,V,Y

[0422] 52 -- A,E,H,K

[0423] 53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0424] 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0425] 55 -- C,F,H,L,P,W,Y

[0426] 56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0427] LCB7 (서열번호 29-30)

[0428] 1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0429] 2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0430] 3 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0431] 4 -- I,T,V

[0432] 5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0433] 6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0434] 7 -- L,P,Y

[0435] 8 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0436] 9 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0437] 10 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0438] 11 -- A

[0439] 12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0440] 13 -- A,L,P

[0441] 14 -- H,L,R,T,Y

[0442] 15 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0443] 16 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0444] 17 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0445] 18 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0446] 19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0447] 20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0448] 21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0449] 22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0450] 23 -- A,S

[0451] 24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0452] 25 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0453] 26 -- C,G,S,V,Y

[0454] 27 -- K,L,M,W

[0455] 28 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0456] 29 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0457] 30 -- A,Y

[0458] 31 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0459] 32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0460] 33 -- A,C,F,I,K,L,V,W

[0461] 34 -- A,H,L

[0462] 35 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0463] 36 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0464] 37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0465] 38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0466] 39 -- A,C,K,L,M,N

[0467] 40 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0468] 41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0469] 42 -- A,C,D,L,V

[0470] 43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0471] 44 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0472] 45 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0473] 46 -- Q,S,V

[0474] 47 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0475] 48 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0476] 49 -- E,L

[0477] 50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0478] 51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0479] 52 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0480] 53 -- I

[0481] 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0482] 55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0483] 56 -- L,M,N,R

[0484] 57 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0485] LCB8 (서열번호 31-32)

[0486] 1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0487] 2 -- C,F,I,L,M,S,V,W,Y

[0488] 3 -- A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0489] 4 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0490] 5 -- A,C,F,G,I,K,L,M,Q,S,T,V,W,Y

[0491] 6 -- H,I,K,L,M

[0492] 7 -- A,H,I,K,L,M,N,P,Q,R,W,Y

[0493] 8 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0494] 9 -- A,C,F,G,I,L,M,S,Y

[0495] 10 -- A,F,H,K,L,M,Q,R,S

[0496] 11 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0497] 12 -- A,C,D,E,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0498] 13 -- A,C,D,E,F,G,H,M,N,Q,S,W,Y

[0499] 14 -- C,D,E,H,N,Q,S

[0500] 15 -- A,D,E,F,H,I,L,M,N,P,Q,S,T,V,W,Y

[0501] 16 -- C,F,M,N,R,Y

[0502] 17 -- A,C,I,L,M,Q,R,V

[0503] 18 -- A,C,F,H,I,L,M,T,V,Y

[0504] 19 -- I,Q,S

[0505] 20 -- D,N

[0506] 21 -- A,C,G,S,V

[0507] 22 -- A,C,I,L,M,V

[0508] 23 -- C,F,R,T,W,Y

[0509] 24 -- A,C,D,E,F,G,H,I,L,M,N,Q,R,S,T,V,W,Y

[0510] 25 -- C,E,S,T,V,Y

[0511] 26 -- A,C,D,E,F,G,H,N,Q,S,T

[0512] 27 -- A,C,D,E,G,H,I,K,L,M,N,Q,R,S,T,V

[0513] 28 -- C,E,F,G,H,I,K,L,M,Q,R,W,Y

[0514] 29 -- A,C,F,G,H,I,K,L,M,N,Q,R,S,T,V,Y

[0515] 30 -- A,C,E,G,H,K,M,N,P,Q,R,T

[0516] 31 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,Y

[0517] 32 -- A,C,D,E,G,H,I,K,N,Q,R,S,T,W

[0518] 33 -- A,C,E,G,H,K,M,N,P,Q,R,S,W,Y

[0519] 34 -- C,D,E,F,H,M,N,W,Y

[0520] 35 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y

[0521] 36 -- A,C,D,E,F,G,H,K,L,M,N,Q,R,S,T,V,W,Y

[0522] 37 -- F,G,H,I,L,M,S,T,Y

[0523] 38 -- D,E,H,Q,W,Y

[0524] 39 -- C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y

[0525] 40 -- A,C,E,G,H,I,K,M,P,V,Y

[0526] 41 -- C,F,H,I,K,L,M,R,S,T,V

[0527] 42 -- E,F,I,T,W,Y

[0528] 43 -- A,C,D,E,F,H,I,L,M,N,Q,R,S,T,V,W,Y

[0529] 44 -- C,G,I,K,L,M,T,V,Y

[0530] 45 -- G,S,W,Y

[0531] 46 -- C,I,K,L,M,N,Q,R,S,T

[0532] 47 -- A,C,E,N,Q,S,T,V

[0533] 48 -- C,D,E,F,H,I,L,M,W

[0534] 49 -- C,D,F,H,K,L,M,N,Q,R,T

[0535] 50 -- A,C,D,E,N,Y

[0536] 51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0537] 52 -- A,C,D,E,G,H,K,L,M,N,Q,R,S,T

[0538] 53 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,S,T,V,W,Y

[0539] 54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0540] 55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,S,T,V,W,Y

[0541] 56 -- C,I,L,M

[0542] 57 -- A,C,D,E,G,I,N,Q,S,T

[0543] 58 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0544] 59 -- A,C,G,P,S

[0545] 60 -- A,C,E,F,G,I,L,M,N,Q,S,T,V

[0546] 61 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0547] 62 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0548] 63 -- A,C,E,F,G,H,I,L,M,N,Q,S,T,V,W,Y

[0549] 64 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,S,T,V

[0550] 65 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,W,Y

[0551] AHB1 (서열번호 33-34)

[0552] 1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0553] 2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0554] 3 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0555] 4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0556] 5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0557] 6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0558] 7 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0559] 8 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0560] 9 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0561] 10 -- A,C,F,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0562] 11 -- F,N,Y

[0563] 12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0564] 13 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0565] 14 -- A,D,G

[0566] 15 -- A,C,D,E,G,H,I,K,L,M,N,Q,R,S,T,V

[0567] 16 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0568] 17 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0569] 18 -- A,C,D,E,F,G,H,I,L,M,N,Q,S,T,V,W,Y

[0570] 19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0571] 20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0572] 21 -- A,C,E,G,S,V

[0573] 22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0574] 23 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0575] 24 -- A,C,D,E,F,H,K,L,M,N,Q,R,S,T,V,Y

[0576] 25 -- A,C,D,F,G,H,L,M,N,Q,R,S,T,V,W,Y

[0577] 26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0578] 27 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0579] 28 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,Y

[0580] 29 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0581] 30 -- A,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0582] 31 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0583] 32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0584] 33 -- A,G,S

[0585] 34 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0586] 35 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0587] 36 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y

[0588] 37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0589] 38 -- A,C,E,G,H,M,P,Q

[0590] 39 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0591] 40 -- A,C,D,E,G,K,N,Q,R,S,T

[0592] 41 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,S,T,V,W,Y

[0593] 42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0594] 43 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,S,T,V,W,Y

[0595] 44 -- E,F,H,Q,S,W,Y

[0596] 45 -- D,N

[0597] 46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0598] 47 -- C,T,V

[0599] 48 -- F,S,W,Y

[0600] 49 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0601] 50 -- A,C,F,H,I,K,L,M,N,Q,R,S,T,V,W,Y

[0602] 51 -- A,D,G,H,N,S

[0603] 52 -- H,K,Q,R

[0604] 53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0605] 54 -- A,C,H,I,K,L,M,N,P,Q,R,S,T,V

[0606] 55 -- A,C,E,G,H,K,N,Q,R,S,T

[0607] 56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0608] 57 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0609] 58 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0610] 59 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0611] 60 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0612] 61 -- A,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0613] 62 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0614] 63 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0615] 64 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0616] 65 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0617] 66 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0618] 67 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0619] 68 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0620] 69 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0621] 70 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0622] 71 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0623] 72 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0624] 73 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0625] 74 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0626] 75 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0627] 76 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0628] 77 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0629] 78 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0630] 79 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0631] 80 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0632] 81 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0633] 82 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0634] 83 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0635] 84 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0636] 85 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

[0637] AHB2 (서열번호 101-102 및 164)

[0638] 1 -- C,G,A,V,F,Y,W,S,Q,D,E,R,K

[0639] 2 -- C,P,G,V,I,M,L,F,Y,W,S,N,Q,D,E,R,H

[0640] 3 -- C,G,A,V,I,F,S,T,D,E,K

[0641] 4 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0642] 5 -- C,P,G,A,V,M,L,Y,W,S,N,Q,D,E,R,K,H

[0643] 6 -- G,A,V,I,F,S,T,D,H

[0644] 7 -- C,P,G,V,I,M,L,F,W,S,T,N,Q,E,R,K,H

[0645] 8 -- C,P,G,A,V,M,L,Y,W,S,T,N,Q,D,E,R,K,H

[0646] 9 -- C,P,G,A,V,I,M,L,F,W,S,T,N,Q,D,E,R,K,H

[0647] 10 -- C,P,G,A,V,I,L,Y,W,S,T,N,E,R,K

[0648] 11 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,H

[0649] 12 -- C,P,G,A,V,I,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0650] 13 -- C,G,A,V,M,L,F,W,S,T,N,E,H

[0651] 14 -- C,P,G,A,V,I,Y,S,T,N,D,E,R,H

[0652] 15 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K

[0653] 16 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0654] 17 -- C,P,G,A,V,L,Y,W,S,T,Q,D,E,R

[0655] 18 -- C,P,A,V,I,M,F,Y,N,Q,R,K,H

[0656] 19 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0657] 20 -- C,P,G,A,V,M,L,Y,W,N,Q,E,R,K,H

[0658] 21 -- C,P,G,A,V,I,M,L,F,Y,W,S,N,Q,E,R,K,H

[0659] 22 -- C,P,G,A,V,M,L,F,Y,S,T,N,Q,D,E,R,K,H

[0660] 23 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,E,R,K

[0661] 24 -- C,P,G,A,V,I,M,L,F,Y,W,S,Q,E,R,H

[0662] 25 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,R,H

[0663] 26 -- C,G,A,V,L,Y,S,N,D,R,K,H

[0664] 27 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0665] 28 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0666] 29 -- C,P,G,V,I,M,L,F,Y,W,S,T,N,Q,D,R,K,H

[0667] 30 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0668] 31 -- C,G,A,V,I,M,L,F,Y,W,S,T,Q,D,E,R,K,H

[0669] 32 -- P,G,A,V,I,L,W,S,T,D,R,H

[0670] 33 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,E,R,K,H

[0671] 34 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0672] 35 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0673] 36 -- C,P,G,A,V,I,L,F,Y,S,T,N,Q,D,E,R,H

[0674] 37 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0675] 38 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,Q,E,R,K

[0676] 39 -- C,P,G,A,V,I,W,S,Q,E,R,H

[0677] 40 -- C,P,G,A,V,I,L,Y,W,S,T,N,D,E,R,K,H

[0678] 41 -- C,P,G,A,V,I,M,L,Y,W,S,T,N,Q,D,E,R,K,H

[0679] 42 -- C,P,G,A,V,M,L,Y,W,S,T,N,Q,D,E,R,K,H

[0680] 43 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0681] 44 -- C,P,G,A,V,I,M,L,F,W,S,T,Q,D,E,R,H

[0682] 45 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0683] 46 -- C,P,G,A,V,I,M,L,F,S,T,Q,E,R,K

[0684] 47 -- C,G,A,V,I,M,L,F,W,S,T,N,Q,D,E,R,H

[0685] 48 -- C,P,G,A,V,I,M,L,F,Y,W,S,N,Q,E,R,K

[0686] 49 -- C,P,G,A,V,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0687] 50 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0688] 51 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0689] 52 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0690] 53 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,D,E,R,K,H

[0691] 54 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0692] 55 -- C,P,G,A,V,I,M,L,F,Y,S,T,N,Q,D,E,R,K,H

[0693] 56 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0694] 57 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0695] 58 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,E,R,K,H

[0696] 59 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0697] 60 -- C,G,A,V,I,M,L,F,Y,W,S,T,Q,D,E,R,K

[0698] 61 -- C,P,G,A,V,I,M,L,F,Y,W,S,N,Q,D,E,R,K,H

[0699] 62 -- C,G,A,V,L,S,T,N,D,E,K,H

[0700] 63 -- C,P,G,A,V,I,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0701] 64 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,H

[0702] 65 -- C,G,A,V,I,M,L,F,Y,S,T,N,R,K,H

[0703] 66 -- C,P,G,A,V,I,M,L,W,T,Q,E,R

[0704] 67 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0705] 68 -- C,P,G,A,V,I,L,F,Y,W,S,T,N,Q,D,E,R,H

[0706] 69 -- P,G,V,I,M,L,Y,W,S,T,Q,R,K

[0707] 70 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

[0708] 71 -- C,G,A,V,L,F,W,S,Q,D,E,R,K

[0709] 72 -- C,V,I,L,S

[0710] 73 -- P,G,A,V,S,T,E

[0711] 74 -- C,A,L,F,Y,S,T,R,H

[0712] 75 -- C,P,G,V,I,L,F,W,S,N,D,E,R,K

[0713] 다양한 디자인 타입들에서 RBD 표적에 대해 8A에 기재된 인터페이스 잔기의 잔기 번호를 **표 2**에 나타낸다. 다른 구현예에서, 표 2에 열거된 인터페이스 잔기들에서 아미노산 잔기는 참조 서열의 잔기와 동일하거나, 또는 보존적인 아미노산 치환에 의해 치환될 수 있다. 이러한 보존적인 아미노산 치환은 잔기를 물리화학적인 특징이 비슷한 잔기로 치환하는 것을 수반하며, 예를 들어 지방족 잔기는 다른 잔기로 (예, Ile, Val, Leu 또는 Ala을 다른 것으로), 또는 극성 잔기를 다른 잔기로 (예, Lys과 Arg 간의; Glu과 Asp 간의; 또는 Gln과 Asn 간의) 치환을 포함한다. 다른 이러한 보존적인 치환, 예를 들어, 소수성 특성이 비슷한 전체 영역의 치환이 알려져 있다. 아미노산은 이의 측쇄 특성의 유사성에 따라 분류할 수 있다 (A. L. Lehninger, in Biochemistry, second ed., pp. 73-75, Worth Publishers, New York (1975)): (1) 비-극성: Ala (A), Val (V), Leu (L), Ile (I), Pro (P), Phe (F), Trp (W), Met (M); (2) 비-하전된 극성: Gly (G), Ser (S), Thr (T), Cys (C), Tyr (Y), Asn (N), Gln (Q); (3) 산성: Asp (D), Glu (E); (4) 염기성: Lys (K), Arg (R), His (H). 대안적으로, 자연 생성 잔기들은 공통된 측쇄 특성에 따라 그룹으로 분류할 수 있다: (1) 소수성: 노르루신, Met, Ala, Val, Leu, Ile; (2) 중성 친수성: Cys, Ser, Thr, Asn, Gln; (3) 산성: Asp, Glu; (4) 염기성: His, Lys, Arg; (5) 쇄 배향성 (chain orientation)에 영향을 미치는 잔기: Gly, Pro; (6) 방향족: Trp, Tyr, Phe. 비-보존적인 치환은 이들 종류 중 한가지의 구성원을 다른 종류로 교체하는 것을 수반할 것이다. 구체적인 보존적인 치환으로는 예를 들어; Ala → Gly 또는 → Ser; Arg → Lys; Asn → Gln 또는 → His; Asp → Glu; Cys → Ser; Gln → Asn; Glu → Asp; Gly → Ala 또는 → Pro; His → Asn 또는 → Gln; Ile → Leu 또는 → Val; Leu → Ile 또는 → Val; Lys → Arg, → Gln 또는 → Glu; Met → Leu, → Tyr 또는 → Ile; Phe → Met, → Leu 또는 → Tyr; Ser → Thr; Thr → Ser; Trp → Tyr; Tyr → Trp; 및/또는 Phe → Val, → Ile 또는 → Leu.

[0714] **표 2: 인터페이스 잔기**

[0715] 'LCB1': [3, 6, 7, 10, 13, 17, 20, 22, 23, 25, 26, 29, 32, 33, 36],

[0716] 'LCB2': [1, 2, 5, 6, 9, 12, 13, 16, 20, 32, 35, 39],

[0717] 'LCB3': [1, 3, 4, 6, 7, 10, 11, 13, 14, 15, 18, 27, 30, 33, 34, 37],

[0718] 'LCB4': [8, 11, 12, 15, 23, 24, 26, 27, 28, 30, 31, 34, 56],

[0719] 'LCB5': [35, 37, 38, 40, 41, 44, 47, 48, 53, 56, 60, 63],

[0720] 'LCB6': [3, 4, 7, 8, 11, 12, 14, 15, 21, 24, 25, 28, 31, 32, 35],

[0721] 'LCB7': [2, 3, 6, 7, 9, 10, 13, 17, 29, 32, 33, 36],

[0722] 'LCB8': [14, 15, 16, 19, 22, 23, 26, 29, 30, 38, 41, 42, 45],

[0723] 'AHB1', [34, 38, 41, 45, 48, 49, 52, 63, 64, 67, 68, 70, 71, 74, 78, 81, 82, 85],

[0724] 'AHB2', [4, 7, 11, 14, 15, 18, 21, 26, 29, 30, 33, 34, 36, 37, 40, 43, 44, 47, 48].

[0725] 일 구현예에서, 표 2에 열거된 인터페이스 잔기에서 아미노산 잔기들은 참조 서열의 잔기와 동일하다.

[0726] 다른 구현예에서, 폴리펩타이드는 서열번호 1-10, 13-17, 19-21, 33-34, 및 100-101로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100%로 동일한 아미노산 서열을 포함한다.

[0727] 일 구현예에서, 폴리펩타이드는 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%

또는 100% 동일한 아미노산 서열을 포함한다 (표 3 참조).

[0728] **표 3: LCB1 변이체 예**

표 1

[0729]

명칭	결합제 단백질
LCB1_4N	DKENILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 102)
LCB1_4K	DKEKILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 103)
LCB1_14K	DKEWILQKIYEIMKLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 104)
LCB1_15T	DKEWILQKIYEIMRTLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 105)
LCB1_18Q	DKEWILQKIYEIMRLLDQLGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 106)
LCB1_18K	DKEWILQKIYEIMRLLDKLGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 107)
LCB1_27Q	DKEWILQKIYEIMRLLDELGHAEASMQVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 108)
LCB1_27Y	DKEWILQKIYEIMRLLDELGHAEASMYVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 109)
LCB1_17E	DKEWILQKIYEIMRLLEELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 110)
LCB1_17R	DKEWILQKIYEIMRLLRELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 111)
LCB1_42N	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDENLLEEAERLLEEVER(서열번호 112)
LCB1_49Q	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAEQLLEEVER(서열번호 113)
LCB1_52Q	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLQEVER(서열번호 114)
LCB1_32L	DKEWILQKIYEIMRLLDELGHAEASMRVSDLLYEFMKKGDERLLEEAERLLEEVER(서열번호 115)
LCB1_28A	DKEWILQKIYEIMRLLDELGHAEASMRASDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 116)
LCB1_v1.3_ACH1	DKENILQKIYEIMKTLEQLGHAEASMYVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 117)
LCB1_v1.3_ACH2	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDENLLEEAERLLEEVER(서열번호 118)
LCB1_v1.3_ACH3	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAEQLLEEVER(서열번호 119)
LCB1_v1.3_ACH4	DKENILQKIYEIMKTLEQLGHAEASMYVSDLIYEFMKQGDENLLEEAEQLLEEVER(서열번호 120)
LCB1_v1.3_ACH5	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDENLLEEAEQLLEEVER(서열번호 121)
LCB1_v1.3_1	DRENILQKIYEIMKELEKLGHAEASMQVSDLIYEFMQDKDERLLEEAERLLEEVKR(서열번호 122)
LCB1_v1.3_2	DRENILQKIYEIMKELRQLGHAEASMQVSDLIYEFMKTKDKRLLEEAERLLEEVKR(서열번호 123)
LCB1_v1.3_3	DRENILQKIYEIMKTLRRLGHAEASMQVSDLIYEFMQDKDKRLLEEAERLLEEVQR(서열번호 124)
LCB1_v1.3_4	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 125)
LCB1_v1.3_5	DRENILQKIYEIMKTLEKLGHAEASMQASDLIYEFMKTKDERLLEEAERLLEEVQR(서열번호 126)
LCB1_v1.3_6	DKENILQKIYEIMKTLRALGHAEASMQVSDLIYEFMQTKDERLLEEAERLLEEVKR(서열번호 127)
LCB1_v1.3_7	DKENVLQKIYEIMKTLEKLGHAEASMQVSDLIYEFMQTKDKRLLEEAERLLEEVQR(서열번호 128)
LCB1_v1.3_15	DRENILQKIYEIMKELEKLGHAEASMQVSDLIYEFMQDKDENLLEEAERLLEEVKR(서열번호 129)
LCB1_v1.3_16	DRENILQKIYEIMKELRQLGHAEASMQVSDLIYEFMKTKDKNLLEEAERLLEEVKR(서열번호 130)
LCB1_v1.3_17	DRENILQKIYEIMKTLRRLGHAEASMQVSDLIYEFMQDKDKNLLEEAERLLEEVQR(서열번호 131)
LCB1_v1.3_19	DRENILQKIYEIMKTLEKLGHAEASMQASDLIYEFMKTKDENLLEEAERLLEEVQR(서열번호 132)
LCB1_v1.3_20	DKENILQKIYEIMKTLRALGHAEASMQVSDLIYEFMQTKDENLLEEAERLLEEVKR(서열번호 133)
LCB1_v1.3_21	DKENVLQKIYEIMKTLEKLGHAEASMQVSDLIYEFMQTKDKNLLEEAERLLEEVQR(서열번호 134)
LCB1_v2.2	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
LCB1_v2.2_ompT	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTR(서열번호 136)

[0730] 폴리펩타이드는 후술한 실시예에 상세히 기술된 바와 같이 결합 활성을 유지하면서 돌연변이를 상당한 수로 가질 수 있다. 일 구현예에서, 폴리펩타이드는 서열번호 1의 아미노산 서열을 기준으로 2, 4, 5, 14, 15, 17, 18, 27, 28, 32, 37, 38, 39, 41, 42, 49, 52, 및 55로 이루어진 군으로부터 선택되는 잔기 1개, 2개, 3개, 4개, 5개, 6개, 7개, 8개, 9개, 10개, 11개, 12개, 13개, 14개, 15개, 16개, 17개 또는 모두 18개로 이루어진 군으로부터 선택되는 아미노산 치환을 포함한다. 다른 구현예에서, 치환은 표 4에 열거된 치환들로부터, 개별적으로 (즉, 표에 열거된 임의의 하나의 돌연변이) 또는 해당 열의 조합으로 선택된다.

[0731] **표 4: LCB1 치환 예**

표 2

[0732]

명칭	기원 서열	WT 대비 돌연변이
LCB1_1	LCB1	W4N R14K L15T E18Q R27Q K38Q
LCB1_2	LCB1	W4N R14K L15T E18Q R27Y K38Q
LCB1_3	LCB1	W4N R14K L15T D17E E18Q R27Q K38Q

LCB1_4	LCB1	W4N R14K L15T D17E E18Q R27Q K38Q R42N R49Q E52Q
LCB1_4N	LCB1	W4N
LCB1_4K	LCB1	W4K
LCB1_14K	LCB1	R14K
LCB1_15T	LCB1	L15T
LCB1_18Q	LCB1	E18Q
LCB1_18K	LCB1	E18K
LCB1_27Q	LCB1	R27Q
LCB1_27Y	LCB1	R27Y
LCB1_38Q	LCB1	K38Q
LCB1_17E	LCB1	D17E
LCB1_17R	LCB1	D17R
LCB1_42N	LCB1	R42N
LCB1_49Q	LCB1	R49Q
LCB1_52Q	LCB1	E52Q
LCB1_32L	LCB1	I32L
LCB1_28A	LCB1	V28A
LCB1_v1.3	LCB1	W4N R14K L15T D17E E18Q R27Q K38Q
LCB1_v1.3_ACH1	LCB1_v1.3	W4N R14K L15T D17E E18Q R27Y K38Q
LCB1_v1.3_ACH2	LCB1_v1.3	W4N R14K L15T D17E E18Q R27Q K38Q R42N
LCB1_v1.3_ACH3	LCB1_v1.3	W4N R14K L15T D17E E18Q R27Q K38Q R49Q
LCB1_v1.3_ACH4	LCB1_v1.3	W4N R14K L15T D17E E18Q R27Y K38Q R42N R49Q
LCB1_v1.3_ACH5	LCB1_v1.3	W4N R14K L15T D17E E18Q R27Q K38Q R42N R49Q
LCB1_v1.3_1	LCB1_v1.3	K2R W4N R14K L15E D17E E18K R27Q K37Q K38D G39K E55K
LCB1_v1.3_2	LCB1_v1.3	K2R W4N R14K L15E D17R E18Q R27Q K38T G39K E41K E55K
LCB1_v1.3_3	LCB1_v1.3	K2R W4N R14K L15T D17R E18R R27Q K37Q K38D G39K E41K E55Q
LCB1_v1.3_4	LCB1_v1.3	W4N I5V R14K L15E D17E E18R R27Q K38T G39K E55K
LCB1_v1.3_5	LCB1_v1.3	K2R W4N R14K L15T D17E E18K R27Q V28A K38T G39K E55Q
LCB1_v1.3_6	LCB1_v1.3	W4N R14K L15T D17R E18A R27Q K37Q K38T G39K E55K
LCB1_v1.3_7	LCB1_v1.3	W4N I5V R14K L15T D17E E18K R27Q K37Q K38T G39K E41K E55Q
LCB1_v1.3_15	LCB1_v1.3	K2R W4N R14K L15E D17E E18K R27Q K37Q K38D G39K R42N E55K
LCB1_v1.3_16	LCB1_v1.3	K2R W4N R14K L15E D17R E18Q R27Q K38T G39K E41K R42N E55K
LCB1_v1.3_17	LCB1_v1.3	K2R W4N R14K L15T D17R E18R R27Q K37Q K38D G39K E41K R42N
LCB1_v1.3_19	LCB1_v1.3	K2R W4N R14K L15T D17E E18K R27Q V28A K38T G39K R42N E55Q
LCB1_v1.3_20	LCB1_v1.3	W4N R14K L15T D17R E18A R27Q K37Q K38T G39K R42N E55K
LCB1_v1.3_21	LCB1_v1.3	W4N I5V R14K L15T D17E E18K R27Q K37Q K38T G39K E41K R42N E55Q
LCB1_v2.2	LCB1_v1.3	W4N I5V R14K L15E D17E E18R R27Q K38T G39K R42N E55K
LCB1_v2.2_ompT	LCB1_v1.3	W4N I5V R14K L15E D17E E18R R27Q K38T G39K R42N E55T

[0733] 다른 구현예에서, 폴리펩타이드는 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다 (표 5 참조).

[0734] **표 5: LCB3 변이체 예**

표 3

[0735]

명칭	결합제 단백질
LCB3_8Q	NDDELHMQMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 137)
LCB3_8T	NDDELHMTMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 138)
LCB3_19K	NDDELHMLMTDLVYEALHKAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 139)
LCB3_19I	NDDELHMLMTDLVYEALHIAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 140)
LCB3_25F	NDDELHMLMTDLVYEALHFAKDEEFKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 141)
LCB3_25M	NDDELHMLMTDLVYEALHFAKDEEMKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 142)
LCB3_26Q	NDDELHMLMTDLVYEALHFAKDEEIQKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 143)
LCB3_28H	NDDELHMLMTDLVYEALHFAKDEEIKKHVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 144)
LCB3_35K	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEKADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 145)
LCB3_37T	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELATKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 146)

LCB3_40R	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKARKNNDRQKLEKVVEELKELLERLLS(서열번호 147)
LCB3_43K	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 148)
LCB3_34G	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFGLADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 149)
LCB3_34Y	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFYLADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 150)
LCB3_34T	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFTLADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 151)
LCB3_49K	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLKKVVEELKELLERLLS(서열번호 152)
LCB3_v1.2_ACH1	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFGKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 153)
LCB3_v1.2_ACH2	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFYKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 154)
LCB3_v2.2	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)
LCB3_v1.3_2	NDDELHMQMTDLVYEALHFAKTEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 156)
LCB3_v1.3_3	NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKARKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 157)
LCB3_v1.3_4	NDDELHMQMTDLVWEALHFAKDEEFQKHVFQLFEKARKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 158)
LCB3_v1.3_5	NDDELHMQMTDLVWEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 159)
LCB3_v1.3_6	NEDELHMQMTDLVWEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 160)
LCB3_v1.3_7	NDDELHMQMTDLVWEALHFAKTEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 161)
LCB3_v1.3_15	NLDELHMQMTDLVYEALHFAKTEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 162)
LCB3_v2.3	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)

[0736] 폴리펩타이드는 후술한 실시예에 상세히 기술된 바와 같이 결합 활성을 유지하면서 돌연변이를 상당한 수로 가질 수 있다. 일 구현예에서, 폴리펩타이드는 서열번호 13의 아미노산 서열을 기준으로 2, 6, 8, 9, 13, 14, 19, 22, 25, 26, 28, 29, 34, 35, 37, 40, 43, 45, 49 및 62로 이루어진 군으로부터 선택되는 잔기 1개, 2개, 3개, 4개, 5개, 6개, 7개, 8개, 9개, 10개, 11개, 12개, 13개, 14개, 15개, 16개, 17개, 18개, 19개 또는 모두 20개로 이루어진 군으로부터 선택되는 아미노산 치환을 포함한다. 다른 구현예에서, 치환은 표 6에 열거된 치환들로부터, 개별적으로 또는 해당 열의 조합으로 선택된다.

[0737] **표 6: LCB3 치환 예**

표 4

[0738]

명칭	기원 서열	WT 대비 돌연변이							
LCB3_1	LCB3	L8Q	I25F	K26Q	R28H	L35K	D37T		
LCB3_2	LCB3	L8Q	K26Q	R28H	L35K	D37T	N43K		
LCB3_3	LCB3	L8Q	I25F	K26Q	R28H	L35K	D37T	N43K	
LCB3_4	LCB3	L8Q	F19K	I25F	K26Q	R28H	L35K	D37T	Y40R,N43K
LCB3_8Q	LCB3	L8Q							
LCB3_8T	LCB3	L8T							
LCB3_19K	LCB3	F19K							
LCB3_19I	LCB3	F19I							
LCB3_25F	LCB3	I25F							
LCB3_25M	LCB3	I25M							
LCB3_26Q	LCB3	K26Q							
LCB3_28H	LCB3	R28H							
LCB3_35K	LCB3	L35K							
LCB3_37T	LCB3	D37T							
LCB3_40R	LCB3	Y40R							
LCB3_43K	LCB3	N43K							
LCB3_34G	LCB3	E34G							
LCB3_34Y	LCB3	E34Y							
LCB3_34T	LCB3	E34T							
LCB3_49K	LCB3	E49K							
LCB3_v1.2	LCB3	L8Q	K26Q	R28H	L35K	D37T	N43K		
LCB3_v1.2_ACH1	LCB3_v1.2	L8Q	K26Q	R28H	E34G	L35K	D37T	N43K	
LCB3_v1.2_ACH2	LCB3_v1.2	L8Q	K26Q	R28H	E34Y	L35K	D37T	N43K	
LCB3_v2.2	LCB3_v1.3	D2L	L8Q	I25F	K26Q	R28H	L35K	D37T	N43K

LCB3_v1.3_2	LCB3_v1.3	L8Q	D22T	I25F	K26Q	R28H	L35K	D37T	N43K
LCB3_v1.3_3	LCB3_v1.3	L8Q	I25F	K26Q	R28H	L35K	D37R	N43K	
LCB3_v1.3_4	LCB3_v1.3	L8Q	Y14W	I25F	K26Q	R28H	L35K	D37R	N43K
LCB3_v1.3_5	LCB3_v1.3	L8Q	Y14W	I25F	K26Q	R28H	L35K	D37T	N43K
LCB3_v1.3_6	LCB3_v1.3	D2E	L8Q	Y14W	I25F	K26Q	R28H	L35K	D37T, N43K
LCB3_v1.3_7	LCB3_v1.3	L8Q	Y14W	D22T	I25F	K26Q	R28H	L35K	D37T, N43K
LCB3_v1.3	LCB3_v1.2	L8Q	I25F	K26Q	R28H	L35K	D37T	N43K	
LCB3_v1.3_15	LCB3_v1.3	D2L	L8Q	D22T	I25F	K26Q	R28H	L35K	D37T,N43K
LCB3_v2.3	LCB1_v2.1	D2I	H6L	L8Q	M9V	V13I	I25F	K26Q	R28H,V29A, L35K, D37T, N43K, R45K, L62I

[0739] 추가적인 구현예에서, 폴리펩타이드는 서열번호 33-34 및 100-101 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다 (표 7 참조).

[0740] **표 7: AHB2 변이체 예**

표 5

[0741] AHB2v2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART (서열번호 164)

[0742] 일 구현예에서, 폴리펩타이드는 서열번호 101의 아미노산 서열에 대해 아미노산 치환을, 63 및 75로 이루어진 군으로부터 선택되는 잔기 또는 양쪽 잔기에서, 포함한다. 추가적인 구현예에서, 치환은 R63A 및/또는 K75T를 포함한다.

[0743] 본원에 개시된 모든 구현예들에서, 폴리펩타이드는 의도한 용도에 적합한 것으로 간주되는 하나 이상의 부가적인 관능기 또는 잔기를 포함할 수 있다. 일 구현예에서, 폴리펩타이드는 N-말단 및/또는 C-말단에 하나 이상의 첨가되는 시스테인 잔기를 추가로 포함할 수 있다. 다른 구현예에서, 폴리펩타이드는 N-연결된 당화 부위 (즉, NX(S/T), 여기서 X는 임의의 아미노산임)를 추가로 포함할 수 있다.

[0744] 다른 구현예에서, 폴리펩타이드는 서열번호 1-17, 19-21, 23-34 및 100-101로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 2 카피 이상 (즉, 2, 3, 4, 5 카피 이상) 포함할 수 있다. 이러한 구현예에서, 결합제가 2개 이상 연결된다. 일 구현예에서, 폴리펩타이드 2 카피 이상이 모두 동일하고; 다른 구현예에서, 폴리펩타이드 2 카피 이상이 모두 동일하지 않다. 임의의 이러한 구현예들에서, 폴리펩타이드 2 카피 이상이 아미노산 링커 서열에 의해 분리되어 있을 수 있지만, 이러한 링커가 필수적인 것은 아니다. 아미노산 링커는 의도한 목적에 적합한 임의 길이 및 아미노산 조성일 수 있다. 일 구현예에서, 아미노산 링커는 독립적으로 아미노산 2-100개 또는 3-100개 길이이다.

[0745] 다른 구현예에서, 아미노산 링커 서열은 Gly-Ser 풍부 (Gly-Ser 잔기가 적어도 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100%임) 아미노산 링커를 포함한다. 추가적인 구현예에서, Gly-Ser 풍부 링커는 GG 및 서열번호 35-46 및 165-171로 이루어진 군으로부터 선택되는 아미노산 서열을 포함한다.

[0746] GSGS (서열번호 35)

[0747] GGSGGS (서열번호 36)

[0748] SGGSGGSGGSG (서열번호 37)

[0749] GGSGGSGSGGSG (서열번호 38)

[0750] GGSGSSGGSGSGSG (서열번호 39)

[0751] GGSGSGGSGSGSGGS (서열번호 40)

[0752] SGGSGSGSGGSGSGS (서열번호 41)

[0753] GGGSGGGSSGGSGGSSGGGSGGGS (서열번호 42)

[0754] GGGSGGGGSGGGGSGGGGSGGGGSGGGGSG (서열번호 43)

[0755] GGGSGGGSGGSGGSGGGSGGGSGSGGSGGGGSGGGS (서열번호 44)

[0756] GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS (서열번호 45)

[0757] SGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS (서열번호 46)

[0758] GGSGGGGSGGGGSGGGGSGG (서열번호 165)

[0759] GGSGGGGSGGGGSGG (서열번호 166)

[0760] GGSGGGGSGG (서열번호 167)

[0761] GGGGSGGGG (서열번호 168)

[0762] GGGSGGG (서열번호 169)

[0763] GGSGG (서열번호 170)

[0764] GGSGSSG (서열번호 171)

[0765] 다른 구현예에서, 아미노산 링커 서열은 Pro-풍부 (Pro 잔기가 적어도 15%, 20%, 25% 이상임) 아미노산 링커를 포함할 수 있다. 비-제한적인 예시적인 구현예는 서열번호 97-98 및 172-176으로 이루어진 군으로부터 선택되는 아미노산 서열을 포함할 수 있다.

[0766] AGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASG (서열번호 97)

[0767] GSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSGGSGNSSGSGGSPVPSTPPTPSPSTPPTPSPSAS (서열번호 98)

[0768] GGASPAAPAPASPAAPAPSAPAGG (서열번호 172)

[0769] GGASPAAPAPASPAGG (서열번호 173)

[0770] GGASPAAPAPGG (서열번호 174)

[0771] GGASPAAPAGG (서열번호 175)

[0772] GGSSGPSTPPTPSPSTPPTPSPSPGGSSG (서열번호 176).

[0773] 추가적인 비-제한적인 구현예들에서, 아미노산 링커는 서열번호 99 및 177-178로 이루어진 군으로부터 선택되는 아미노산 서열을 포함할 수 있다.

[0774] GGSSAGSPTSTGTSSATPSGSGTGG (서열번호 177)

[0775] GGSSGEAAAKEAAAKEAAAKGSSGG (서열번호 178)

[0776] GGSSGQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGSSG (서열번호 99)

[0777] 일 구현예에서, 폴리펩타이드는 식 Z1-Z2-Z3를 포함하고, 여기서

[0778] Z1은 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

[0779] Z2는 선택적인 아미노산 링커를 포함하고;

[0780] Z3는 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동

일한 아미노산 서열을 포함하며;

[0781] 여기서, Z1과 Z3는 서로 동일하거나 또는 상이할 수 있다. 일 구현예에서, Z1과 Z3는 동일하고; 다른 구현예에서, Z1과 Z3는 서로 상이하다. Z1과 Z3가 서로 다른 구현예에서, 이들 각각은 주어진 출발 단량체의 변이체일 수 있다 (예, Z1은 서열번호 1 (LCB1)의 아미노산 서열을 포함하고, Z3는 서열번호 102-136의 아미노산 서열을 포함함). 본원에 개시된 단량체들의 임의 조합을 이용할 수 있다. 폴리펩타이드는 본원에 개시된 임의의 구현예의 단량체를 2, 3, 4 또는 5개 이상 포함할 수 있을 것으로 추가로 이해될 것이다. 단량체가 3개 이상인 구현예들에서, 단량체 3개 모두 동일할 수 있거나; 단량체 2개는 동일하고 하나는 상이할 수 있거나, 또는 단량체 3개 모두 상이할 수 있다.

[0782] LCB1 및 이의 변이체와 관련한 일 구현예에서,

[0783] Z1은 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

[0784] Z3는 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0785] LCB3 및 이의 변이체와 관련한 다른 구현예에서,

[0786] Z1은 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

[0787] Z3는 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0788] AHB 및 이의 변이체와 관련한 다른 구현예에서,

[0789] Z1은 서열번호 33-34, 100-101, 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

[0790] Z3는 서열번호 33-34, 100-101, 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0791] 일 구현예에서, Z1 및 Z3 중 하나는 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

[0792] Z1 및 Z3 중 다른 하나는 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0793] 다른 구현예에서, Z1 및 Z3 중 하나는 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

[0794] Z1 및 Z3 중 다른 하나는 서열번호 33-34, 100-100, 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0795] 추가적인 구현예에서, Z1 및 Z3 중 하나는 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고;

[0796] Z1 및 Z3 중 다른 하나는 서열번호 33-34, 100-100, 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0797] 본원에 개시된 임의의 다른 구현예들에 대한 다른 구현예에서, 폴리펩타이드는 단량체 3개 이상 (즉, 3, 4 또는 5개 이상)을 포함한다. 이러한 일 구현예에서, 폴리펩타이드는 식 B1-B2-Z1-Z2-Z3-B3-B4를 포함하고, 여기서:

[0798] Z1, Z2, 및 Z3는 상기에서 정의된 바와 같이 정의되고;

[0799] B2 및 B3는 선택적인 아미노산 링커를 포함하고;

[0800] B1 및 B4 중 하나 또는 둘다는 독립적으로 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하되, B1 및 B4 중 하나는 생략될 수 있다. 일 구현예에서, B1 및 B4 중 하나가 생략된다. 다른 구현예에서, B1 및 B4 둘다 존재한다. 일 구현예에서, B1 및 B4는 독립적으로 서열번호 1-17, 19-21, 23-34 및 100-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다. 이러한 구현예에서, B1 및 B4는 서로 동일하거나 또는 서로 상이할 수 있다. 일 구현예에서, 존재하는 경우 B1 및 존재하는 경우 B4는 Z1 및 Z3 중 하나 또는 둘다와 동일하다. 다른 구현예에서, 존재하는 경우 B1 및 존재하는 경우 B4는 Z1 및 Z3 중 어느 하나와 동일하지 않다.

[0801] 일 구현예에서, 존재하는 경우 B1 및 존재하는 경우 B4는 독립적으로 서열번호 1-10, 13-17, 19-21, 33-34, 100-101, 및 102-164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0802] 다른 구현예에서, 존재하는 경우 B1 및 존재하는 경우 B4는, 독립적으로 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0803] 추가적인 구현예에서, 존재하는 경우 B1 및 존재하는 경우 B4는, 독립적으로 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0804] 또 다른 구현예에서, 존재하는 경우 B1 및 존재하는 경우 B4는, 독립적으로 서열번호 33-34, 100-101, 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0805] 다양한 구현예들에서, B1 및 B4 둘다 존재하는 경우,

[0806] · B1 및 B4 중 하나는 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고, 다른 하나는 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하거나;

[0807] · B1 및 B4 중 하나는 서열번호 1-10 및 102-136으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고, 다른 하나는 서열번호 33-34, 100-101, 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함거나, 또는

[0808] · B1 및 B4 중 하나는 서열번호 13-17, 19-21 및 137-163으로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하고, 다른 하나는 서열번호 33-34, 100-101, 및 164로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다.

[0809] 다양한 비-제한적인 구현예들에서, 폴리펩타이드는 서열번호 47-60, 193-355 및 454-588로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열, 및 표 8의 우측 칸에 언급된 것들로부터 선택되는 유형을 포함하고, 이러한 유형에서 위치 X1, X2, X3 및 X4는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 아미노산 1개 이상으로 된 임의 서열일 수 있다. 모든 구현예들에서, 폴리펩타이드에서 임의의 N-말단 메티오닌 잔기는 존재하거나 또는 생략될 수 있다. 일 구현예에서, 폴리펩타이드에서 임의의 N-말단 메티오닌 잔기는 생략된다.

[0810] >LCB1-6GS-LCB1: DKEWILQKIY EIMRLLDELG HAEASMRVSD LIYEFMKKGD ERLLEEAERL LEEVERGGSG GSDKEWILQK IYEIMRLLDE LGHAEASMRV SDLIYEFMKK GDERLLEEAE RLLEEVER (서열번호 47)

[0811] >LCB1-12GS-LCB1: DKEWILQKIY EIMRLLDELG HAEASMRVSD LIYEFMKKGD ERLLEEAERL LEEVERGGSG GSGSGGSGDK EWILQKIYEI MRLLDELGHA EASMRVSDLI YEFMKKGDER LLEEAERLLE EVER (서열번호 48)

[0812] >LCB1-24GS-LCB1: DKEWILQKIY EIMRLLDELG HAEASMRVSD LIYEFMKKGD ERLLEEAERL LEEVERGGGS GGGSSGGSGG SSGGGSGGGS DKEWILQKIY EIMRLLDELG HAEASMRVSD LIYEFMKKGD ERLLEEAERL LEEVER (서열번호 49)

[0813] >LCB1-36GS-LCB1: DKEWILQKIY EIMRLLDELG HAEASMRVSD LIYEFMKKGD ERLLEEAERL LEEVERGGGS GGGSGGSGGS GGGSGGGSGS GGSGGGGSGG GSDKEWILQK IYEIMRLLDE LGHAEASMRV SDLIYEFMKK GDERLLEEAE RLLEEVER (서열번호 50)

[0814] >LCB1_v1.1-GSLCB1_v1.1(1GS1): DKENILQKIY EIMKTLDQLG HAEASMQVSD LIYEFMKQGD ERLLEEAERL LEEVERGGGG SGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SDKENILQKI YEIMKTLDQL GHAEASMQVS DLIYEFMKQG DERLLEEAER LLEEVER (서열번호 51)

[0815] >LCB1_v1.1-PRO-LCB1_v1.1(1PRO1): DKENILQKIY EIMKTLDQLG HAEASMQVSD LIYEFMKQGD ERLLEEAERL LEEVERAGSG GSGGSGGSPV PSTPPTPSPS TPPTPSPSPV PSTPPTPSPS TPPTPSPSPV PSTPPTPSPS TPPTPSPSAS GDKENILQKI YEIMKTLDQL GHAEASMQVS DLIYEFMKQG DERLLEEAER LLEEVER (서열번호 52)

[0816] >LCB3_v1.2-GS3-LCB3_v1.2(3GS3): NDDELHMQMT DLVYEALHFA KDEEIQKHVF QLFEKATKAY KNKDRQKLEK VVEELKELLE RLLSGGGGSG GGGSGGGGSG GGGSGGGGSG GGGSGGGGSG GGGSGGGGSG GGGSGGGGSG GGGSGGGGSN DDELHMQMTD LVYEALHFAK DEEIQKHVFQ LFEKATKAYK NKDRQKLEKV VEELKELLER LLS (서열번호 53)

[0817] >LCB3_v1.2-PRO-LCB3_v1.2(3PRO3): NDDELHMQMT DLVYEALHFA KDEEIQKHVF QLFEKATKAY KNKDRQKLEK VVEELKELLE RLLSAGSGGS GGSGGSPVPS TPPTPSPSTP PTPSPSPVPS TPPTPSPSTP PTPSPSPVPS TPPTPSPSTP PTPSPSASGN DDELHMQMTD LVYEALHFAK DEEIQKHVFQ LFEKATKAYK NKDRQKLEKV VEELKELLER LLS (서열번호 54)

[0818] >LCB1_v1.1-GS-LCB3_v1.2(1GS3): DKENILQKIY EIMKTLDQLG HAEASMQVSD LIYEFMKQGD ERLLEEAERL LEEVERGGGG SGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SNDDELHMQM TDLVYEALHF AKDEEIQKHV FQLFEKATKA YKNKDRQKLE KVVEELKELL ERLLS (서열번호 55)

[0819] >LCB3_v1.2-GS-LCB1_v1.1(3GS1): NDDELHMQMT DLVYEALHFA KDEEIQKHVF QLFEKATKAY KNKDRQKLEK VVEELKELLE RLLSGGGGSG GGGSGGGGSG GGGSGGGGSG GGGSGGGGSG GGGSGGGGSG GGGSGGGGSG GGGSGGGGSD KENILQKIYE IMKTLDQLGH AEASMQVSDL IYEFMKQGDE RLLEEAERLL EEVER (서열번호 56)

[0820] >LCB3_v1.2-10GS-LCB1_v1.1(LCB3-GS10-LCB1): NDDELHMQMT DLVYEALHFA KDEEIQKHVF QLFEKATKAY KNKDRQKLEK VVEELKELLE RLLSGGSGGS GGSGDKENIL QKIYEIMKTL DQLGHAEASM QVSDLIYEFM KQGDERLLEE AERLLEEVER (서열번호 57)

[0821] >LCB1_v1.1-PRO-LCB3_v1.2(1PRO3): DKENILQKIY EIMKTLDQLG HAEASMQVSD LIYEFMKQGD ERLLEEAERL LEEVERAGSG GSGGSGGSPV PSTPPTPSPS TPPTPSPSPV PSTPPTPSPS TPPTPSPSPV PSTPPTPSPS TPPTPSPSAS GNDDELHMQM TDLVYEALHF AKDEEIQKHV FQLFEKATKA YKNKDRQKLE KVVEELKELL ERLLS (서열번호 58)

[0822] >LCB3_v1.2-PRO-LCB1_v1.1(3PRO1): NDDELHMQMT DLVYEALHFA KDEEIQKHVF QLFEKATKAY KNKDRQKLEK VVEELKELLE RLLSAGSGGS GGSGGSPVPS TPPTPSPSTP PTPSPSPVPS TPPTPSPSTP PTPSPSPVPS TPPTPSPSTP PTPSPSASGD KENILQKIYE IMKTLDQLGH AEASMQVSDL IYEFMKQGDE RLLEEAERLL EEVER (서열번호 59)

[0823] >36175(5_LCB1_링커14): DKEWILQKIY EIMRLLDELG HAEASMRVSD LIYEFMKKGD ERLLEEAERL LEEVERGGSG SSGGSGSGSG DKEWILQKIY EIMRLLDELG HAEASMRVSD LIYEFMKKGD ERLLEEAERL LEEVERGGSG SSGGSGSGSG DKEWILQKIY EIMRLLDELG HAEASMRVSD LIYEFMKKGD ERLLEEAERL LEEVERGGSG SSGGSGSGSG DKEWILQKIY EIMRLLDELG HAEASMRVSD LIYEFMKKGD ERLLEEAERL LEEVERGGSG SSGGSGSGSG DKEWILQKIY EIMRLLDELG HAEASMRVSD LIYEFMKKGD ERLLEEAERL LEEVER (서열번

호 60)

[0824] **표 8. Daisy 쇄 디자인**

표 6

[0825]

명칭	단백질	주석: X1, X2, X3 및 X4는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 아미노산 1개 이상으로 된 임의 서열일 수 있음
1GS1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 193)	X1-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 4)-X2-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 4)
1PRO1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 194)	X1-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 4)-X2-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 4)
3GS3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 195)	X1-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (서열번호 15)-X2-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (서열번호 15)
3PRO3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 196)	X1-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 15)-X2-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 15)
1GS3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 197)	X1-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 4)-X2-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 15)
3GS1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 198)	X1-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 15)-X2-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 4)
1PRO3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 199)	X1-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 4)-X2-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 15)
3PRO1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 200)	X1-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 15)-X2-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 4)
CSL-LCB1-GS15-LCB1	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSGGGGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 201)	X1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)
CSL-LCB3-GS15-LCB3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 202)	X1-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS (서열번호 13)-X2-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)

CSL-LCB1-GS20-LCB1	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSGGGGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 203)	X1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)
CSL-LCB3-GS20-LCB3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 204)	X1-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X2-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)
CSL-LCB1-GS20-LCB1-GS20-LCB1	MEKKISAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSGSGSSGSGSSGSGSSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSSGGSSSGGSSSGGSSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 205)	X1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X3-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)
CSL-LCB3-GS20-LCB3-GS20-LCB3	MEKKISAWSHPQFEKGGSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSSGSGSSGSGSSGSGSSGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSSGGSSSGGSSSGGSSSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 206)	X1-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X2-DDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X3-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)
CSL-LCB1-XTENx2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSAGGSPAGSPTSTGTSTSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 207)	X1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)
CSL-LCB1-XTENx3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSAGGSPAGSPTSTGTSGSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSAGGSPAGSPTSTGTSGSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 208)	x1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X3-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)
CSL-LCB3-XTENx2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSAGGSPAGSPTSTGTSGSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 209)	X1-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X2-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)
CSL-LCB3-XTENx3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSAGGSPAGSPTSTGTSGSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSAGGSPAGSPTSTGTSGSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 210)	X1-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X2-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X3-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)
C-LCB1-GS20-LCB1-GS20-LCB1-LS	MEKKISSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSGSGSSGSGSSGSGSSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSGGSSSGGSSSGGSSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSGSSGSAWSHPQFEK(서열번호 211)	X1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X3-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1) -X4
C-LCB3-GS20-LCB3-GS20-LCB3-LS	MEKKISSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSGSGSSGSGSSGSGSSGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSSGGSSSGGSSSGGSSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGSGSSGSAWSHPQFEK(서열번호 212)	X1-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X2-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X3-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X4
CSL-LCB1-XTEN25x3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPSGSGTGGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPSGSGTGGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 213)	X1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)-X3 DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(서열번호 1)

CSL-LCB3-XTEN25x3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGSSAGSPTSTGTSSATPSGSGTGGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGSSAGSPTSTGTSSATPSGSGTGGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 214)	X1NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X2-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)-X3-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(서열번호 13)
LCB1_v1.3_GS_2X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGGGSSGGGSSGGGSSGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 215)	X1-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 8)-X2-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)
LCB1_v1.3_XTEN_2X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 216)	X1-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X2-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)
LCB1_v1.3_EAAAK_2X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGEAAAKEAAAKEAAAKGSSGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 217)	X1-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X2-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)
LCB1_v1.3_Pro_2X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 218)	X1-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X2-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)
LCB1_v1.3_Ub_2X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 219)	X1-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X2-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)
LCB1_v1.3_XTEN_3X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 220)	X1-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X2-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X3-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)
LCB1_v1.3_EAAAK_3X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGEAAAKEAAAKEAAAKGSSGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGEAAAKEAAAKEAAAKGSSGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 221)	X1-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X2-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X3-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)
LCB1_v1.3_Pro_3X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 222)	X1-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X2-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X3-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)
LCB1_v1.3_Ub_3X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 223)	X1-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X2-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)-X3-DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 8)
1GS1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 224)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)

1Pro1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 225)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
3GS3_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 226)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)
3Pro3_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 227)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)
1GS1_CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 228)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
1Pro1_CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 229)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
3GS3_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 230)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
3Pro3_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 231)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
1GS1GS1_NTS	MEKKISAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 232)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
1Pro1Pro1_NTS	MEKKISAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 233)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
3GS3GS3_NTS	MEKKISAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 234)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)
3Pro3Pro3_NTS	MEKKISAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 235)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)
1GS1GS1_CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEK(서열번호 236)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4

1Pro1Pro1_CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEK(서열번호 237)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4
3GS3GS3_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGSSGSAWSHPQFEK(서열번호 238)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X4
3Pro3Pro3_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGSSGSAWSHPQFEK(서열번호 239)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X4
1GS3_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 240)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)
1Pro3_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 241)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)X-2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)
3GS1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 242)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
3Pro1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 243)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
1GS3_CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 244)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
1Pro3_CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 245)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
3GS1_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 246)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
3Pro1_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 247)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
3-GS10-1-L_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 248)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)

3-GS10-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 249)	X1-}NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
3-GS15-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 250)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
3-GS20-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 251)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
1-GS10-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 252)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
1-GS15-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 253)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
1-GS20-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 254)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-1_GS10	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 255)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)
2-1_GS15	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 256)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)
2-1_GS20	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 257)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)
2-2-1_GS10	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 258)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3
2-2-1_GS15	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 259)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3
2-2-1_GS20	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 260)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3
2-2_GS10	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 261)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)

2-2_GS15	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 262)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-2_GS20	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 263)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-2-2_GS10	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 264)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-2-2_GS15	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 265)	X1ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-2-2_GS20	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 266)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
AHB2-AHB2_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 267)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
LCB3-LCB1_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 268)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)
AHB2-LCB1_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 269)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)
AHB2_3x_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 270)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)

3-2-1_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 271)	X1NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3
2-3-1_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 272)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
1-1-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 273)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-2-2_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 274)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
3-3-3_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 275)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)
2-2-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 276)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDE-REIREIEEEARRILEHLEELARK(서열번호 101)X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-2_PAS16	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 277	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-2_PAS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 278)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
3-1_PAS16	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 279)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)
3-1_PAS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 280)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)

2-1_PAS16	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 281)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)
2-1_PAS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 282)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)
3v2.3-2-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 283)	X1-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS (서열번호 163)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3
2-3v2.3-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 284)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3
2-2-2_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 285)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)
1-1-1_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTRGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTRGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTR(서열번호 286)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (서열번호 125)
3v2.3-2-1_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 287)	X1-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X3
2-3v2.3-1_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(서열번호 288)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3
3v2.3-2-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 289)	X1-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS (서열번호 163)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3v2.3-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 290)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)

3v2.3-2-1_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 291)	X1-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3v2.3-1_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 292)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3v2.3-1_PAS24_N-His-TEV	MEKKIHHHHHHSGENLYFQSGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 293)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3v2.3-1_PAS24_ompT_N-His-TEV	MEKKIHHHHHHSGENLYFQSGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 294)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3-1_PAS24_NTSF	MEKKIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 295)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3-1_PAS24_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 296)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3-1_PAS24_NTSM	MEKKIEQKLISEEDLGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 297)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS24-3-PAS16-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 298)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS16-3-PAS16-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 299)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)

2-PAS11-3-PAS16-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 300)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS24-3-PAS11-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 301)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS16-3-PAS11-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 302)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS11-3-PAS11-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 303)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-2_G4	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 304)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-2_G2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 305)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-3_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 306)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)
2-3_PAS16	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 307)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)
2-3_PAS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 308)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(서열번호 163)
1-2-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGASPAAPAPASPAAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 309)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)

2-PAS24-3-PAS24-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 310)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS24-3-PAS16-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 311)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS16-3-PAS24-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGG (서열번호 155)GGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 312)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS16-3-PAS16-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 313)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS11-3-PAS16-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 314)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS24-3-PAS11-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 315)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS16-3-PAS11-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 316)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-PAS11-3-PAS11-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 317)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3-1_PAS7	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 318)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)

2-3-1_GS7	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 319)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3-1_GS5	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 320)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3-1_GS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGSGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 321)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-2-2_PAS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 322)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-2-2_GS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 323)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-2-2_GS8	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 324)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-2-2_GS5	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 325)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
2-3-1_GGGGS15	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 326)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)

2-3-1_GGGGS12	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 327)	X1-E-LEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3-1_GGGGS9	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 328)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
2-3-1_GGGGS7	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 329)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLG (서열번호 135)HAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
1-1_GGGGS25	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 330)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
1-1_GGGGS20	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 331)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
1-1_GGGGS15	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 332)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
1-1_GGGGS10	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 333)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
2-1_GGGGS10	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 334)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
3-1_GGGGS10	MEKKIGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 335)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
2-3_GGGGS10	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 336)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
3-2_GGGGS10	MEKKIGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEARRILEHLEELARKGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 337)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3
2-3-1_GGGGS10	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 338)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4

3-2-1_GGGGS10	MEKKIGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 339)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4
2-3-1_GGGGS15	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 340)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4
3-2-1_GGGGS15	MEKKIGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 341)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4
LCB3-LCB1_PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 342)	X1NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
AHB2-LCB1_PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 343)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3
AHB2-LCB3_PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 344)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
LCB3-AHB2_PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 345)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3
AHB2-LCB3-LCB1_PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 346)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4
LCB3-AHB2-LCB1_PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 347)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4
LCB3-AHB2-LCB1_PAS24	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 348)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4
AHB2v2-LCB1_PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 349)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X3

AHB2v2-LCB3_PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 350)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
LCB3-AHB2v2_PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 351)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART (서열번호 164)-X3
AHB2v2-LCB3-LCB1_PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 352)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR (서열번호 135)-X4
LCB3-AHB2v2-LCB1_PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 353)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4
AHB2v2-LCB3-LCB1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 354)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
LCB3-AHB2v2-LCB1_PAS24	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 355)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X4

[0826] **표 8A**

표 7

[0827]

서열번호	명칭	서열
51	1GS1	DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
52	1PRO1	DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
53	3GS3	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
54	3PRO3	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
55	1GS3	DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
56	3GS1	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER

58	1PRO3	DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGSGGSPVPSTPPTPS PSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEI QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
59	3PRO1	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGSGGSGGSPV PSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGDKENILQKIYEIMKTLD QLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
454	CSL-LCB1-GS15-LCB1	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSDKEWILQ KIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER
455	CSL-LCB3-GS15-LCB3	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGG SNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS
456	CSL-LCB1-GS20-LCB1	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGGSGGGGSGGGGSGGGGSDK EWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER
457	CSL-LCB3-GS20-LCB3	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGG SGGGGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS
458	CSL-LCB1-GS20-LCB1-GS20-LCB1	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSGSGSSGSGSSGSGSSGSDK EWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSSGGSSSGGSSSGGSSSGDKEW ILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER
459	CSL-LCB3-GS20-LCB3-GS20-LCB3	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSGSGSSGSGSSG SGSSGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSSGGSS SGGSSSGGSSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS
460	CSL-LCB1-XTENx2	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSAGGSPAGSPTSTGTSTSGDK EWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER
461	CSL-LCB1-XTENx3	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSAGGSPAGSPTSTGTSGSGDK EWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSAGGSPAGSPTSTGTSGSGDKEW ILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER
462	CSL-LCB3-XTENx2	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSAGGSPAGSPTST GTSGSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS
463	CSL-LCB3-XTENx3	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSAGGSPAGSPTST GTSGSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSAGGSPA GSPTSTGTSGSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS
458	C-LCB1-GS20-LCB1-GS20-LCB1-LS	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSGSGSSGSGSSGSGSSGSDK EWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSSGGSSSGGSSSGGSSSGDKEW ILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER
459	C-LCB3-GS20-LCB3-GS20-LCB3-LS	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSGSGSSGSGSSG SGSSGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSSGGSS SGGSSSGGSSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS
464	CSL-LCB1-XTEN25x3	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPSGSG TGGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPS GSGTGGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER
465	CSL-LCB3-XTEN25x3	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGSSAGSPTSTGTS SATPSGSGTGGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGS SAGSPTSTGTSSATPSGSGTGGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELK ELLERLLS
466	LCB1_v1.3_GS_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGGGSSGGGSSGGGSSGGG SSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
467	LCB1_v1.3_XTEN_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPSGSG TGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
468	LCB1_v1.3_EAAAK_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGEAAAKEAAAKEAAAKGS SGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
469	LCB1_v1.3_Pro_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGPSTPPTPSPSTPPTPSP SPGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
470	LCB1_v1.3_Ub_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGQIFVKTLTGKTITLEVE PSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGSSGDKENILQKIYEIMKT LEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
471	LCB1_v1.3_XTEN_3X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPSGSG TGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPS GSGTGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
472	LCB1_v1.3_EAAAK_3X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGEAAAKEAAAKEAAAKGS SGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGEAAAKEAAAKEAAA KGSSGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
473	LCB1_v1.3_Pro_3X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGPSTPPTPSPSTPPTPSP SPGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGPSTPPTPSPS TPPTPSPSPGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER

474	LCB1_v1.3_Ub_3X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSSGQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
475	1GS1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
476	1Pro1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
477	3GS3_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
478	3Pro3_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
475	1GS1_CTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
476	1Pro1_CTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
477	3GS3_CTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
478	3Pro3_CTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
479	1GS1GS1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
480	1Pro1Pro1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
481	3GS3GS3_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
482	3Pro3Pro3_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
479	1GS1GS1_CTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
480	1Pro1Pro1_CTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
481	3GS3GS3_CTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
482	3Pro3Pro3_CTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
483	1GS3_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
484	1Pro3_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
485	3GS1_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
486	3Pro1_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
483	1GS3_CTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
484	1Pro3_CTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
485	3GS1_CTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR

486	3Pro1_CTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSP STPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
487	3-GS10-1-L_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGSGGDKEN VLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
488	3-GS10-1_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGDKEN VLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
489	3-GS15-1_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSS GDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
490	3-GS20-1_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSS GGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
491	1-GS10-1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
492	1-GS15-1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGDKENVLQ KIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
493	1-GS20-1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
494	2-1_GS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
495	2-1_GS15	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
496	2-1_GS20	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
497	2-2-1_GS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEE LARKGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
498	2-2-1_GS15	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEV KR
499	2-2-1_GS20	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEE ARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLL EEAERLLEEVKR
500	2-2_GS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEE LARK
501	2-2_GS15	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARK
502	2-2_GS20	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEE ARRILEHLEELARK
503	2-2-2_GS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEE LARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARR ILEHLEELARK
504	2-2-2_GS15	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDERE IREIEEEARRILEHLEELARK
505	2-2-2_GS20	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS SGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEE ARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMML ELIKSDDEREIREIEEEARRILEHLEELARK
506	AHB2-AHB2_PAS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARK
507	LCB3-LCB1_PAS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPA APAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
508	AHB2-LCB1_PAS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
509	AHB2_3x_PAS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFN WWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK

510	3-2-1_PAS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPA APAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH LEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEA ERLLEEVKR
511	2-3-1_PAS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEA ERLLEEVKR
512	1-1-1_PAS24	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGASPAAPAPASPAAPSAPA GGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGASPAAPAPASPAAPSA PAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
509	2-2-2_PAS24	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFN WWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
513	3-3-3_PAS24	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPA APAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGAS PAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKEL LERLLS
514	2-2-1_PAS24	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFM KTKDENLLEEAERLLEEVKR
515	2-2_PAS16	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPASPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRI LEHLEELARK
516	2-2_PAS11	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK
517	3-1_PAS16	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPA GGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
518	3-1_PAS11	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKE NVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
519	2-1_PAS16	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
520	2-1_PAS11	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
521	3v2.3-2-1_PA S24	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPA APAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH LEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEA ERLLEEVKR
522	2-3v2.3-1_PA S24	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE LLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEA ERLLEEVKR
523	2-2-2_PAS24_ ompT	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGA SPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFN WWATEMMLELIKSDDEREIREIEEEAARILEHLEELART
524	1-1-1_PAS24_ ompT	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTRGGASPAAPAPASPAAPSAPA GGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTRGGASPAAPAPASPAAPSA PAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTR
525	3v2.3-2-1_PA S24_ompT	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPA APAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEH LEELARTGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEA ERLLEEVKR
526	2-3v2.3-1_PA S24_ompT	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGA SPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE LLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEA ERLLEEVKR
527	3v2.3-2-1_PA S24	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPA APAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH LEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEA ERLLEEVKR

528	2-3v2.3-1_PAS24	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
529	3v2.3-2-1_PAS24_ompT	NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
530	2-3v2.3-1_PAS24_ompT	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
538	2-3v2.3-1_PAS24_N-His-TEV	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
530	2-3v2.3-1_PAS24_ompT_N-His-TEV	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
531	2-3-1_PAS24_NTSF	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
531	2-3-1_PAS24_NTS3F	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
531	2-3-1_PAS24_NTSM	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
532	2-PAS24-3-PAS16-1_NTS3F	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
533	2-PAS16-3-PAS16-1_NTS3F	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
534	2-PAS11-3-PAS16-1_NTS3F	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
535	2-PAS24-3-PAS11-1_NTS3F	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
536	2-PAS16-3-PAS11-1_NTS3F	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
537	2-PAS11-3-PAS11-1_NTS3F	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
538	2-2_G4	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
539	2-2_G2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
540	2-3_PAS24	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS
541	2-3_PAS16	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS
542	2-3_PAS11	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS
543	1-2-1_PAS24	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR

544	2-PAS24-3-PAS24-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
545	2-PAS24-3-PAS16-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
546	2-PAS16-3-PAS24-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
547	2-PAS16-3-PAS16-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
548	2-PAS11-3-PAS16-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
549	2-PAS24-3-PAS11-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
550	2-PAS16-3-PAS11-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
551	2-PAS11-3-PAS11-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
552	2-3-1_PAS7	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
553	2-3-1_GS7	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
554	2-3-1_GS5	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
555	2-3-1_GS11	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGSGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
556	2-2-2_PAS11	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
557	2-2-2_GS11	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
558	2-2-2_GS8	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
559	2-2-2_GS5	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
560	2-3-1_GGGGS15	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
561	2-3-1_GGGGS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
562	2-3-1_GGGGS9	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR

563	2-3-1_GGGGS7	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGG SGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGDKE NVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
564	1-1_GGGGS25	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGGGSGGGGSGGGG SGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
565	1-1_GGGGS20	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGGGSGGGGSGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
566	1-1_GGGGS15	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGGGSGGDKENVLQ KIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
567	1-1_GGGGS10	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
568	2-1_GGGGS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS GGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
569	3-1_GGGGS10	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGDKEN VLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
570	2-3_GGGGS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS GGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
571	3-2_GGGGS10	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGELEE QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
572	2-3-1_GGGGS1 0	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS GGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGG SGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
573	3-2-1_GGGGS1 0	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGELEE QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGG SGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
560	2-3-1_GGGGS1 5	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGS GGGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG SGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
574	3-2-1_GGGGS1 5	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGSG GELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG SGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
575	LCB3-LCB1_PA S12	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
576	AHB2-LCB1_PA S12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
577	AHB2-LCB3_PA S12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
578	LCB3-AHB2_PA S12	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGEL EEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
579	AHB2-LCB3-LC B1_PAS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGA SPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASP AAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
580	LCB3-AHB2-LC B1_PAS12	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGEL EEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASP AAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
581	LCB3-AHB2-LC B1_PAS24	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPA APAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH LEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEA ERLLEEVKR
582	AHB2v2-LCB1_ PAS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGA SPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
583	AHB2v2-LCB3_ PAS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGA SPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
584	LCB3-AHB2v2_ PAS12	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGEL EEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART
585	AHB2v2-LCB3- LCB1_PAS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGA SPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASP AAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
586	LCB3-AHB2v2- LCB1_PAS12	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGEL EEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASP AAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
587	AHB2v2-LCB3- LCB1_PAS24	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGA SPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEA ERLLEEVKR

588	LCB3-AHB2v2-LCB1_PAS24	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR

[0828] 일부 구현예에서, 폴리펩타이드는 표 8의 가운데 칸에 언급된 것들로부터 선택되는 유형의 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다. 이들 구현예에서, X1, X2, X3 (유형에 언급된 경우) 및 X4 (유형에 언급된 경우)는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 아미노산 1개 이상으로 된 임의 서열일 수 있다. 예를 들어, 표 8에서 제1열 가운데 칸의 유형은 X1-(서열번호 4)-X2-(서열번호 4)이다. 이러한 구현예에서, X2는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는, (예를 들어) 적절한 것으로 간주되는 임의의 적절한 길이와 아미노산 조성을 가진 아미노산 링커를 포함할 수 있다. X1은 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 리더 서열, 검출가능한 태그, 정제 태그 등을 포함하나 이들로 제한되는 것은 아닌 적절한 것으로 간주되는 임의의 아미노산 잔기 또는 잔기들을 포함할 수 있다.

[0829] 다른 예로서, 표 8에서 마지막 열 가운데 칸에서 유형은 X1-(서열번호 155)-X2-(서열번호 164)-X3-(서열번호 135)-X4이다. 이러한 구현예에서, X2 및 X3는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는, (예를 들어) 적절한 것으로 간주되는 임의의 적절한 길이와 아미노산 조성을 가진 아미노산 링커를 포함할 수 있다. X1 및 X4는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 리더 서열, 검출가능한 태그, 정제 태그, 분비 신호 등을 포함하나 이들로 제한되는 것은 아닌 적절한 것으로 간주되는 임의의 아미노산 잔기 또는 잔기들을 포함할 수 있다.

[0830] 일부 구현예에서, 단량체 도메인들 사이에 존재하는 선택적인 도메인이 존재하고, 아미노산 링커를 포함할 수 있다. 이러한 구현예에서, (a) 상기 제1 예에서, X2는 존재할 것이며, 임의의 적절한 길이와 아미노산 조성을 가진 아미노산 링커를 포함하고, X1은 존재하거나 또는 생략될 수 있으며; (b) 상기 제2 예에서, X2 및 X3 중 하나 또는 둘다 존재할 것이며, 임의의 적절한 길이와 아미노산 조성을 가진 아미노산 링커를 포함하고, X1 및 X4는 독립적으로 존재할 수 있거나 또는 생략될 수 있다.

[0831] 본원에 개시된 폴리펩타이드 구현예들 중 임의 구현예 또는 구현예 조합에서, 폴리펩타이드는 하나 이상의 추가적인 기능성 펩타이드 도메인을 추가로 포함할 수 있다. 임의의 이러한 추가적인 기능성 펩타이드 도메인은 의도한 목적에 적절한 경우에 이용할 수 있다. 다양한 비-제한적인 구현예에서, 추가적인 기능성 펩타이드 도메인은 예를 들어 표적화 도메인, 검출가능한 도메인, 스캐폴드 도메인, 분비 신호, Fc 도메인 또는 추가의 치료학적 펩타이드 도메인을 포함할 수 있다. 일 구현예에서, 추가적인 기능적인 도메인은 Fc 도메인을 포함하며, 이는 비-제한적으로 서열번호 64의 아미노산 서열을 포함하는 Fc 도메인을 포함한다.

[0832] **Fc 도메인:**
EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (서열번호 64)

[0833] 다른 구현예에서, 추가되는 기능성 도메인은 올리고머화 도메인을 포함할 수 있다. 임의의 올리고머화 도메인은 의도한 목적에 적합한 올리고머를 생성하기에 적합한 바와 같이 이용할 수 있다. 비-제한적인 일 구현예에서, 올리고머화 도메인은 동형삼량체화 도메인 (homotrimerization domain)을 포함할 수 있다. 올리고머화 도메인의 예는 서열번호 179-189 및 589-594로 이루어진 군으로부터 선택되는 아미노산 서열을 포함할 수 있다.

[0834] 1rfo: GYIPEAPRDGQAYVRKDGEWVLLSTFL (서열번호 179)

[0835] 1na0_int2-R3: EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 180)

[0836] 1na0_int2:
EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 181)

[0837] 6msr: GSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK(서열번호 182)

[0838] 1gcm: RMKQIEDKIEEILSKIYHIENEIARIKKLIGER (서열번호 183)

[0839] pRO-2-noHis: GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK(서열번호 184)

[0840] 1na0_3: NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 185)

[0841] 4pn9: GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (서열번호 186)

[0842] SB175: SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)

[0843] SB175.1: SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK(서열번호 188)

[0844] SB175.2: SEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR(서열번호 189)

[0845] 5L6HC3_1: SEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR (서열번호 589)

[0846] 36729.2: EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL(서열번호 590)

[0847] 1na0_int2-R3 v2: EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAKQNLGNAKQKQ (서열번호 591)

[0848] 1na0_int2-R3 v3: EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEIEYYQKALELDPNNAEAKQNLGNAKQKQ (서열번호 592)

[0849] 1na0_int2 v2: EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNKQKQ(서열번호 593)

[0850] 6msr v2: EYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIK(서열번호 594).

[0851] 일 구현예에서, 폴리펩타이드는 서열번호 356-453 및 595-692로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열, 및 표 9의 우측 칸에 언급된 것들로부터 선택되는 유형을 포함하되, 유형에서 위치 X1, X2, X3 및 X4는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 아미노산 1개 이상으로 된 임의 서열일 수 있다. 모든 구현예들에서, 폴리펩타이드에 임의의 N-말단 메티오닌 잔기가 존재하거나 또는 생략될 수 있다. 일 구현예에서, 폴리펩타이드에서 임의의 N-말단 메티오닌 잔기가 생략된다.

[0852] **표 9. 동형삼량체 디자인**

표 8

[0853]

명칭	단백질	**주석:** X1, X2, X3 및 X4는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 아미노산 1개 이상으로 된 임의 서열일 수 있음
AHB2-6GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 356)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL (서열번호 179)-X3
AHB2-28GS-AHB2-6GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 357)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X4

AHB2-5GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGGYIPEAPRDGQAAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 358)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X3
AHB2-4GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 359)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X3
AHB2-3GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 360)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X3
AHB2-28GS-AHB2-3GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 361)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X4
AHB2-4GS-5L6HC3_1	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 362)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR (서열번호 589)
AHB2-5GS-5L6HC3_1	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 363)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR (서열번호 589)
AHB2-28GS-AHB2-4GS-5L6HC3_1	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 364)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3
AHB2-28GS-AHB2-5GS-5L6HC3_1	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 365)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3
LCB3-6GS-1rfo	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 366)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X3
LCB3-5GS-1rfo	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 367)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X3
LCB3-4GS-1rfo	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 368)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X3
LCB3-5GS-5L6HC3_1	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 369)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-SEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR (서열번호 589)

LCB3-28GS-LCB3-4GS-5L6HC3_1	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 370)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
LCB3-28GS-LCB3-5GS-5L6HC3_1	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 371)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
36729.2_LCB1v2.2_6GS	MEKKIEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 372)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL (서열번호 590)
36729.2_LCB1v2.2_4GS	MEKKIEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 373)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL (서열번호 590)
36729.2_LCB1v2.2_2GS	MEKKIEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 374)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL (서열번호 590)
LCB3-PAS24-LCB3-4GS-5L6HC3_1	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 375)	-X1NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
LCB3-PAS24-LCB3-5GS-5L6HC3_1	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 376)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
LCB1-10GS-AHB2-4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 377)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X4
LCB1-28GS-AHB2-4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 378)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X4
LCB3-10GS-AHB2-4GS-1rfo	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 379)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X4

LCB3-16GS-AHB2-4GS-1rfo	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 380)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X4
36729.2_6GS_LCB1v2.2-28GS-LCB3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGMEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 381)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)
36729.2_6GS_LCB1v2.2-9GS-LCB3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGMEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 382)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)
36729.2_6GS_LCB1v2.2-28GS-AHB2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGMEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 383)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
36729.2_6GS_LCB1v2.2-9GS-AHB2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGMEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 384)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)
LCB1-10GS-LCB3-4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 385)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X4
LCB1-28GS-LCB3-4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 386)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3 GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X4
AHB2-10GS-LCB3-4GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 387)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X4
AHB2-16GS-LCB3-4GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 388)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 179)-X4

LCB1-9GS-LCB3-5GS-5L6HC3_1	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 389)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
AHB2-9GS-LCB3-5GS-5L6HC3_1	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 390)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X3
AHB2-4GS-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 391)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAKQNLGNAKQKQ (서열번호 591)
AHB2-6GS-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 392)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEIEYYQKALELDPNNAEAKQNLGNAKQKQ (서열번호 _592)
AHB2-4GS-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAKQNLGNKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 393)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNKQKQ (서열번호 593)
AHB2-6GS-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 394)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNKQKQ (서열번호 593)
AHB2-4GS-6msr	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 395)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIK (서열번호 594)
AHB2-6GS-6msr	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 396)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIK (서열번호 594)
36729.2_LCB1v2.2_6GS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 397)	X1-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL (서열번호 590)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
36729.2_LCB1v2.2_4GS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 398)	X1-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL (서열번호 590)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)

36729.2_LCB1v2.2_2GS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR (서열번호 399)	X1-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL (서열번호 590)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
AHB2-8GS-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 400)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 180)-X3
AHB2-8GS-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 401)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 181)-X3
AHB2-8GS-6msr	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 402)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)-X2-GSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK(서열번호 182)-X3
AHB2-10GS-6msr	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 403)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)-X2-GSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK(서열번호 182)-X3
AHB2-10GS-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 404)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 180)-X3
AHB2-10GS-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 405)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 181)-X3
AHB2-4GS-1gcm	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSRMKQIEDKIEEILSKIYHIENEIARIKKLIGERGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 406)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)-X2-RMKQIEDKIEEILSKIYHIENEIARIKKLIGER (서열번호 183)-X3
AHB2-8GS-1gcm	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSRMKQIEDKIEEILSKIYHIENEIARIKKLIGERGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 407)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)-X2-RMKQIEDKIEEILSKIYHIENEIARIKKLIGER(서열번호 183)-X3
AHB2-4GS-pRO-2-noHis	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 408)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)-X2-GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK(서열번호 184)-X3
AHB2-8GS-pRO-2-noHis	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 409)	X1ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (서열번호 101)-X2-GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK(서열번호 184)-X3

AHB2-6GS-1na0_3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 410)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 185)-X3
AHB2-10GS-1na0_3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 411)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 185)-X3
AHB2-6GS-4pn9	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGEIAKSLKEIAKSLKEIAWSLKEIAKSLKGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 412)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (서열번호 186)-X3
AHB2-10GS-4pn9	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGEIAKSLKEIAKSLKEIAWSLKEIAKSLKGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 413)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (서열번호 186)-X3
AHB2-GGGGS5-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 414)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 180)-X3
AHB2-GGGGS7-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 415)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 180)-X3
AHB2-GGGGS9-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGGGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 416)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 180)-X3
AHB2-GGGGS5-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 417)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 181)-X3
AHB2-GGGGS7-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 418)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 181)-X3
AHB2-GGGGS9-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGGGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 419)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 181)-X3

AHB2-GGGGS5-6msr	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 420)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK(서열번호 182)-X3
AHB2-GGGGS7-6msr	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 421)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK(서열번호 182)-X3
AHB2-GGGGS9-6msr	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGGGGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 422)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK(서열번호 182)-X3
AHB2-GGGGS5-1gcm	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGERGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK (서열번호 423)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-RMKQIEDKIEEILSKIYHIENEIARIKKLIGER(서열번호 183)-X3
AHB2-GGGGS7-1gcm	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGERGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 424)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-RMKQIEDKIEEILSKIYHIENEIARIKKLIGER(서열번호 183)-X3
AHB2-GGGGS9-1gcm	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGGGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGERGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 425)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-RMKQIEDKIEEILSKIYHIENEIARIKKLIGER(서열번호 183)-X3
AHB2-GGGGS5-pRO-2-noHis	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 426)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK(서열번호 184)-X3
AHB2-GGGGS7-pRO-2-noHis	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 427)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK(서열번호 184)-X3
AHB2-GGGGS9-pRO-2-noHis	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGGGGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 428)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK(서열번호 184)-X3
AHB2-GGGGS5-1na0_3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 429)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 185)-X3
AHB2-GGGGS7-1na0_3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 430)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 185)-X3

AHB2-GGGGS9-1na0_3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGGGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 431)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG (서열번호 185)-X3
AHB2-GGGGS5-4pn9	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 432)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (서열번호 186)-X3
AHB2-GGGGS7-4pn9	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 433)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (서열번호 186)-X3
AHB2-GGGGS9-4pn9	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGGGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 434)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (서열번호 186)-X3
AHB2-2GS-SB175	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 435)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK (서열번호 187)-X3
AHB2-4GS-SB175	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 436)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)-X3
AHB2-6GS-SB175	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 437)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)-X3
AHB2-2GS-SB175.1	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 438)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK(서열번호 188)-X3
AHB2-4GS-SB175.1	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSSPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 439)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK(서열번호 188)-X3
AHB2-6GS-SB175.1	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGSPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 440)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK(서열번호 188)-X3
AHB2-2GS-SB175.2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 441)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR(서열번호 189)-X3
AHB2-4GS-SB175.2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSSEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 442)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR(서열번호 189)-X3

AHB2-6GS-SB175.2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGSGSEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 443)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK-X2-SEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR(서열번호 189)-X3
SB175-6GS-LCB1v2.2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGGGSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 444)	X1-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
SB175-10GS-LCB1v2.2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGGGSGGGGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 445)	X1-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
SB175.1-6GS-LCB1v2.2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGSPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAKGGGGSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 446)	X1-SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK(서열번호 188)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
SB175.1-10GS-LCB1v2.2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGSPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAKGGGGSGGGGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 447)	X1-SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK(서열번호 188)-X2DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 135)
LCB3-8GS-SB175	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGASPAAPAGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 448)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)-X3
LCB3-6GS-SB175	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGASPAAPAGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 449)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)-X3
LCB3-4GS-SB175	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGASPAAPAGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 450)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)-X3
LCB3-2GS-SB175	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGASPAAPAGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 451)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(서열번호 155)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)-X3
AHB2v1-2GS-SB175	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 452)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(서열번호 101)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)-X3
AHB2v2-2GS-SB175	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(서열번호 453)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(서열번호 164)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 187)-X3

[0854] **표 9A**

표 9

[0855]

서열번호	명칭	서열
595	AHB2-6GS-1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
596	AHB2-28GS-AHB2-6GS-1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL

597	AHB2-5GS-1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGGYIPEAPRDGQAYVRKDGEWVLLSTFL
598	AHB2-4GS-1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGYIPEAPRDGQAYVRKDGEWVLLSTFL
599	AHB2-3GS-1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GGYIPEAPRDGQAYVRKDGEWVLLSTFL
600	AHB2-28GS-AHB2-3 GS-1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDD EREIREIEEEARRILEHLEELARKGSGGYIPEAPRDGQAYVRKDGEWVLLSTFL
601	AHB2-4GS-5L6HC3_ 1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKE ESRKIADESR
602	AHB2-5GS-5L6HC3_ 1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAK EESRKIADESR
603	AHB2-28GS-AHB2-4 GS-5L6HC3_1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDD EREIREIEEEARRILEHLEELARKGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIR EEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR
604	AHB2-28GS-AHB2-5 GS-5L6HC3_1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDD EREIREIEEEARRILEHLEELARKGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTI REEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR
605	LCB3-6GS-1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGYIPEAP RDGQAYVRKDGEWVLLSTFL
606	LCB3-5GS-1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGGYIPEAPR DGQAYVRKDGEWVLLSTFL
607	LCB3-4GS-1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRD GQAYVRKDGEWVLLSTFL
608	LCB3-5GS-5L6HC3_ 1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVA DLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR
609	LCB3-28GS-LCB3-4 GS-5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGSGSGSG SGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERL LSGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIR RAKEESRKIADESR
610	LCB3-28GS-LCB3-5 GS-5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGSGSGSG SGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERL LSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEI RRAKEESRKIADESR
611	36729.2_LCB1v2.2 _6GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
612	36729.2_LCB1v2.2 _4GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSDKENVLQKIYEIMKEL ERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
613	36729.2_LCB1v2.2 _2GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSDKENVLQKIYEIMKELER LGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
614	LCB3-PAS24-LCB3- 4GS-5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASP AAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGS GSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKE ESRKIADESR
615	LCB3-PAS24-LCB3- 5GS-5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASP AAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGS GSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAK EESRKIADESR
616	LCB1-10GS-AHB2-4 GS-1rfo	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSGGELEEQVMHVLD QVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRD GQAYVRKDGEWVLLSTFL
617	LCB1-28GS-AHB2-4 GS-1rfo	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSG SGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
618	LCB3-10GS-AHB2-4 GS-1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGSGGELE EQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSG YIPEAPRDGQAYVRKDGEWVLLSTFL

619	LCB3-16GS-AHB2-4GS-1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGSGSGSG SGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELAR KGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
620	36729.2_6GS_LCB1v2.2-28GS-LCB3	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHM QMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
621	36729.2_6GS_LCB1v2.2-9GS-LCB3	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGNLDELHMQMTDLVYEALHFAKDEEFQ KHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
622	36729.2_6GS_LCB1v2.2-28GS-AHB2	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVM HVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
623	36729.2_6GS_LCB1v2.2-9GS-AHB2	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGELEEQVMHVLDQVSELAHELLHKLTG EELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
624	LCB1-10GS-LCB3-4GS-1rfo	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSGGNLDELHMQMTD LVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEW VLLSTFL
625	LCB1-28GS-LCB3-4GS-1rfo	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSG SGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGY IPEAPRDGQAYVRKDGEWVLLSTFL
626	AHB2-10GS-LCB3-4GS-1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSG YIPEAPRDGQAYVRKDGEWVLLSTFL
627	AHB2-16GS-LCB3-4GS-1rfo	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLL SGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
628	LCB1-9GS-LCB3-5GS-5L6HC3_1	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGNLDELHMQMTDL VYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELARK LLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR
629	AHB2-9GS-LCB3-5GS-5L6HC3_1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGSGSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGS EELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESR KIADESR
630	AHB2-4GS-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAKQN LGNAKQKQ
631	AHB2-6GS-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEIEYYQKALELDPNNAEAK QNLGNAKQKQ
632	AHB2-4GS-1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYN LGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNKQKQ
633	AHB2-6GS-1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNKQKQ
634	AHB2-4GS-6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIK
635	AHB2-6GS-6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGS GSGSGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRA IK
636	36729.2_LCB1v2.2_6GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
637	36729.2_LCB1v2.2_4GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSDKENVLQKIYEIMKEL ERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
638	36729.2_LCB1v2.2_2GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSDKENVLQKIYEIMKELER LGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR

639	AHB2-8GS-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
640	AHB2-8GS-1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
641	AHB2-8GS-6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
642	AHB2-10GS-6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
643	AHB2-10GS-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
644	AHB2-10GS-1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
645	AHB2-4GS-1gcm	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSRMKQIEDKIEEILSKIYHIENEIARIKKLIGER
646	AHB2-8GS-1gcm	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSRMKQIEDKIEEILSKIYHIENEIARIKKLIGER
647	AHB2-4GS-pRO-2-noHis	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK
648	AHB2-8GS-pRO-2-noHis	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK
649	AHB2-6GS-1na0_3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
650	AHB2-10GS-1na0_3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
651	AHB2-6GS-4pn9	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
652	AHB2-10GS-4pn9	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
653	AHB2-GGGGS5-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
654	AHB2-GGGGS7-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
655	AHB2-GGGGS9-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
656	AHB2-GGGGS5-1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
657	AHB2-GGGGS7-1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
658	AHB2-GGGGS9-1na0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
659	AHB2-GGGGS5-6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
660	AHB2-GGGGS7-6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
661	AHB2-GGGGS9-6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK

662	AHB2-GGGGS5-1gcm	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG SGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGER
663	AHB2-GGGGS7-1gcm	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GSGGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGER
664	AHB2-GGGGS9-1gcm	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GGSGGGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGER
665	AHB2-GGGGS5-pRO-2-noHis	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG SGGGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRA IK
666	AHB2-GGGGS7-pRO-2-noHis	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GSGGGGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIV RAIK
667	AHB2-GGGGS9-pRO-2-noHis	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GGSGGGGGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLEL IVRAIK
668	AHB2-GGGGS5-1na0_3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG SGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
669	AHB2-GGGGS7-1na0_3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GSGGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAE AWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
670	AHB2-GGGGS9-1na0_3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GGSGGGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNN AEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
671	AHB2-GGGGS5-4pn9	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG SGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
672	AHB2-GGGGS7-4pn9	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GSGGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
673	AHB2-GGGGS9-4pn9	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GGSGGGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
674	AHB2-2GS-SB175	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK
675	AHB2-4GS-SB175	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GSSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK
676	AHB2-6GS-SB175	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GGSGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK
677	AHB2-2GS-SB175.1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK
678	AHB2-4GS-SB175.1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GSSPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK
679	AHB2-6GS-SB175.1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GGSGSPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK
68041	AHB2-2GS-SB175.2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG SEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR
681	AHB2-4GS-SB175.2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GSSEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR
682	AHB2-6GS-SB175.2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG GGSGSEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR
683	SB175-6GS-LCB1v2.2	SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGGGSGDKENVLQK IYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
684	SB175-10GS-LCB1v2.2	SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLKGGGGSGGGGSDKEN VLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
685	SB175.1-6GS-LCB1v2.2	SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAKGGGGSGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
686	SB175.1-10GS-LCB1v2.2	SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAKGGGGSGGGGSDKENVLQKIY EIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
687	LCB3-8GS-SB175	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGSEALE ELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK
688	LCB3-6GS-SB175	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGSEALEEL EKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK
689	LCB3-4GS-SB175	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSSEALEELEK ALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK
690	LCB3-2GS-SB175	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSEALEELEKAL RELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK

691	AHB2v1-2GS-SB175	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGG SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK
692	AHB2v2-2GS-SB175	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGG SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK

[0856] 일부 구현예에서, 폴리펩타이드는 표 9의 중간 칸에 언급된 것들로부터 선택되는 유형의 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함한다. 이들 구현예에서, X1, X2, X3 (유형에 언급된 경우) 및 X4 (유형에 언급된 경우)는 존재하거나 또는 생략될 수 있으며, 존재하는 경우에는 표 8에 열거된 구현예에 전술된 바와 같이, 아미노산 1개 이상으로 된 임의 서열일 수 있다. 일부 구현예에서, 단량체 도메인 사이에 존재하는 선택적인 도메인이 존재하고, 표 8에 열겨된 구현예들에 대해 전술한 바와 같이 아미노산 링커를 포함할 수 있다.

[0857] 다른 구현예에서, 폴리펩타이드는 서열번호 693-701로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함하되, 임의의 N-말단 메티오닌 잔기가 생략되거나 또는 존재할 수 있으며, 괄호 안 잔기는 존재하거나 또는 생략될 수 있으며 (바람직하게는 생략됨), 동일성 % 결정에 고려되지 않는다. 일 구현예에서, N-말단 메티오닌 잔기가 생략되고, 선택적인 잔기가 생략된다.

[0858] **표 9B**

표 10

[0859]

명칭	서열
C389_AHB2v1_2GS-SB175	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSEAL EELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK (서열번호 693)
AHB2v2_12PAS_LCB3v2.2_12PAS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPA APAPGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGG DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR (서열번호 694)
AHB2v2_24PAS_LCB3v2.2_24PAS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPA APAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS GGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 695)
C398_SB175_6GS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSSE ALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 696)
AHB2v1_10GS_LCB3v2.2_10GS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGG GSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGSGGDKEN VLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 697)
C390-AHB2v1-4GS-SB175	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSSE ALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRIIAKVLK(서열번호 696)
C326-AHB2v1-4GS-1rfo	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGY IPEAPRDGQAYVRKDGEWVLLSTFL(서열번호 698)
AHB2v1-10GS-LCB3_v2.3-10GS-LCB1_v2.2 + His Tev tag	(MSHHHHHHHHHSENLYFQSGG)ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEE EARRILEHLEELARKGGGSGGGSGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE LLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(서열번호 699)
LCB1v3 + His Tev tag	(MSHHHHHHHHHSENLYFQSGGG)DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(서열번호 700)
LCB1-Fc9 + 신호 서열 리더 제거	DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSGSGSGGSEPKSSDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK(서열번호 701)

[0860] 본원에 기술된 구현예들 중 임의 구현예 또는 구현예들의 조합에 따른 폴리펩타이드는 개체에 투여시 잔류 시간 연장을 촉진하기 위해 안정화 도메인이 추가로 연결될 수 있다. 임의의 적합한 안정화 도메인이 의도한 목적으로 사용될 수 있다. 안정화 도메인에 대한 예로는 폴리에틸렌 글리콜 (PEG), 알부민, 하이드록시에틸 전분 (HES), 아미노산 Pro, Ala 및/또는 Ser으로 된 ('PASylation') 입체구조적으로 무질서한 폴리펩타이드 서열 (conformationally disordered polypeptide sequence), 및/또는 아미노산 Lys 및 Ala으로 구성되고 Glu이 첨가 또는 비-첨가된 뮤신 확산성 (mucin diffusivity) 폴리펩타이드를 포함하지만, 이들로 한정되는 것은 아니다.

[0861] 이러한 뮤신 확산성 폴리펩타이드에 대한 비-제한적인 예는 하기 서열을 포함하지만, 이로 제한되는 것은 아니다:

[0862] Mucin 도메인: AKAKAKAKAKAKAKAKAKGG (서열번호 61); GGAKAKAKAKAKAKAKAKAK (서열번호 62)

[0863] 이들 구현예에 따른 폴리펩타이드의 예는, 예를 들어, 서열번호 65-96로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 100% 동일한 아미노산 서열을 포함할 수 있으며, 분비 신호 (MARAWIFFLLCLAGRALA; 서열번호 63)가 존재하는 일 구현예에서는 임의의 다른 분비 신호로 대체될 수 있다.

[0864] LCB1_v1.1_Cys_: AKAKAKAKAKAKAKAKAKGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERC (서열번호 65)

[0865] >Mucin_LCB1_v1.3: AKAKAKAKAKAKAKAKAKGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 66)

[0866] >LCB1_v1.3_Mucin: DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGAKAKAKAKAKAKAKAKAK (서열번호 67)

[0867] FC 융합체 (**진한 서열 = 분비 신호**, 밑줄 = LCB, 노란색=GS 링커, 녹색=Fc)

[0868] >LCB1-Fc1 (BM40-LCB1-GS4-Fc-Opt-WT)(LCB1 서열 = 제1 경우의 **LCB1-1**):
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSGSEPKSSDKTHTCPPCPAPELLGGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK (서열번호 68)

[0869] > LCB1-Fc2 (BM40-LCB1-GS15-Fc-Opt-WT)(LCB1 서열 = 제1 경우의 **LCB1-1**):
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSGSGGSGSGSGGSEPKSSDKTHTCPP
CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK (서열번호 69)

[0870] >LCB1-Fc3 (BM40-Fc-Opt- GS15-2-LCB1-WT)(LCB1 서열 = 제1 경우의 **LCB1-1**):
MARAWIFFLLCLAGRALAEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGSGSGSGGSGSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDE
RLLEEAERLLEEVER (서열번호 70)

[0871] >LCB1-Fc4 (BM40-LCB1-GS15-Fc-Opt-GS15-2-LCB1-WT)(LCB1 서열 = 제1 경우의 **LCB1-1**):
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSGSGGSGSGSGGSEPKSSDKTHTCPP
CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGKSGGSGSGSGGSGSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER (서열번호 71)

[0872] >LCB1-Fc5 (BM40-LCB1-GS4-Fc-Opt-Q38)(LCB1 서열 = 제1 경우의 **LCB1-3**):
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVERGSGSEPKSSDKTHTCPPCPAPELLGGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK (서열번호 72)

[0873] >LCB1-Fc6 (BM40-LCB1-GS15-Fc-Opt-Q38)(LCB1 서열 = 제1 경우의 **LCB1-3**):
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSGSGSGGSEPKSSDKTHTCPP
CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK (서열번호 73)

[0874] >LCB1-Fc7 (BM40-Fc-Opt-GS15-2-LCB1-Q38)(LCB1 서열 = 제1 경우의 **LCB1-3**):

MARAWIFFLLCLAGRALAEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGSGSGSGGSGSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDE RLLEEAERLLEEVER (서열번호 74)

[0875] >LCB1-Fc8 (BM40-LCB1-Q38-GS15-Fc-Opt-GS15-2-LCB1-Q38)(LCB1 서열 = 제1 경우의 **LCB1-3**): **MARAWIFFLLCLAGRALA**DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSGSGSGGSEPKSSDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGKSGGSGSGSGGSGSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVER (서열번호 75)

[0876] > LCB1-6M-Fc9 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GS15-Fc-Opt)(LCB1 서열 = **이 경우의 LCB1_v1.1₩**): **MARAWIFFLLCLAGRALA**DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSGSGSGGSEPKSSDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK (서열번호 76)

[0877] > LCB1-6M-Ngly-Fc10 (BM40-LCB1-6M-Ngly -4N,14K,15T,18Q,**27N**,38Q -GS15-Fc-Opt)(LCB1 서열 = **오리지널 경우의 LCB1-5 =** LCB1_v1.1 = LCB1-4 + N-연결된 당화): **MARAWIFFLLCLAGRALA**DKENILQKIYEIMKTLDQLGHAEASM**N**VSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSGSGSGGSEPKSSDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK (서열번호 77)

[0878] > LCB3-6M-Fc11 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GS15-Fc-Opt)(LCB 서열은 제1 경우의 **LCB3-3**와 동일):
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGSGGSGSGSGGSEPKSS DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK (서열번호 78)

[0879] > LCB3-6M-NGly-Fc12 (BM40-LCB3-6M-Ngly-8Q,26Q,28H,35N,37T,43K -GS15-Fc-Opt)(LCB 서열은 LCB3-3 + N-연결된 당화인 제1 경우의 **LCB3-4**와 동일):
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFENATKAYKNKDRQKLEKVVEELKELLERLLSGGSGSGGSGSGSGGSEPKSS DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK (서열번호 79)

[0880] > LCB1-6M-GPGcP-Fc13 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GPGcP-Fc-Opt)(LCB 서열은 제1 경우의 **LCB3-3**와 동일):
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGSGGSPVPSTPPTPSPSTPPT PSPSGGSGNSSGSGGSPVPSTPPTPSPSTPPTPSPSASEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (서열번호 80)

[0881] > LCB3-6M-GPGcP-Fc14 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GPGcP-Fc-Opt) (LCB 서열은 제1 경우의 **LCB3-3**와 동일):
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGSGGSGGSPVPSTPPT PSPSTPPTPSPSGGSGNSSGSGGSPVPSTPPTPSPSTPPTPSPSASEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (서열번호 81)

[0882] > LCB1-6M-GS30-Fc15 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GS30-Fc-Opt)LCB1-4: **MARAWIFFLLCLAGRALA**DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGSGGGGSGGGGSGGGGSGGGGSGGGG SGEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN

GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (서열번호 82)

[0883] > LCB3-6M-GS30-Fc16 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GS30-Fc-Opt) (LCB 서열은 제1 경우의 **LCB3-3**와 동일):
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGGSGGGGSGGGGSG
GGGSGGGGSGEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (서열번호 83)

[0884] > LCB1-v1.3-Fc17 (BM40-LCB1-v1.3 -4N,14K,15T,17E,18Q,27Q,38Q -GS15-Fc-Opt):
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSGSGSGGSEPKSSDKTHTCPP
CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK (서열번호 84)

[0885] > LCB1-v1.3-Ngly-Fc18 (BM40-LCB1-v1.3 Ngly -4N,14K,15T,17E,18Q,27N,38Q -GS15-Fc-Opt)(>LCB1_v1.5 (= LCB1_v1.3 + N-연결된 당화):
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMNVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSGSGSGGSEPKSSDKTHTCPP
CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK (서열번호 85)

[0886] > LCB1-v1.3-GPGcP-Fc19 (BM40-LCB1-v1.3-Fc19 -4N,14K,15T,17E,18Q,27Q,38Q－GPGcP-Fc-Opt):
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGSGGSPVPSTPPTPSPSTPPT
PSPSGGSGNSSGSGGSPVPSTPPTPSPSTPPTPSPSASEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (서열번호 86)

[0887] > LCB1-v1.3-GS30-Fc20 (BM40-LCB1-v1.3 -4N,14K,15T,17E,18Q,27Q,38Q -GS30-Fc-Opt):
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGSGGGGSGGGGSGGGGSGGGGSGGGG
SGEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (서열번호 87)

[0888] Fc21-LCB1v2.2-FcIgG1_WT:
MARAWIFFLLCLAGRALADKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPP
CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK (서열번호 88)

[0889] Fc22-LCB1v2.2-FcIgG3_WT:
MARAWIFFLLCLAGRALADKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPR
CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEAL
HNRFTQKSLSLSPGK (서열번호 89)

[0890] Fc23_LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_WT:
MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIY
EIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (서열번호
90)

[0891] Fc24_AHB2-10GS-LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_WT:
MARAWIFFLLCLAGRALAELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDERELREIEEEARRILEHLEELARKGGGSGGGSG

GNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQ
VSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK(서열번호 91)

[0892] Fc25_LCB3_v2.3-10GS-AHB2-10GS-LCB1_v2.2_FcIgG1_WT:
MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGELEEQVMHVL
DQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQ
VSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK(서열번호 92)

[0893] Fc26_LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_GA:
MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIY
EIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELLAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK(서열번호 93)

[0894] Fc27_LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_GRLR:
MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIY
EIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELLRGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKARPAPIEKTISKAKGQPREPQVYTLPPSRDEL
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK(서열번호 94)

[0895] Fc28_LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_GAALIE:
MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIY
EIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELLAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPLPEEKTISKAKGQPREPQVYTLPPSRDEL
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK(서열번호 95)

[0896] Fc29_LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_GAALIELS:
MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIY
EIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELLAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPLPEEKTISKAKGQPREPQVYTLPPSRDEL
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK(서열번호
96).

[0897] 본 발명은 본원의 임의 구현예 또는 구현예들의 조합에 따른 폴리펩타이드의 올리고머를 추가로 제공한다. 일 구현예에서, 올리고머는 올리고머화 도메인을 포함하는 본원에 개시된 폴리펩타이드의 올리고머이다. 일 구현예에서, 올리고머는 동형삼량체를 포함하나 이로 제한되는 것은 아닌 삼량체를 포함한다.

[0898] 다른 구현예에서, 본 발명은 나노입자 또는 바이러스 유사 입자와 같은 폴리펩타이드 입자 지지체를 포함하나 이로 제한되지 않는 지지체에 부착된, 본원의 임의 구현예 또는 구현예들의 조합에 따른 폴리펩타이드를 2, 3 또는 4 카피 이상으로 포함하는 조성물을 제공한다.

[0899] 본원에 기술된 바와 같이, 폴리펩타이드는 SARS-CoV-2 스파이크 당단백질에 결합하며, 따라서 (예를 들어) SARS-CoV-2 감염을 치료하기 위한 치료제로서 유용하다. 일 구현예에서, 폴리펩타이드는 첨부된 실시예에 기술된 바와 같이 측정시 적어도 10 nM의 친화성으로 SARS-CoV-2 스파이크 당단백질에 결합한다.

[0900] 다른 측면에서, 본 발명은 본 발명의 폴리펩타이드를 암호화하는 핵산을 제공한다. 핵산 서열은 RNA (예, mRNA) 또는 DNA를 포함할 수 있다. 이러한 핵산 서열은, 비-제한적으로, 폴리A 서열, 변형된 Kozak 서열, 에피토프 태그 암호화 서열, 유출 신호 암호화 서열, 분비 신호 암호화 서열, 핵 위치화 신호를 암호화하는 서열 및 원형질막 위치화 신호를 암호화하는 서열 등의, 암호화된 폴리펩타이드의 발현 및/또는 정제를 촉진하는데 유용한 부가적인 서열을 포함할 수 있다. 당해 기술 분야의 당업자라면, 본원의 교시 내용에 기반하여, 어떤 핵산 서열이 본 발명의 단백질을 암호화할 것인지 자명할 것이다.

[0901] 다른 측면에서, 본 발명은 적절한 조절 서열에 작동가능하게 연결된 본 발명의 임의 구현예 또는 구현예들의 조

합에 따른 핵산을 포함하는 발현 벡터를 제공한다. "발현 벡터"는 유전자 산물의 발현을 구현할 수 있는 임의의 조절 서열에 핵산 암호화 영역 또는 유전자를 작동가능하게 연결한 벡터를 포함한다. 본 발명의 핵산 서열에 작동가능하게 연결되는 "조절 서열"은 핵산 분자의 발현을 구현할 수 있는 핵산 서열이다. 조절 서열은 발현을 지시하는 기능을 수행하는 한 핵산 서열과 인접해야 하는 것은 아니다. 따라서, 예를 들어, 프로모터 서열과 핵산 서열 사이에 전사되지만 번역되진 않는 개입 서열들이 존재할 수 있으며, 프로모터 서열은 여전히 암호화 서열에 "작동가능하게 연결된" 것으로 간주할 수 있다. 다른 이러한 조절 서열로는, 비-제한적으로, 폴리아데닐화 신호, 종결 신호 및 리보솜 결합부를 포함한다. 이러한 발현 벡터는, 비-제한적으로, 플라스미드 및 바이러스-기반의 발현 벡터를 비롯해 당해 기술 분야에서 공지된 임의 유형의 것일 수 있다. 포유류 시스템에서 개시된 핵산 서열의 발현을 인가하기 위해 사용되는 조절 서열은 (비-제한적으로, CMV, SV40, RSV, 액틴, EF 등의 다양한 임의의 프로모터에 의해 구동되는) 구성적 또는 (비-제한적으로, 테트라사이클린, 엑다이손 (ecdysone), 스테로이드-응답성 등의 다수의 임의의 유도성 프로모터에 의해 구동되는) 유도성일 수 있다.

[0902] 일 측면에서, 본 발명은 본원의 임의 구현예 또는 구현예들의 조합에 따른 폴리펩타이드, 조성물, 핵산, 및/또는 발현 벡터를 포함하는 세포를 제공하며, 세포는 포유류 세포와 같은 원핵 생물 또는 진핵 생물일 수 있다. 일 구현예에서, 세포는 본원의 핵산 또는 발현 벡터로 일시적으로 또는 안정적으로 형질감염될 수 있다. 원핵생물 및 진핵생물 세포에 발현 벡터의 형질감염은 당해 기술 분야에서 공지된 임의 기법을 통해 달성할 수 있다. 본 발명에 따른 폴리펩타이드 생산 방법은 본 발명의 추가적인 일부이다. 본 방법은 (a) 본 발명의 이러한 측면에 따른 숙주를 폴리펩타이드의 발현을 촉진하는 조건 하에 배양하는 단계, 및 (b) 선택적으로, 발현된 폴리펩타이드를 회수하는 단계를 포함한다. 다른 구현예에서, 폴리펩타이드는, 비-제한적으로, 무-세포성 단백질 합성 (cell-free protein synthesis)(또는 시험관내 전사 및 번역)을 이용하는 등의 임의의 다른 적절한 기법을 통해 생산할 수 있다.

[0903] 다른 측면에서, 본 발명은 하기를 포함하는 약학적 조성물/백신을 제공한다:

[0904] (a) 본원의 임의 구현예 또는 구현예들의 조합에 따른 폴리펩타이드, 핵산, 발현 벡터 및/또는 숙주 세포; 및

[0905] (b) 약제학적으로 허용가능한 담체.

[0906] 조성물은 (a) 동결보호제; (b) 계면활성제; (c) 증량제; (d) 긴장도 조정제; (e) 안정화제; (f) 보존제, 및/또는 (g) 완충제를 더 포함할 수 있다. 일부 구현예에서, 약학적 조성물에서 완충제는 트리스 완충제, 히스티딘 완충제, 포스페이트 완충제, 사이트레이트 완충제 또는 아세테이트 완충제이다. 또한, 조성물은 동결보호제, 예를 들어 슈크로스, 소르비톨 또는 트레할로스를 함유할 수 있다. 특정 구현예에서, 조성물은 보존제, 예를 들어 벤즈알코늄 클로라이드, 벤즈에토늄, 클로로헥시딘, 페놀, m-크레졸, 벤질 알코올, 메틸파라벤, 프로필파라벤, 클로로부탄올, o-크레졸, p-크레졸, 클로로크레졸, 페닐머큐릭 나이트레이트, 티메로살, 벤조산 및 이들의 다양한 혼합물을 함유한다. 다른 구현예들에서, 조성물은 글리신과 같은 증량제를 함유한다. 또 다른 구현예에서, 조성물은 계면활성제, 예를 들어, 폴리소르베이트-20, 폴리소르베이트-40, 폴리소르베이트-60, 폴리소르베이트-65, 폴리소르베이트-80, 폴리소르베이트-85, 폴록사머-188, 소르비탄 모노라우레이트, 소르비탄 모노팔미테이트, 소르비탄 모노스테아레이트, 소르비탄 모노올레이트, 소르비탄 트리라우레이트, 소르비탄 트리스테아레이트, 소르비탄 트리올레이트, 또는 이들의 조합을 함유한다. 또한, 조성물은 긴장도 조정제, 예를 들어, 제형을 인간 혈액과 실질적으로 등장성 또는 삼투 등장성 (isoosmotic)으로 만드는 화합물을 함유할 수 있다. 예시적인 긴장도 조정제로는 슈크로스, 소르비톨, 글리신, 메티오닌, 만니톨, 덱스트로스, 이노시톨, 소듐 클로라이드, 아르기닌 및 아르기닌 하이드로클로라이드 등이 있다. 다른 구현예들에서, 조성물은, 추가적으로 안정화제, 예를 들어, 동결건조된 형태 또는 액체 형태에서 나노구조의 화학적 및/또는 물리적 불안정성을 실질적으로 낮추거나 또는 방지하는 분자를 함유한다. 예시적인 안정화제로는 슈크로스, 소르비톨, 글리신, 이노시톨, 소듐 클로라이드, 메티오닌, 아르기닌 및 아르기닌 하이드로클로라이드 등이 있다.

[0907] 폴리펩타이드, 핵산, 발현 벡터, 및/또는 숙주 세포는 조성물에서 단독 활성 물질일 수 있거나, 또는 의도한 용도에 적합한 하나 이상의 다른 물질이 조성물에 추가로 포함될 수 있다.

[0908] 다른 측면에서, 본 발명은 필요한 개체에 임의 청구항에 따른 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리고머, 조성물 및/또는 약학적 조성물을 감염을 치료하기에 유효한 함량으로 투여하는 것을 포함하는, 중증 급성 호흡기 증후군 (SARS) 코로나바이러스 감염 (SARS-Co-V 및 SARS-CoV-2 포함)의 치료 방법을 제공한다. 일 구현예에서, SARS 코로나바이러스는 SARS-CoV-2를 포함한다.

[0909] 다른 측면에서, 본 발명은 필요한 개체에 임의 청구항에 따른 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리

고머, 조성물 및/또는 약학적 조성물을 감염을 치료하기에 유효한 함량으로 투여하는 것을 포함하는 중증 급성 호흡기 증후군 (SARS) 코로나바이러스 감염 (SARS-Co-V 및 SARS-CoV-2 포함)의 진행을 제한하는 방법을 제공한다. 일 구현예에서, SARS 코로나바이러스는 SARS-CoV-2를 포함한다.

[0910] 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 및/또는 약학적 조성물은 주치의가 적절한 것으로 간주한 임의의 적합한 투여 경로를 통해 투여될 수 있다. 일 구현예에서, 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리고머, 조성물 및/또는 약학적 조성물은 비강내로 투여된다. 다른 구현예에서, 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 올리고머, 조성물 및/또는 약학적 조성물은 전신으로 투여된다.

[0911] 본 방법이 SARS 코로나바이러스 감염의 치료를 포함하는 경우, 하나 이상의 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 및/또는 약학적 조성물을 SARS 코로나바이러스 감염된 것으로 이미 진단된 개체에 투여한다. 본원에서 사용된 바와 같이, "치료한다" 또는 "치료하는"은 (1) 개체에서 감염 증상의 중증도 저하; (b) 개체에서 증상의 증가 제한; (c) 생존성 증가; (d) 증상의 기간 감소; (e) 증상 진행의 제한 또는 방지; 및 (f) 감염을 치료하기 위한 입원 필요성 및/또는 입원 기간의 감소 중 하나 이상을 달성하는 것을 의미한다.

[0912] 본 방법이 SARS 코로나바이러스 감염의 진행 제한을 포함하는 경우, 하나 이상의 폴리펩타이드, 핵산, 발현 벡터, 숙주 세포, 및/또는 약학적 조성물은 SARS 코로나바이러스 감염이 확인되진 않았지만 이러한 감염 위험이 있을 수 있는 개체에 예방적으로 투여된다. 본원에서 사용된 바와 같이, "제한"은 임의 개체일 수 있는, 감염 위험이 있는 개체에서 SARS 코로나바이러스 감염의 진행 제한을 의미한다.

[0913] 개체는 인간 개체와 같은 임의 개체일 수 있다.

[0914] SARS-CoV-2 감염에 대한 증상의 예로는, 비-제한적으로, 발열, 피로, 기침, 숨가쁨, 가슴 압박 및/또는 통증, 후각 상실 또는 감소, 미각 상실 또는 감소, 및 호흡기 관련 문제, 비-제한적인 예로, 폐렴, 기관지염, 중증 급성 호흡기 증후군 (SARS), 및 상기도 및 하기도 감염을 포함한다.

[0915] 본원에서 사용된 바와 같이, "유효량"은 SARS-CoV-2 감염을 치료 및/또는 제한하는데 효과적인 조성물의 양을 의미한다. 본원의 임의의 구현예에 따른 폴리펩타이드, 조성물, 핵산 또는 조성물은 전형적으로 전술한 바와 같이 약학적 조성물로 제형화되며, 경구, 비경구, 흡입 분무, 직장 또는 국소 등의 임의의 적합한 경로를 통해 통상적인 약제학적으로 허용가능한 담체, 보강제 및 비히클을 함유한 투약 단위 제형으로 투여될 수 있다. 본원에서 사용된 바와 같이, 용어 비경구는 피하, 정맥내, 동맥내, 근육내, 흉골내, 힘줄내, 척수내, 두개강내, 흉강내, 주입 기법 또는 복막내를 포함한다. 폴리펩타이드 조성물은 또한 미소구, 리포좀, 면역-자극 복합체 (ISCOM), 또는 적절한 조직 (예, 혈액)으로 도입되는 기타 미세입자 전달 시스템 또는 지속 방출형 제형으로 투여될 수 있다. 투여량 용법은 최적의 원하는 반응 (예를 들어, 치료학적 또는 예방학적 반응)을 제공하도록 조정될 수 있다. 적합한 투여량 범위는 예를 들어 폴리펩타이드 또는 이의 나노입자 0.1 ㎍/체중 kg 내지 100 mg/체중 kg일 수 있다. 조성물은 단일 볼루스로 전달되거나, 또는 주치의가 결정한 바에 따라 1회보다 더 많은 횟수 (예를 들어, 2, 3, 4, 5 또는 그 이상)로 투여될 수 있다.

[0916] 본 발명의 내용은 또한 후술한 실시예에 기술된 바와 같은 단계들을 포함하는, SARS-Cov-2의 수용체 결합 부위 (RBD)에 결합하는 폴리펩타이드를 설계하는 방법을 제공한다. 이러한 방법은 폴리펩타이드 설계 (실시예에서 임의 구현예 또는 구현예들의 조합으로 기술된 바와 같이), 무세포성 합성 및 임의의 적절한 기법을 이용한 SARS-Cov-2 RBD 결합 평가 단계를 포함할 수 있다.

[0917] **실시예**

[0918] **개요**

[0919] 효과적인 SARS-CoV-2 치료제가 요구되고 있다. 본 발명자들은 전산적 단백질 설계 (computational protein design)를 이용해, 세포 도입에 필수적인 Ace2 수용체와의 상호작용을 차단하는, SARS-CoV-2의 수용체 결합 부위 (RBD)에 대한 고 친화성 결합제를 구축하고자 하였다. 본 발명자들은 2가지 전략을 이용해 RBD 상의 Ace2 결합 부위에 대해 상보적인 형태를 가진 소형 단백질 스캐폴드를 제작하였다: 첫째, RBD와의 상호작용 대부분을 형성하는 Ace2의 나선을 둘러싸는 스캐폴드를 구축하였으며, 2번째에서는, 잔기 65개 미만 길이의 다양한 드 보노 설계된 스캐폴드를 이 영역에 도킹시켰다. 이들 2가지 경우에서, RBD 인터페이스에 위치한 스캐폴드 잔기들은 고 친화성 결합에 대해 최적화하였으며, 단백질의 나머지 부분의 잔기들은 표적 구조로의 접힘 및 안정성에 대해 최적화하였다. 바이러스에 가장 강하게 결합할 것으로 예측되는 디자인 50,000개를 큰 올리고뉴클레오티드 어레이에 코딩한 다음 RBD 결합성에 대해 형광 활성화된 세포 분류를 이용해 효모 표면 디스플레이로 스크리닝하였으며; 분류하기 전 및 분류한 후 집단에 대한 심층 서열분석을 통해 표적에 결합하는 디자인 수백개를 식별

하였다. (분류에 의해 대부분 농화된) 가장 높은 친화성 결합제의 결합 방식을 고 해상도 서열 맵핑에 의해 검증하고, 유익한 치환 1-4개를 조합해 친화성을 추가로 증가시켰다. RBD 상의 Ace2 계면을 둘러싸는 여러가지 결합 부위와 완전히 다른 서열을 가진 최적화된 디자인 8종을 E. coli에서 고 수준으로 발현시켰으며, 100pM 내지 10nM 범위의 Kd로 RBD에 결합한다는 것을 밝혔다. 이들 디자인은 10nM 내지 20pM 범위의 IC50으로 살아있는 바이러스의 Vero-6 세포 감염을 차단하였다. 따라서, 이들 폴리펩타이드는 예를 들어 비강내 및 전신 SARS-CoV-2 치료제로서 모두 유용하며, 본 발명의 결과는 보다 일반적으로는 대유행 위협에 대항하여 신속하게 잠재적인 치료학적 후보 물질을 제작하는 전산적 단백질 설계 능력을 입증해준다.

[0920] SARS-CoV-2 감염은 보통 코에서 시작해, 여기서 수회 바이러스 복제한 다음 더 넓은 호흡계로 전파되는 것으로 보인다. 일반적으로 바이러스 저해제를 고 농도로 코 및 호흡계에 전달하여, 잠재적으로 예방학적 보호를, 그리고 감염 초기에 치료학적 효능을 제공할 수 있으며, 의료 종사자 및 감염된 개체와 자주 접촉하는 사람에게 특히 유용할 수 있다. 다수의 단일클론 항체들이 전신성 SARS-CoV-2 치료제로서 개발 중이지만, 항체는 크고 종종 매우 안정적인 분자가 아니며 결합 부위의 밀도가 낮으므로 (150Kd 항체 당 2개), 이들 화합물은 비강내 전달에는 이상적이지 않으며; Fc 도메인은 추가적인 이점을 거의 제공하지 않는다. 단일클론 바이러스에 대해 친화성이 매우 높지만, 저해 도메인의 밀도를 극대화하고 분무를 통해 호흡계에 직접 전달할 수 있도록 크기가 매우 작은 단백질 저해제가 더 바람직할 것이다.

[0921] 본 발명자들은 Ace2 결합과 경쟁하는 RBD에 대한 고 친화성 결합제를 데 노보 설계하는데 착수하였다. 본 발명자들은 2가지 전략을 조사하였다: 먼저, RBD와의 상호작용 대부분을 형성하는 Ace2의 나선을 둘러싸는 스캐폴드에 대해 더 높은 친화성을 달성하기 위해 RBD와의 부가적인 상호작용을 형성하는 작은 단백질 형태를 설계하고자 시도하였으며, 2번째로, RBD와의 임의의 공지된 결합 상호작용을 포함하지 않는 결합제를 완전히 처음부터 설계하고자 하였다. 2번째 전략의 이점은, 설계 가능한 범위가 훨씬 더 넓어, 잠재적으로 친화성이 더 높은 결합 방식을 식별할 수 있다는 것이다. 첫번째 방식에서는 본 발명자들은 Rosetta™ 블루 프린트 빌더를 이용해 Ace2 나선을 통합한 소형 단백질을 제작하였으며, 2번째 방식에서는 거대한 미니단백질 라이브러리를 이용해 RIF 도킹 및 디자인을 제작하였다. 디자인은 Ace2 결합 부위를 둘러싼 RBD 표면의 구분된 영역들과 상호작용한다 (**도 1**). 방식 1에서 디자인들은 긴 올리고뉴클레오티드에 암호화하고, 효모 세포 표면 상의 형광 태깅된 RBD에 대한 결합을 스크리닝하였다. 심층 서열분석을 통해 Ace2 나선 스캐폴드 디자인 3종을 동정하였으며 (방식 1), RBD 결합에 대해 FACS 분류를 통해 명확하게 농화된 데 노보 인터페이스 디자인 150종을 동정하였다 (방식 2). 디자인들은 *E. coli*에서 발현시켜 정제하였으며, 이들 다수가 용해성으로 발현되었으며, 생물층 간섭 측정 실험에서 RBD에 결합하는 것으로 확인되었고, 이는 RBD에의 결합에 대해 ACE-2와 효과적으로 경쟁할 수 있었다 (도 2에 나타낸 실시예). BLI 데이터에 기반하여 (예, **도 2** 참조), 미니결합제의 RBD 결합 친화성은 다음과 같다: LCB1 <1nM, LCB3 <1nM. LCB2, LCB4, LCB5, LCB6, LCB7, LCB8의 친화성은 1~20nM 범위이고, 여러가지 결합제들의 상대적인 강도는 LCB4 > LCB2 > LCB9 = LCB5 > LCB6 > LCB7이다.

[0922] 디자인들이 설계한 인터페이스를 통해 RBD에 결합하는지를 확인하기 위해, 각 디자인에서 모든 잔기들을 아미노산 20개 중 하나로 하나씩 치환시킨 부위 포화 라이브러리를 구축하고, 이를 RBD 결합에 대해 FACS 분류를 수행하였다. 심층 서열분석 결과, 결합 인터페이스 잔기와 단백질 코어 잔기들이 이러한 부위 포화 라이브러리 (SSM)가 구축된 다수의 디자인들에 보존되어 있는 것으로, 밝혀졌다 (SSM은 표 1에서 아미노산 변동에 대해 허용가능한 위치를 정의하는데 이용됨). 대부분의 디자인들 경우, FACS 분류에서 적은 수의 치환이 농화되었는데, 이는 이들 치환이 RBD에 대한 결합 친화성을 증가시킴을 시사한다. 방식 1의 디자인들, 그리고 방식 2의 디자인들 중 9종에 대해 최고 친화성을 달성하기 위해, 이들 치환을 병합한 조합 라이브러리를 구축하여, 다시 FACS로 결합성을 스크리닝하였으며; 결합 친화성이 매우 높아, 분류시 이용한 농도는 최저 20pM 였다. 각 라이브러리는 밀접하게 관련성 있는 서열 수개로 수렴되었으며, 각 디자인에 대해 최적화된 변이체 하나를 *E. coli*에서 발현시켜 정제하였다.

[0923] RBD에 대해 서로 다른 결합 방식을 가진 최적화된 디자인 8종의 결합성을 생물층 간섭측정으로 조사하였다 (도 1). 다수의 디자인들은 Kd가 1-20nM 범위였으며, 나머지는 Kd가 1nM 미만으로, 너무 강해 이러한 기법으로 신뢰성있게 측정하기 어려웠다 (도 2 참조). 디자인들의 원이색성 스펙트럼은 디자인 모형과 일치하였으며, 이들 디자인은 실온에서 수일 후에도 완전한 결합 활성을 유지하였다 (**도 3**).

[0924] 본 발명자들은 이들 디자인이 살아있는 바이러스에 의한 인간 세포 감염을 차단하는 능력을 조사하였다. 설계한 결합제가 다양한 함량으로 존재하는 조건 하에 vero 세포 $2.5\text{-}3x10^4$개에 SARS-CoV-2를 100 FFU로 첨가하였다. 상세한 내용은 도 4에 범례로 제공된다. 본 발명자들은 디자인들 모두에서 강력한 감염 저해를 관찰하였으며,

IC50은 1 nM 내지 0.02 nM 범위였다.

[0925] 구체적인 디자인에 대한 상세 설명을 표 10에 제시한다.

[0926] **표 10**

표 11

[0927]

구조체 명칭	서열번호	발현 숙주	벡터	발현 방법	용해성 생산 수준 추정치 (mg / L)	RBD에 대한 Kd 추정치 (nM)	스파이크에 대한 Kd 추정치 (nM) 항원항체 결합력	SARS-CoV-2 중화 IC50 (nM)
LCB1-1	(서열번호 1)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1-2	(서열번호 2)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1-3	(서열번호 3)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1-4	(서열번호 4)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1-5	(서열번호 5)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1_v1.1_Cys	(서열번호 6)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1_v1.2	(서열번호 7)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1_v1.3	(서열번호 8)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1_v1.4	(서열번호 9)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1_v1.5 (LCB1_v1.3 + N-연결된 당화)	(서열번호 10)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB2-1	(서열번호 11)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB2-2	(서열번호 12)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3-1	(서열번호 13)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3-2	(서열번호 14)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3-3	(서열번호 15)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3-4	(서열번호 16)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3_v1.1	(서열번호 17)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3_v1.2	(서열번호 15)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3_v1.3	(서열번호 19)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3_v1.4	(서열번호 20)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3_v1.5	(서열번호 21)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3-4	(서열번호 16)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB4-1	(서열번호 23)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB4-2	(서열번호 24)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB5-1	(서열번호 25)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB5-2	(서열번호 26)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB6-1	(서열번호 27)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB6-2	(서열번호 28)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB7-1	(서열번호 29)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB7-2	(서열번호 30)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB8-1	(서열번호 31)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB8-2	(서열번호 32)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
AHB1-1	(서열번호 33)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
AHB1-2	(서열번호 34)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
AHB2-1	(서열번호 100)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
AHB2-2	(서열번호 101)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1-6GS-LCB1	(서열번호 47)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1-12GS-LCB1	(서열번호 48)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1-24GS-LCB1	(서열번호 49)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1-36GS-LCB1	(서열번호 50)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1_v1.1-GSLCB1_v1.1(1GS1)	(서열번호 51)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1_v1.1-PRO-LCB1_v1.1(1PRO1)	(서열번호 52)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01

LCB3_v1.2-GS3-LCB3_v1.2 (3GS3)	(서열번호 53)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3_v1.2-PRO-LCB3_v1.2 (3PRO3)	(서열번호 54)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1_v1.1-GS-LCB3_v1.2 (1GS3)	(서열번호 55)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3_v1.2-GS-LCB1_v1.1 (3GS1)	(서열번호 56)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3_v1.2-10GS-LCB1_v1.1(LCB3-GS10-LCB1)	(서열번호 57)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1_v1.1-PRO-LCB3_v1.2 (1PRO3)	(서열번호 58)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB3_v1.2-PRO-LCB1_v1.1 (3PRO1)	(서열번호 59)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
(5_LCB1_링커14)	(서열번호 60)	E. coli	pET	자기유도 37℃	20.38	0.2	0.1	0.01141
Mucin_LCB1_v1.1_Cys	(서열번호 65)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
Mucin_LCB1_v1.3	(서열번호 66)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1_v1.3_Mucin	(서열번호 67)	E. coli	pET	자기유도 37℃	10	0.2	0.1	0.01
LCB1-Fc1 (BM40-LCB1-GS4-Fc-Opt-WT)(LCB1 서열 = 제1 경우의 LCB1-1)	(서열번호 68)	인간 293 세포	pCMVR	일시적 형질감염 37℃	12	0.2	0.1	0.01
LCB1-Fc2 (BM40-LCB1-GS15-Fc-Opt-WT)(LCB1 서열 = 제1 경우의 LCB1-1)	(서열번호 69)	인간 293 세포	pCMVR	일시적 형질감염 37℃	12	0.2	0.1	0.01
LCB1-Fc3 (BM40-Fc-Opt-GS15-2-LCB1-WT)(LCB1 서열 = 제1 경우의 LCB1-1)	(서열번호 70)	인간 293 세포	pCMVR	일시적 형질감염 37℃	12	0.2	0.1	0.01
LCB1-Fc4 (BM40-LCB1-GS15-Fc-Opt-GS15-2-LCB1-WT)(LCB1 서열 = 제1 경우의 LCB1-1)	(서열번호 71)	인간 293 세포	pCMVR	일시적 형질감염 37℃	2	0.2	0.1	0.01
LCB1-Fc5 (BM40-LCB1-GS4-Fc-Opt-Q38) (LCB1 서열 = 제1 경우의 **LCB1-3**)	(서열번호 72)	인간 293 세포	pCMVR	일시적 형질감염 37℃	6	0.2	0.1	0.01
LCB1-Fc6 (BM40-LCB1-GS15-Fc-Opt-Q38) (LCB1 서열 = 제1 경우의 **LCB1-3**)	(서열번호 73)	인간 293 세포	pCMVR	일시적 형질감염 37℃	5	0.2	0.1	0.01
LCB1-Fc7 (BM40-Fc-Opt-GS15-2-LCB1-Q38) (LCB1 서열 = 제1 경우의 **LCB1-3**)	(서열번호 74)	인간 293 세포	pCMVR	일시적 형질감염 37℃	10	0.2	0.1	0.01
LCB1-Fc8 (BM40-LCB1-Q38-GS15-Fc-Opt-GS15-2-LCB1-Q38)(LCB1 서열 = 제1 경우의 **LCB1-3**)	(서열번호 75)	인간 293 세포	pCMVR	일시적 형질감염 37℃	1	0.2	0.1	0.01
LCB1-6M-Fc9 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GS15-Fc-Opt)	(서열번호 76)	인간 293 세포	pCMVR	일시적 형질감염 37℃	20	0.2	0.1	0.01
LCB1-6M-Ngly-Fc10 (BM40-LCB1-6M-Ngly -4N,14K,15T,18Q,**27N**,38Q -GS15-Fc-Opt) (LCB1 서열 = 오리지널 경우의 **LCB1-5 =** LCB1_v1.1 = LCB1-4 + N-연결된 당화)	(서열번호 77)	인간 293 세포	pCMVR	일시적 형질감염 37℃	20	0.2	0.1	0.01

LCB3-6M-Fc11 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GS15-Fc-Opt) (LCB 서열은 제1 경우의 LCB3-3와 동일)	(서열번호 78)	인간 293 세포	pCMVR	일시적 형질감염 37℃	5	0.2	0.1	0.01
LCB3-6M-NGly-Fc12 (BM40-LCB3-6M-Ngly -8Q,26Q,28H,35N,37T,43K -GS15-Fc-Opt) (LCB 서열은 제1 경우의 **LCB3-4**와 동일, 즉 LCB3-3 + N-연결된 당화)	(서열번호 79)	인간 293 세포	pCMVR	일시적 형질감염 37℃	5	0.2	0.1	0.01
LCB1-6M-GPGcP-Fc13 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GPGcP-Fc-Opt) (LCB 서열은 제1 경우의 **LCB3-3와 동일**	(서열번호 80)	인간 293 세포	pCMVR	일시적 형질감염 37℃	2	0.2	0.1	0.01
LCB3-6M-GPGcP-Fc14 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GPGcP-Fc-Opt) (LCB 서열은 제1 경우의 **LCB3-3** 와 동일)	(서열번호 81)	인간 293 세포	pCMVR	일시적 형질감염 37℃	2	0.2	0.1	0.01
LCB1-6M-GS30-Fc15 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GS30-Fc-Opt)LCB1-4	(서열번호 82)	인간 293 세포	pCMVR	일시적 형질감염 37℃	1	0.2	0.1	0.01
LCB3-6M-GS30-Fc16 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GS30-Fc-Opt) (LCB 서열은 제1 경우의 **LCB3-3**와 동일)	(서열번호 83)	인간 293 세포	pCMVR	일시적 형질감염 37℃	1	0.2	0.1	0.01
LCB1-v1.3-Fc17 (BM40-LCB1-v1.3 -4N,14K,15T,17E,18Q,27 Q,38Q -GS15-Fc-Opt)	(서열번호 84)	인간 293 세포	pCMVR	일시적 형질감염 37℃	5	0.2	0.1	0.01
LCB1-v1.3-Ngly-Fc18 (BM40-LCB1-v1.3 Ngly -4N,14K,15T,17E,18Q,27 N,38Q -GS15-Fc-Opt) (>LCB1_v1.5 (= LCB1_v1.3 + N-연결된 당화)	(서열번호 85)	인간 293 세포	pCMVR	일시적 형질감염 37℃	5	0.2	0.1	0.01
LCB1-v1.3-GPGcP-Fc19 (BM40-LCB1-v1.3-Fc19 -4N,14K,15T,17E,18Q,27 Q,38Q－GPGcP-Fc-Opt)	(서열번호 86)	인간 293 세포	pCMVR	일시적 형질감염 37℃	5	0.2	0.1	0.01
LCB1-v1.3-GS30-Fc20 (BM40-LCB1-v1.3 -4N,14K,15T,17E,18Q,27 Q,38Q -GS30-Fc-Opt)	(서열번호 87)	인간 293 세포	pCMVR	일시적 형질감염 37℃	5	0.2	0.1	0.01

[0928] 설계한 결합제들은 항체에 비해 잠재적인 치료제로서 몇가지 이점을 가진다. 요컨대, 이들 결합제는 다양한 결합 방식을 망라하여, 조합시 바이러스 탈출이 거의 불가능하다. 승온된 온도에서 연장된 시간 경과 이후에도 활성이 유지되어, 이들 결합제에 저온 유통이 필요하지 않을 것으로 보인다. 이들 디자인은 전장 항체 분자보다 20배 작고, 그래서 동일 질량에서 잠재적인 중화 부위가 20배 이상 더 많으므로, 국소 투여된 약물의 잠재적인 효능이 증가한다. 항체와 달리, 적절한 접힘을 위해 포유류 세포에서 발현시킬 필요가 없는 매우 단순한 미니단백질의 경우, 상품의 단가 및 상당한 대량 생산으로의 규모 확장 필요성이 더 낮을 것이다. 작은 크기와 높은 안정성은 분무에 의한 호흡계로의 직접 전달을 가능하게 한다. 면역원성은 임의의 외래 분자가 가진 잠재적인 문제이지만, 기존에 특성화된 작은 데 노보 설계된 단백질들에서는, 아마도 작은 크기와 더불어 높은 용해성 및

안정성이 이를 수지상 세포 상에 제시할 가능성이 거의 없게 만들어, 면역 반응이 거의 또는 전혀 관찰되지 않았다.

[0929] **참조문헌**

[0930] 1. Yuan M, Wu NC, Zhu X, Lee CD, So RTY, Lv H, Mok CKP, Wilson IA: **A highly conserved cryptic epitope in the receptor binding domains of SARS-CoV-2 and SARS-CoV**. *Science* 2020, **368**(6491):630-633.

[0931] 2. Case JB, Rothlauf PW, Chen RE, Liu Z, Zhao H, Kim AS, Bloyet L-M, Zeng Q, Tahan S, Droit L *et al*: **Neutralizing antibody and soluble ACE2 inhibition of a replication-competent VSV-SARS-CoV-2 and a clinical isolate of SARS-CoV-2**. *bioRxiv* 2020:2020.2005.2018.102038.

[0932] **수용체-결합 도메인을 표적으로 하는 초강력 미니단백질은 SARS-CoV-2 감염 및 질환으로부터 보호한다.**

[0933] COVID-19 대유행을 완화하기 위한 공중 보건 조치와 스파이크 단백질-기반의 백신의 도입에도 불구하고, SARS-CoV-2 감염과 사망은 계속 증가하고 있다. 여기서, 본 발명자들은, 선두 결합제 한종 LCB1에 대한 변형된 버전이, 인간 ACE2-발현성 형질전환 마우스에서 SARS-CoV-2-매개 폐 질환으로부터 보호하는 능력을 조사하였다. LCB1-Fc의 전신 투여는 바이러스 부담을 감소시켜 세포 침윤과 염증을 감소시켰으며, 폐 질환 및 병리를 완전히 방지하였다. LCB1v1.3의 비강내 1회 투여는, 바이러스 접종하기 전 최대 5일 또는 접종한 후 최대 2일에 제공된 경우에도, 폐에서 SARS-CoV-2 감염을 감소시켰다. 중요하게도, LCB1v1.3는 원형 균주 (WA1/2020), 신생 B.1.1.7 균주 및 핵심적인 E484K 및 N501Y 스파이크 단백질 치환을 코딩하는 균주로부터 생체내 보호하였다. 이들 데이터는 SARS-CoV-2 감염을 예방 또는 치료하는데 있어 LCB1v1.3의 용도를 뒷받침해준다.

[0934] 중증 급성 호흡기 증후군 코로나바이러스 2 (SARS-CoV-2)는 코로나바이러스 질환 2019 (COVID-19) 대유행의 원인으로서, 전 세계적으로 질환, 고통 및 경제적인 어려움을 초래하였다. 공중 보건 조치에도 불구하고, SARS-CoV-2 전파는 기본적으로 인간에서 인간으로의 전파를 통해 계속 이루어지고 있다 (Day, 2020; Li et al., 2020; Standl et al., 2020). SARS-CoV-2-유발성 임상 증상은 무증상 감염에서부터 중증 폐렴, 다기관 장애 및 사망에 이른다. 질환 중증도를 결정짓는 기저 기전에 대해서는 거의 파악되지 않았지만, 면역력이 약한 개체, 노인 그리고 특정 합병증을 가진 개체 (예, 심혈관 질환, 당뇨병 또는 비만 병력)가 예후 불량 위험성이 높다 (Zhou et al., 2020).

[0935] 본원에서, 인간 ACE2 (hACE2)-발현성 형질전환 마우스에서 엄격한 SARS-CoV-2 질환 발병 모델을 이용해 (Golden et al., 2020; Winkler et al., 2020a), 본 발명자들은 예시적인 미니단백질 결합제, LCB1의 생체내 효과를 평가하였다. 생체내 실험을 위해, 본 발명자들은 LCB1의 2가지 버전을 조사하였다: (a) Fc-변형된 2가 형태로서, 생체내 반감기를 연장하고 면역 시스템의 작동자 부분 (effector arm)과 연관시킨, LCB1-hIgG-Fc9 (LCB1-Fc); 및 (b) 추가로 최적화한, Fc 도메인이 결핍된 단량체 형태로서, LCB1v1.3. SARS-CoV-2 노출하기 하루 전 또는 노출한 후 다음날 LCB1-Fc의 복막내 투여는 체중 감소의 부재, 검출 한계에 달하는 바이러스 부담 감소 및 폐 염증과 병리의 저해 등의 실질적인 보호를 제공하였다. LCB1v1.3의 비강내 전달은 무려 SARS-CoV-2 접종하기 5일 전 또는 접종한 후 2일째에도 보호를 제공하였다. 투여 실험 결과, LCB1v1.3는 약리학적으로 달성가능한 농도에서 효능을 유지하며, 면역원성은 약한 것으로, 드러났다. 가장 중요하게는, LCB1v1.3는 문제가 되는 남아프리카 (B.1.351) 및 브라질 변종 (B.1.1.248)에 존재하는 주요 스파이크 치환 E484K 및 N501Y을 코딩하는 SARS-CoV-2 균주와 현재 발생하는 B.1.1.7 영국 변종으로부터 동물을 보호하였다. 요컨대, 이러한 연구를 통해 LCB1-Fc 및 LCB1v1.3가 SARS-CoV-2 질환을 예방 또는 완화하기 위한 가능성 있는 치료제로서 확정되었다.

[0936] **결과**

[0937] **LCB1v1.3 예방은 바이러스 부담과 임상 질환을 제한한다.** 본 발명자들은 LCB1을 변형하여, 생체내 검사용 2가지 버전을 제작하였다: (a) RBD 결합성은 변형시키지 않으면서 발현 수율 및 용해성을 높이기 위해 LCB1에 극성 돌연변이를 도입하였으며 (LCB1v1.3), (b) 생체이용성을 강화하기 위해 LCB1을 인간 IgG1 Fc 도메인과 융합함으로써 LCB1을 변형하였다 (LCB1-Fc). LCB1v1.3 및 LCB1-Fc는 S 삼량체의 단일 RBD에 강하게 결합하며 (**도 5A**), 해리 상수 (K_D)는 각각 625 pM 및 156 pM 미만이었다 (**도 5B**). LCB1v1.3 및 LCB1-Fc는 또한 어센틱 SARS-CoV-2 분리주 (2019n-CoV/USA_WA1/2020 [WA1/2020])를 강하게 중화하였다 (EC_{50}은 각각 14.4 및 71.8 pM임; **도 5C**).

[0938] SARS-CoV-2에 대한 이들 미니단백질의 보호 잠재성을 확인하기 위해, 본 발명자들은 K18 인간 hACE2-발현성 형질전환 마우스를 이용하였으며, 이에 SARS-CoV-2를 비강내 접종하여 중증 폐 감염 및 질환을 유발하였다 (Golden et al., 2020; Winkler et al., 2020a). 예방 실험에서, SARS-CoV-2 WA1/2020을 10^3 PFU로 비강내

(i.n.) 접종하기 하루 전에, LCB1-Fc 250 mg (10 mg/kg)을 단일 용량으로 복막내 주사 (i.p.)에 의해 투여한 바, 비슷한 전산적 방법을 이용해 설계한 대조군 단백질 (인플루엔자 A 바이러스 헤마글루티닌 미니결합제)이 투여된 동물과 비교해, 체중 감소가 방지되었다 (**도 5D**). LCB1-Fc 예방 후, 감염시킨 바이러스는 감염 후 4 또는 7일차 (dpi)에 검출되지 않은 반면, 대조군 단백질을 투여한 동물에서는 높은 수준으로 관찰되었다 (**도 5E,** *상단 및 하단*). 마찬가지로, LCB1-Fc 처리 동물의 폐, 심장, 비장 및 뇌에서 바이러스 RNA 수준은 4 또는 7 dpi에 분석의 검출 한계 수준이거나 또는 그 근처였다 (**도 5F-I**). LCB1-Fc 처리는 4 dpi에 입수한 코 세척액 샘플에서 바이러스 RNA 수준에는 효과가 없었으며 (**도 5J**), 이는 햄스터에서 최근 인간 항체 중화 실험과 비슷한 결과였다 (Zhou et al., 2021). 그러나, 바이러스 RNA 수준은 7 dpi에 감소하였으며, 이는 LCB1-Fc 처리가 상기도에서 바이러스 제거를 가속화하거나 또는 전파를 방지함을 시사해준다.

[0939] COVID-19 폐 질환의 증상은 미만성 폐포 손상, 염증 및 폐렴이며, 호흡 곤란과 기계적 인공호흡 필요성으로 이어진다 (Johnson et al., 2020; Kordzadeh-Kermani et al., 2020). 본 발명자들은 K18-hACE2 마우스에 SARS-CoV-2 감염 후 관찰되는 폐 기능 손상을 방지하는 LCB1-Fc의 능력을 평가하였다 (Winkler et al., 2020a). 7 dpi에 LCB1-Fc 처리 동물에서 폐 생체역학에 대한 기계적 인공호흡 검사를 수행한 결과, 나이브 동물과는 차이가 관찰되지 않은 반면 (**도 6A**), 대조군 결합제 단백질이 제공된 마우스에서는 최대흡기량 및 폐 유순도 감소뿐 아니라 폐 저항, 탄력성 및 조직 저항의 증가가 관찰되었는데, 이는 모두 폐 기능 손상과 일치하였다. 이러한 생물물리학적 특성으로 인해 대조군 결합제 및 LCB1-Fc 처리 동물 또는 나이브 동물 간에 전혀 다른 압력-용량 곡선이 수득되었다. 또한, 본 발명자들은 SARS-CoV-2-유발성 폐 병리에 대한 LCB1-Fc 처리 효과를 평가하였다. SARS-CoV-2 노출 후 7 dpi에 수집한 동물의 폐 단편에서는 LCB1-Fc 비-처리한 대조군 단백질-처리 마우스 또는 나이브 마우스에서 세포 침윤 및 기강경화 (airspace consolidation)를 특징으로 하는 광범위하게 확산된 염증이 관찰되었다 (**도 6B**). 4 dpi에, 대조군 결합제 처리 동물이 아닌 LCB1-Fc 처리 동물에서는 폐에서 염증성 사이토카인과 케모카인 RNA 시그니처는 나타나지 않았으며, 이는 LCB1-Fc 처리가 폐에서 바이러스 감염 및 염증을 방지함을 시사해준다 (**도 6C 및 11**).

[0940] **항--RBD 결합제를 이용한 노출-후 요법은 바이러스 부담을 감소시킨다.** 노출-후 상황에서 그 효과를 평가하기 위해, 1 dpi에 LCB1-Fc를 i.p. 주사에 의해 투여하였다. LCB1-Fc를 이용한 요법은 체중 감소를 방지하였으며 (**도 7A**), 4 및 7 dpi에 검사한 모든 조직들에서 바이러스 부담을 감소시켰다 (**도 7B-G**). 각 시점에 수집한 LCB1-Fc 처리 동물의 폐에서는 감염성 바이러스가 회수되지 않았다. 폐 조직 단편에서, LCB1-Fc 요법이 병리학적 결과를 향상시키는 것으로 검증되었다 (**도 7H**). 7 dpi에 LCB1-Fc 처리 동물의 폐 조직 단편에서 면역 세포 침윤은 관찰되지 않았지만, 대조군 결합제-처리 동물에서는 그렇지 않았다.

[0941] 본 발명자들은 다음으로 노출 후 i.n. 전달 요법으로서 LCB1v1.3의 효능을 조사하였다. I.n. 전달은 항-SARS-CoV-2 생물제제의 자가-투여를 가능하게 할 수 있다. 실제, 인플루엔자 바이러스에 대한 미니단백질 저해제는 코 미스트로서 효능이 입증된 바 있다 (Chevalier et al., 2017). 이러한 실험들에서, LCB1v1.3가 주어진 질량 용량에 대해 더 많은 수의 RBD 분자에 결합하여 중화 활성 증가를 달성할 수 있어, 본 발명자들은 LCB1v1.3을 이용하였다 (**도 5C**). 7 dpi에 대조군 결합제-처리 동물의 폐 및 기타 말초 조직에서 SARS-CoV-2 RNA가 높은 수준으로 검출된 반면, LCB1v1.3 투여 동물에서는 SARS-CoV-2 접종 후 D+1 또는 D+2에 i.n. 투여에 의해 감염이 감소하였다 (**도 7I 및 12**). LCB1v1.3 처리 동물의 코 세척액에서는 대조군 결합제-처리 동물과 비교해 처리 후 D+1에 바이러스 RNA 수준이 감소하였지만, D+2에는 그렇지 않았다 (**도 7J**).

[0942] **LCB1v1.3의 비강내 전달은 감염 후 최대 5일 투여시까지 SARS-CoV-2로부터 보호를 제공한다.** 본 발명자들은 다음으로 i.n. 예방으로 투여된 LCB1v1.3의 내구성을 조사하였다. SARS-CoV-2를 10^3 PFU로 접종하기 5일전, 3일전, 1일전 또는 6시간 전에, K18-hACE2 형질전환 마우스에 LCB1v1.3 또는 대조군 결합제를 50 μg 1회 i.n. 용량으로 투여하였다. 4 또는 7 dpi에, 조직에서 바이러스 부담을 RT-qPCR에 의해 확인하였다. 예상한 바와 같이, SARS-CoV-2 노출 시점에 인접하여 투여한 경우에는 바이러스 부담 및 체중 감소에 대한 더 높은 저하로 확인된 바와 같이 LCB1v1.3에 의한 보호가 더 우수하였다 (**도 8A-D 및 S3**). 그러나, 접종하기 5일전에 LCB1v1.3를 투여하고 7 dpi에 수집한 마우스에서도, 대조군 결합제 처리 동물과 비교해, 폐에서 바이러스 RNA 수준 저하가 관찰되었다. 수집 시점과 무관하게, SARS-CoV-2 접종하기 3일 전에 LCB1v1.3를 투여한 동물에서도 폐 바이러스 RNA 수준이 감소하였다.

[0943] 본 발명자들은 LCB1v1.3 i.i. 용량 범위에서 효능을 조사하였다 (**도 8E-J**). LCB1v1.3를 2 mg (0.1 mg/kg) 정도로 소량 처리한 경우 SARS-CoV-2-유발성 체중 감소가 방지되었다. LCB1v1.3 투여량 2 및 10 mg (0.1 - 0.5 mg/kg)은, 대조군-결합제-처리 동물과 비교해, 7 dpi에 폐, 심장 및 비장 내 바이러스 RNA 수준을 감소시켰다.

아울러, LCB1v1.3를 50 ㎍ 용량으로 투여한 동물에서는 있더라도 최소의 폐 염증이 관찰되었다 (**도 8K**). 요컨대, 이러한 결과는, 노출 전 i.n. 경로로 투여시 LCB1v1.3 저용량으로도 SARS-CoV-2 감염 및 질환을 엄격한 K18-hACE 형질전환 마우스 발병 모델에서 제한할 수 있음을, 보여준다.

[0944] **LCB1v1.3는 면역원성이 낮고, 반복 투여 후 보호 활성을 유지한다.** 본 발명자들은 K18-hACE2 형질전환 마우스에 대조군 결합제 또는 LCB1v1.3를 50 ㎍으로 총 18일 동안 3일 간격으로 투여하였다 (**도 9A**). 이 시점에, 혈청을 수집하여, 항-LCB1v1.3 항체의 존재를 확인하였다. 마우스 10마리 중 단 1마리에서만 LCB1v1.3에 대한 IgG 항체가 만들어졌다 (**도 9B**). 반복 투여가 LCB1v1.3-매개 보호를 제공하는지를 확인하기 위해, 코호트에 SARS-CoV-2를 10^3 PFU로 기회 감염시켰다. 재차, 체중 감소 (**도 9C**) 및 폐 및 다른 장기에서 바이러스 감염에 대한 실질적인 보호가 LCB1v1.3 투여 동물 전체에서 관찰되었다 (**도 9D-H**).

[0945] **LCB1v1.3는 신생 SARS-CoV-2 변종으로부터 보호한다.** 본 발명자들은 69-70 및 144-145의 결손 및 N501Y, A570D, D614G 및 P681H 치환을 가진 B.1.1.7 분리주, 그리고 B.1.351 및 B.1.248 변종에서 잔기 E484K, N501Y 및 D614G에 존재하는 주요 치환을 가진 재조합 WA1/2020 균주에 대한 LCB1v1.3의 활성을 조사하였다 (Xie et al., 2021a). B.1.1.7 및 E484K/N501Y/D614G 균주에 대한 LCB1v1.3의 중화 활성이 WA1/2020 균주에서보다 약 45-50배 낮았음에도 불구하고, EC_{50} 값은 여전히 각각 ~800 pM 및 667 pM이었다 (**도 10A**). LCB1v1.3가 문제되는 스파이크 단백질 치환을 가진 SARS-CoV-2 균주로부터 생체내 보호할 수 있는지를 확인하기 위해, K18-hACE2 형질전환 마우스에 LCB1v1.3 또는 대조군 결합제를 1회 i.n. 50 ㎍ 용량으로 B.1.1.7 또는 E484K/N501/D614G SARS-CoV-2 10^3 PFU 접종하기 하루 전에 투여하였다. 특히, 어느 한가지 변종을 기회 감염시키기 전에 사전 LCB1v1.3 처리시 6 dpi에 수집한 모든 조직들에서 바이러스 감염 (**도 10C-G 및 10I-M**) 및 체중 감소 (**도 10B 및 10H**)가 방지되었다. 즉, LCB1v1.3는 SARS-CoV-2의 신생 균주 및 순환 균주 모두에 대해 효과적이다.

[0946] **고찰**

[0947] 본원에서, 본 발명자들은, 엄격한 K18-hACE2 마우스의 SARS-CoV-2 발병 모델을 이용해, LCB1-Fc가 바이러스 접종하기 하루 전 또는 접종한 후 다음날 투여시 SARS-CoV-2 감염 및 질환을 방지함을 입증해 주었다. LCB1-Fc 처리 마우스의 폐 생체역학은 검사한 모든 매개변수에서 나이브 동물의 결과를 나타내었다.

[0948] 또한, 본 발명자들은 Fc 도메인이 없는 LCB1의 최적화된 단량체 형태인 LCB1v1.3의 효능을 평가하였다. LCB1v1.3 1회 i.n. 용량을 무려 SARS-CoV-2 감염하기 5일전 또는 감염한 후 2일차에 투여하였을 경우, 바이러스 부담이 감소되었다. 본 발명의 i.n. 전달 방식은 독특하다. SARS-CoV-2의 i.n. 요법은 햄스터 질환 모델에서 1형 인터페론을 이용한 경우에만 보고된 바 있으며 (Hoagland et al., 2021), 효능은 제한적이었다. K18-hACE2 마우스 모델은 폐 염증 및 저하된 폐 기능 등의 중증 COVID-19의 몇가지 특징들을 나타낸다 (Golden et al., 2020; Winkler et al., 2020a). K18-hACE2 마우스는 감염에 매우 취약하므로, 처치의 치료학적 범위가 제한적이며 (Winkler et al., 2020b), 본 발명의 미니단백질의 경우에는 바이러스 감염만 억제할지 모른다. 중요하게도, 본 발명의 데이터는, 감염 전 또는 감염 후 LCB1v1.3 결합제 처리가 면역 세포 침윤 및 폐 염증을 제한하여, 조직 손상 및 호흡 기능 저하를 방지함을 입증해주었다. 코 예방에 대한 원리 증명 연구의 일환으로, LCB1v1.3의 낮은 면역원성이 관찰되었으며, 이는 반복 투여가 가능할 수 있음을 시사한다.

[0949] 수종의 항체-기반의 요법들이 SARS-CoV-2에 유망한 것으로 입증되고 일부는 EUA 승인되었음에도 불구하고, 바이러스 진화는 영국 (B.1.1.7), 남아프리카 (B.1.351), 브라질 (B.1.248) 및 기타 지역에서의 신생 변종에서 입증된 바와 같이 이러한 개입에 위협이 될 수 있다. 실제, 본 발명자 및 다른 사람들은, 수많은 단일클론 항체 및 다클론 항체가 이들 변종 수종에 대해 중화 활성 저하를 보임을 관찰한 바 있다 (Chen et al., 2021; Wang et al., 2021a; Wang et al., 2021b; Wibmer et al., 2021; Xie et al., 2021b). 이와 비교해, LCB1v1.3는 초기 (WA1/2020) 및 신생 (B.1.1.7 및 E484K/N501Y/D614G) SARS-CoV-2 균주들에 대해 모두 효과가 있었다. SARS-CoV-2 RBD와의 복합체를 형성한 오리지널 LCB1 결합제의 cryo-EM 구조에 기반하면 (Cao et al., 2020), N501Y 돌연변이만 결합에 영향을 미치는 것으로 예상된다. 본 발명자들은 신생 변종에서 LCB1v1.3의 중화 활성 감소를 관찰하였지만, EC_{50} 값이 여전히 800 pM 미만으로, 상당한 효능이 유지되는 것으로 보인다.

[0950] 다른 잠재적인 SARS-CoV-2 항체에 기반한 치료와 비교해, 미니단백질은 몇가지 이점을 가진다: (a) 크기가 작아, 하나의 삼량체 스파이크의 각 프로토머에 결합해 주어진 용량에서 더 높은 효력을 제공할 수 있으며; (b) 비율 효율적으로 제조할 수 있으며; 및 (c) 링커 단백질을 이용해 혼성함으로써 내성을 제한하는 다량체 구조를 제작할 수 있다.

[0951] **실험 모델 및 개체에 대한 상세 설명**

[0952] **세포 및 바이러스.** Vero E6 (CRL-1586, American Type Culture Collection (ATCC), Vero CCL81 (ATCC), Vero-furin (Mukherjee et al., 2016) 및 Vero-hACE2-TMPRSS2 (A. Creanga and B. Graham의 선물, NIH)는, 10% 소 태아 혈청 (FBS), 10 mM HEPES pH 7.3, 1 mM 소듐 피루베이트, 1x 비-필수 아미노산 및 100 U/ml 페니실린-스트렙토마이신이 첨가된 둘베코의 변형된 이글 배지 (DMEM)에서 37℃에서 배양하였다. 또한, Vero-hACE2-TMPRSS2 세포는 5 μg/mL 푸로마이신의 존재 하에 배양하였다. SARS-CoV-2의 WA1/202 (2019n-CoV/USA_WA1/2020) 분리주는 미국 질환 방제 센터 (CDC)에서 입수하였다. B.1.1.7 및 WA1/2020 E484K/N501Y/D614G 바이러스는 이전에 언급된 바 있다 (Chen et al., 2021; Xie et al., 2021a). Vero CCL81 또는 Vero-hACE2-TMPRSS2 세포를 접종하여 감염성 원액을 증폭시켰다. 상층액을 수집하여 분액한 다음 -80℃에서 보관하였다. 감염성 SARS-CoV-2를 이용한 모든 작업은 워싱턴 의학 대학의 생물안전위원회-허가 BSL3 및 A-BSL3 시설에서 양압 공기 호흡기 및 보호 장비를 수반하여 수행하였다.

[0953] **마우스 실험.** 동물 실험은 국립보건원의 실험 동물 관리 이용 지침의 권고안에 따라 수행하였다. 프로토콜은 워싱턴 의학 대학의 동물 관리 이용 위원회로부터 승인받았다 (보증 번호 A3381-01). 케타민 염산염 및 자일라진으로 마취를 유도하여 유지시킨 상태에서 바이러스를 접종하였으며, 동물 통증을 최소화하기 위한 모든 시도를 행하였다.

[0954] 이형접합성 K18-hACE c57BL/6J 마우스 (균주: 2B6.Cg-Tg(K18-ACE2)2Prlmn/J)는 Jackson Laboratory에서 입수하였다. 동물은 군으로 사육하고, 표준 사료 (chow diet)를 제공하였다. 다양한 나이의 암컷 및 수컷 마우스에 SARS-CoV-2를 10^3 PFU로 비강내 투여를 통해 투여하였다.

[0955] **방법에 대한 상세한 설명**

[0956] **미니단백질 제조.** LCB1-Fc를 합성하고, GenScript 사에서 pCMVR 플라스미드에 카나마이신 내성을 이용해 클로닝하였다. 플라스미드는 *E. coli*의 NEB 5-alpha 균주 (New England Biolabs)에 형질전환하여, Expi293F 포유류 세포에 일시적으로 형질감염하기 위한 DNA를 회수하였다. Expi293F 세포는 Expi293F 발현 배지 (Life Technologies)를 이용해 150 rpm으로 교반하면서 33℃, 70% 습도 및 8% CO_2 하에 현탁 배양하였다. 배양물을 PEI-MAX (Polyscience)를 이용해, 3 x 10^6 세포/mL 밀도로 배양한 세포에 형질감염시켜, 3일간 배양하였다. 이를 원심분리 (4000 x *g*에서 5분, PDADMAC 용액을 최종 농도 0.0375%로 첨가 (Sigma Aldrich, #409014), 및 2차 스핀 (5분, 4000 x *g*))하여, 상층액을 청징 처리하였다. 청징 처리된 상층액을 MabSelect PrismA™ 2.6x5 cm 컬럼 (Cytiva)을 이용해 AKTA Avant150 FPLC (Cytiva)에서 정제하였다. 결합한 단백질은 5 컬럼 부피의 20 mM $NaPO_4$ 및 150 mM NaCl pH 7.2와 이후 5 컬럼 부피의 20 mM $NaPO_4$ 및 1 M NaCl pH 7.4로 헹군 후, 3 컬럼 부피의 100 mM 글리신 (pH 3.0)으로 용출시켰다. 용출물은 2 M 트리스 베이스를 사용해 최종 농도 50 mM로 중화하였다. SDS-PAGE를 이용해 단백질 순도를 평가하였다. 단백질은 0. 22 ㎛ 필터를 통과시켜, 사용시까지 4℃에서 보관하였다.

[0957] 오리지널 LCB1에 대해 극성 돌연변이 (4N, 14K, 15T, 17E, 18Q, 27Q, 38Q)를 가진 LCB1v1.3를 pet29b 벡터에 클로닝하였다. LCB1v1.3는 Lemo21(DE3)(NEB)에서 테리픽 브로스 배지 (terrific broth media) 중에 발현시키고, 2 L 배플드 셰이크 플라스크에서 배양하였다. 박테리아는 37℃에서 O.D.600 ~0.8까지 증식시킨 후 1 mM IPTG를 첨가하여 유도하였다. 발현 온도를 18℃로 낮추고, 세포를 ~16 h 동안 교반하였다. 세포를 회수하여 열 처리를 통해 세포용해한 다음 80℃에서 10분간 교반하면서 인큐베이션하였다. 세포용해물을 24,000 *x g*로 30분간 원심분리하여 청징 처리한 다음 IMAC 사에서 AKTA Avant150 FPLC 시스템 (Cytiva)에서 정제하기 위해 2.6x10 cm Ni Sepharose™ 6 FF 컬럼 (Cytiva)에 로딩하였다. 단백질을 50 mM Tris pH 8.0 및 500 mM NaCl 완충제 중의 이미다졸 30 mM -> 500 mM 선형 농도 구배를 이용해 용출시켰다. 피크 분획들을 모아 10 kDa MWCO 원심분리 필터 (Millipore)에서 농축한 다음 멸균 여과 (0.22 μm)하여 Superdex™ 200 Increase 10/300 또는 HiLoad S200 pg GL SEC 컬럼 (Cytiva)에 50 mM 포스페이트 pH 7.4, 150 mM NaCl 완충제를 사용해 적용하였다. 크기 배제 크로마토그래피를 실시한 후, 박테리아-유래 성분을 검사해 낮은 수준의 내독소를 검증하였다.

[0958] **생물층 간섭측정.** 생물층 간섭측정 데이터는 Octet™ RED96 (ForteBio)을 이용해 수집하고, 장치에 통합된 소프트웨어를 이용해 처리하였다. 간략하게는, 바이오틴화된 RBD (Acro Biosystems)를 스트렙타비딘-코팅된 바이오센서 (SA ForteBio)에 20 nM로 결합 완충제 (10 mM HEPES (pH 7.4), 150 mM NaCl, 3 mM EDTA, 0.05% 계면활성

제 P20 및 0.5% 탈지유 분말) 중에 360초간 로딩하였다. 분석 단백질 (LCB1v1.3 또는 LCB1-Fc)을 농축 원액으로부터 결합 완충제로 희석하였다. 결합 완충제 단독에서 베이스라인을 측정한 후, 바이오센서를 표적 단백질이 지정된 농도로 수용된 웰에 3,600 s 동안 침지한 (결합 단계) 다음 바이오센서를 다시 베이스라인/완충제에 7,200 s 동안 침지하여 (해리), 결합 동역학을 모니터링하였다.

[0959] **플라크 분석**. Vero-furin 세포 (Mukherjee et al., 2016)를 바닥이 평평한 12웰 조직 배양 플레이트에서 각 웰에 세포 $2.5x10^5$의 밀도로 접종하였다. 다음날, 배지를 제거하고, DMEM+2% FBS에 10배 연속 희석한 적정할 물질의 희석물 200 ㎕로 교체한 다음 플레이트를 주기적으로 흔들면서 37℃에서 인큐베이션하였다. 1시간 후, 메틸셀룰로스 1 mL을 적층하였다. 플레이트를 37℃에서 72시간 동안 인큐베이션한 다음 PBS 중의 4% 파라포름알데하이드 (최종 농도)로 20분간 고정하였다. 고정된 세포 단일층을 20% 메탄올 중의 0.05% (w/v) 크리스탈 바이올렛으로 염색하고, 멸균한 탈이온수로 2번 헹구었다.

[0960] **바이러스 부담 측정.** 조직의 무게를 측정하고, MagNA Lyser™ 장치 (Roche Life Science)에서 2% 열-불활화된 FBS가 첨가된 DMEM 배지 1,000 ㎕ 중에 지르코니아 비드를 사용해 균질화하였다. 조직 균질물을 10,000 rpm으로 5분간 원심분리하여 청징 처리한 다음 -80℃에서 보관하였다. KingFisher Flex 추출 로봇 (Thermo Scientific)에서 MagMax mirVana™ 총 RNA 단리 키트 (Thermo Scientific)를 이용해 RNA를 추출하였다. RNA를 역 전사하고, TaqMan™ RNA-to-CT 1-스텝 키트 (ThermoFisher)를 사용해 증폭시켰다. 역 전사는 48℃에서 15분 및 이후 95℃에서 2분간 처리하여 수행하였다. 증폭은 다음과 같이 사이클 50회로 수행하였다: 95℃에서 15초 및 60℃에서 1분. 샘플에서 SARS-CoV-2 N 유전자 RNA 카피를 이전에 공개된 분석을 이용해 확인하였다 (Case et al., 2020; Hassan et al., 2020). 간략하게는, N 유전자의 고도로 보존된 영역을 표적화하기 위해 TaqMan™ 분석을 설계하였다 (정방향 프라이머: ATGCTGCAATCGTGCTACAA (서열번호 190); 역방향 프라이머: GACTGCCGCCTCTGCTC (서열번호 191); 프로브: /56-FAM/TCAAGGAAC/ZEN/AACATTGCCAA/3IABkFQ/) (서열번호 192). 이 영역은 반응 당 카피수 10개 미만으로 카피수 측정 가능하도록 RNA 가닥에 포함시켰다. 반응 혼합물은 프라이머 및 프로브를 최종 농도 각각 500 및 100 nM로 포함하였다.

[0961] **사이토카인 및 케모카인 mRNA 측정**. 전술한 바와 같이 폐 균질물로부터 RNA를 단리하였다. DNAse-처리된 RNA로부터 고-효율 cDNA 역 전사 키트 (Thermo Scientific) 및 첨가된 RNase 저해제를 제조사의 프로토콜에 따라 이용해 cDNA를 합성하였다. TaqMan™ Fast Universal PCR 마스터 믹스 (Thermo Scientific) 및 *IFN-g* (IDT: Mm.PT.58.41769240), *IL-6* (Mm.PT.58.10005566), *IL-1b* (Mm.PT.58.41616450), *Tnfa* (Mm.PT.58.12575861), *CXCL10* (Mm.PT.58.43575827), *CCL2* (Mm.PT.58.42151692), *CCL5* (Mm.PT.58.43548565), *CXCL11* (Mm.PT.58.10773148.g), *Ifnb* (Mm.PT.58.30132453.g), *CXCL1* (Mm.PT.58.42076891)에 특이적인 시판 프라이머/프로브 세트를 이용해 사이토카인 및 케모카인 발현을 측정하고, 결과를 *GAPDH* (Mm.PT.39a.1) 수준에 대해 표준화하였다. $2^{-\Delta\Delta Ct}$ 방법을 이용해 처리 마우스와 나이브 대조군을 비교해 배수 변화를 결정하였다.

[0962] **폐 병리학.** 조직 회수 및 고정하기 전 동물을 안락사시켰다. 좌측 폐를 먼저 좌측 주 기관지에서 묶어, 바이러스 RNA를 분석하기 위해 수집하였다. 우측 폐에는 10% 중성 완충화된 포르말린 약 1.2 mL을 3-mL 시린지와 기도에 삽입된 카테터를 사용해 주입하여 부풀렸다. 조직을 파라핀으로 함침하고, 단편을 헤마톡실린 및 에오신으로 염색하였다. Hamamatsu NanoZoomer™ 슬라이드 스캐닝 시스템을 사용해 슬라이드를 스캔하고, NDP 뷰 소프트웨어 (ver.1.2.46)로 이미지를 획득하였다.

[0963] **호흡 역학.** 마우스를 케타민/자일라진 (각각 100 mg/kg 및 10 mg/kg)으로 마취하였다. 목 영역을 절개하여 기도를 단리하고, 18게이지의 블런트 금속 캐뉼러 (전형적인 저항 0.18 $cmH_2O.s/mL$)를 사용해 캐뉼러를 삽입하였으며, 나일론 봉합사로 고정하였다. 그런 후, FX 어댑터 Y-튜빙에 부착된 캐뉼러를 통해 flexiVent™ 컴퓨터-제어되는 피스톤 호흡기 (SCIREQ Inc.)를 마우스에 연결하였다. 기계적 인공 호흡을 개시하였으며, 마우스에 케타민 100 mg/kg 및 마비성 판쿠로늄 브로마이드 0.1 mg/마우스를 복막내 경로로 투여하여, 인공 호흡에 반하는 호흡을 측정 중에 억제시켰다. 마우스는 마우스에 대한 디폴트 설정을 이용해 인공 호흡을 실시하였으며, 이는 호기 종말 양압 3 cm H_2O, 10 mL/kg 1회 호흡량 (Vt), 호흡율 150회/분 (bpm) 및 흡기 산소분율 (FiO_2) 0.21 (즉, 실내 공기)로 구성된다. 호흡 역학은 강제 진동 기법을 이용해 이전에 언급된 (McGovern et al., 2013) 바와 같이, 최신 버전의 flexiVent™ 오퍼레이팅 소프트웨어 (flexiWare v8.1.3)를 이용해 분석하였다. 압력-용량 곡

선 및 최대흡기량 측정을 수행하였다.

[0964] **중화 분석.** 결합제 단백질의 연속 희석물을 SARS-CoV-2 10^2 FFU (focus-forming unit)와 함께 37℃에서 1시간 동안 인큐베이션하였다. 96웰 플레이트에서 결합제-바이러스 복합체를 Vero E6 (WA1/2020) 또는 Vero-hACE2-TMPRSS2 (B.1.1.7 및 WA1/2020 E484K/N501Y/D614G) 세포 단일층에 첨가하여, 37℃에서 1시간 동안 인큐베이션하였다. 그 후, 세포에 2% FBS 첨가된 MEM 중의 1% (w/v) 메틸셀룰로스를 적층하였다. 24-30시간 후 적층을 제거하여 플레이트를 회수한 다음 PBS 중의 4% PFA로 실온에서 20분간 고정하였다. 플레이트를 헹군 다음 0.1% 사포닌 및 0.1% 소 혈청 알부민 첨가된 PBS 중에 SARS2-2, SARS2-11, SARS2-16, SARS2-31, SARS2-38, SARS2-57 및 SARS2-71 항-스파이크 단백질 항체의 올리고클로날 풀 (Zhou et al., 2021) 및 HRP-접합된 염소 항-마우스 IgG와 연속 인큐베이션하였다. SARS-CoV-2-감염된 세포 포커스를 TrueBlue™ 퍼옥시다제 기질 (KPL)을 사용해 가시화하고, ImmunoSpot™ 미세분석기 (Cellular Technologies)로 정량하였다. Prism™ 소프트웨어 (GraphPad Prism™ 8.0)로 데이터를 가공 처리하였다.

[0965] **ELISA.** C-말단 바이오틴화된 LCB1.1v3를 스트렙타비딘-코팅된 플레이트 (RayBiotech #7C-SCP-1)에 총 부피 100 ㎕ 중의 2.5 ㎍/mL로 고정한 다음 4℃에서 밤새 인큐베이션하였다. 플레이트를 세척 완충제 (TBS + 0.1% (w/v) BSA + 0.05% (v/v) Tween20)로 헹구고, 차단 완충제 (TBS + 2% (w/v) BSA + 0.05% (v/v) Tween20) 200 ㎕/웰로 실온에서 1시간 동안 차단 처리하였다. 플레이트를 세척 완충제로 200 ㎕/웰로 헹군 다음 차단 완충제에서 1:100 희석한 혈청 샘플 100 ㎕를 각각의 웰에 첨가하였다. 양성 대조군의 경우, Fc-RBD를 차단 완충제 100 ㎕에서 240 ng/mL부터 시작해 1:5로 연속 희석하였다. 샘플 모두 실온에서 1시간 동안 인큐베이션하였다. 플레이트를 세척 완충제 200 ㎕/웰로 헹구었다. 혈청 샘플의 경우, HRP-접합된 말 항-마우스 IgG 항체 (Vector Laboratories #PI-2000-1)를 차단 완충제에 1:200로 희석하여, 각 웰에 100 ㎕ 씩 넣어 실온에서 30분간 인큐베이션하였다. 양성 대조군의 경우, HRP-접합된 마우스 항-인간 IgG 항체 (Invitrogen #05-4220)를 차단 완충제에 1:500로 희석하고, 각 웰에 100 ㎕ 씩 첨가하여 실온에서 30분간 인큐베이션하였다. 플레이트를 세척 완충제로 헹구고, 각 웰에 TMB (SeraCare) 100 ㎕를 첨가하여 2분간 두었다. 1N HCl 100 ㎕를 첨가해 반응을 정지시켰다. Synergy Neo2™ 플레이트 리더 (BioTek Instruments)에서 450 nm 광학 밀도를 측정하였다.

[0966] **정량 및 통계 분석**

[0967] Prism™ Version 8 (GraphPad)을 이용해 P 값이 >0.05일 경우 통계학적으로 유의한 것으로 간주하였다. 검사, 동물 수, 중앙값 및 통계학적 비교 군들을 각 도면의 범례에 나타낸다. 체중 변화 분석은 이원식 ANOVA에 의해 수행하였다. 기능적 매개변수 또는 면역 매개변수의 변화를 대조군-결합제-처리 동물과 비교하였으며, 일원식 ANOVA 및 다중 비교 검정으로 분석하였다. 양쪽 군 간의 바이러스 부담에 대한 통계 분석은 만-휘트니 검정으로 수행하였다.

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[1003] **다가 디자인**

[1004] SARS-CoV-2의 탈출 변종은 COVID-19 대유행을 상당히 연장하는 위협이 되고 있다. 본원에서 본 발명자들은 이러한 문제를 해결하기 위해 잠재적인 예방학적 및 치료학적 물질로서 다가 미니결합제를 개발하였다. 본 발명자들은 스파이크 삼량체에 기하구조적으로 매칭되는, 미니결합제를 3카피 (자가-조립된 동형삼량체) 또는 서로 다른 부위를 표적화하는 개별 미니결합제들이 3개 연결된 (다중-도메인 융합) 다가 미니결합제를 설계하였으며, 신속한 무세포 발현 및 평가 워크플로우를 이용해 이들의 구성을 최적화하였다. 최적화된 디자인들은 SARS-CoV-2-S-당단백질로부터 매우 느린 해리 속도를 나타내었으며, 복합체의 반감기는 2주 이상이었다. 구조 Cryo-EM 결과, 동형삼량체 및 융합 미니결합제 구조체들은 모두 단일 스파이크 단백질 상의 RBD 3종 모두에 결합할 수 있는 것으로, 확인되었다. 상위 삼량체 및 융합제 후보물질들은 문제가 되는 B.1.1.7, B.1.351, B.1.1.28 변종뿐 아니라 야생형 SARS-CoV-2 바이러스를 중화하였으며, IC50은 낮은 pM 범위였다. 아울러, 상위 동형삼량체 후보물질들은 인간 ACE2-발현성 형질전환 마우스에서 동일한 변종에 대해 예방학적 보호를 제공하였다. 본 발명의 방식

은 문제가 되는 광범위하게 유행하는 변종을 널리 중화할 수 있는 강력한 다가 저해제를 설계하기 위해 신속한 실험 프로토타이핑과 연계된 전산적 단백질 설계 유용성을 부각시켜준다.

[1005] 본 발명자들은 숙주 수용체 ACE2와 SARS-CoV-2 수용체 결합 도메인 (RBD) 간의 상호작용을 차단하는 전산적으로 설계한 미니단백질에 대한 다가 버전을 개발하고자 하였다. 원칙적으로, 설계한 미니결합제의 작은 크기는 하나의 스파이크 단백질 삼량체 내 복수의 RBD에 동시적으로 결합 가능하게 한다. 본 발명자들은, 이러한 다가 결합이 단량체 카운트파트와 비교해 탈출 돌연변이에 대해 내성인 초-고 친화성 저해제를 달성할 수 있을 것으로 가설을 세웠다. 이러한 다가 상호작용으로부터 구현되는 항체 항원 결합성은 개별 도메인으로부터 벗어난 돌연변이의 효과를 완화할 수 있었다. 아울러, 복수의 개별 에피토프들을 포함하거나 또는 표적 에피토프와 서로 다른 접촉 세트를 포함하는 단일 단백질은 돌연변이 탈출에 대한 디자인들의 견고성을 추가로 높일 수 있었다. LCB1, AHB2 및 LCB3 미니결합제 (이하 각각 M1, M2 및 M3으로 언급됨; 표 11) 및 이의 공지된 결합 방식에 기반하여, 다가 저해제, 자기-조립된 동형삼량체 및 다중-도메인 융합체를 설계하는 2가지 병렬적인 전략을 추구하였다.

표 12

[1006]

ID	단백질
M1	LCB1_v2.2
M2	AHB2
M3	LCB3_v2.2
F23-P12	AHB2_v2-PAS12-LCB3_v2.2
F31-P12	LCB3_v2.2-PAS12-LCB1_v2.2
F231-P12	AHB2_v2-PAS12-LCB3_v2.2-PAS12-LCB1_v2.2
F231-P24	AHB2_v2-PAS24-LCB3_v2.2-PAS24-LCB1_v2.2
F23-G10	AHB2_v2-GS10-LCB3_v2.2
F31-F10	LCB3_v2.2-GS10-LCB1_v2.2
F231-G10	AHB2_v2-GS10-LCB3_v2.2-GS10-LCB1_v2.2
H1-1	SB175-6GS-LCB1_v2.2
H2-0	AHB2-4GS-1rfo
H2-1	AHB2-2GS-SB175
H3-1	LCB3_v2.2-6GS-SB175

[1007] **표 11.** 다가 미니결합제를 설명하기 위해 사용된 약어 목록

[1008] 설계한 단백질의 프로토타이핑을 신속하게 수행할 수 있도록, 본 발명자들은 대유행의 긴급성에 보다 부합되는 매우 단축된 설계-구축-검사 사이클을 가능하게 하는 무세포성 DNA 조립 및 단백질 발현 워크플로우를 개발하였다. 본 워크플로우는 깁슨 조립을 이용한 무세포성 DNA 조립 단계 후 무세포성 단백질 합성 (CFPS)을 구동하는 데 사용되는 선형 발현 주형을 구축하기 위한 PCR을 병합하였다. 개발한 워크플로우로, 단 6시간 안에 합성 DNA를 정제된 단백질로 번역할 수 있으며, 고-처리량 방식 (예, 96웰 또는 384웰 플레이트)으로 쉽게 규모 확장가능하며, 자동화된 액체 처리가 가능하다. 아울러, 본 발명자들은 단량체 RNA 또는 삼량체 hexapro SARS-CoV-2-S-당단백질 (S6P)에 대해 설계한 단백질의 해리 속도를 비교할 수 있도록, 무세포성 워크플로우를 AlphaLISA™ 단백질-단백질 상호작용 (PPI) 경쟁 분석과 결합시켰다. 다가 (multivalency)는 주로 상호작용의 해리 속도 상수에만 영향을 미치므로, 인-솔루션 오프-속도 (in-solution off-rate) 스크린으로 1가 결합을 다가 결합으로부터 구분할 수 있을 것으로 추정하였다. 구축한 워크플로우는 다가 단백질 후보물질을 주당 수백종 평가할 수 있다.

[1009] **다가 결합제의 설계와 검증**

[1010] 제1 전략으로, 스파이크 삼량체의 RBD 3개와 기하구조적으로 매칭되는, M1, M2 및 M3 미니단백질의 자기-조립되는 삼량체 버전을 설계하였다 (이하, H[결합 도메인 #]-[동형삼량체#]로 언급됨; 예를 들어, H1-1은 동형삼량체 도메인 1을 가진 M1의 동형삼량체임, 표 11). 본 발명자들은 다양한 동형삼량체화 도메인과 링커 길이를 가진 백종 이상의 단백질을 본 발명의 무세포성 발현 및 다가 스크린 워크플로우를 이용해 설계, 발현 및 평가하였다. 본 발명자들은 각 동형삼량체에서 다가 결합을 잠재적으로 의미하는 해리 속도가 느린 버전들을 동정하였다 (도 14).

[1011] 2번째 전략으로, 유연한 링커에 의해 분리된 M1, M2 및 M3 결합 도메인의 2- 및 3-도메인 융합체들을 제작하였

다 (이하, F[결합 도메인 #s]-[링커]로 언급됨; 예를 들어, F231-P12는 모두 PAS12 링커에 의해 분리된 M2-M2-M1 융합체를 의미함, 표 11). RBD의 "열린" 및 "닫힌" 상태에 결합하였을 때 도메인들의 말단 사이의 거리를 망라하도록 선정된 다양한 링커 길이들을 평가하였다. 또한, 다가성을 최적화하기 위해 결합 도메인 연결성 및 링커 길이가 다양한 디자인 백종 이상을 발현시켜 평가하였다. 식별된 2- 및 3-도메인 융합체 수종이 전술한 동형-삼량체 구조에와 비슷한 느린 해리 속도를 나타내었다 (도 14).

[1012] 각각의 전략에서 우수한 후보물질들은 경쟁자와 14일간 두었을 때, 전혀 내지 거의 해리되지 않았으며, 추가적인 측정은 S6P의 안정성으로 제한적이었다. 이들 데이터에 따라, 복합체들은 해리 속도 상수가 $1x10^{-7}$ s^{-1} 보다 느린 것으로 추정되었다. 본 발명자들이 인지하는 한, 이는 이전에 보고된 합성 단백질-단백질 상호작용에서 측정된 가장 느린 해리 속도 상수이다.

[1013] 다음으로, 본 발명자들은 S6P와 상위 후보물질 미니결합제 구조체 간의 복합체의 특징을 규명하기 위해 단일 입자 저온-전자 현미경 (cryo-EM) 검경을 이용하였다 (도 15). H2-1, F31-G10 및 F231-P24 구조체의 Cryo-EM 구조는 각각 해상도 2.6, 4.5 및 3.9 Å에서 결정하였다. H2-1은 RBD 3개 모두에 동시에 결합하여, RBD 3종 모두 열린 상태를 취하도록 유발하는 것으로 밝혀졌다. 설계 모형은 관찰된 구조와 거의 정확하게 일치하였다. F31-G10은 RBD 2개에 결합하였으며, 둘다 결합시 열린 형태를 취하는 것으로 나타났다. 구조는 이 링커 길이가 본래의 상태에서 RBD 2개에 동시에 결합할 수 있다는 것을 보여준다. 3번째 자유 RBD는 구조에서 열린 형태 또는 닫힌 형태를 취하였다. F231-P24는 RBD 3개에 결합하였으며, M1은 닫힌 형태의 RBD에 결합하고, M2와 M3는 열린 형태의 RBD에 결합하였다. 이는 링커 길이가 결합 도메인 3개가 천연 상태의 유의한 왜곡없이 RBD 3개 모두에 동시에 결합하기에 충분히 길다는 것을 의미한다. F31-G10 및 F231-P24 둘다, 유연한 링커가 도메인의 연결을 검증하기 위해 EM 맵에서 밀도를 나타내지 않음에도 불구하고, 맵에서 다가 결합이 강하게 시사되었다.

[1014] **다가 미니결합제는 광범위하게 유행하는 SARS-CoV-2 변종을 중화한다**

[1015] 본 발명자들은 다음으로 다가 변이체가 SARS-CoV-2 변종을 중화하는 능력을 확인하고자 하였다. 본 발명자들은 돌연변이 스파이크 단백질 패널에서 최상의 다가 미니결합제의 해리 속도를 스크리닝하였다 (도 16). 동형삼량체가 최대 돌연변이 내성을 나타내었으며, H2 동형삼량체는 임의의 돌연변이 스파이크에 대해 24시간 후 거의 해리되지 않았다. 2-도메인 융합체는 검사한 점 돌연변이에 대해 증가된 회복탄력성 (resilience)을 거의 나타내지 않았다. 3-도메인 융합체는 일부는 여전히 결합에 영향을 미쳤지만 검사한 점 돌연변이에 대해 상당히 더 일관된 결합성을 나타내었다.

[1016] 본 발명자들은 실제 SARS-CoV-2 분리주와 더불어 SARS-CoV-2 HIV 슈도바이러스 둘다에 대해 중화 분석을 통해 이들 단백질의 효능을 추가적으로 평가하였다 (도 16). H2-0 및 H2-1 동형삼량체는 검사한 모든 구조체들에서 일관적으로 최상의 성능을 나타내었으며, IC_{50}은 낮은 pM 범위였다. 3-도메인 융합체들 역시 양호한 성능을 나타내었으며, 검사한 모든 변이체들에서 IC_{50}은 nM 범위였다. H2 동형삼량체의 중화 범위가 클수록 고유한 이점인 M2 단량체에 의한 ACE2 결합부를 단백질 설계에 의해 더 잘 모방함을 반영하는 것일 수 있다.

[1017] **다가 미니결합제는 바이러스 탈출에 대해 저항한다.**

[1018] 본 발명자들은, 상위 후보물질이 현재 유행하는 SARS-CoV-2 돌연변이를 중화하는 능력을 평가하는 것 외에도, 저해제가 바이러스 탈출에 대해 저항하는 능력 역시 검사하였다 (도 17). 이를 위해, 플라크 분석을 Vero E6 세포에서 복제한 VSV-SARS-CoV-2 키메라 바이러스로 수행하였다. 저해제에 내성인 돌연변이를 선별하기 위해, 비-내성 바이러스의 복제를 중지시키기 위해 적층에 저해제를 포함시켰다. 양성 대조군 중화 항체 (2B04)의 경우, 플레이트 당 복수의 탈출 돌연변이를 선별하였다. F231-P12 및 H2-1 둘다에서 각 저해제에 대한 레플리케이트 웰 35개에서 탈출 돌연변이는 분리되지 않았다.

[1019] **H2-0는 인간 ACE2-발현성 형질전환 마우스에서 예방학적 보호를 제공한다.**

[1020] 본 발명의 다가 미니결합제가 생체내 모델에서 보호를 제공하는 능력을 확인하기 위해, 본 발명자들은 인간 ACE2-발현성 형질전환 마우스에서 노출-전 예방학적 치료를 평가하였다 (도 17). SARS-CoV-2 변종 B.1.1.7, B1.351, B.1.1.24을 10^3 FFU로 접종하기 전날, H2-0를 1회 50 μg 용량으로 비강내 (i.n.) 투여하였다. 모든 경우에, H2-0의 i.n. 투여는 SARS-CoV-2-유도성 체중 감소로부터 마우스를 보호하였다. 감염 후 6일차에, 다양한 조직들에서 RT-qPCR에 의해 바이러스 부담을 측정하였다. 특히, 모든 사례들에서 폐 내 바이러스 부담이 감소하였다. 이들 결과는, i.n. 투여에 의해 제공된 H2-0가 관련 마우스 모델에서 SARS-CoV-2 감염에 대해 예방학적

보호를 제공할 수 있음을 보여준다.

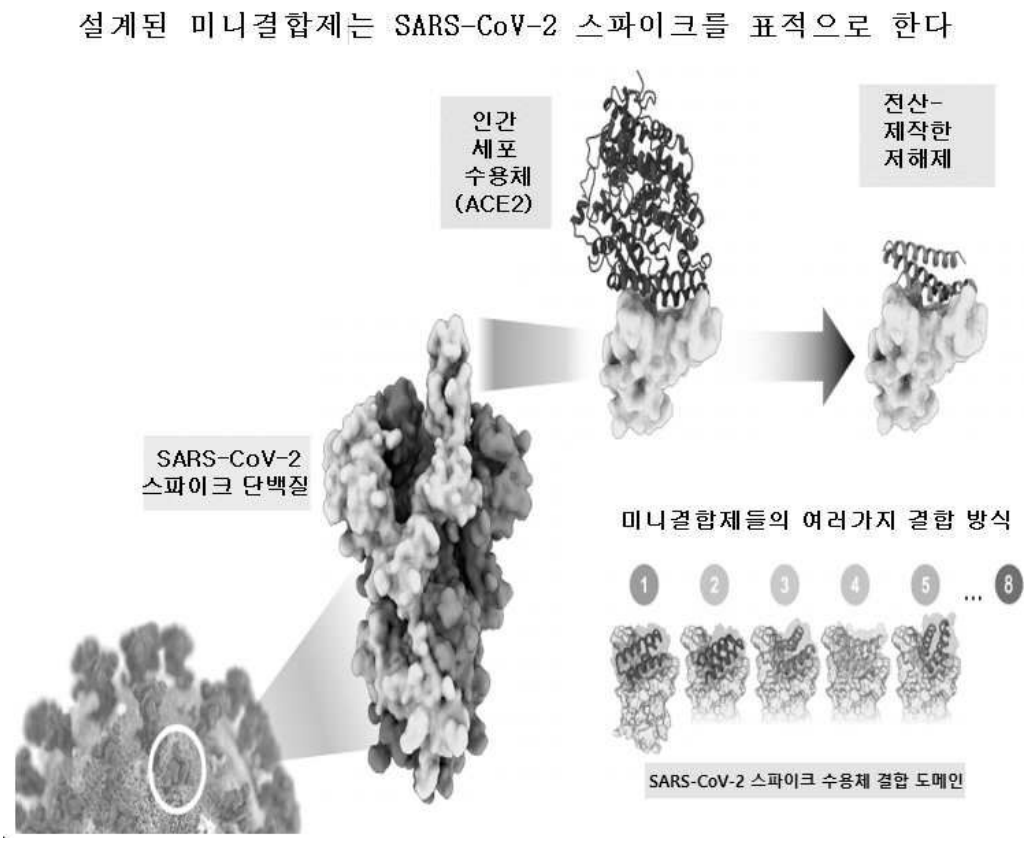
[1021] **결론**

[1022] 본 발명자들은, 개별 단백질 변이체 평가가 프로세스를 제한하는 단계인 여러가지 다양한 응용 분야들에서 무세포성 단백질 발현 및 평가 워크플로우의 유용성을 찾을 수 있을 것으로, 기대한다. 아울러, 본 발명에서 개발한 다가 스크린은 연구자가 다가 단백질 치료제를 개발하는 능력을 촉진할 것이다.

[1023] 설계한 단백질 구조체들은 COVID-19 감염을 예방 및 치료하는데 단일클론 항체에 비해 여러가지 이점을 가질 수 있다. 1) 호흡계에 직접 투여, 2) 상품의 낮은 단가와 상당한 대규모 생산 가능성, 3) 높은 안정성과 저온 유통 불필요성, 및 4) 단일 화합물에서 탈출 돌연변이에 대한 매우 광범위한 저항성. 보다 일반적으로, 설계한 고 친화성의 다가 미니결합제는 바이러스 대유행을 퇴치하기 위한 강력한 플랫폼을 제공할 수 있다.

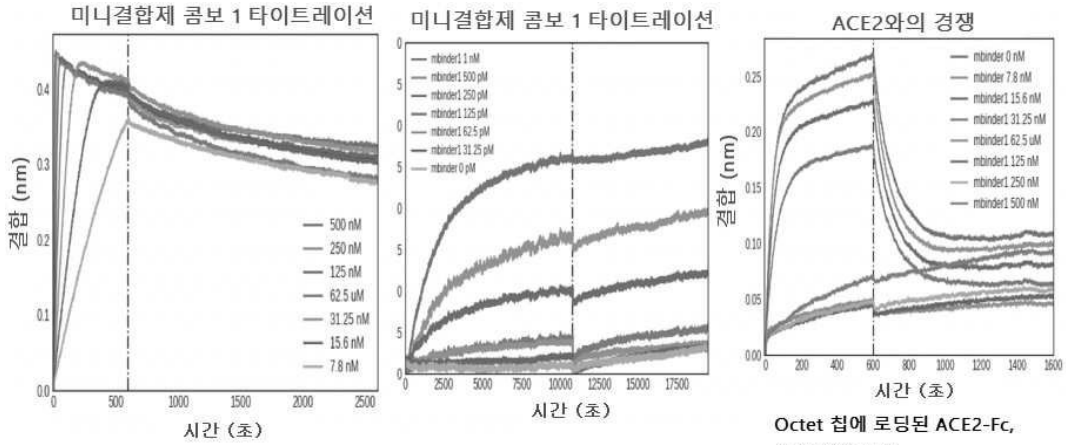
도면

도면1



도면2

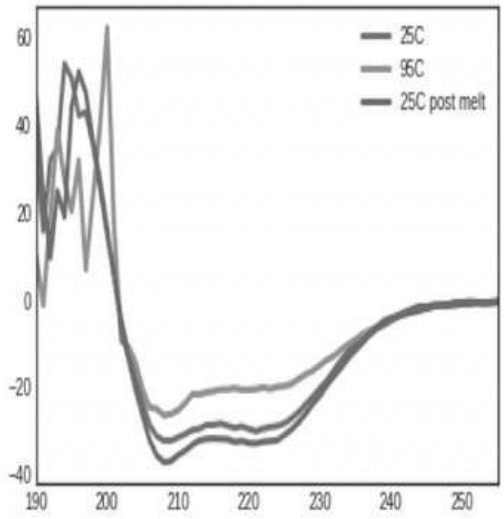
55 잔기 디자인은 ~300pM 친화성으로 RBD에 결합하고
ACE2와 결합에 대해 경쟁한다



콤보 1 미니결합제에 대한 생물층 간섭측정 (BLI) 데이터는 스파이크 RBD에 대해 ~300 pM 친화성을 나타내며, ACE-2에 의한 RBD 결합에 대해 경쟁한다

도면3

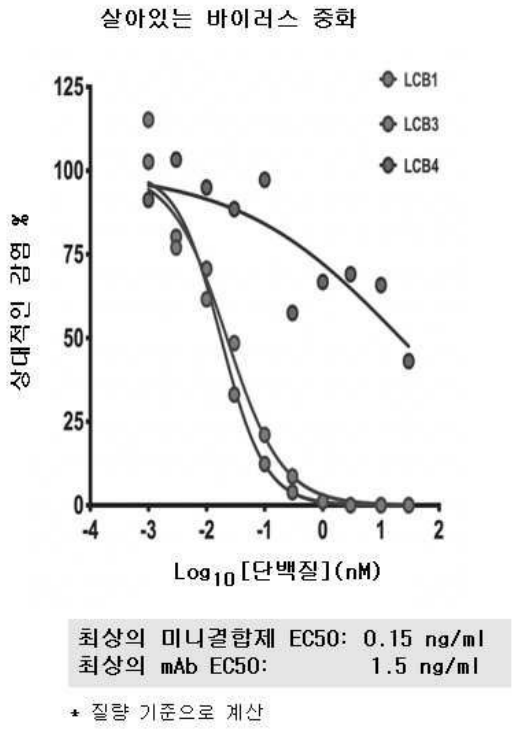
55 잔기 스파이크 RBD 미니결합제는 높은 열 안정성을 가진다



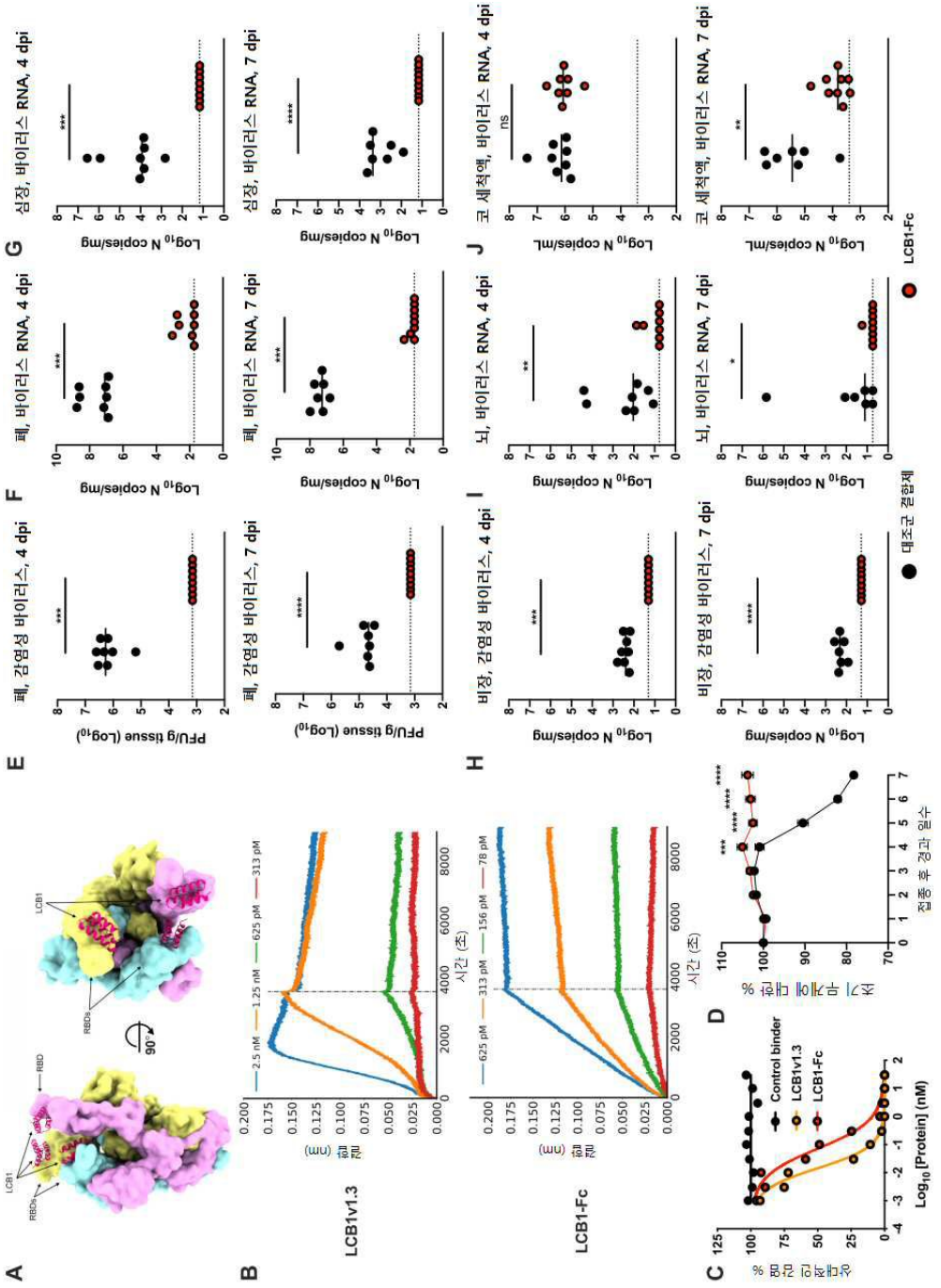
콤보 1 미니결합제에 대한 원이색성 (CD) 스펙트럼은 최대 95℃의 극도의 열 안정성을 나타낸다

도면4

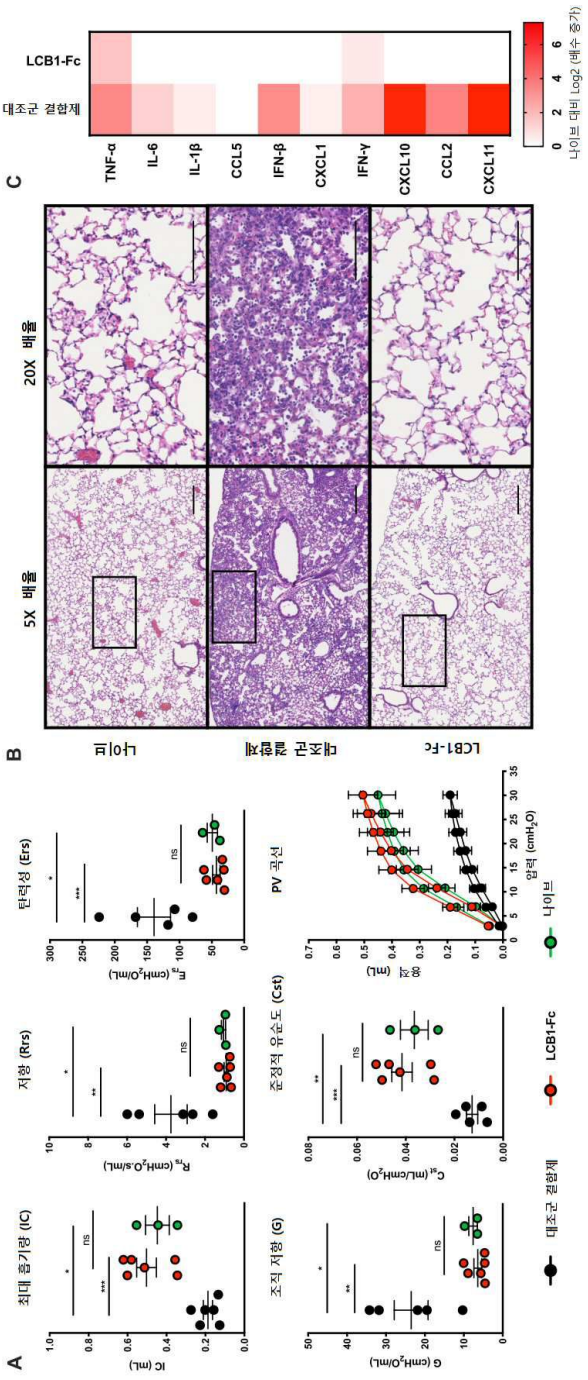
미니결합제는 살아있는 코로나바이러스를 강하게 중화한다



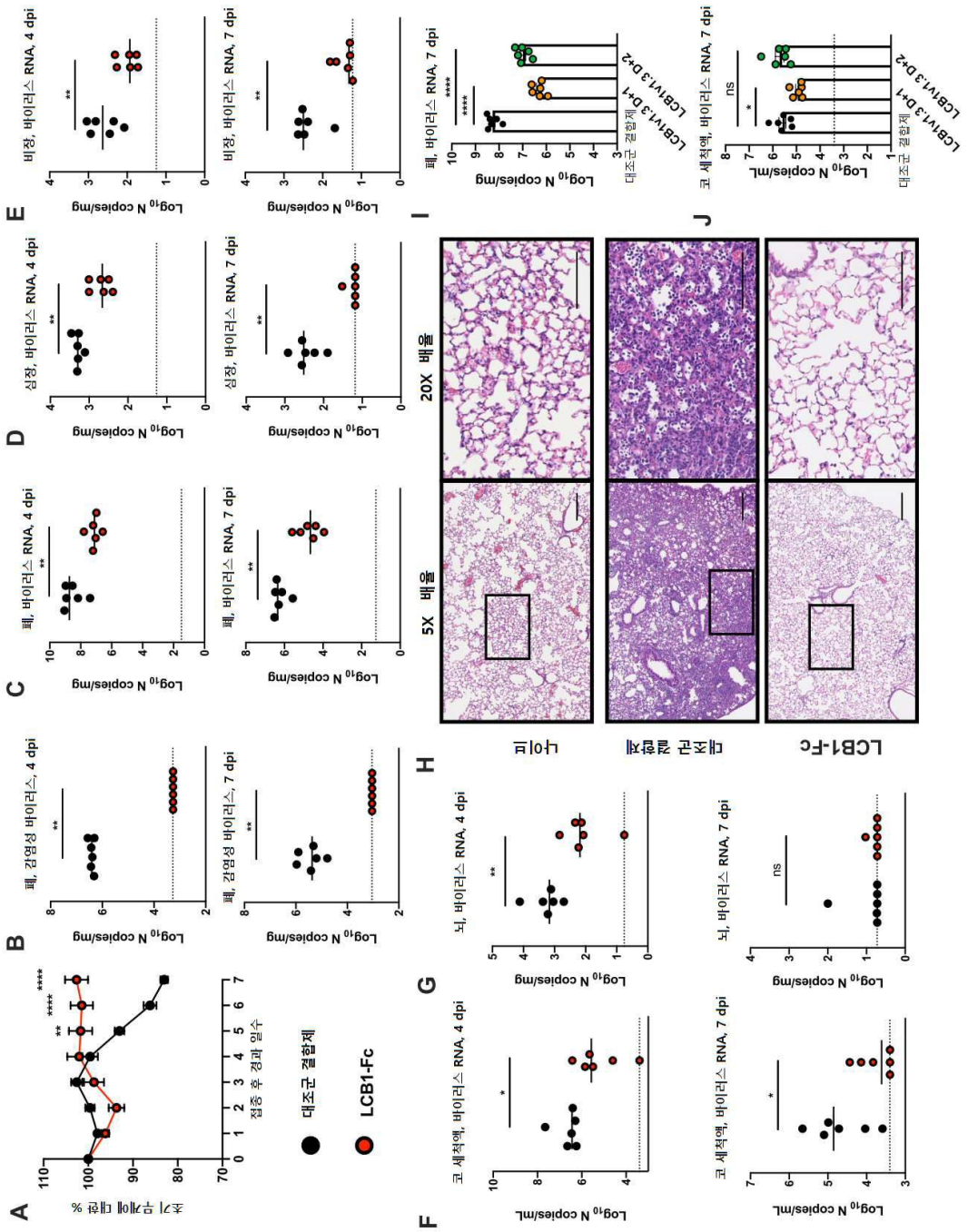
도면5


A
LCB1
RBD
RBD
LCB1
90°
B
LCB1v1.3
2.5 nM
1.25 nM
625 pM
313 pM
결합 (nm)
시간 (초)
LCB1-Fc
625 pM
313 pM
156 pM
78 pM
결합 (nm)
시간 (초)
C
중화활성 감염 %
Control binder
LCB1v1.3
LCB1-Fc
Log10 [Protein] (nM)
D
생존 %
접종 후 경과 일수
E
폐, 감염성 바이러스, 4 dpi
PFU/g tissue (Log10)
폐, 감염성 바이러스, 7 dpi
PFU/g tissue (Log10)
F
폐, 바이러스 RNA, 4 dpi
Log10 N copies/mg
폐, 바이러스 RNA, 7 dpi
Log10 N copies/mg
G
심장, 바이러스 RNA, 4 dpi
Log10 N copies/mg
심장, 바이러스 RNA, 7 dpi
Log10 N copies/mg
H
비장, 감염성 바이러스, 4 dpi
Log10 N copies/mg
비장, 감염성 바이러스, 7 dpi
Log10 N copies/mg
I
뇌, 바이러스 RNA, 4 dpi
Log10 N copies/mg
뇌, 바이러스 RNA, 7 dpi
Log10 N copies/mg
J
코 세척액, 바이러스 RNA, 4 dpi
Log10 N copies/mL
코 세척액, 바이러스 RNA, 7 dpi
Log10 N copies/mL
대조군 결합체
LCB1-Fc

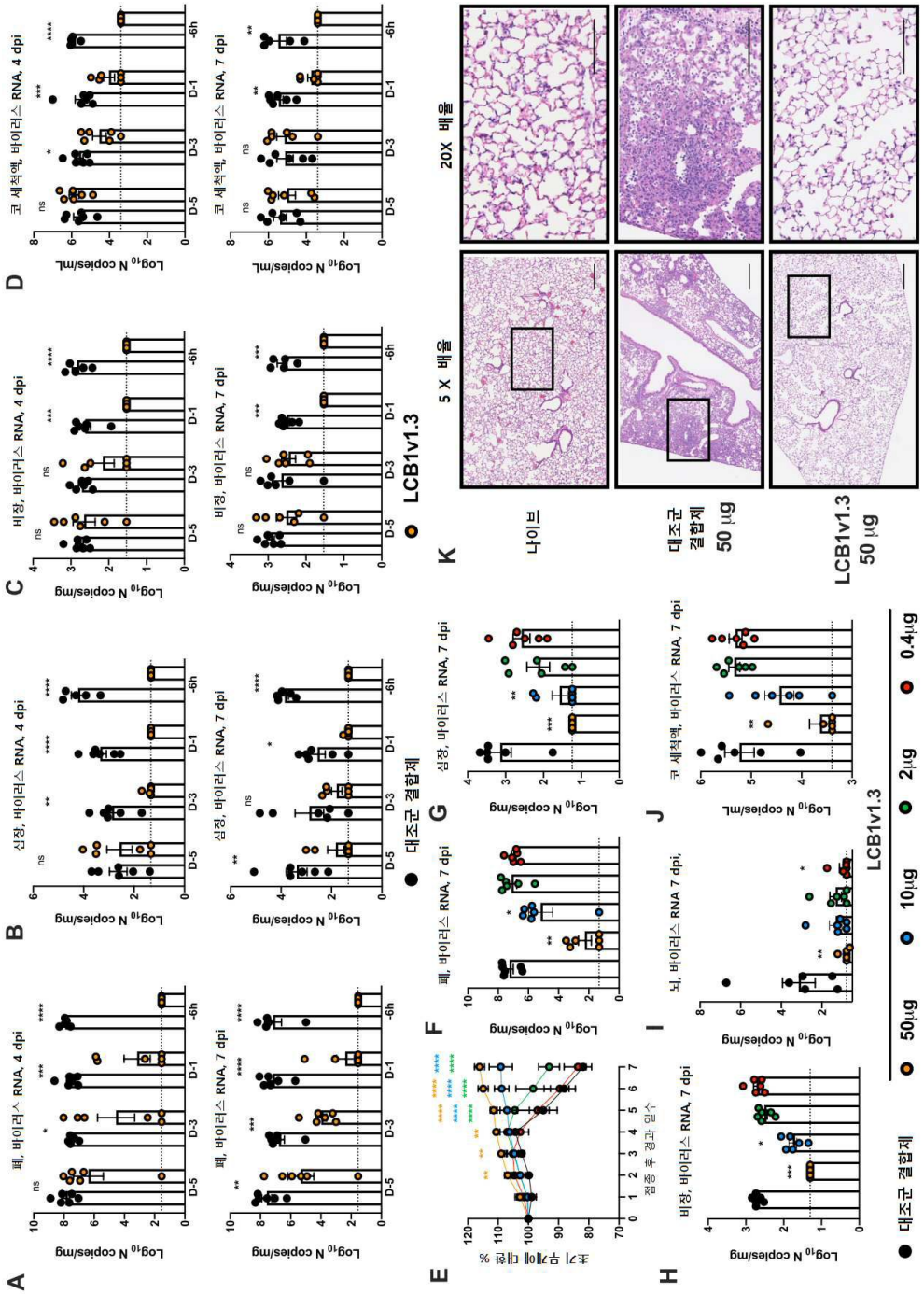
도면6


A
최대 흡기량 (IC)
IC (mL)
조직 저항 (G)
G (cmH2O/mL)
저항 (Rrs)
R5 (cmH2O.s/mL)
준정적 유순도 (Cst)
Cst (mL/cmH2O)
탄력성 (Ers)
E5 (cmH2O/mL)
PV 곡선
용적 (mL)
압력 (cmH2O)
나이브
대조군 결합제
LCB1-Fc
B
나이브
대조군 결합제
LCB1-Fc
5X 배율
20X 배율
C
LCB1-Fc
대조군 결합제
TNF-α
IL-6
IL-1β
CCL5
IFN-β
CXCL1
IFN-γ
CXCL10
CCL2
CXCL11
나이브 대비 Log2 (배수 증가)

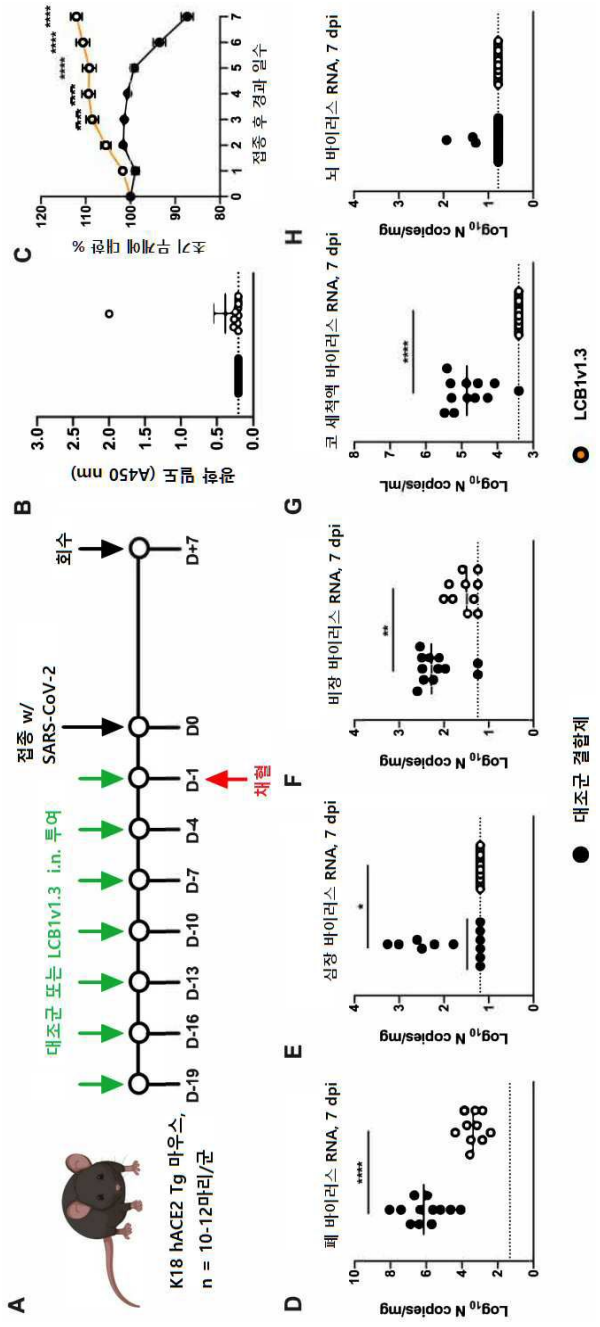
도면7


A
초기 무게에 대한 %
감염 후 경과 일수
대조군 결합제
LCB1-Fc
B
폐, 감염성 바이러스, 4 dpi
폐, 감염성 바이러스, 7 dpi
C
폐, 바이러스 RNA, 4 dpi
폐, 바이러스 RNA, 7 dpi
D
심장, 바이러스 RNA, 4 dpi
심장, 바이러스 RNA, 7 dpi
E
비장, 바이러스 RNA, 4 dpi
비장, 바이러스 RNA, 7 dpi
F
코 세척액, 바이러스 RNA, 4 dpi
코 세척액, 바이러스 RNA, 7 dpi
G
뇌, 바이러스 RNA, 4 dpi
뇌, 바이러스 RNA, 7 dpi
H
5X 배율
20X 배율
나이브
대조군 결합제
LCB1-Fc
I
폐, 바이러스 RNA, 7 dpi
대조군 결합제
LCB1v1.3 D+1
LCB1v1.3 D+2
J
코 세척액, 바이러스 RNA, 7 dpi
대조군 결합제
LCB1v1.3 D+1
LCB1v1.3 D+2

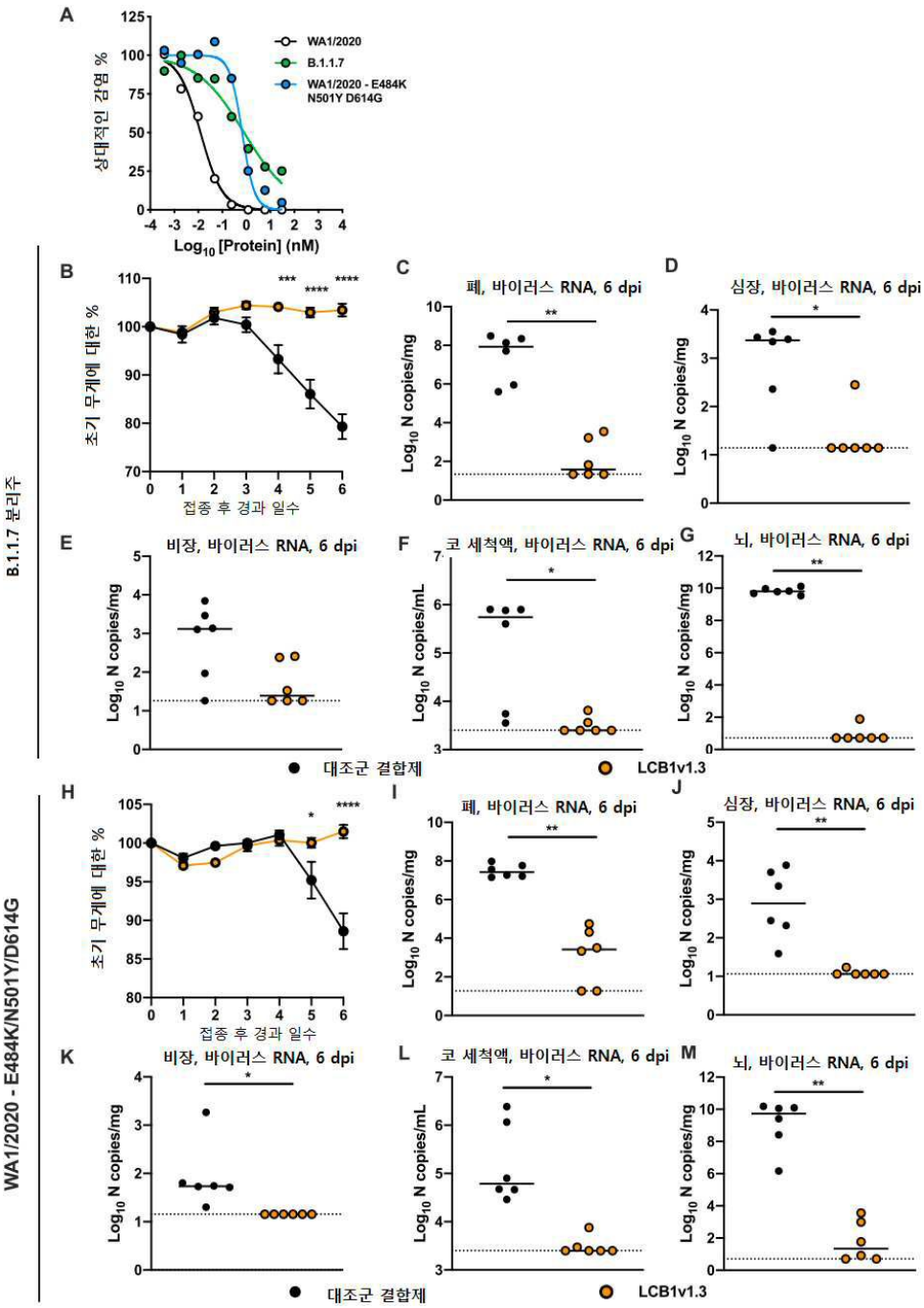
도면8


A
B
C
D
E
F
G
H
I
J
K
폐, 바이러스 RNA, 4 dpi
폐, 바이러스 RNA, 7 dpi
심장, 바이러스 RNA, 4 dpi
심장, 바이러스 RNA, 7 dpi
비장, 바이러스 RNA, 4 dpi
비장, 바이러스 RNA, 7 dpi
코 세척액, 바이러스 RNA, 4 dpi
코 세척액, 바이러스 RNA, 7 dpi
뇌, 바이러스 RNA 7 dpi,
Log10 N copies/mg
Log10 N copies/mL
D-5
D-3
D-1
-6h
대조군 결합제
LCB1v1.3
50μg
10μg
2μg
0.4μg
초기 무게에 대한 %
접종 후 경과 일수
5 X 배율
20X 배율
나이브
대조군 결합제 50 μg
LCB1v1.3 50 μg

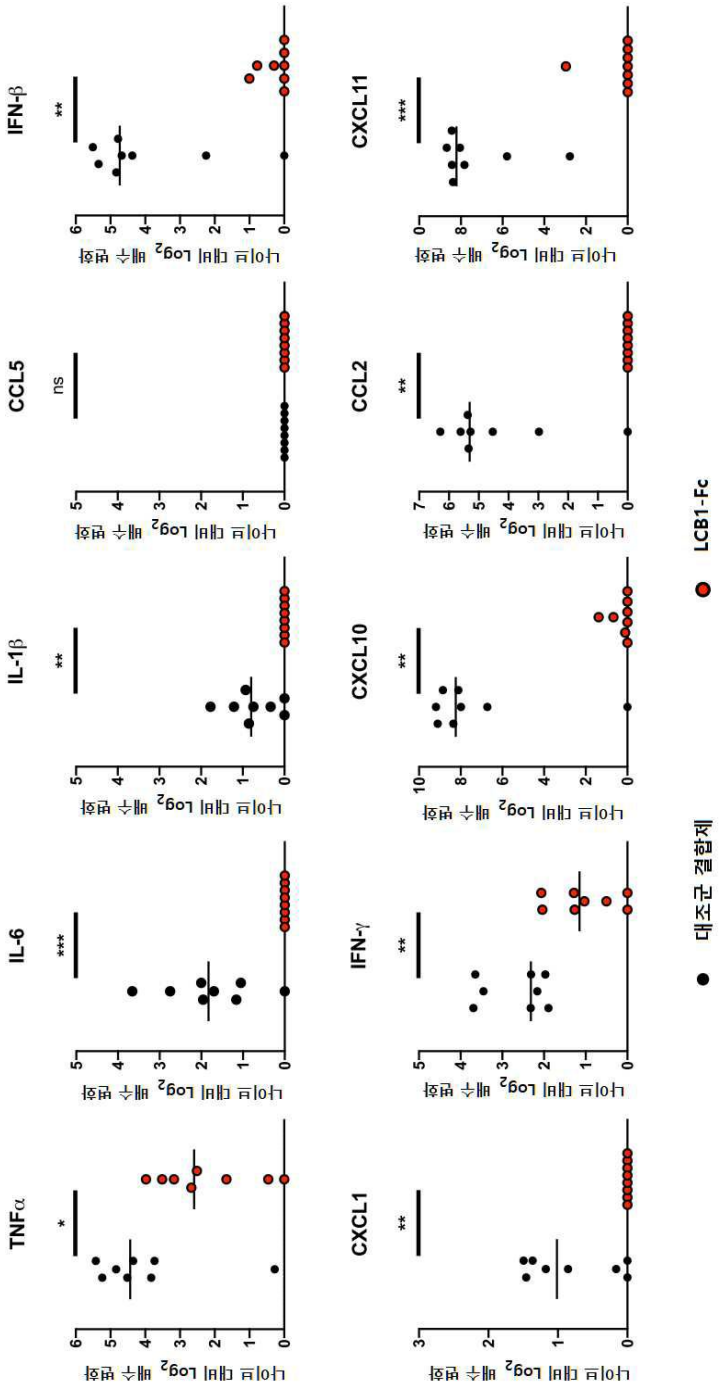
도면9


A
K18 hACE2 Tg 마우스,
n = 10-12마리/군
대조군 또는 LCB1v1.3 i.n. 투여
D-19
D-16
D-13
D-10
D-7
D-4
D-1
D0
D+7
접종 w/
SARS-CoV-2
회수
채혈
B
항체 밀도 (A450 nm)
C
초기 무게에 대한 %
접종 후 경과 일수
D
폐 바이러스 RNA, 7 dpi
Log10 N copies/mg
E
심장 바이러스 RNA, 7 dpi
Log10 N copies/mg
F
비장 바이러스 RNA, 7 dpi
Log10 N copies/mg
G
코 세척액 바이러스 RNA, 7 dpi
Log10 N copies/mL
H
뇌 바이러스 RNA, 7 dpi
Log10 N copies/mg
대조군 결합제
LCB1v1.3

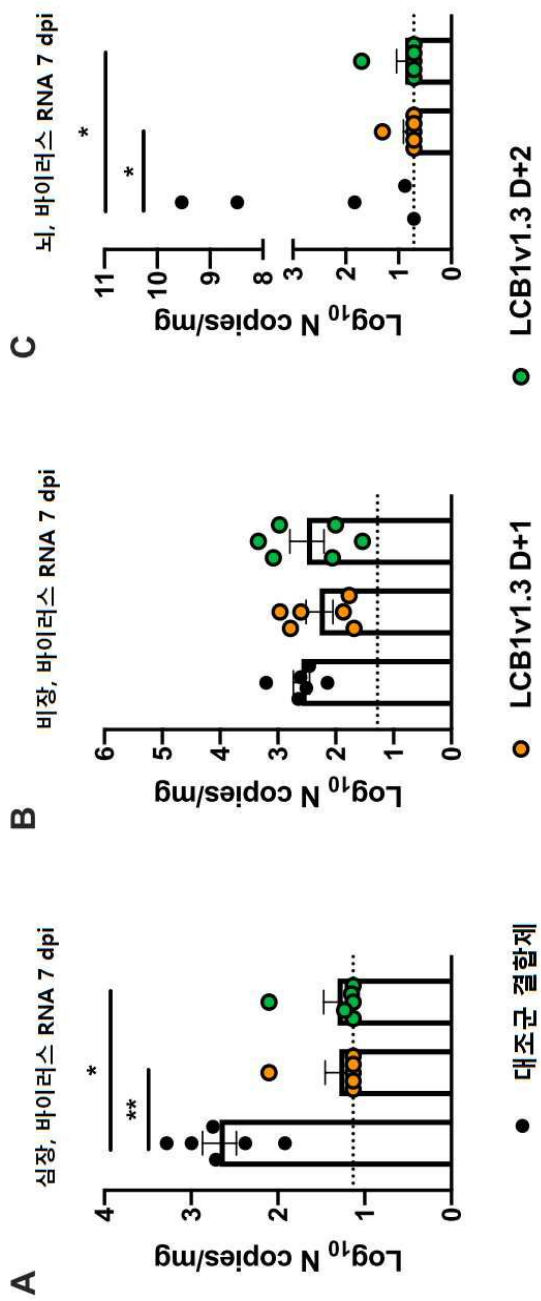
도면10


A
상대적인 감염 %
WA1/2020
B.1.1.7
WA1/2020 - E484K
N501Y D614G
Log10 [Protein] (nM)
B.1.1.7 분리주
B
초기 무게에 대한 %
접종 후 경과 일수
C
폐, 바이러스 RNA, 6 dpi
Log10 N copies/mg
D
심장, 바이러스 RNA, 6 dpi
Log10 N copies/mg
E
비장, 바이러스 RNA, 6 dpi
Log10 N copies/mg
F
코 세척액, 바이러스 RNA, 6 dpi
Log10 N copies/mL
G
뇌, 바이러스 RNA, 6 dpi
Log10 N copies/mg
대조군 결합제
LCB1v1.3
WA1/2020 - E484K/N501Y/D614G
H
초기 무게에 대한 %
접종 후 경과 일수
I
폐, 바이러스 RNA, 6 dpi
Log10 N copies/mg
J
심장, 바이러스 RNA, 6 dpi
Log10 N copies/mg
K
비장, 바이러스 RNA, 6 dpi
Log10 N copies/mg
L
코 세척액, 바이러스 RNA, 6 dpi
Log10 N copies/mL
M
뇌, 바이러스 RNA, 6 dpi
Log10 N copies/mg
대조군 결합제
LCB1v1.3

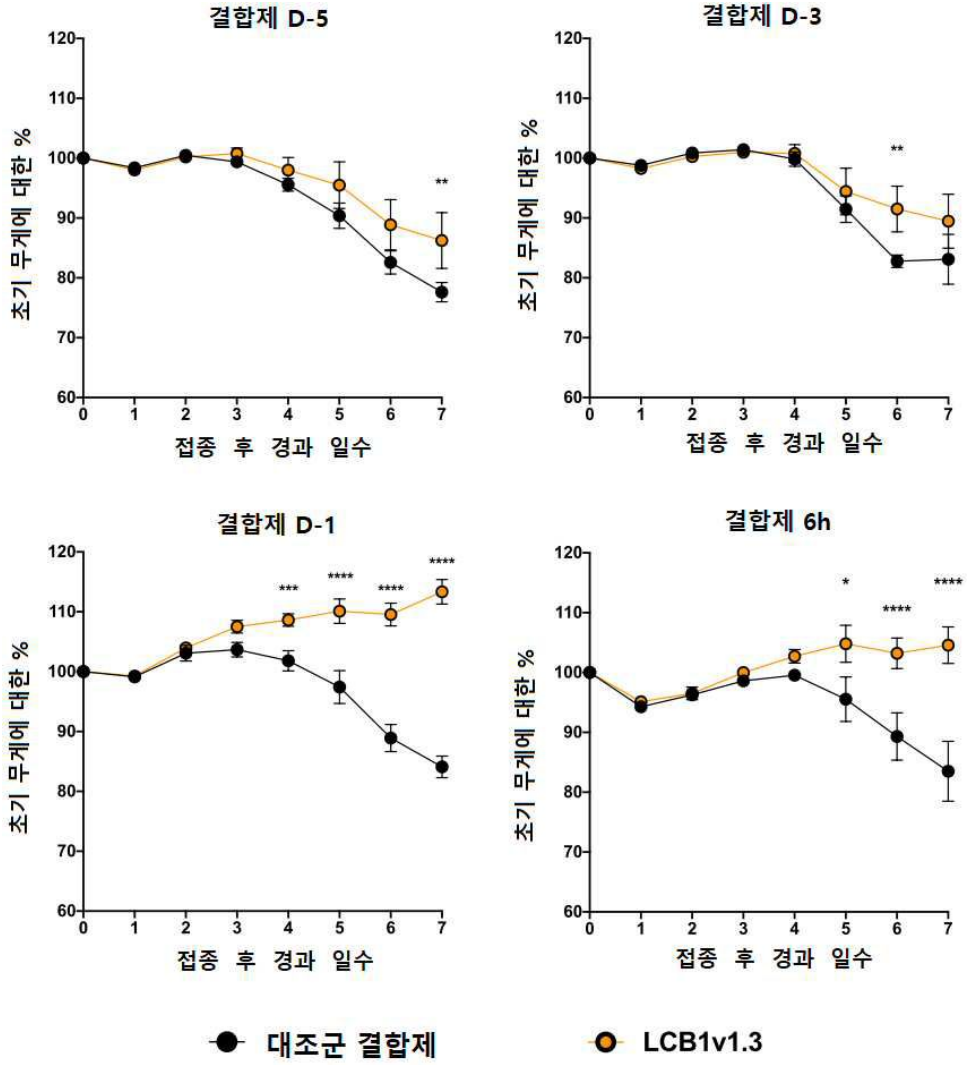
도면11


TNFα
IL-6
IL-1β
CCL5
IFN-β
CXCL1
IFN-γ
CXCL10
CCL2
CXCL11
나이브 대비 log2 배수 변화
대조군 결합제
LCB1-Fc

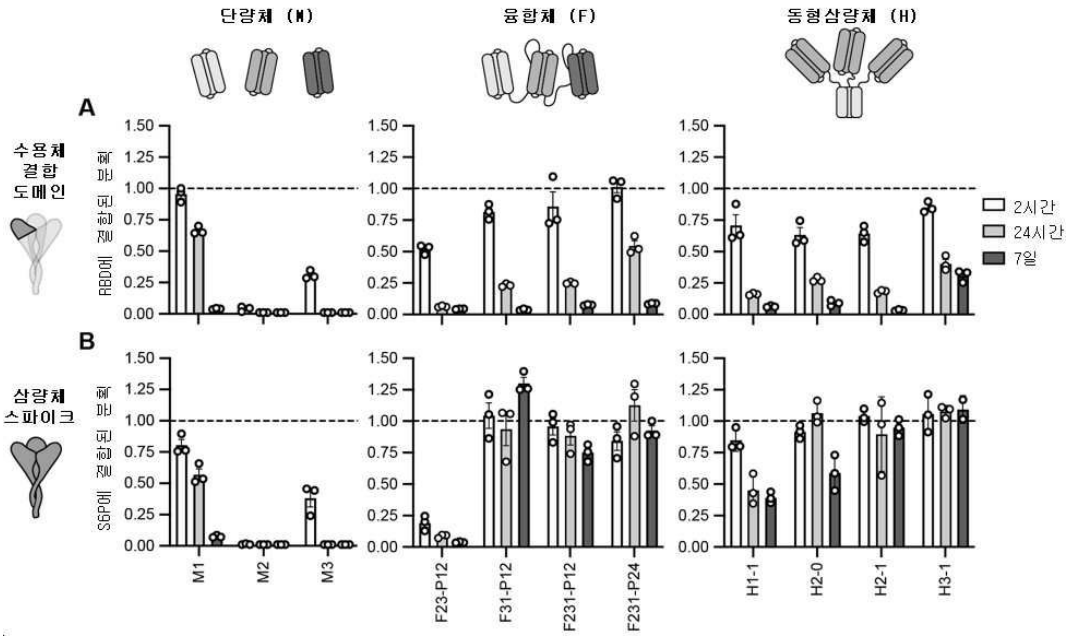
도면12


A
심장, 바이러스 RNA 7 dpi
Log10 N copies/mg
B
비장, 바이러스 RNA 7 dpi
Log10 N copies/mg
C
뇌, 바이러스 RNA 7 dpi
Log10 N copies/mg
대조군 결합제
LCB1v1.3 D+1
LCB1v1.3 D+2

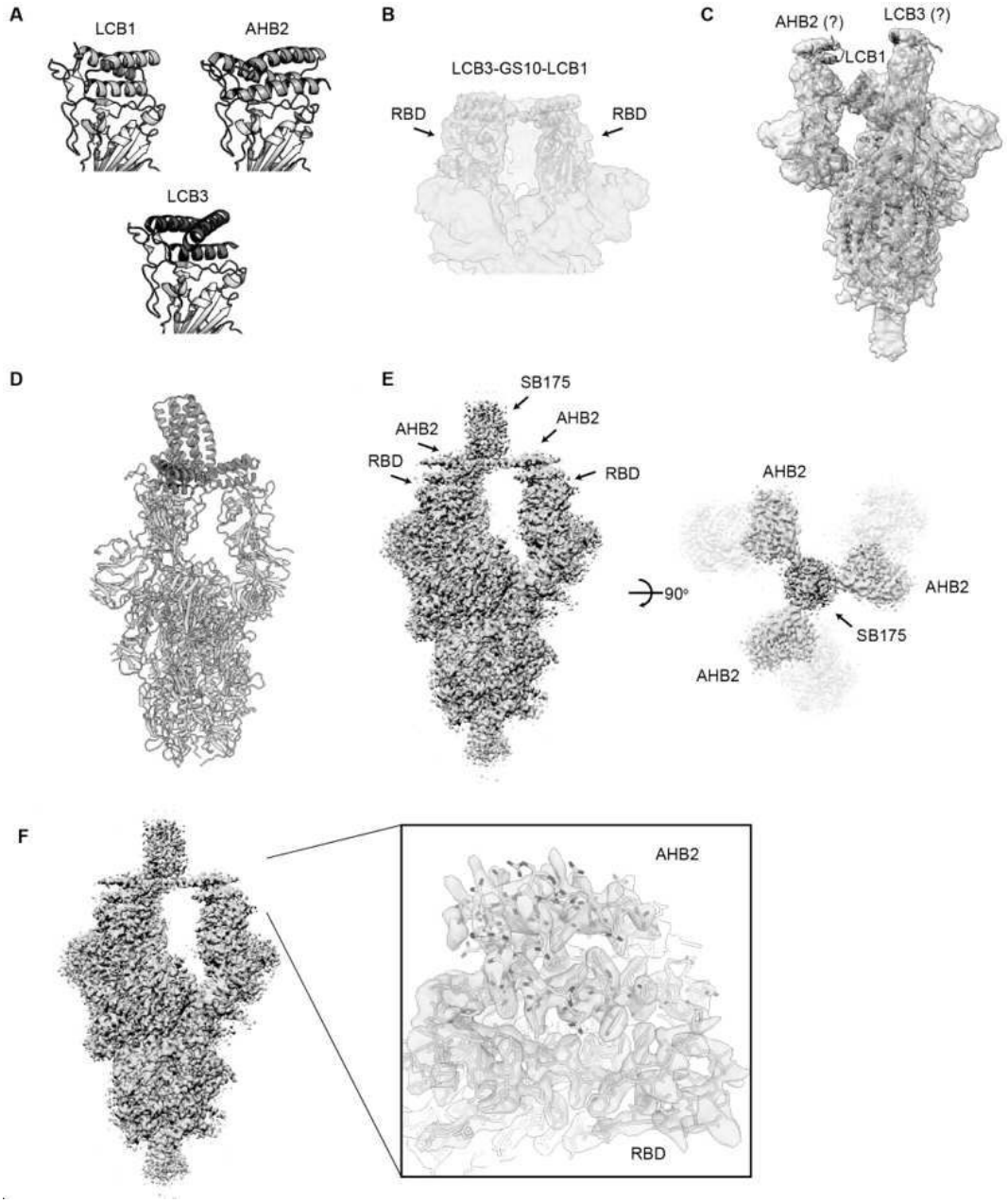
도면13


결합제 D-5
결합제 D-3
결합제 D-1
결합제 6h
초기 무게에 대한 %
접종 후 경과 일수
대조군 결합제
LCB1v1.3

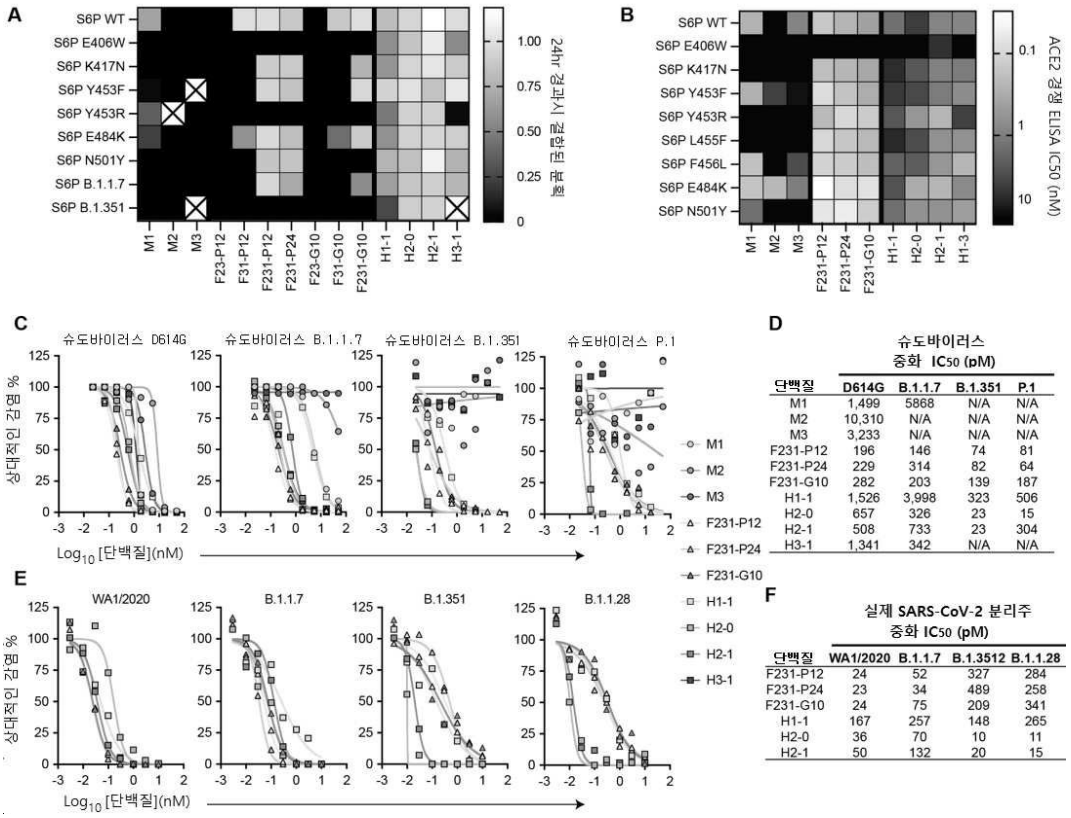
도면14


단량체 (M)
융합체 (F)
동형삼량체 (H)
A
수용체 결합 도메인
RBD에 결합된 분획
B
삼량체 스파이크
S6P에 결합된 분획
2시간
24시간
7일
M1
M2
M3
F23-P12
F31-P12
F231-P12
F231-P24
H1-1
H2-0
H2-1
H3-1

도면15


A
LCB1
AHB2
LCB3
B
LCB3-GS10-LCB1
RBD
RBD
C
AHB2 (?)
LCB3 (?)
LCB1
D
E
SB175
AHB2
AHB2
RBD
RBD
90°
AHB2
AHB2
SB175
AHB2
F
AHB2
RBD

도면16



D

슈도바이러스 중화 IC50 (pM)

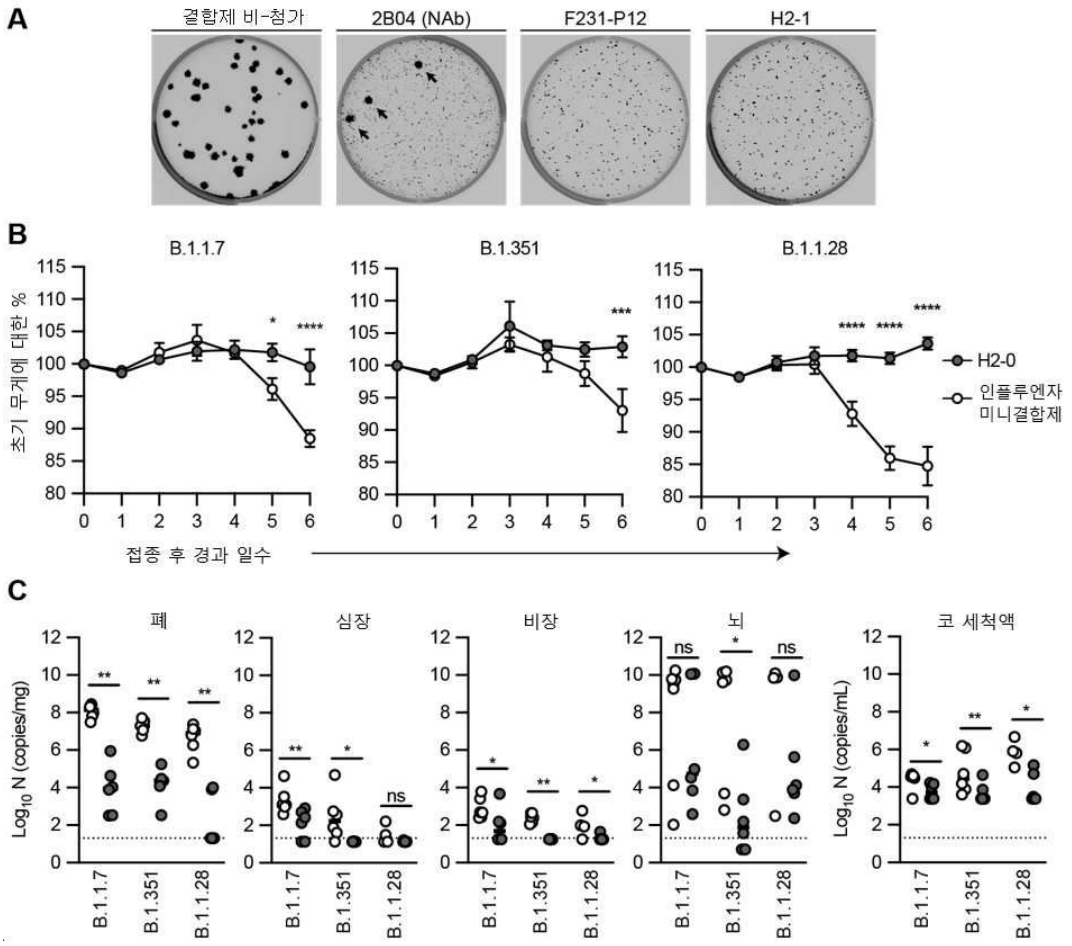
단백질	D614G	B.1.1.7	B.1.351	P.1
M1	1,499	5868	N/A	N/A
M2	10,310	N/A	N/A	N/A
M3	3,233	N/A	N/A	N/A
F231-P12	196	146	74	81
F231-P24	229	314	82	64
F231-G10	282	203	139	187
H1-1	1,526	3,998	323	506
H2-0	657	326	23	15
H2-1	508	733	23	304
H3-1	1,341	342	N/A	N/A

F

실제 SARS-CoV-2 분리주 중화 IC50 (pM)

단백질	WA1/2020	B.1.1.7	B.1.3512	B.1.1.28
F231-P12	24	52	327	284
F231-P24	23	34	489	258
F231-G10	24	75	209	341
H1-1	167	257	148	265
H2-0	36	70	10	11
H2-1	50	132	20	15

도면17



서 열 목 록

SEQUENCE LISTING

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<120> SARS-COV-2 inhibitors

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<150> 63/067593

<151> 2020-08-19

<150> 63/051474

<151> 2020-07-14

<160> 701

<170> PatentIn version 3.5

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Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

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

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

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Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

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Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

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Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

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1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Asn Val Ser Asp Leu Ile

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

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1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Cys

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1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Tyr Val Ser Asp Leu Ile

20 25 30

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35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

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1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

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

1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Gln Leu Leu Gln Glu Val Glu Arg

50 55

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1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Asn Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

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1 5 10 15

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

20 25 30

Ala Glu Phe Ile Ala Lys Arg Asn Asn Asn Glu Glu Leu Glu Arg Leu

35 40 45

Val Arg Glu Val Lys Lys Arg Leu

50 55

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

20 25 30

Ala Glu Phe Ile Ala Lys Arg Asn Asn Asn Glu Glu Leu Glu Arg Leu

35 40 45

Val Arg Glu Val Lys Lys Arg Leu

50 55

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<211> 64

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1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 14

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1 5 10 15

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

20 25 30

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

35 40 45

Ser Lys Val Val Ser Glu Leu Lys Glu Leu Leu Glu Arg Leu Gln

50 55 60

<210> 15

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<400> 15

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

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 16

<211> 64

<212> PRT

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1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 17

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1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

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1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

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

1 5 10 15

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

20 25 30

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

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1 5 10 15
Leu His Lys Ala Lys Asp Glu Glu Met Gln Lys Arg Val Phe Gln Leu

20 25 30
Phe Glu Gln Ala Asp Lys Ala Tyr Lys Thr Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

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

1 5 10 15
Ile Glu Arg Asn Asp Pro Tyr Leu Met Phe Asp Val Ala Val Glu Met
20 25 30

Leu Arg Leu Ala Glu Glu Asn Asn Asp Glu Arg Ile Ile Glu Arg Ala

35 40 45

Lys Arg Ile Leu Glu Glu Tyr Glu

50 55

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

1 5 10 15

Val Glu Arg Asn Asp Pro Tyr Leu Ile Phe Asp Val Ala Ile Glu Leu

20 25 30

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

35 40 45

Lys Arg Ile Leu Glu Glu Val Glu

50 55

<210> 25

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Ser Leu Glu Glu Leu Lys Glu Gln Val Lys Glu Leu Lys Lys Glu Leu

1 5 10 15

Ser Pro Glu Met Arg Arg Leu Ile Glu Glu Ala Leu Arg Phe Leu Glu

20 25 30

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

35 40 45

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

50 55 60

Thr

65

<210> 26

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Ser Pro Glu Asp Arg Arg Leu Ile Glu Glu Ala Leu Arg Leu Leu Glu
20 25 30

Glu Gly Asn Pro Ala Met Ala Ser Met Val Leu Ser Asp Leu Val Phe
35 40 45

Leu Leu Gly Asp Pro Arg Val Ile Glu Leu Leu Met Leu Val Thr Lys

50 55 60

Thr

65

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Asp Arg Glu Gln Arg Leu Val Arg Phe Leu Val Arg Leu Ala Ser Lys
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Phe Asn Leu Ser Pro Glu Gln Ile Leu Gln Leu Phe Glu Val Leu Glu
20 25 30

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

35 40 45

Glu Glu Val Ala Lys Glu Leu Gly

50 55

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Asp Arg Glu Gln Arg Leu Val Arg Phe Leu Val Arg Leu Ala Ser Lys
1 5 10 15

Phe Asn Leu Ser Met Glu Gln Ile Leu Ile Leu Phe Asp Val Leu Glu
20 25 30

Glu Leu Leu Glu Arg Gly Val Ser Glu Glu Glu Ile Arg Lys Ile Leu
35 40 45

Glu Glu Val Ala Lys Glu Leu
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20 25 30

Leu Ala Glu Arg Leu Gly Met Glu Glu Leu Leu Lys Glu Val Arg Glu
35 40 45

Leu Leu Arg Lys Ile Glu Glu Leu Arg
50 55

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1 5 10 15

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

20 25 30

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

35 40 45

Leu Leu Arg Lys Ile Glu Glu Leu Arg

50 55

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<211> 65

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<400> 31

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

1 5 10 15

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

20 25 30

Gly Asp Pro Arg Leu Glu Glu Val Leu Tyr Leu Ile Trp Arg Ala Leu

35 40 45

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

50 55 60

Arg

65

<210> 32

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Pro Val Thr Glu Leu Leu Arg Glu Ala Lys Glu Lys Asn Asp Pro Met

1 5 10 15

Ala Ile Ser Asp Ala Leu Phe Leu Val Phe Glu Leu Ala Gln Arg Thr

20 25 30

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

35 40 45

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

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Asp Glu Asp Leu Glu Glu Leu Glu Arg Leu Tyr Arg Lys Ala Glu Glu

1 5 10 15

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

20 25 30

Ala Lys Glu Gln Met Glu Arg Ala Met Arg Leu Phe Asp Gln Val Phe

35 40 45

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

50 55 60

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

65 70 75 80

Tyr Gln Arg Val Arg

85

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1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Tyr Gln Arg Val Arg

85

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Gly Ser Gly Ser

1

<210> 36

<211> 6

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<213> Artificial Sequence

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<400> 36

Gly Gly Ser Gly Gly Ser

1 5

<210> 37

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Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly

1 5 10

<210> 38

<211> 12

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Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser

1 5 10 15

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Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser

1 5 10 15

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<211> 24

<212> PRT

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Gly Gly Gly Ser Gly Gly Gly Ser Ser Gly Gly Ser Gly Gly Ser Ser

1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Ser

20

<210> 43

<211> 30

<212> PRT

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Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

20 25 30

<210> 44

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1 5 10 15

Gly Ser Gly Gly Gly Ser Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser

20 25 30

Gly Gly Gly Ser

35

<210> 45

<211> 75

<212> PRT

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1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

65 70 75

<210> 46

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Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10 15

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

20 25 30

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

35 40 45

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

50 55 60

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

65 70 75

<210> 47

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 47

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

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

Leu Glu Glu Val Glu Arg
115

<210> 48

<211> 124

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 48

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15
Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

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

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
115 120

<210> 49
<211> 136
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 49
Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15
Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

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

100 105 110

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

115 120 125

Arg Leu Leu Glu Glu Val Glu Arg

130 135

<210> 50

<211> 148

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 50

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Ser Gly Gly Gly Ser

50 55 60

Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser

65 70 75 80

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Lys Glu Trp

85 90 95

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

100 105 110

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met

115 120 125

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

130 135 140

Glu Val Glu Arg

145

<210> 51

<211> 187

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 51

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

Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly

50 55 60

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
65 70 75 80

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
85 90 95

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met
130 135 140

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

Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu
165 170 175

Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
180 185

<210> 52

<211> 187

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 52

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

Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser Gly Gly

50 55 60

Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
65 70 75 80

Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr
85 90 95

Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser
100 105 110

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser

115 120 125

Ala Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met
130 135 140

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

Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu
165 170 175

Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
180 185

<210> 53

<211> 203

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 53

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
85 90 95

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Asp Asp Glu Leu
130 135 140

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
145 150 155 160

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

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

180 185 190

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
195 200

<210> 54

<211> 203

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 54

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser
65 70 75 80

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
85 90 95

Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
100 105 110

Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
115 120 125

Thr Pro Pro Thr Pro Ser Pro Ser Ala Ser Gly Asn Asp Asp Glu Leu
130 135 140

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
145 150 155 160

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

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
180 185 190

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
195 200

<210> 55

<211> 195

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 55

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

1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly

50 55 60

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

65 70 75 80

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

85 90 95

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val

130 135 140

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val

145 150 155 160

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

165 170 175

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg

180 185 190

Leu Leu Ser

195

<210> 56

<211> 195

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 56

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
85 90 95

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu Asn Ile
130 135 140

Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His
145 150 155 160

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
165 170 175

Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

180 185 190

Val Glu Arg
195

<210> 57

<211> 130

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 57

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Asp Lys Glu Asn Ile Leu
65 70 75 80

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His Ala
85 90 95

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
100 105 110

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
115 120 125

Glu Arg
130

<210> 58

<211> 195

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 58

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

Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser Gly Gly

50 55 60

Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser

65 70 75 80

Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr

85 90 95

Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser

100 105 110

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser

115 120 125

Ala Ser Gly Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val

130 135 140

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val

145 150 155 160

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

165 170 175

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg

180 185 190

Leu Leu Ser

195

<210> 59

<211> 195

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 59

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

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser

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

130 135 140
Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His
145 150 155 160
Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
165 170 175
Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
180 185 190
Val Glu Arg
195
<210> 60
<211> 336

<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 60
Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15
Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Ser Gly Gly

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly

115 120 125

Ser Gly Ser Ser Gly Gly Ser Gly Ser Gly Ser Gly Asp Lys Glu Trp

130 135 140

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

145 150 155 160

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met

165 170 175

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

180 185 190

Glu Val Glu Arg Gly Gly Ser Gly Ser Ser Gly Gly Ser Gly Ser Gly

195 200 205

Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg

210 215 220

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

225 230 235 240

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

245 250 255

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Ser

260 265 270

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

275 280 285

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

290 295 300

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

305 310 315 320

Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg

325 330 335

<210> 61

<211> 22

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 61

Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys

1 5 10 15

Ala Lys Ala Lys Gly Gly

20

<210> 62

<211> 22

<212

> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 62

Gly Gly Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys

1 5 10 15

Ala Lys Ala Lys Ala Lys

20

<210> 63

<211> 18

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 63

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1 5 10 15

Leu Ala

<210> 64

<211> 232

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 64

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

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

50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

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

115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

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

180 185 190

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

195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys

225 230

<210> 65

<211> 79

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 65

Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys

1 5 10 15

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

20 25 30

Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met

35 40 45

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

50 55 60

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Cys

65 70 75

<210> 66

<211> 79

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 66

Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys

1 5 10 15

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

20 25 30

Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met
35 40 45

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg
50 55 60
Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Cys
65 70 75
<210> 67
<211> 78
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 67
Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15
Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30
Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ala Lys Ala Lys Ala Lys
50 55 60
Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys Ala Lys
65 70 75
<210> 68
<211> 310
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic
<400> 68
Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15
Leu Ala Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
20 25 30

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
35 40 45
Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu
50 55 60

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

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

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
260 265 270
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys

275 280 285

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

290 295 300

Ser Leu Ser Pro Gly Lys

305 310

<210> 69

<211> 321

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 69

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys

85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro

100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser

115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp

130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn

145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val

165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu

180 185 190

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

195 200 205

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

210 215 220

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr

225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu

245 250 255

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

260 265 270

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

275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu

290 295 300

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

305 310 315 320

Lys

<210> 70

<211> 321

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 70

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1 5 10 15

Leu Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys

20 25 30

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

35 40 45

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
50 55 60

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
65 70 75 80

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
85 90 95

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
100 105 110

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
115 120 125

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
130 135 140

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
145 150 155 160

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
165 170 175

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
180 185 190

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
195 200 205

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
210 215 220

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
225 230 235 240

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Ser Gly Ser
245 250 255

Gly Ser Gly Gly Ser Gly Ser Gly Ser Asp Lys Glu Trp Ile Leu Gln
260 265 270

Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu
275 280 285

Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly
290 295 300

Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu
305 310 315 320
Arg

<210> 71
<211> 392
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 71
Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15
Leu Ala Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
20 25 30

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

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

145 150 155 160

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

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

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

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
355 360 365
Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
370 375 380
Arg Leu Leu Glu Glu Val Glu Arg
385 390

<210> 72

<211> 310

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 72

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
20 25 30

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
35 40 45

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

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

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
85 90 95

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
100 105 110

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
115 120 125

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
130 135 140

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
145 150 155 160

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
165 170 175

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
180 185 190

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

195 200 205

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
275 280 285
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
290 295 300
Ser Leu Ser Pro Gly Lys
305 310

<210> 73
<211> 321
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 73

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

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

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

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

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

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

<210> 74

<211> 321

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 74

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

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

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

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

195 200 205

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

210 215 220

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

225 230 235 240

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Ser Gly Ser

245 250 255

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

260 265 270

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

275 280 285

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

290 295 300

Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu

305 310 315 320

Arg

<210> 75

<211> 392

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 75

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys

85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro

100 105 110

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser

115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp

130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn

145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val

165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu

180 185 190

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

195 200 205

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

210 215 220

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr

225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu

245 250 255

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

260 265 270

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

275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu

290 295 300

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

305 310 315 320

Lys Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser
325 330 335
Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
340 345 350
Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
355 360 365

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
370 375 380
Arg Leu Leu Glu Glu Val Glu Arg
385 390

<210> 76
<211> 321
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 76

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
115 120 125

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
145 150 155 160

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

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
290 295 300
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
305 310 315 320
Lys

<210> 77
<211> 321
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 77

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

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

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

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

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

245 250 255

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

260 265 270

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

275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu

290 295 300

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

305 310 315 320

Lys

<210> 78

<211> 329

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 78

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu

65 70 75 80

Leu Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly

85 90 95

Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

100 105 110

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

115 120 125

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
325

<210> 79
<211> 329
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 79

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
20 25 30

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

Gln Leu Phe Glu Asn Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
65 70 75 80

Leu Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly
85 90 95

Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
100 105 110

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
115 120 125

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
130 135 140

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
145 150 155 160

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
165 170 175

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
180 185 190

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
195 200 205

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
210 215 220

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu

225 230 235 240

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
245 250 255

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
260 265 270

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
275 280 285

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
290 295 300

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305 310 315 320

Lys Ser Leu Ser Leu Ser Pro Gly Lys
325

<210> 80

<211> 372

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 80

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
20 25 30

Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
35 40 45

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

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser
65 70 75 80

Gly Gly Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser
85 90 95

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

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

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

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

340 345 350

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

Ser Pro Gly Lys
370

<210> 81

<211> 380

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 81

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
20 25 30

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

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
65 70 75 80

Leu Ser Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val
85 90 95

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
100 105 110

Pro Ser Gly Gly Ser Gly Asn Ser Ser Gly Ser Gly Gly Ser Pro Val
115 120 125

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
130 135 140

Pro Ser Ala Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
145 150 155 160

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

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

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
355 360 365
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

<210> 82
<211> 336
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 82

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
20 25 30

Thr Leu Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
35 40 45

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

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Ser Gly Gly
65 70 75 80

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
85 90 95

Gly Ser Gly Gly Gly Gly Ser Gly Glu Pro Lys Ser Ser Asp Lys Thr
100 105 110

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
115 120 125

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
130 135 140

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
145 150 155 160

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
165 170 175

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
180 185 190

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
195 200 205

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
210 215 220

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

225 230 235 240

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys

245 250 255

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

260 265 270

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

275 280 285

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

290 295 300

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

305 310 315 320

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

325 330 335

<210> 83

<211> 344

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 83

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu

65 70 75 80

Leu Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

85 90 95

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

100 105 110

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

115 120 125

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

130 135 140

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

145 150 155 160

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

165 170 175

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln

180 185 190

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln

195 200 205

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

210 215 220

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

225 230 235 240

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr

245 250 255

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

260 265 270

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

275 280 285

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

290 295 300

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

305 310 315 320

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

325 330 335

Ser Leu Ser Leu Ser Pro Gly Lys

340

<210> 84

<211> 321

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 84

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
20 25 30

Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
35 40 45

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

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
195 200 205

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
210 215 220

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
290 295 300
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
305 310 315 320
Lys

<210> 85
<211> 321
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 85
Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

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

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys
85 90 95

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
195 200 205

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
210 215 220

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
245 250 255

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
260 265 270

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
275 280 285

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
290 295 300

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
305 310 315 320

Lys

<210> 86

<211> 372

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 86

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

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser
65 70 75 80
Gly Gly Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser
85 90 95
Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Gly Gly Ser Gly Asn Ser
100 105 110
Ser Gly Ser Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser
115 120 125

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

180 185 190

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

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

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

<210> 87
<211> 336
<212> PRT
<213> Artificial Sequence
<220><223>
Synthetic
<400> 87

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

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

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

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

245 250 255

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

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 88
<211> 321
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 88

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

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

100 105 110

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

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

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

290 295 300
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
305 310 315 320
Lys

<210> 89
<211> 321
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 89

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

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

20 25 30

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
35 40 45

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
50 55 60

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

Gly Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys

85 90 95

Thr His Thr Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
100 105 110

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
130 135 140

Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly Val Glu Val His Asn

145 150 155 160

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
165 170 175

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
180 185 190

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
195 200 205

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

210 215 220

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr

225 230 235 240

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu

245 250 255

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

260 265 270

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

275 280 285

Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu

290 295 300

Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

305 310 315 320

Lys

<210> 90

<211> 395

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 90

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly

100 105 110

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

115 120 125

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

130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser

145 150 155 160

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro

165 170 175

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

195 200 205

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

210 215 220

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

225 230 235 240

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

245 250 255

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

260 265 270

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

275 280 285

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

290 295 300

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

305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

325 330 335

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

340 345 350

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
355 360 365

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
385 390 395

<210> 91
<211> 480
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 91

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

Leu Ala Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser
20 25 30

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu
35 40 45

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu

50 55 60

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala
65 70 75 80

Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly
85 90 95

Ser Gly Gly Gly Ser Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val
100 105 110

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

115 120 125

Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
130 135 140

Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
145 150 155 160

Leu Leu Glu Arg Ile Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

165 170 175

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

180 185 190

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

195 200 205

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

210 215 220

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly

225 230 235 240

Ser Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr

245 250 255

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser

260 265 270

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg

275 280 285

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro

290 295 300

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala

305 310 315 320

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

325 330 335

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr

340 345 350

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr

355 360 365

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

370 375 380

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys

385 390 395 400

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

405 410 415

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

420 425 430

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

435 440 445

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

450 455 460

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

465 470 475 480

<210> 92

<211> 480

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 92

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu

85 90 95

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

100 105 110

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

115 120 125

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu

130 135 140

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

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

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

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
385 390 395 400

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

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475 480
<210> 93
<211> 395
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 93
Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15
Leu Ala Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr
20 25 30
Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe

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

100 105 110

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

115 120 125

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

130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser

145 150 155 160

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro

165 170 175

Cys Pro Ala Pro Glu Leu Leu Ala Gly Pro Ser Val Phe Leu Phe Pro

180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

195 200 205

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

210 215 220

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

225 230 235 240

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

245 250 255

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

260 265 270

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

275 280 285

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

290 295 300

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

305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

325 330 335

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

340 345 350

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

355 360 365

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

385 390 395

<210> 94

<211> 395

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 94

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly

100 105 110

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

115 120 125

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

130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser

145 150 155 160

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro

165 170 175

Cys Pro Ala Pro Glu Leu Leu Arg Gly Pro Ser Val Phe Leu Phe Pro

180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

195 200 205

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

210 215 220

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

225 230 235 240

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

245 250 255

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

260 265 270

Asn Lys Ala Arg Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

275 280 285

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

290 295 300

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

305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

325 330 335

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

340 345 350

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

355 360 365

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

385 390 395

<210> 95

<211> 395

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 95

Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

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

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe
35 40 45

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

50 55 60

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile
65 70 75 80

Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn
85 90 95

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
100 105 110

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

115 120 125

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser
145 150 155 160

Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
165 170 175

Cys Pro Ala Pro Glu Leu Leu Ala Gly Pro Ser Val Phe Leu Phe Pro

180 185 190

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
195 200 205

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
210 215 220
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
225 230 235 240
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val

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

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

370 375 380
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
385 390 395

<210> 96
<211> 395
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 96
Met Ala Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala
1 5 10 15

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

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

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

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

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

260 265 270

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

275 280 285

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

290 295 300

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

305 310 315 320

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

325 330 335

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

340 345 350

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

355 360 365

Asn Val Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr

370 375 380

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

385 390 395

<210> 97

<211> 75

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 97

Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser

1 5 10 15

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser

20 25 30

Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr

35 40 45

Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser

50 55 60

Thr Pro Pro Thr Pro Ser Pro Ser Ala Ser Gly

65 70 75

<210> 98

<211> 65

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 98

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser Thr
1 5 10 15

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Gly
20 25 30

Gly Ser Gly Asn Ser Ser Gly Ser Gly Gly Ser Pro Val Pro Ser Thr
35 40 45

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Ala

50 55 60

Ser

65

<210> 99

<211> 85

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 99

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

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

Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile

35 40 45

Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn
50 55 60

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

65 70 75 80

Gly Gly Ser Ser Gly

85

<210> 100

<211> 75

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 100

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

1 5 10 15

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

20 25 30

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

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75

<210> 101

<211> 75

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 101

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75

<210> 102

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 102

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

<210> 103

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 103

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

1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

<210> 104

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 104

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Leu Leu
1 5 10 15
Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 105

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 105

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Thr Leu
1 5 10 15
Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 106

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 106

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

Asp Gln Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

<210> 107

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 107

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

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

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

<210> 108

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 108

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

<210> 109

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 109

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

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

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

<210> 110

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 110

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

Glu Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

<210> 111

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 111

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15
Arg Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 112

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 112

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15
Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 113

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 113

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Gln Leu Leu Glu Glu Val Glu Arg

50 55

<210> 114

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 114

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Gln Glu Val Glu Arg

50 55

<210> 115

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 115

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

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

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

<210> 116

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 116

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

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

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

<210> 117

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 117

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

1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Tyr Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg

50 55

<210> 118

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 118

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

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg
50 55

<210> 119

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 119

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

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Gln Leu Leu Glu Glu Val Glu Arg
50 55

<210> 120

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 120

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

1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Tyr Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Gln Leu Leu Glu Glu Val Glu Arg

50 55

<210> 121

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 121

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

1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Gln Leu Leu Glu Glu Val Glu Arg

50 55

<210> 122

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 122

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

1 5 10 15

Glu Lys Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Gln Asp Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Lys Arg

50 55

<210> 123

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 123

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

1 5 10 15

Arg Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Lys Arg

50 55

<210> 124

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 124

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu

1 5 10 15

Arg Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Gln Asp Lys Asp Lys Arg Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Gln Arg

50 55

<210> 125

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 125

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg
50 55

<210> 126

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 126

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Lys Leu Gly His Ala Glu Ala Ser Met Gln Ala Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Gln Arg
50 55

<210> 127

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 127

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

1 5 10 15

Arg Ala Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Lys Arg

50 55

<210> 128

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 128

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

1 5 10 15

Glu Lys Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Gln Arg

50 55

<210> 129

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 129

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

1 5 10 15

Glu Lys Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Lys Arg

50 55

<210> 130

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 130

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

1 5 10 15

Arg Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Lys Asn Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Lys Arg

50 55

<210> 131

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 131

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu

1 5 10 15

Arg Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Gln Arg

50 55

<210> 132

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 132

Asp Arg Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Lys Leu Gly His Ala Glu Ala Ser Met Gln Ala Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Gln Arg
50 55

<210> 133

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 133

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

Arg Ala Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Gln Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg
50 55

<210> 134

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 134

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

1 5 10 15

Glu Lys Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

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

35 40 45

Arg Leu Leu Glu Glu Val Gln Arg

50 55

<210> 135

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 135

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

1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Lys Arg

50 55

<210> 136

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 136

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

1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Thr Arg

50 55

<210> 137

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 137

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

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 138

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 138

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

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 139

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 139

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

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 140

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 140

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

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 141

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 141

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

<210> 142
<211> 64
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 142
Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Met Lys Lys Arg Val Phe Gln Leu
20 25 30
Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 143
<211> 64
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 143
Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys Arg Val Phe Gln Leu
20 25 30
Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 144

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 144

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys His Val Phe Gln Leu
20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 145

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 145

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 146

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 146

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

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

20 25 30

Phe Glu Leu Ala Thr Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 147

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 147

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

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

20 25 30

Phe Glu Leu Ala Asp Lys Ala Arg Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 148

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 148

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

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 149

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 149

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

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 150

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 150

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

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 151

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 151

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

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 152

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 152

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

1 5 10 15

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

20 25 30

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

35 40 45

Lys Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 153

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 153

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu
20 25 30

Phe Gly Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 154

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 154

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

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

20 25 30

Phe Tyr Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 155

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 155

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 156

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 156

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

1 5 10 15

Leu His Phe Ala Lys Thr Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 157

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 157

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 158

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 158

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Trp Glu Ala

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 159

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 159

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Trp Glu Ala

1 5 10 15

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

20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

<210> 160

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 160

Asn Glu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Trp Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 161

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 161

Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Trp Glu Ala
1 5 10 15

Leu His Phe Ala Lys Thr Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

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

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 162

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 162

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Thr Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

<210> 163

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 163

Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
50 55 60

<210> 164

<211> 75

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 164

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

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

<210> 165
<211> 20
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 165
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
1 5 10 15
Gly Ser Gly Gly
20
<210> 166
<211> 15
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 166
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10 15
<210> 167

<211> 10
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 167
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

1 5 10

<210> 168

<211> 9

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 168

Gly Gly Gly Gly Ser Gly Gly Gly Gly

1 5

<210> 169

<211> 7

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 169

Gly Gly Gly Ser Gly Gly Gly

1 5

<210> 170

<211> 5

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 170

Gly Gly Ser Gly Gly

1 5

<210> 171

<211> 7

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 171

Gly Gly Ser Gly Ser Ser Gly

1 5

<210> 172

<211> 24

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 172

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro

1 5 10 15

Ala Pro Ser Ala Pro Ala Gly Gly

20

<210> 173

<211> 16

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 173

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly

1 5 10 15

<210> 174

<211> 12

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 174

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly

1 5 10

<210

> 175

<211> 11

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 175

Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly

1 5 10

<210> 176

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 176

Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr

1 5 10 15

Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly

20 25

<210> 177

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 177

Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser Ser Ala

1 5 10 15

Thr Pro Ser Gly Ser Gly Thr Gly Gly

20 25

<210> 178

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 178

Gly Gly Ser Ser Gly Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu

1 5 10 15

Ala Ala Ala Lys Gly Ser Ser Gly Gly

20 25

<210> 179

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 179

Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys

1 5 10 15

Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu

20 25

<210> 180

<211> 85

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 180

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

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

20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

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

50 55 60

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

65 70 75 80

Lys Gln Lys Gln Gly

85

<210> 181

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 181

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

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

20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

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

50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

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

100 105 110

Asn Ala Lys Gln Lys Gln Gly

115

<210> 182

<211> 76

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 182

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

1 5 10 15

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

20 25 30

Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg

35 40 45

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

50 55 60

Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys

65 70 75

<210> 183

<211> 33

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 183

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
1 5 10 15

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
20 25 30

Arg

<210> 184

<211> 76

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 184

Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser
1 5 10 15

Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg Ala Ser Thr Glu
20 25 30

Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg
35 40 45

Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn Asn Arg Ile Ile
50 55 60

Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
65 70 75

<210> 185

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 185

Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn Ala Met Tyr Arg Lys

1 5 10 15

Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr Leu Ala Leu Leu Lys

20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Ala Tyr

35 40 45

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

50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

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

100 105 110

Asn Ala Lys Gln Lys Gln Gly

115

<210> 186

<211> 30

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 186

Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Glu

1 5 10 15

Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Gly

20 25 30

<210> 187

<211> 63

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 187

Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys
1 5 10 15
Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro
20 25 30

Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn
35 40 45
Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
50 55 60

<210> 188
<211> 57
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 188
Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
1 5 10 15
Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu

20 25 30
Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile
35 40 45
Val Glu Val Leu Arg Ile Ile Ala Lys
50 55

<210> 189
<211> 50
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 189
Ser Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu
1 5 10 15

Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu Val
20 25 30

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val

35 40 45

Leu Arg

50

<210> 190

<211> 20

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic

<400> 190

atgctgcaat cgtgctacaa 20

<210> 191

<211> 17

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic

<400> 191

gactgccgcc tctgctc 17

<210> 192

<211> 11

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic

<400> 192

aacattgcca a 11

<210> 193

<211> 234

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 193

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu

1 5 10 15

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

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

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

Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
210 215 220
Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
225 230
<210> 194
<211> 234
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 194

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
1 5 10 15
Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

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

85 90 95
Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser Gly Gly Ser
100 105 110
Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
115 120 125
Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro
130 135 140
Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr

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

210 215 220
Ala Glu Arg Leu Leu Glu Glu Val Glu Arg

225 230

<210> 195

<211> 250

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 195

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
1 5 10 15
Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
20 25 30

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

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly
100 105 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
165 170 175
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Asp Asp Glu Leu His
180 185 190
Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp

195 200 205

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

210 215 220

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

225 230 235 240

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

245 250

<210> 196

<211> 250

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 196

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu

1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asn

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser Thr

115 120 125

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro

130 135 140

Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro

145 150 155 160

Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr

165 170 175

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

180 185 190

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

195 200 205

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

210 215 220

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

225 230 235 240

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

245 250

<210> 197

<211> 242

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 197

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu

1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asp

35 40 45

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

50 55 60

Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr

65 70 75 80

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

85 90 95

Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly

100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

165 170 175

Gly Ser Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr

180 185 190

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

195 200 205

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

210 215 220

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu

225 230 235 240

Leu Ser

<210> 198

<211> 242

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 198

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu

1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asn

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly

100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

165 170 175

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

180 185 190

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His Ala

195 200 205

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

210 215 220

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

225 230 235 240

Glu Arg

<210> 199

<211> 242

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 199

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asp
35 40 45

Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp
50 55 60

Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
65 70 75 80

Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg
85 90 95

Leu Leu Glu Glu Val Glu Arg Ala Gly Ser Gly Gly Ser Gly Gly Ser
100 105 110

Gly Gly Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
115 120 125

Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro
130 135 140

Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr
145 150 155 160

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Ala
165 170 175

Ser Gly Asn Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
180 185 190

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe
195 200 205

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
210 215 220

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
225 230 235 240

Leu Ser

<210> 200

<211> 242

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 200

Met Glu Lys Lys Ile Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu
1 5 10 15

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
20 25 30

Pro Gln Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Asn
35 40 45

Asp Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu
50 55 60

His Phe Ala Lys Asp Glu Glu Ile Gln Lys His Val Phe Gln Leu Phe
65 70 75 80

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu
85 90 95

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Ala
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser Thr
115 120 125

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro
130 135 140

Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro
145 150 155 160

Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
165 170 175

Pro Pro Thr Pro Ser Pro Ser Ala Ser Gly Asp Lys Glu Asn Ile Leu
180 185 190

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Asp Gln Leu Gly His Ala
195 200 205

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
210 215 220
Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
225 230 235 240
Glu Arg

<210> 201
<211> 169
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 201
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

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

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95
Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
100 105 110
Ser Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu
115 120 125
Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu

130 135 140

Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala
145 150 155 160
Glu Arg Leu Leu Glu Glu Val Glu Arg
165

<210> 202
<211> 185
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 202

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

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

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

145 150 155 160

Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu
165 170 175

Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185

<210> 203

<211> 174

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 203

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Trp Ile Leu
35 40 45

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

Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr
115 120 125

Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met
130 135 140

Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg
145 150 155 160

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
165 170

<210> 204

<211> 190

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 204

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

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

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

145 150 155 160
Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys
165 170 175
Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185 190

<210> 205

<211> 230

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 205

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Ser Gly Ser Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr
20 25 30

Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met
35 40 45

Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg
50 55 60

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Ser
65 70 75 80

Ser Gly Ser Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Gly Ser Ser
85 90 95

Gly Ser Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
100 105 110

Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
115 120 125

Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu
130 135 140

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Ser Ser Gly Gly
145 150 155 160

Ser Ser Ser Gly Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly Asp Lys
165 170 175

Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu
180 185 190

Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu
195 200 205

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

210 215 220

Leu Glu Glu Val Glu Arg

225 230

<210> 206

<211> 254

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 206

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Ser Gly Ser Ser Gly Asn Asp Asp Glu Leu His Met Leu Met Thr

20 25 30

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

35 40 45

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

50 55 60

Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu

65 70 75 80

Leu Glu Arg Leu Leu Ser Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser

85 90 95

Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Asn Asp Asp Glu Leu His

100 105 110

Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp

115 120 125

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

130 135 140

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

145 150 155 160

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Ser Ser Gly Gly

165 170 175

Ser Ser Ser Gly Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly Asn Asp

180 185 190

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

195 200 205

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

210 215 220

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

225 230 235 240

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

245 250

<210> 207

<211> 174

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 207

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys

65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

85 90 95

Glu Arg Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr

100 105 110

Gly Thr Ser Thr Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr

115 120 125

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

130 135 140

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

145 150 155 160

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg

165 170

<210> 208

<211> 250

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 208

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys

65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

85 90 95

Glu Arg Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr

100 105 110

Gly Thr Ser Gly Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr

115 120 125

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

130 135 140

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

145 150 155 160

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

Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu
225 230 235 240
Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
245 250

<210> 209
<211> 190
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 209
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

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

85 90 95
Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Ala Gly Gly Ser
100 105 110

Pro Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser Gly Ser Gly Asn Asp
115 120 125

Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His
130 135 140

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

145 150 155 160

Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys
165 170 175

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185 190

<210> 210

<211> 274

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 210

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Asp Asp Glu Leu His
35 40 45

Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys
65 70 75 80

Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Ala Gly Gly Ser
100 105 110

Pro Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser Gly Ser Gly Asn Asp
115 120 125

Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His
130 135 140

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

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

Leu Ser

<210> 211
<211> 233
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 211
Met Glu Lys Lys Ile Ser Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys
1 5 10 15
Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala
20 25 30
Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp

35 40 45

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

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

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

<210> 212
<211> 257
<212> PRT

<213> Artificial Sequence
<220><223> Synthetic
<400> 212

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

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

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

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

245 250 255

Lys

<210> 213

<211> 260

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 213

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys

65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

85 90 95

Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser

100 105 110

Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly Gly Asp Lys Glu Trp Ile

115 120 125

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

130 135 140

Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

145 150 155 160

Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

165 170 175

Val Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr

180 185 190

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

195 200 205

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

210 215 220

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met

225 230 235 240

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

245 250 255

Glu Val Glu Arg

260

<210> 214

<211> 284

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 214

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp

50 55 60

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

65 70 75 80

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

85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Ala Gly

100 105 110

Ser Pro Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly

115 120 125

Thr Gly Gly Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val

130 135 140

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

145 150 155 160

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

165 170 175

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg

180 185 190

Leu Leu Ser Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr

195 200 205

Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly Gly Asn Asp Asp Glu

210 215 220

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

225 230 235 240

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

245 250 255

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

260 265 270

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

275 280

<210> 215

<211> 179

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 215

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

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

Val Glu Arg

<210> 216
<211> 179
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 216
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45

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

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

Val Glu Arg

<210> 217
<211> 179
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 217
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45

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

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

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

Val Glu Arg

<210> 218
<211> 183
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 218
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
50 55 60
Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95
Glu Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro
100 105 110

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

Leu Leu Glu Glu Val Glu Arg
180

<210> 219
<211> 239
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 219
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45

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

Glu Arg Gly Gly Ser Ser Gly Gln Ile Phe Val Lys Thr Leu Thr Gly
100 105 110

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

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

<210> 220
<211> 260
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 220
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45
Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala

50 55 60

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

65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

85 90 95

Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser

100 105 110

Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly Gly Asp Lys Glu Asn Ile

115 120 125

Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His

130 135 140

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

145 150 155 160

Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

165 170 175

Val Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr

180 185 190

Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly Gly Asp Lys Glu Asn

195 200 205

Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly

210 215 220

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

225 230 235 240

Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

245 250 255

Glu Val Glu Arg

260

<210> 221

<211> 260

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 221

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45

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

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Glu Arg Gly Gly Ser Ser Gly Glu Ala Ala Ala Lys Glu Ala Ala Ala
100 105 110

Lys Glu Ala Ala Ala Lys Gly Ser Ser Gly Gly Asp Lys Glu Asn Ile
115 120 125

Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His
130 135 140

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
145 150 155 160

Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
165 170 175

Val Glu Arg Gly Gly Ser Ser Gly Glu Ala Ala Ala Lys Glu Ala Ala
180 185 190

Ala Lys Glu Ala Ala Ala Lys Gly Ser Ser Gly Gly Asp Lys Glu Asn
195 200 205

Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly
210 215 220

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

225 230 235 240

Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

245 250 255

Glu Val Glu Arg

260

<210> 222

<211> 268

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 222

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

85 90 95

Glu Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro

100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp

115 120 125

Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu

130 135 140

Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr

145 150 155 160

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

165 170 175

Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro
180 185 190
Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly
195 200 205
Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile

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

<210> 223
<211> 380
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic

<400> 223
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
35 40 45
Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
50 55 60

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

Lys Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val
115 120 125

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

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

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

Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile
325 330 335
Met Lys Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val
340 345 350
Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu

355 360 365

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg

370 375 380

<210> 224

<

211> 179

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 224

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

50 55 60

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

65 70 75 80

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

85 90 95

Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser

100 105 110

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val

115 120 125

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

130 135 140

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

145 150 155 160

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

165 170 175

Val Lys Arg

<210> 225

<211> 183

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 225

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

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

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro
100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp
115 120 125

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
130 135 140

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
145 150 155 160

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
165 170 175

Leu Leu Glu Glu Val Lys Arg
180

<210> 226

<211> 195

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 226

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly
100 105 110

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
115 120 125

Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
130 135 140

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

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
165 170 175

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
180 185 190

Leu Leu Ser
195

<210> 227

<211> 199

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 227

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

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

35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro

100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro
115 120 125

Ser Pro Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met
130 135 140

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
145 150 155 160

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

165 170 175

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
180 185 190

Leu Leu Glu Arg Leu Leu Ser
195

<210> 228

<211> 179

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 228

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15
Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

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

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

145 150 155 160
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
165 170 175
Phe Glu Lys

<210> 229

<211> 183

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 229

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15
Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

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

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

145 150 155 160
Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp
165 170 175
Ser His Pro Gln Phe Glu Lys
180

<210> 230

<211> 195

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 230

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn Leu
85 90 95

Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His
100 105 110

Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu
115 120 125

Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys
130 135 140

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly
145 150 155 160

Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
165 170 175

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
180 185 190

Phe Glu Lys
195

<210> 231

<211> 199

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 231

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

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

20 25 30

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

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr

65 70 75 80

Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser

85 90 95

Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr

100 105 110

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

115 120 125

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

130 135 140

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu

145 150 155 160

Leu Ser Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln

165 170 175

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp

180 185 190

Ser His Pro Gln Phe Glu Lys

195

<210> 232

<211> 240

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 232

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
20 25 30

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
35 40 45

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

50 55 60

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly
65 70 75 80

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser
85 90 95

Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
100 105 110

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser

115 120 125

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
130 135 140

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

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
165 170 175

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

180 185 190

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
195 200 205

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
210 215 220

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

225 230 235 240

<210> 233

<211> 248

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 233

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
20 25 30

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
35 40 45

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
50 55 60

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly
65 70 75 80

Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro
85 90 95

Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu Asn Val
100 105 110

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
115 120 125

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
130 135 140

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
145 150 155 160

Val Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser
165 170 175

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly
180 185 190

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
195 200 205

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
210 215 220

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
225 230 235 240

Arg Leu Leu Glu Glu Val Lys Arg
245

<210> 234

<211> 264

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 234

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
20 25 30

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
35 40 45

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
50 55 60

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
65 70 75 80

Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly
85 90 95

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn
100 105 110

Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu
115 120 125

His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe
130 135 140

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

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

Glu Leu Leu Glu Arg Leu Leu Ser
260

<210> 235
<211> 272
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 235
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
20 25 30
Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
35 40 45

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
50 55 60
Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
65 70 75 80

Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro
85 90 95
Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly
100 105 110

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

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

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
245 250 255
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
260 265 270

<210> 236
<211> 240
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 236

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

20 25 30

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

35 40 45

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

50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser

65 70 75 80

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

85 90 95

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met

100 105 110

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

115 120 125

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly

130 135 140

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser

145 150 155 160

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

165 170 175

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser

180 185 190

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

195 200 205

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

210 215 220

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

225 230 235 240

<210> 237

<211> 248

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 237

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

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

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

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

Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala
225 230 235 240
Trp Ser His Pro Gln Phe Glu Lys
245

<210> 238
<211> 264
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 238

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

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

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

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser
165 170 175

Ser Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met
180 185 190

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
195 200 205

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
210 215 220

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
225 230 235 240

Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Ser Ser Gly Ser Ala
245 250 255

Trp Ser His Pro Gln Phe Glu Lys
260

<210> 239

<211> 272

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 239

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr
65 70 75 80

Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser
85 90 95

Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
100 105 110

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
115 120 125
Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
130 135 140

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

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

<210> 240
<211> 187
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 240
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

50 55 60

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

65 70 75 80

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

85 90 95

Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser

100 105 110

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu

115 120 125

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

130 135 140

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

145 150 155 160

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

165 170 175

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

180 185

<210> 241

<211> 191

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 241

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

50 55 60

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

65 70 75 80

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

85 90 95

Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro

100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asn

115 120 125

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

130 135 140

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

145 150 155 160

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

165 170 175

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

180 185 190

<210> 242

<211> 187

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 242

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly

100 105 110

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly

115 120 125

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

130 135 140

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

145 150 155 160

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

165 170 175

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

180 185

<210> 243

<211> 191

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 243

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Pro

100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro

115 120 125

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

130 135 140

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser

145 150 155 160

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

165 170 175

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

180 185 190

<210> 244

<211> 187

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 244

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

1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

20 25 30

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

35 40 45

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

50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser

65 70 75 80

Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr

85 90 95

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

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
165 170 175
Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
180 185

<210> 245
<211> 191
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 245
Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
1 5 10 15
Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

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

85 90 95
Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
100 105 110

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

145 150 155 160
Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
165 170 175
Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
180 185 190

<210> 246

<211> 187

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 246

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

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

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

Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu
130 135 140

Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp
145 150 155 160
Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
165 170 175
Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
180 185

<210> 247
<211> 191
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 247
Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

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

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

130 135 140

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

145 150 155 160

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly

165 170 175

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

180 185 190

<210> 248

<211> 172

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 248

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Gly Ser Gly Gly

100 105 110

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

115 120 125

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

130 135 140

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

145 150 155 160

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

165 170

<210> 249

<211> 172

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 249

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly

100 105 110

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

115 120 125

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

130 135 140

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

145 150 155 160

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

165 170

<210> 250

<211> 177

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 250

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly
100 105 110

Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln
115 120 125

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
130 135 140

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
145 150 155 160

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
165 170 175

Arg

<210> 251

<211> 182

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 251

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly
100 105 110

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys
115 120 125

Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg
130 135 140

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu
145 150 155 160

Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu
165 170 175

Leu Glu Glu Val Lys Arg
180

<210> 252

<211> 164

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 252

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
35 40 45

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

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95

Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn
100 105 110

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

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
130 135 140

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
145 150 155 160

Glu Val Lys Arg

<210> 253

<211> 169

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 253

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

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

Glu Arg Leu Leu Glu Glu Val Lys Arg
165

<210> 254
<211> 174
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 254
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu

35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

50 55 60

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

65 70 75 80

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

85 90 95

Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser

100 105 110

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

115 120 125

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met

130 135 140

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

145 150 155 160

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

165 170

<210> 255

<211> 183

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 255

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

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

Leu Leu Glu Glu Val Lys Arg
180

<210> 256
<211> 188
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 256
Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

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

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
130 135 140

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

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu
165 170 175

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
180 185

<210> 257

<211> 193

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 257

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

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

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly

115 120 125

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

130 135 140

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

145 150 155 160

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

165 170 175

Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys

180 185 190

Arg

<210> 258

<211> 268

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 258

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu

115 120 125

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

130 135 140

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala

145 150 155 160

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

165 170 175

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile

180 185 190

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly

195 200 205

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

210 215 220

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

225 230 235 240

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

245 250 255

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

260 265

<210> 259

<211> 278

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 259

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly

115 120 125

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln

130 135 140

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu

145 150 155 160

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu

165 170 175

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu

180 185 190

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly

195 200 205

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys

210 215 220

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

225 230 235 240

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu

245 250 255

Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu

260 265 270

Leu Glu Glu Val Lys Arg

275

<210> 260

<211> 288

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 260

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met
130 135 140

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

Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala
165 170 175

Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile
180 185 190

Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu
195 200 205

Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
210 215 220

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

<210> 261
<211> 202
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 261
Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

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

115 120 125

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

130 135 140

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala

145 150 155 160

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

165 170 175

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile

180 185 190

Leu Glu His Leu Glu Glu Leu Ala Arg Lys

195 200

<210> 262

<211> 207

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 262

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly

115 120 125

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln

130 135 140

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu

145 150 155 160

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu

165 170 175

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu

180 185 190

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

195 200 205

<210> 263

<211> 212

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 263

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly

115 120 125

Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met

130 135 140

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

145 150 155 160

Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala

165 170 175

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

180 185 190

Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu

195 200 205

Leu Ala Arg Lys

210

<210> 264

<211> 287

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 264

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu

115 120 125

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

130 135 140

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala

145 150 155 160

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

165 170 175

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile

180 185 190

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly

195 200 205

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln

210 215 220

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu

225 230 235 240

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu

245 250 255

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu

260 265 270

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

275 280 285

<210> 265

<211> 297

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 265

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly

115 120 125

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln

130 135 140

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu

145 150 155 160

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu

165 170 175

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu

180 185 190

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly

195 200 205

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu

210 215 220

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

225 230 235 240

Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr

245 250 255

Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp
260 265 270
Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu
275 280 285
Glu His Leu Glu Glu Leu Ala Arg Lys
290 295

<210> 266
<211> 307
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 266

Met Ser Lys Ile Lys Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

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

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

130 135 140
His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys
145 150 155 160

Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala
165 170 175
Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile
180 185 190
Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu

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

260 265 270
Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
275 280 285
Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
290 295 300
Ala Arg Lys
305

<210> 267
<211> 216
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 267
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

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

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu

130 135 140

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

145 150 155 160

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe

165 170 175

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

180 185 190

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu

195 200 205

His Leu Glu Glu Leu Ala Arg Lys

210 215

<210> 268

<211> 186

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 268

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala

115 120 125

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

130 135 140

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

145 150 155 160

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

165 170 175

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

180 185

<210> 269

<211> 197

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 269

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

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

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu

130 135 140

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

145 150 155 160

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe

165 170 175

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

180 185 190

Glu Glu Val Lys Arg

195

<210> 270

<211> 315

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 270

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

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

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu

130 135 140

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

145 150 155 160

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe

165 170 175

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

180 185 190

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu

195 200 205

His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro

210 215 220

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly

225 230 235 240

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

245 250 255

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

260 265 270

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

275 280 285

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
290 295 300

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
305 310 315

<210> 271

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 271

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asn Leu Asp Glu Leu His
35 40 45

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
50 55 60

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

65 70 75 80

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
85 90 95

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala
100 105 110

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala
115 120 125

Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser

130 135 140

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu
145 150 155 160

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu
165 170 175

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala
180 185 190
Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala

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

260 265 270
Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
275 280 285
<210> 272
<211> 285
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 272
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

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

85 90 95

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

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

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

<210> 273

<211> 258

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 273

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

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

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

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

245 250 255

Lys Arg

<210> 274

<211> 315

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 274

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

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

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu

130 135 140

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

145 150 155 160

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe

165 170 175

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

180 185 190

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu

195 200 205

His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro

210 215 220

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly

225 230 235 240

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

245 250 255

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

260 265 270

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

275 280 285

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

290 295 300

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

305 310 315

<210> 275

<211> 282

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 275

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala

115 120 125

Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr

130 135 140

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

145 150 155 160

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

165 170 175

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu

180 185 190

Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala

195 200 205

Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His

210 215 220

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

225 230 235 240

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

245 250 255

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

260 265 270

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

275 280

<210> 276

<211> 296

<212

> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 276

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

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

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu
130 135 140

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
145 150 155 160

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
165 170 175

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

180 185 190

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu
195 200 205

His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro
210 215 220

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
225 230 235 240

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

245 250 255

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

260 265 270

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

275 280 285

Arg Leu Leu Glu Glu Val Lys Arg

290 295

<210> 277

<211> 208

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 277

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

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

115 120 125

Ser Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp

130 135 140

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

145 150 155 160

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

165 170 175

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

180 185 190

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

195 200 205

<210> 278

<211> 203

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 278

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

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

115 120 125

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

130 135 140

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

145 150 155 160

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

165 170 175

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

180 185 190

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

195 200

<210> 279

<211> 178

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 279

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

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

115 120 125

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

130 135 140

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

145 150 155 160

Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

165 170 175

Lys Arg

<210> 280

<211> 173

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 280

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

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

115 120 125

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

130 135 140

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

145 150 155 160

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

165 170

<210> 281

<211> 189

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 281

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

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

115 120 125

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

130 135 140

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

145 150 155 160

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

165 170 175

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

180 185

<210> 282

<211> 184

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 282

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

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

115 120 125

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

130 135 140

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

145 150 155 160

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

165 170 175

Arg Leu Leu Glu Glu Val Lys Arg

180

<210> 283

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 283

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

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

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

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

195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser

210 215 220

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

225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

245 250 255

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

260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

275 280 285

<210> 284

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 284

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

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

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

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

<210> 285
<211> 315
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 285

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu

130 135 140

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

145 150 155 160

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe

165 170 175

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

180 185 190

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu

195 200 205

His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro

210 215 220

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly

225 230 235 240

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

245 250 255

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

260 265 270

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

275 280 285

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg

290 295 300

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr

305 310 315

<210> 286

<211> 258

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 286

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

50 55 60

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

65 70 75 80

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

85 90 95

Thr Arg Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala

100 105 110

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

115 120 125

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

130 135 140

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

145 150 155 160

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

165 170 175

Thr Arg Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala

180 185 190

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

195 200 205

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

210 215 220

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

225 230 235 240

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

245 250 255

Thr Arg

<210> 287

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 287

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp

50 55 60

Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys

65 70 75 80

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

85 90 95

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

100 105 110

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

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

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

<210> 288
<211> 285
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 288

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

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

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

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

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

260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

275 280 285

<210> 289

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 289

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp

50 55 60

Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys

65 70 75 80

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

85 90 95

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

100 105 110

Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala

115 120 125

Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser

130 135 140

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu

145 150 155 160

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu

165 170 175

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala

180 185 190

Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala

195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser

210 215 220

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

225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

245 250 255

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

260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

275 280 285

<210> 290

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 290

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

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

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

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

195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser

210 215 220

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

225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

245 250 255

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

260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

275 280 285

<210> 291

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 291

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

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

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

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

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

260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

275 280 285

<210> 292

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 292

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

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

35 40 45

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

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

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

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp

130 135 140

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

145 150 155 160

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

165 170 175

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

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

<210> 293
<211> 270
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic
<400> 293

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

Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg
65 70 75 80
Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu
85 90 95

Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro
100 105 110
Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile
115 120 125

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

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

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
260 265 270

<210> 294
<211> 270
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 294
Met Glu Lys Lys Ile His His His His His His Ser Gly Glu Asn Leu
1 5 10 15
Tyr Phe Gln Ser Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln
20 25 30

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

35 40 45

His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp

50 55 60

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

65 70 75 80

Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu

85 90 95

Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro

100 105 110

Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile

115 120 125

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

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro

195 200 205

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

210 215 220

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met

225 230 235 240

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

245 250 255

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

260 265 270

<210> 295

<211> 297

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 295

Met Glu Lys Lys Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly
1 5 10 15

Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
20 25 30

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
35 40 45

Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu
50 55 60

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
65 70 75 80

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
85 90 95

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
100 105 110

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
115 120 125

Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala
130 135 140

Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met
145 150 155 160

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

Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala
180 185 190

Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu
195 200 205

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

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
275 280 285
Glu Arg Leu Leu Glu Glu Val Lys Arg
290 295

<210> 296
<211> 311
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 296

Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
1 5 10 15
His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser

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

85 90 95
Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu

115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly

130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala

145 150 155 160

Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val

165 170 175

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

180 185 190

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

195 200 205

Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu

210 215 220

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

225 230 235 240

Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp

245 250 255

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu

260 265 270

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr

275 280 285

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

290 295 300

Leu Leu Glu Glu Val Lys Arg

305 310

<210> 297

<211> 299

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 297

Met Glu Lys Lys Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly
1 5 10 15
Ser Gly Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly

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

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

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

210 215 220
Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
225 230 235 240
Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met

245 250 255

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

260 265 270

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

275 280 285

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

290 295

<210> 298

<211> 303

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 298

Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp

1 5 10 15

His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser

20 25 30

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly

35 40 45

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser

50 55 60

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln

65 70 75 80

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu

85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu

100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu

115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly

130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala

145 150 155 160

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

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

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
290 295 300

<210> 299
<211> 295
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 299
Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
1 5 10 15
His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser
20 25 30
Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly

35 40 45

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser

50 55 60

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln

65 70 75 80

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu

85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu

100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu

115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly

130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn

145 150 155 160

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

165 170 175

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

180 185 190

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

195 200 205

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

210 215 220

Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp

225 230 235 240

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu

245 250 255

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr

260 265 270

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

275 280 285

Leu Leu Glu Glu Val Lys Arg

290 295

<210> 300

<211> 290

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 300

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

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

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

180 185 190

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

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

<210> 301
<211> 298
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 301
Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp

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

65 70 75 80
Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
100 105 110
Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
115 120 125
Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly

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

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

260 265 270
Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
275 280 285
Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
290 295

<210> 302
<211> 290
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 302

Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp
1 5 10 15

His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser
20 25 30

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
35 40 45

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser
50 55 60

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
65 70 75 80

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly
130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn
145 150 155 160

Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu
165 170 175

His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe
180 185 190

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu
195 200 205

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly
210 215 220

Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu
225 230 235 240

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

245 250 255

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

260 265 270

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

275 280 285

Lys Arg

290

<210> 303

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 303

Met Glu Lys Lys Ile Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp

1 5 10 15

His Asp Ile Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ser Gly Ser Ser

20 25 30

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly

35 40 45

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Ser

50 55 60

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln

65 70 75 80

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu

85 90 95

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu

100 105 110

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu

115 120 125

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly

130 135 140

Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu

145 150 155 160

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

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

<210> 304

<211> 196

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 304

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

50 55 60

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

115 120 125
His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys
130 135 140
Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala
145 150 155 160
Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile
165 170 175
Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu

180 185 190
Leu Ala Arg Lys
195

<210> 305
<211> 194
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 305
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110
Glu Leu Ala Arg Lys Gly Gly Glu Leu Glu Glu Gln Val Met His Val
115 120 125
Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr
130 135 140
Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu
145 150 155 160
Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu

165 170 175
Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala
180 185 190
Arg Lys

<210> 306
<211> 205
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 306
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110
Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125
Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Ile Asp
130 135 140
Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe

145 150 155 160
Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys
165 170 175
Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val
180 185 190
Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
195 200 205

<210> 307
<211> 197
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic
<400> 307

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110
Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp
130 135 140
Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
145 150 155 160
His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
165 170 175
Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
180 185 190

Glu Arg Ile Leu Ser
195

<210> 308
<211> 192
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 308
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly
115 120 125
Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala
130 135 140
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu
145 150 155 160
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu
165 170 175

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
180 185 190

<210> 309
<211> 277
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 309

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Asp Lys Glu Asn Val Leu

35 40 45
Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
50 55 60

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
65 70 75 80
Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
85 90 95
Lys Arg Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala

100 105 110
Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val
115 120 125
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
130 135 140
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
145 150 155 160
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

165 170 175
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
180 185 190
Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
195 200 205
Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu
210 215 220
Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu

225 230 235 240
Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
245 250 255
Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
260 265 270
Glu Glu Val Lys Arg
275

<210> 310
<211> 285
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 310

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp

130 135 140

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe

145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys

165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val

180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala

195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser

210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu

260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

275 280 285

<210> 311

<211> 277

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 311

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp

130 135 140

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe

145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
165 170 175
Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
180 185 190
Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala
195 200 205
Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp Lys Glu
210 215 220

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
225 230 235 240
Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
245 250 255
Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
260 265 270
Glu Glu Val Lys Arg
275

<210> 312
<211> 277
<212> PRT
<213> Artificial Sequence
<220
><223> Synthetic
<400> 312

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110
Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
130 135 140
Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
145 150 155 160
His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
165 170 175
Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
180 185 190

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
195 200 205
Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu
210 215 220
Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
225 230 235 240
Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
245 250 255

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
260 265 270
Glu Glu Val Lys Arg
275
<210> 313
<211> 269
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 313

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125

Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
130 135 140

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
145 150 155 160

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
165 170 175

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
180 185 190

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
195 200 205

Ser Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
210 215 220

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

225 230 235 240

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu

245 250 255

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

260 265

<210> 314

<211> 264

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 314

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly

115 120 125

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

130 135 140

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

145 150 155 160

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

165 170 175

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

180 185 190

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly

195 200 205

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

210 215 220

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

225 230 235 240

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

245 250 255

Arg Leu Leu Glu Glu Val Lys Arg

260

<210> 315

<211> 272

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 315

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp

130 135 140

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe

145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys

165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val

180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala

195 200 205

Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys

210 215 220

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala

225 230 235 240

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

245 250 255

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

260 265 270

<210> 316

<211> 264

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 316

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110
Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
115 120 125
Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
130 135 140
Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
145 150 155 160

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
165 170 175
Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
180 185 190
Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly
195 200 205
Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
210 215 220

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
225 230 235 240
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
245 250 255
Arg Leu Leu Glu Glu Val Lys Arg
260

<210> 317

<211> 259

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 317

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly
115 120 125

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
130 135 140

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
145 150 155 160

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
165 170 175

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185 190

Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
195 200 205

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

210 215 220

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

225 230 235 240

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

245 250 255

Val Lys Arg

<210> 318

<211> 251

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 318

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Ala Gly Gly Asn Leu Asp Glu

115 120 125

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala

130 135 140

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala

145 150 155 160

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val

165 170 175

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser

180 185 190

Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met

195 200 205

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser

210 215 220

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu

225 230 235 240

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

245 250

<210> 319

<211> 253

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 319

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Ser Gly Gly Asn Leu Asp

115 120 125

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe

130 135 140

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys

145 150 155 160

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val

165 170 175

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser

180 185 190

Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

195 200 205

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

210 215 220

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu

225 230 235 240

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

245 250

<210> 320

<211> 247

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 320

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His
115 120 125
Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
130 135 140
Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
145 150 155 160
Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
165 170 175

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Asp
180 185 190
Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
195 200 205
Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
210 215 220
Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
225 230 235 240

Leu Leu Glu Glu Val Lys Arg
245

<210> 321
<211> 259
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 321

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
115 120 125
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
130 135 140
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
145 150 155 160
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
165 170 175

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
180 185 190
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Asp Lys Glu Asn Val
195 200 205
Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
210 215 220
Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
225 230 235 240

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

245 250 255

Val Lys Arg

<210> 322

<211> 289

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 322

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly
115 120 125

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
130 135 140

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
145 150 155 160

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
165 170 175

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

180 185 190

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

195 200 205

Ala Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu

210 215 220

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly

225 230 235 240

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met

245 250 255

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile

260 265 270

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg

275 280 285

Lys

<210> 323

<211> 289

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 323

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly

115 120 125

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

130 135 140

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

145 150 155 160

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

165 170 175

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

180 185 190

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly

195 200 205

Ser Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu

210 215 220

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly

225 230 235 240

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met

245 250 255

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile

260 265 270

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg

275 280 285

Lys

<210> 324

<211> 283

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 324

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110
Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Ser Gly Gly Glu Leu Glu
115 120 125

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
130 135 140
Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
145 150 155 160
Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp
165 170 175
Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu
180 185 190

His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Ser Gly Gly
195 200 205
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
210 215 220
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
225 230 235 240

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
245 250 255

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
260 265 270

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
275 280

<210> 325

<211> 277

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 325

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val
115 120 125

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
130 135 140

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

145 150 155 160

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

165 170 175

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

180 185 190

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val

195 200 205

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

210 215 220

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

225 230 235 240

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

245 250 255

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

260 265 270

Glu Leu Ala Arg Lys

275

<210

> 326

<211> 267

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 326

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu

130 135 140

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His

145 150 155 160

Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp

165 170 175

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu

180 185 190

Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

195 200 205

Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met

210 215 220

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser

225 230 235 240

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu

245 250 255

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

260 265

<210> 327

<211> 261

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 327

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu

130 135 140

Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln

145 150 155 160

Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys

165 170 175

Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu

180 185 190

Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Asp Lys Glu

195 200 205

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu

210 215 220

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe

225 230 235 240

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu

245 250 255

Glu Glu Val Lys Arg
260

<210> 328

<211> 255

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 328

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110

Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Asn Leu
115 120 125

Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His
130 135 140

Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu
145 150 155 160

Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys
165 170 175

Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly
180 185 190

Gly Gly Ser Gly Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
195 200 205

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
210 215 220
Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
225 230 235 240
Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
245 250 255

<210> 329
<211> 251
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 329
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30
Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
35 40 45
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
50 55 60
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
85 90 95
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
100 105 110
Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly Gly Gly Asn Leu Asp Glu
115 120 125
Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala

130 135 140

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala
145 150 155 160

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val
165 170 175

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Gly Ser
180 185 190

Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met

195 200 205

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
210 215 220

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
225 230 235 240

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
245 250

<210> 330

<211> 182

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 330

Met Glu Lys Lys Ile Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys
1 5 10 15

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
20 25 30

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
35 40 45

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
50 55 60

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
65 70 75 80

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln

85 90 95

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu

100 105 110

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys

115 120 125

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys

130 135 140

Arg Gly Gly Gly Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe

145 150 155 160

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser

165 170 175

His Pro Gln Phe Glu Lys

180

<210> 331

<211> 177

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 331

Met Glu Lys Lys Ile Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys

1 5 10 15

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala

20 25 30

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

35 40 45

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

50 55 60

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

65 70 75 80

Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile

85 90 95

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val

100 105 110

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu

115 120 125

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser

130 135 140

Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly

145 150 155 160

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu

165 170 175

Lys

<210> 332

<211> 172

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 332

Met Glu Lys Lys Ile Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys

1 5 10 15

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala

20 25 30

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

35 40 45

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

50 55 60

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp

65 70 75 80

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu

85 90 95

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr

100 105 110

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg

115 120 125

Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Ala
130 135 140
Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser
145 150 155 160
Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
165 170

<210> 333
<211> 167
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 333
Met Glu Lys Lys Ile Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys

1 5 10 15
Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala
20 25 30
Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp
35 40 45
Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
50 55 60
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu

65 70 75 80
Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
85 90 95
Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
100 105 110
Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
115 120 125
Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln

130 135 140

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp
145 150 155 160
Ser His Pro Gln Phe Glu Lys
165

<210> 334
<211> 186
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 334

Met Glu Lys Lys Ile Gly Gly Gly Glu Leu Glu Glu Gln Val Met His
1 5 10 15
Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
20 25 30
Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
35 40 45
Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
50 55 60
Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
65 70 75 80
Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu
85 90 95
Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
100 105 110
Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
115 120 125
Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
130 135 140
Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Ala Trp Ser

145 150 155 160
His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
165 170 175

Ser Ala Trp Ser His Pro Gln Phe Glu Lys
180 185

<210> 335

<211> 175

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 335

Met Glu Lys Lys Ile Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln
1 5 10 15

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
20 25 30

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
35 40 45

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
50 55 60

Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys
85 90 95

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
100 105 110

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
115 120 125

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly
130 135 140

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
145 150 155 160

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
165 170 175

<210> 336

<211> 194

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 336

Met Glu Lys Lys Ile Gly Gly Gly Glu Leu Glu Glu Gln Val Met His
1 5 10 15
Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu

20 25 30
Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
35 40 45
Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
50 55 60
Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
65 70 75 80
Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asn Leu Asp

85 90 95
Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
100 105 110
Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
115 120 125
Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
130 135 140
Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Gly

145 150 155 160
Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly
165 170 175
Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe
180 185 190
Glu Lys

<210> 337

<211> 194

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 337

Met Glu Lys Lys Ile Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln

1 5 10 15

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu

20 25 30

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr

35 40 45

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys

50 55 60

Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser

65 70 75 80

Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser

85 90 95

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu

100 105 110

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu

115 120 125

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala

130 135 140

Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly

145 150 155 160

Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly

165 170 175

Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe

180 185 190

Glu Lys

<210> 338

<211> 260

<

212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 338

Met Glu Lys Lys Ile Gly Gly Gly Glu Leu Glu Glu Gln Val Met His
1 5 10 15

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
20 25 30

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
35 40 45

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg

50 55 60

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
65 70 75 80

Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asn Leu Asp
85 90 95

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
100 105 110

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys

115 120 125

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
130 135 140

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser
145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
165 170 175

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser

180 185 190

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
195 200 205

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly

210 215 220

Gly Gly Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

225 230 235 240

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro

245 250 255

Gln Phe Glu Lys

260

<210> 339

<211> 260

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 339

Met Glu Lys Lys Ile Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln

1 5 10 15

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu

20 25 30

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr

35 40 45

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys

50 55 60

Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser

65 70 75 80

Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser

85 90 95

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu

100 105 110

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu

115 120 125

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala

130 135 140

Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser

145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile

165 170 175

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser

180 185 190

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu

195 200 205

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly

210 215 220

Gly Gly Ser Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

225 230 235 240

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro

245 250 255

Gln Phe Glu Lys

260

<210> 340

<211> 270

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 340

Met Glu Lys Lys Ile Gly Gly Gly Glu Leu Glu Glu Gln Val Met His

1 5 10 15

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu

20 25 30

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr

35 40 45

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg

50 55 60

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu

65 70 75 80

Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

85 90 95

Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr

100 105 110

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe

115 120 125

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln

130 135 140

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu

145 150 155 160

Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

165 170 175

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu

180 185 190

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu

195 200 205

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala

210 215 220

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly

225 230 235 240

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly

245 250 255

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

260 265 270

<210> 341

<211> 270

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 341

Met Glu Lys Lys Ile Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln

1 5 10 15

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu

20 25 30

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr

35 40 45

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys

50 55 60

Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser

65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val

85 90 95

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr

100 105 110

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu

115 120 125

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu

130 135 140

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala

145 150 155 160

Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

165 170 175

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu

180 185 190

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu

195 200 205

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala

210 215 220

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly

225 230 235 240

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly

245 250 255

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
260 265 270

<210> 342

<211> 174

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 342

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly
65 70 75 80

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
85 90 95

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu

100 105 110

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
115 120 125

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly
130 135 140

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

165 170

<210> 343

<211> 185

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 343

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn
85 90 95

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
100 105 110

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
115 120 125

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His
145 150 155 160

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
165 170 175

Ala Trp Ser His Pro Gln Phe Glu Lys
180 185

<210> 344

<211> 193

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 344

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu
85 90 95

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
100 105 110

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala
115 120 125

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val
130 135 140

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly
145 150 155 160

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
165 170 175

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
180 185 190

Lys

<210> 345

<211> 193

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 345

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15
Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30
His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45
Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60
Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly
65 70 75 80
Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu

85 90 95
Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
100 105 110
Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
115 120 125
Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg
130 135 140
Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly

145 150 155 160
Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
165 170 175
Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
180 185 190
Lys

<210> 346

<211> 261

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 346

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu

85 90 95

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala

100 105 110

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala

115 120 125

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val

130 135 140

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser

145 150 155 160

Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys

165 170 175

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala

180 185 190

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

195 200 205

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

210 215 220

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu

225 230 235 240

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

245 250 255

Pro Gln Phe Glu Lys

260

<210

> 347

<211> 261

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 347

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly

65 70 75 80

Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu

85 90 95

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg

100 105 110

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile

115 120 125

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg

130 135 140

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser

145 150 155 160

Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys

165 170 175

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala

180 185 190

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

195 200 205

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

210 215 220

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu

225 230 235 240

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

245 250 255

Pro Gln Phe Glu Lys

260

<210> 348

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 348

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

65 70 75 80

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu

85 90 95

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu

100 105 110

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe

115 120 125

Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp

130 135 140

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu

145 150 155 160

His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro

165 170 175

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly

180 185 190

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

195 200 205

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

210 215 220

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

225 230 235 240

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser

245 250 255

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly

260 265 270

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

275 280 285

<210> 349

<211> 185

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 349

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr

65 70 75 80

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn

85 90 95

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly

100 105 110

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met

115 120 125

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

130 135 140

Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His

145 150 155 160

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser

165 170 175

Ala Trp Ser His Pro Gln Phe Glu Lys

180 185

<210> 350

<211> 193

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 350

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr

65 70 75 80

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu

85 90 95

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala

100 105 110

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala

115 120 125

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val

130 135 140

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly

145 150 155 160

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly

165 170 175

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu

180 185 190

Lys

<210> 351

<211> 193

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 351

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly

65 70 75 80

Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu

85 90 95

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg

100 105 110

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile

115 120 125

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala

130 135 140

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ser Gly

145 150 155 160

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly

165 170 175

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu

180 185 190

Lys

<210> 352

<211> 261

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 352

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr

65 70 75 80

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu

85 90 95

Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala

100 105 110

Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala

115 120 125

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val

130 135 140

Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser

145 150 155 160

Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys

165 170 175

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala

180 185 190

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

195 200 205

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

210 215 220

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu

225 230 235 240

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

245 250 255

Pro Gln Phe Glu Lys

260

<210> 353

<211> 261

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 353

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly

65 70 75 80

Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu

85 90 95

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg

100 105 110

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile

115 120 125

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala

130 135 140

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser

145 150 155 160

Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys

165 170 175

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala

180 185 190

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

195 200 205

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

210 215 220

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu

225 230 235 240

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

245 250 255

Pro Gln Phe Glu Lys

260

<210

> 354

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 354

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

35 40 45

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

50 55 60

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

65 70 75 80

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

85 90 95

Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu

100 105 110

Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

115 120 125

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp

130 135 140

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe

145 150 155 160

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys

165 170 175

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val

180 185 190

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala

195 200 205

Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser

210 215 220

Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

225 230 235 240

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

245 250 255

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu

260 265 270

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

275 280 285

<210> 355

<211> 285

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 355

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

65 70 75 80

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu

85 90 95

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu

100 105 110

Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe

115 120 125

Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp

130 135 140

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu

145 150 155 160

His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro

165 170 175

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly

180 185 190

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

195 200 205

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

210 215 220

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

225 230 235 240

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser

245 250 255

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly

260 265 270

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

275 280 285

<210> 356

<211> 150

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 356

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly
85 90 95

Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe
100 105 110

Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
115 120 125

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
130 135 140

His Pro Gln Phe Glu Lys
145 150

<210> 357

<211> 253

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 357

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser

85 90 95

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu

100 105 110

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu

115 120 125

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn

130 135 140

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu

145 150 155 160

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His

165 170 175

Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly Ser Gly Tyr Ile

180 185 190

Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu

195 200 205

Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser

210 215 220

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly

225 230 235 240

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

245 250

<210> 358

<211> 149

<212> PRT

<213> Artificial Sequence

<220

><223> Synthetic

<400> 358

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln
85 90 95

Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
100 105 110

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu
115 120 125

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His
130 135 140

Pro Gln Phe Glu Lys
145

<210> 359

<211> 148

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 359

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala
85 90 95

Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly
100 105 110
Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
115 120 125
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
130 135 140
Gln Phe Glu Lys
145

<210> 360

<211> 147

<212> PRT

<213> Artificial Sequence

<220><223
> Synthetic

<400> 360

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr

85 90 95

Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly

100 105 110

Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

115 120 125

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

130 135 140

Phe Glu Lys

145

<210> 361

<211> 250

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 361

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser

85 90 95

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu
100 105 110
Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
115 120 125
Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn
130 135 140
Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
145 150 155 160

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His
165 170 175
Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Gly Tyr Ile Pro Glu Ala
180 185 190
Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
195 200 205
Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
210 215 220

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225 230 235 240
Ser Ala Trp Ser His Pro Gln Phe Glu Lys
245 250

<210> 362
<211> 206
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 362
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg

85 90 95

Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu

100 105 110

Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp

115 120 125

Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys

130 135 140

Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu

145 150 155 160

Ser Arg Lys Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser Ser Gly

165 170 175

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly

180 185 190

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

195 200 205

<210> 363

<211> 207

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 363

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln
85 90 95
Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg
100 105 110
Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr
115 120 125

Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser
130 135 140
Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu
145 150 155 160
Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser Ser
165 170 175
Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
180 185 190

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200 205
<210> 364
<211> 309
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 364
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser

85 90 95

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu

100 105 110

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu

115 120 125

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn

130 135 140

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu

145 150 155 160

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His

165 170 175

Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Ser Glu Glu Leu Arg

180 185 190

Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu

195 200 205

Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg

210 215 220

Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg

225 230 235 240

Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu

245 250 255

Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg

260 265 270

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu

275 280 285

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

290 295 300

Pro Gln Phe Glu Lys

305

<210> 365

<211> 310

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 365

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser

85 90 95

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu

100 105 110

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu

115 120 125

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn

130 135 140

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu

145 150 155 160

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His

165 170 175

Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly Ser Glu Glu Leu

180 185 190

Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys

195 200 205

Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val

210 215 220

Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile

225 230 235 240

Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu

245 250 255

Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser

260 265 270

Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe

275 280 285

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser

290 295 300

His Pro Gln Phe Glu Lys

305 310

<210> 366

<211> 139

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 366

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu

65 70 75 80

Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val

85 90 95

Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp

100 105 110

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly

115 120 125

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

130 135

<210> 367

<211> 138

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 367

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Gly Tyr Ile Pro Glu Ala

65 70 75 80

Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu

85 90 95

Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser

100 105 110

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly

115 120 125

Ser Ala Trp Ser His Pro Gln Phe Glu Lys

130 135

<210> 368

<211> 137

<212

> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 368

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro

65 70 75 80

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu

85 90 95

Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His

100 105 110

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser

115 120 125

Ala Trp Ser His Pro Gln Phe Glu Lys

130 135

<210> 369

<211> 196

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 369

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala
65 70 75 80

Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu
85 90 95

Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys
100 105 110

Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys
115 120 125

Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile
130 135 140

Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg Gly
145 150 155 160

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
165 170 175

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro
180 185 190

Gln Phe Glu Lys
195

<210> 370

<211> 287

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 370

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
85 90 95

Ser Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu
100 105 110

Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln
115 120 125

Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys
130 135 140

Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu
145 150 155 160

Ser Gly Ser Gly Ser Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln
165 170 175

Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg
180 185 190

Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr
195 200 205

Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser
210 215 220

Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu
225 230 235 240
Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser Ser
245 250 255
Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
260 265 270

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
275 280 285

<210> 371
<211> 288
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 371
Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15
Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30
His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45
Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60
Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
65 70 75 80
Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
85 90 95
Ser Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu

100 105 110
Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln
115 120 125
Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys
130 135 140

Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu
145 150 155 160
Ser Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu

165 170 175
Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala
180 185 190
Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu
195 200 205
Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu
210 215 220
Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys

225 230 235 240
Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser
245 250 255
Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser
260 265 270
Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
275 280 285
<210> 372
<211> 238
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic
<400> 372
Met Glu Lys Lys Ile Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
1 5 10 15
Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg
20 25 30
Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
35 40 45
Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr

50 55 60

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
65 70 75 80
Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
85 90 95
Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
100 105 110
Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
115 120 125

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly
130 135 140
Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
145 150 155 160
Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
165 170 175
Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
180 185 190

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly
195 200 205
Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
210 215 220
Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
225 230 235

<210> 373
<211> 236
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 373
Met Glu Lys Lys Ile Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu

1 5 10 15

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg
20 25 30
Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
35 40 45
Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
50 55 60
Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr

65 70 75 80
Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
85 90 95
Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
100 105 110
Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
115 120 125
Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Asp

130 135 140
Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
145 150 155 160
Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
165 170 175
Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
180 185 190
Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala

195 200 205
Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser
210 215 220
Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
225 230 235
<210> 374
<211> 234
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 374

Met Glu Lys Lys Ile Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
1 5 10 15

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg
20 25 30

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
35 40 45

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
50 55 60

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
65 70 75 80

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
85 90 95

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
100 105 110

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
115 120 125

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Gly Ser Asp Lys Glu
130 135 140

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
145 150 155 160

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
165 170 175

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
180 185 190

Glu Glu Val Lys Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
195 200 205

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
210 215 220

Ser Ala Trp Ser His Pro Gln Phe Glu Lys

225 230

<210> 375

<211> 283

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 375

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15
Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30
His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45
Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60
Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala
65 70 75 80
Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp

85 90 95
Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe
100 105 110
Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys
115 120 125
Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val
130 135 140
Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly

145 150 155 160
Ser Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile
165 170 175
Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu
180 185 190
Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr

195 200 205

Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val

210 215 220

Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys

225 230 235 240

Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp

245 250 255

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly

260 265 270

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

275 280

<210> 376

<211> 284

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 376

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala

65 70 75 80

Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp

85 90 95

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe

100 105 110

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys

115 120 125

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val

130 135 140

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly

145 150 155 160

Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn

165 170 175

Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu

180 185 190

Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys

195 200 205

Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile

210 215 220

Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg

225 230 235 240

Lys Ile Ala Asp Glu Ser Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala

245 250 255

Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser

260 265 270

Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

275 280

<210> 377

<211> 214

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 377

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu

35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly

50 55 60

Ser Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val

65 70 75 80

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr

85 90 95

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu

100 105 110

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu

115 120 125

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala

130 135 140

Arg Lys Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly

145 150 155 160

Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe

165 170 175

Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe

180 185 190

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser

195 200 205

His Pro Gln Phe Glu Lys

210

<210> 378

<211> 232

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 378

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu

35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly

50 55 60

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met

85 90 95

His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys

100 105 110

Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala

115 120 125

Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile

130 135 140

Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu

145 150 155 160

Leu Ala Arg Lys Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg

165 170 175

Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser

180 185 190

Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro

195 200 205

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala

210 215 220

Trp Ser His Pro Gln Phe Glu Lys

225 230

<210> 379

<211> 222

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 379

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60

Glu Arg Leu Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Glu
65 70 75 80

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
85 90 95

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
100 105 110

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
115 120 125

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
130 135 140

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly Tyr
145 150 155 160

Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly
165 170 175

Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly
180 185 190

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
195 200 205

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
210 215 220

<210> 380

<211> 228

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 380

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
1 5 10 15
Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30
His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
35 40 45
Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
50 55 60
Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
65 70 75 80
Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val Leu Asp

85 90 95
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
100 105 110
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
115 120 125
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
130 135 140
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

145 150 155 160
Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala
165 170 175
Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly
180 185 190
Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200 205

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro

210 215 220

Gln Phe Glu Lys

225

<210> 381

<211> 331

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 381

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Met Glu Glu Ala Glu Leu

35 40 45

Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile

50 55 60

Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala

65 70 75 80

Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr

85 90 95

Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn

100 105 110

Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly

115 120 125

Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp

130 135 140

Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys

145 150 155 160

Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu

165 170 175

Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile

180 185 190

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser

195 200 205

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu

210 215 220

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly

225 230 235 240

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

245 250 255

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Asp Glu Leu

260 265 270

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys

275 280 285

Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr

290 295 300

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu

305 310 315 320

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

325 330

<210> 382

<211> 312

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 382

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Met Glu Glu Ala Glu Leu

35 40 45

Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile

50 55 60

Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala

65 70 75 80

Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr

85 90 95

Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn

100 105 110

Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly

115 120 125

Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp

130 135 140

Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys

145 150 155 160

Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu

165 170 175

Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile

180 185 190

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser

195 200 205

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu

210 215 220

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly

225 230 235 240

Ser Gly Ser Gly Ser Gly Ser Gly Asn Leu Asp Glu Leu His Met Gln

245 250 255

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu

260 265 270

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr

275 280 285

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
290 295 300

Glu Leu Leu Glu Arg Leu Leu Ser
305 310

<210> 383

<211> 342

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 383

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Met Glu Glu Ala Glu Leu
35 40 45

Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile
50 55 60

Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala
65 70 75 80

Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr
85 90 95

Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn
100 105 110

Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly
115 120 125

Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp
130 135 140

Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys
145 150 155 160

Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu
165 170 175

Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile
180 185 190
Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
195 200 205

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
210 215 220
Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly
225 230 235 240
Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
245 250 255
Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln
260 265 270

Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu
275 280 285
His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp
290 295 300
Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg
305 310 315 320
Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu
325 330 335

Glu Glu Leu Ala Arg Lys
340

<210> 384
<211> 323
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 384
Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Met Glu Glu Ala Glu Leu
35 40 45

Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile
50 55 60
Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala
65 70 75 80
Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr
85 90 95
Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn
100 105 110

Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly
115 120 125
Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp
130 135 140
Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys
145 150 155 160
Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu
165 170 175

Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile
180 185 190
Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
195 200 205
Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
210 215 220
Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly
225 230 235 240

Ser Gly Ser Gly Ser Gly Ser Gly Glu Leu Glu Glu Gln Val Met His
245 250 255
Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
260 265 270
Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr

275 280 285

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg

290 295 300

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu

305 310 315 320

Ala Arg Lys

<210> 385

<211> 203

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 385

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu

35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly

50 55 60

Ser Gly Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met

65 70 75 80

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe

85 90 95

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys

100 105 110

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu

115 120 125

Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu

130 135 140

Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val

145 150 155 160

Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp
165 170 175
Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
180 185 190
Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200

<210> 386
<211> 221
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 386

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

1 5 10 15
Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
20 25 30
Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
35 40 45
Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly
50 55 60
Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

65 70 75 80
Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Asp Glu Leu His Met
85 90 95
Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu
100 105 110
Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala
115 120 125
Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu

130 135 140

Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr Ile
145 150 155 160
Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu
165 170 175
Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly Ser
180 185 190
Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly

195 200 205
Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
210 215 220

<210> 387
<211> 222
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 387
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His
85 90 95

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
100 105 110
Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
115 120 125

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
130 135 140
Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr
145 150 155 160

Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly
165 170 175
Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Gly Ser Ser Gly
180 185 190
Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly
195 200 205
Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
210 215 220

<210> 388
<211> 228
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 388
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
85 90 95
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
100 105 110

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

115 120 125

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

130 135 140

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

145 150 155 160

Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala

165 170 175

Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly

180 185 190

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

195 200 205

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro

210 215 220

Gln Phe Glu Lys

225

<210> 389

<211> 261

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 389

Met Glu Lys Lys Ile Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

1 5 10 15

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

20 25 30

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu

35 40 45

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly

50 55 60

Ser Gly Ser Gly Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr

65 70 75 80

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln

85 90 95

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn

100 105 110

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu

115 120 125

Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg

130 135 140

Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu

145 150 155 160

Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg

165 170 175

Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg

180 185 190

Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu

195 200 205

Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg

210 215 220

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu

225 230 235 240

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

245 250 255

Pro Gln Phe Glu Lys

260

<210

> 390

<211> 280

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 390

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Asn Leu Asp Glu Leu His Met

85 90 95

Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu

100 105 110

Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala

115 120 125

Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu

130 135 140

Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Glu

145 150 155 160

Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala

165 170 175

Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp

180 185 190

Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu

195 200 205

Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala

210 215 220

Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp

225 230 235 240

Glu Ser Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro

245 250 255

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala

260 265 270

Trp Ser His Pro Gln Phe Glu Lys

275 280

<210> 391

<211> 205

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 391

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu

85 90 95

Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile

100 105 110

Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly

115 120 125

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln

130 135 140

Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu

145 150 155 160

Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly Ser Ser Gly Ser

165 170 175

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
180 185 190

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200 205

<210> 392

<211> 207

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 392

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly
85 90 95

Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr
100 105 110

Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn
115 120 125

Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ile Glu Tyr
130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln
145 150 155 160

Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly Ser Ser
165 170 175

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
180 185 190

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200 205

<210> 393

<211> 238

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 393

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu
85 90 95

Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile
100 105 110

Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
115 120 125

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln
130 135 140

Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
145 150 155 160

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr

165 170 175

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln

180 185 190

Asn Leu Gly Asn Lys Gln Lys Gln Gly Gly Gly Ser Gly Ser Ser Gly

195 200 205

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly

210 215 220

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

225 230 235

<210> 394

<211> 240

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 394

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly

85 90 95

Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr

100 105 110

Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn

115 120 125

Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr

130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
145 150 155 160
Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
165 170 175

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
180 185 190
Lys Gln Asn Leu Gly Asn Lys Gln Lys Gln Gly Gly Gly Ser Gly Ser
195 200 205
Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser
210 215 220
Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
225 230 235 240

<210> 395
<211> 196
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 395
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu
85 90 95
Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg

100 105 110

Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val

115 120 125

Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn

130 135 140

Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys Gly

145 150 155 160

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

165 170 175

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro

180 185 190

Gln Phe Glu Lys

195

<210> 396

<211> 198

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 396

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu

85 90 95

Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser

100 105 110

Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala

115 120 125

Leu Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val

130 135 140

Glu Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile

145 150 155 160

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe

165 170 175

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser

180 185 190

His Pro Gln Phe Glu Lys

195

<210> 397

<211> 238

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 397

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Glu Ala Glu Leu Ala

35 40 45

Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala

50 55 60

Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu

65 70 75 80

Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp

85 90 95

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn

100 105 110

Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp

115 120 125

Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro

130 135 140

Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln

145 150 155 160

Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu

165 170 175

Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr

180 185 190

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met

195 200 205

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn

210 215 220

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

225 230 235

<210> 398

<211> 236

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 398

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Glu Ala Glu Leu Ala

35 40 45

Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala

50 55 60

Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu
65 70 75 80
Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp
85 90 95

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn
100 105 110
Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp
115 120 125
Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro
130 135 140
Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln
145 150 155 160

Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu
165 170 175
Gly Ser Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
180 185 190
Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
195 200 205
Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu
210 215 220

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 399
<211> 234
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 399

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Glu Glu Ala Glu Leu Ala

35 40 45

Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala

50 55 60

Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu

65 70 75 80

Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp

85 90 95

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn

100 105 110

Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp

115 120 125

Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro

130 135 140

Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln

145 150 155 160

Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu

165 170 175

Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys

180 185 190

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp

195 200 205

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu

210 215 220

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

225 230

<210> 400

<211> 210

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 400

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu
85 90 95

Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg
100 105 110

Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp
115 120 125

Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala
130 135 140

Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu
145 150 155 160

Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser
165 170 175

Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly
180 185 190

Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe
195 200 205

Glu Lys
210

<210> 401

<211> 244

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 401

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Ser Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu

85 90 95
Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg
100 105 110
Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp
115 120 125
Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala
130 135 140
Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu

145 150 155 160
Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp
165 170 175
Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn
180 185 190
Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly
195 200 205
Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

210 215 220

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro

225 230 235 240

Gln Phe Glu Lys

<210> 402

<211> 201

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 402

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys

85 90 95

Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr

100 105 110

Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu

115 120 125

Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile

130 135 140

Ile Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val

145 150 155 160

Arg Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His

165 170 175

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser

180 185 190

Ala Trp Ser His Pro Gln Phe Glu Lys

195 200

<210> 403

<211> 203

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 403

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile

85 90 95

Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg

100 105 110

Ala Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro

115 120 125

Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu His Asn

130 135 140

Ala Ile Ile Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu

145 150 155 160

Ile Val Arg Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp

165 170 175

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly

180 185 190

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

195 200

<210> 404

<211> 212

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 404

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala

85 90 95

Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala

100 105 110

Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu

115 120 125

Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp

130 135 140

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn

145 150 155 160

Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly

165 170 175

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

180 185 190

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro

195 200 205

Gln Phe Glu Lys

210

<210> 405

<211> 246

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 405

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala

85 90 95

Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala

100 105 110

Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu

115 120 125

Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp

130 135 140

Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn

145 150 155 160

Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp

165 170 175

Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro

180 185 190

Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln

195 200 205

Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe

210 215 220

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser

225 230 235 240

His Pro Gln Phe Glu Lys

245

<210> 406

<211> 154

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 406

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile

85 90 95

Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys

100 105 110

Leu Ile Gly Glu Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser

115 120 125

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly

130 135 140

Ser Ala Trp Ser His Pro Gln Phe Glu Lys

145 150

<210> 407

<211> 158

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 407

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Arg Met Lys Gln Ile Glu Asp Lys

85 90 95

Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala

100 105 110

Arg Ile Lys Lys Leu Ile Gly Glu Arg Gly Gly Ser Gly Ser Ser Gly

115 120 125

Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly

130 135 140

Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

145 150 155

<210> 408

<211> 197

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 408

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu

85 90 95

Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg

100 105 110

Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val

115 120 125

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn

130 135 140

Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys

145 150 155 160

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu

165 170 175

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

180 185 190

Pro Gln Phe Glu Lys

195

<210> 409

<211> 201

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 409

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys

85 90 95

Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr

100 105 110

Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu

115 120 125

Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile

130 135 140

Ile Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val

145 150 155 160

Arg Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His

165 170 175

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser

180 185 190

Ala Trp Ser His Pro Gln Phe Glu Lys

195 200

<210> 410

<211> 242

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 410

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly

85 90 95

Asn Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr

100 105 110

Thr Leu Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn

115 120 125

Leu Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu

130 135 140

Ala Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp

145 150 155 160

Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala

165 170 175

Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu

180 185 190

Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser

195 200 205

Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly

210 215 220

Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe

225 230 235 240

Glu Lys

<210> 411

<211> 246

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 411

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Ala Glu Lys Met

85 90 95

Tyr Lys Ala Gly Asn Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala

100 105 110

Ile Ile Ala Tyr Thr Leu Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu

115 120 125

Ala Trp Tyr Asn Leu Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp

130 135 140

Glu Ala Ile Glu Ala Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn

145 150 155 160

Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp

165 170 175

Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro

180 185 190

Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln

195 200 205

Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe

210 215 220

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser

225 230 235 240

His Pro Gln Phe Glu Lys

245

<210> 412

<211> 153

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 412

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile
85 90 95
Ala Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys
100 105 110
Ser Leu Lys Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His
115 120 125
Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
130 135 140

Ala Trp Ser His Pro Gln Phe Glu Lys
145 150

<210> 413
<211> 157
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 413
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Glu Ile Ala Lys Ser
85 90 95
Leu Lys Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys

100 105 110

Glu Ile Ala Lys Ser Leu Lys Gly Gly Gly Ser Gly Ser Ser Gly Ser
115 120 125

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
130 135 140

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155

<210> 414

<211> 207

<212> PRT

<213> Artificial Sequence

<220

><223> Synthetic

<400> 414

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
85 90 95

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg
100 105 110

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
115 120 125

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln
145 150 155 160

Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly Ser Ser

165 170 175

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly

180 185 190

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

195 200 205

<210> 415

<211> 209

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 415

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu

85 90 95

Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala

100 105 110

Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr

115 120 125

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile

130 135 140

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala

145 150 155 160

Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly

165 170 175

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly

180 185 190

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu

195 200 205

Lys

<210> 416

<211> 211

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 416

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr

85 90 95

Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile

100 105 110

Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala

115 120 125

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu

130 135 140

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala

145 150 155 160

Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly

165 170 175

Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

180 185 190

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

195 200 205

Phe Glu Lys

210

<210> 417

<211> 241

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 417

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Ser Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu

85 90 95

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg

100 105 110

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu

115 120 125

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr

130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr

145 150 155 160

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile

165 170 175

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala

180 185 190

Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly

195 200 205

Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly

210 215 220

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu

225 230 235 240

Lys

<210> 418

<211> 243

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 418

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu

85 90 95

Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala

100 105 110

Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr

115 120 125

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile

130 135 140

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala

145 150 155 160

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu

165 170 175

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala

180 185 190

Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly

195 200 205

Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

210 215 220

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

225 230 235 240

Phe Glu Lys

<210> 419

<211> 245

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 419

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr

85 90 95

Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile

100 105 110

Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala

115 120 125

Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu

130 135 140

Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala

145 150 155 160

Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr

165 170 175

Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn

180 185 190

Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly

195 200 205

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu

210 215 220

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

225 230 235 240

Pro Gln Phe Glu Lys

245

<210> 420

<211> 198

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 420

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu
85 90 95

Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu
100 105 110

Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu
115 120 125

Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu
130 135 140

Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile
145 150 155 160

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
165 170 175

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
180 185 190

His Pro Gln Phe Glu Lys
195

<210> 421

<211> 200

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 421

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala

85 90 95
Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala
100 105 110
Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp
115 120 125
Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile
130 135 140
Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg

145 150 155 160
Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro
165 170 175
Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala
180 185 190
Trp Ser His Pro Gln Phe Glu Lys
195 200

<210> 422

<211> 202

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 422

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg

85 90 95

Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala

100 105 110

Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser

115 120 125

Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala

130 135 140

Ile Ile Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile

145 150 155 160

Val Arg Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser

165 170 175

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly

180 185 190

Ser Ala Trp Ser His Pro Gln Phe Glu Lys

195 200

<210> 423

<211> 155

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 423

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Ser Gly Gly Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu
85 90 95

Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys
100 105 110

Lys Leu Ile Gly Glu Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp
115 120 125

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly
130 135 140

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155

<210> 424

<211> 157

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 424

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Ser Gly Gly Gly Arg Met Lys Gln Ile Glu Asp Lys Ile
85 90 95
Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg
100 105 110
Ile Lys Lys Leu Ile Gly Glu Arg Gly Gly Ser Gly Ser Ser Gly Ser
115 120 125
Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
130 135 140

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155

<210> 425
<211> 159
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 425
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Gly Gly Gly Ser Gly Gly Gly Gly Arg Met Lys Gln Ile Glu Asp
85 90 95
Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile

100 105 110
Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Gly Gly Ser Gly Ser Ser
115 120 125
Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
130 135 140
Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150 155
<210> 426
<211> 198
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic
<400> 426
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Gly Ser Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu
85 90 95

Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu
100 105 110
Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu
115 120 125

Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu
130 135 140
Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile
145 150 155 160
Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
165 170 175
Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
180 185 190

His Pro Gln Phe Glu Lys
195

<210> 427
<211> 200
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 427
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala
85 90 95

Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala
100 105 110

Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp
115 120 125
Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile
130 135 140
Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg
145 150 155 160
Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro
165 170 175

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala
180 185 190
Trp Ser His Pro Gln Phe Glu Lys
195 200
<210> 428
<211> 202
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 428
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg

85 90 95

Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser
100 105 110
Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser
115 120 125
Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala
130 135 140
Ile Ile Val Glu Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile
145 150 155 160

Val Arg Ala Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
165 170 175
His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
180 185 190
Ser Ala Trp Ser His Pro Gln Phe Glu Lys
195 200

<210> 429
<211> 241
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 429

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Ser Gly Gly Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn
85 90 95
Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr
100 105 110
Leu Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
115 120 125
Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala

130 135 140
Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
145 150 155 160
Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
165 170 175
Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
180 185 190
Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly Ser Gly

195 200 205
Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
210 215 220
Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu
225 230 235 240
Lys

<210> 430
<211> 243
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 430
Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80
Gly Gly Gly Ser Gly Gly Gly Asn Leu Ala Glu Lys Met Tyr Lys Ala
85 90 95
Gly Asn Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala
100 105 110
Tyr Thr Leu Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr
115 120 125
Asn Leu Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile

130 135 140
Glu Ala Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
145 150 155 160
Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu
165 170 175
Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala
180 185 190
Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly Gly Gly

195 200 205
Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
210 215 220
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
225 230 235 240
Phe Glu Lys

<210> 431
<211> 245
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 431

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Asn Leu Ala Glu Lys Met Tyr

85 90 95

Lys Ala Gly Asn Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile

100 105 110

Ile Ala Tyr Thr Leu Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala

115 120 125

Trp Tyr Asn Leu Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu

130 135 140

Ala Ile Glu Ala Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala

145 150 155 160

Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr

165 170 175

Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn

180 185 190

Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly

195 200 205

Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu

210 215 220

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

225 230 235 240

Pro Gln Phe Glu Lys

245

<210> 432

<211> 152

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 432

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Ser Gly Gly Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala

85 90 95

Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser

100 105 110

Leu Lys Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro

115 120 125

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala

130 135 140

Trp Ser His Pro Gln Phe Glu Lys

145 150

<210> 433

<211> 154

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 433

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60
Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80
Gly Gly Gly Ser Gly Gly Gly Gly Glu Ile Ala Lys Ser Leu Lys Glu
85 90 95
Ile Ala Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala

100 105 110
Lys Ser Leu Lys Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser
115 120 125
His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
130 135 140
Ser Ala Trp Ser His Pro Gln Phe Glu Lys
145 150

<210> 434

<211> 156

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400

> 434

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Glu Ile Ala Lys Ser Leu

85 90 95

Lys Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu

100 105 110

Ile Ala Lys Ser Leu Lys Gly Gly Gly Ser Gly Ser Ser Gly Ser Ala

115 120 125

Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser

130 135 140

Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

145 150 155

<210> 435

<211> 182

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 435

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu

85 90 95

Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys

100 105 110

Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu

115 120 125

Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu

130 135 140

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe

145 150 155 160

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser

165 170 175

His Pro Gln Phe Glu Lys

180

<210> 436

<211> 184

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 436

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Ser Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg

85 90 95

Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu

100 105 110

Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile

115 120 125

Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys

130 135 140

Val Leu Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro

145 150 155 160

Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala

165 170 175

Trp Ser His Pro Gln Phe Glu Lys

180

<210> 437

<211> 186

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 437

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Gly Ser Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala

85 90 95

Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu

100 105 110

Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg

115 120 125

Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile

130 135 140

Ala Lys Val Leu Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser

145 150 155 160

His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly

165 170 175

Ser Ala Trp Ser His Pro Gln Phe Glu Lys

180 185

<210> 438

<211> 176

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 438

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser

85 90 95

Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser

100 105 110

Pro Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys

115 120 125

Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Gly Gly Ser Gly Ser

130 135 140

Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser

145 150 155 160

Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

165 170 175

<210> 439

<211> 178

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 439

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Ser Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys

85 90 95

Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn

100 105 110

Gly Ser Pro Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn

115 120 125

Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Gly Gly Ser

130 135 140

Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly

145 150 155 160

Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe

165 170 175

Glu Lys

<210> 440

<211> 180

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 440

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Gly Ser Gly Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu

85 90 95

Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu

100 105 110

Lys Asn Gly Ser Pro Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val

115 120 125

Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Gly

130 135 140

Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

145 150 155 160

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro

165 170 175

Gln Phe Glu Lys

180

<210> 441

<211> 169

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 441

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Ser Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu

85 90 95

Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala

100 105 110

Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val

115 120 125

Glu Val Leu Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His

130 135 140

Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser

145 150 155 160

Ala Trp Ser His Pro Gln Phe Glu Lys

165

<210> 442

<211> 171

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 442

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Gly Ser Ser Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr

85 90 95

Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro

100 105 110

Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile

115 120 125

Ile Val Glu Val Leu Arg Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp

130 135 140

Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly

145 150 155 160

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

165 170

<210> 443

<211> 173

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 443

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
65 70 75 80

Gly Gly Gly Gly Ser Gly Ser Glu Lys Ala Leu Arg Glu Leu Lys Lys
85 90 95

Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly
100 105 110

Ser Pro Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn
115 120 125

Lys Ile Ile Val Glu Val Leu Arg Gly Gly Ser Gly Ser Ser Gly Ser
130 135 140

Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
165 170

<210> 444

<211> 167

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 444

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln
20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Ser Glu Ala Leu Glu Glu
35 40 45

Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu
50 55 60

Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val
65 70 75 80

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val
85 90 95

Leu Arg Ile Ile Ala Lys Val Leu Lys Gly Gly Gly Gly Ser Gly Asp
100 105 110

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
115 120 125

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
130 135 140

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
145 150 155 160

Leu Leu Glu Glu Val Lys Arg
165

<210> 445

<211> 171

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 445

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Ser Glu Ala Leu Glu Glu

35 40 45

Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu

50 55 60

Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val

65 70 75 80

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val

85 90 95

Leu Arg Ile Ile Ala Lys Val Leu Lys Gly Gly Gly Gly Ser Gly Gly

100 105 110

Gly Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met

115 120 125

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser

130 135 140

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu

145 150 155 160

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

165 170

<210> 446

<211> 161

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 446

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Ser Pro Glu Leu Glu Lys

35 40 45

Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr

50 55 60

Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu Val Glu Asn Asn

65 70 75 80

Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile

85 90 95

Ile Ala Lys Gly Gly Gly Gly Ser Gly Asp Lys Glu Asn Val Leu Gln

100 105 110

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu

115 120 125

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys

130 135 140

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys

145 150 155 160

Arg

<210> 447

<211> 165

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 447

Met Glu Lys Lys Ile Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

20 25 30

Phe Glu Lys Gly Gly Ser Gly Ser Ser Gly Ser Pro Glu Leu Glu Lys

35 40 45

Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr

50 55 60

Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu Val Glu Asn Asn

65 70 75 80

Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile

85 90 95

Ile Ala Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu

100 105 110

Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu

115 120 125

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe

130 135 140

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu

145 150 155 160

Glu Glu Val Lys Arg

165

<210> 448

<211> 181

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 448

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Ala

65 70 75 80

Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp

85 90 95

Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp

100 105 110

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile

115 120 125

Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys Gly Gly Ala Ser

130 135 140

Pro Ala Ala Pro Ala Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu

145 150 155 160

Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His

165 170 175

Pro Gln Phe Glu Lys

180

<210> 449

<211> 179

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 449

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Gly Gly Ser Gly Ser Glu Ala Leu Glu

65 70 75 80

Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu

85 90 95

Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu

100 105 110

Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu

115 120 125

Val Leu Arg Ile Ile Ala Lys Val Leu Lys Gly Gly Ala Ser Pro Ala

130 135 140

Ala Pro Ala Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly

145 150 155 160

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln

165 170 175

Phe Glu Lys

<210> 450

<211> 177

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 450

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Gly Ser Ser Glu Ala Leu Glu Glu Leu

65 70 75 80

Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg

85 90 95

Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu

100 105 110

Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu

115 120 125

Arg Ile Ile Ala Lys Val Leu Lys Gly Gly Ala Ser Pro Ala Ala Pro

130 135 140

Ala Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly

145 150 155 160

Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu

165 170 175

Lys

<210> 451

<211> 175

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 451

Met Glu Lys Lys Ile Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

1 5 10 15

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

20 25 30

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

35 40 45

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

50 55 60

Glu Arg Leu Leu Ser Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys

65 70 75 80

Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr

85 90 95

Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn

100 105 110

Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile

115 120 125

Ile Ala Lys Val Leu Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly

130 135 140

Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly

145 150 155 160

Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys

165 170 175

<210> 452

<211> 182

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 452

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp

1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

50 55 60

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

65 70 75 80

Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu

85 90 95

Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys

100 105 110

Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu

115 120 125

Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu

130 135 140

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe

145 150 155 160

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser

165 170 175

His Pro Gln Phe Glu Lys
180

<210> 453

<211> 182

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 453

Met Glu Lys Lys Ile Glu Leu Glu Glu Gln Val Met His Val Leu Asp
1 5 10 15

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
20 25 30

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
35 40 45

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
50 55 60

Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr
65 70 75 80

Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu
85 90 95

Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys
100 105 110

Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu
115 120 125

Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu
130 135 140

Lys Gly Gly Ser Gly Ser Ser Gly Ser Ala Trp Ser His Pro Gln Phe
145 150 155 160

Glu Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser
165 170 175

His Pro Gln Phe Glu Lys
180

<210> 454

<211> 127

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 454

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly
50 55 60

Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu Trp Ile Leu Gln Lys Ile
65 70 75 80

Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser
85 90 95

Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu
100 105 110

Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
115 120 125

<210> 455

<211> 143

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 455

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn

65 70 75 80

Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala Leu

85 90 95

His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu Phe

100 105 110

Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu

115 120 125

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

130 135 140

<210> 456

<211> 132

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 456

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly

50 55 60

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu Trp

65 70 75 80

Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly

85 90 95

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met

100 105 110

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

115 120 125

Glu Val Glu Arg

130

<210> 457

<211> 148

<212> PRT

<213> Artificial Sequence

<220><223

> Synthetic

<400> 457

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu

20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

65 70 75 80

Gly Gly Gly Ser Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu

85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg

100 105 110

Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp

115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu

130 135 140

Arg Leu Leu Ser

145

<210> 458

<211> 208

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 458

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15
Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Ser Gly Ser Gly Ser Ser
50 55 60
Gly Ser Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Asp Lys Glu Trp
65 70 75 80
Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly
85 90 95

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110
Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
115 120 125
Glu Val Glu Arg Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly Gly Ser
130 135 140
Ser Ser Gly Gly Ser Ser Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys
145 150 155 160

Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala
165 170 175
Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp
180 185 190
Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg

195 200 205

<210> 459

<211> 232

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 459

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu

20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Gly Ser Ser Gly Ser Gly

65 70 75 80

Ser Ser Gly Ser Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu

85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg

100 105 110

Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp

115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu

130 135 140

Arg Leu Leu Ser Gly Ser Ser Ser Gly Gly Ser Ser Ser Gly Gly Ser

145 150 155 160

Ser Ser Gly Gly Ser Ser Ser Gly Asn Asp Asp Glu Leu His Met Leu

165 170 175

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu

180 185 190

Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr

195 200 205

Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys

210 215 220

Glu Leu Leu Glu Arg Leu Leu Ser

225 230

<210> 460

<211> 132

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 460

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Ala Gly Gly Ser Pro Ala

50 55 60

Gly Ser Pro Thr Ser Thr Gly Thr Ser Thr Ser Gly Asp Lys Glu Trp

65 70 75 80

Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly

85 90 95

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met

100 105 110

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

115 120 125

Glu Val Glu Arg

130

<210> 461

<211> 208

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 461

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu

1 5 10 15

Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Ser Ala Gly Gly Ser Pro Ala

50 55 60

Gly Ser Pro Thr Ser Thr Gly Thr Ser Gly Ser Gly Asp Lys Glu Trp

65 70 75 80

Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly

85 90 95

His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met

100 105 110

Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

115 120 125

Glu Val Glu Arg Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr

130 135 140

Ser Thr Gly Thr Ser Gly Ser Gly Asp Lys Glu Trp Ile Leu Gln Lys

145 150 155 160

Ile Tyr Glu Ile Met Arg Leu Leu Asp Glu Leu Gly His Ala Glu Ala

165 170 175

Ser Met Arg Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp

180 185 190

Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg

195 200 205

<210> 462

<211> 148

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 462

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Gly Thr
65 70 75 80

Ser Gly Ser Gly Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu
85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg
100 105 110

Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp
115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140

Arg Leu Leu Ser
145

<210> 463

<211> 232

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 463

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30
Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Gly Thr
65 70 75 80

Ser Gly Ser Gly Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu
85 90 95
Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg
100 105 110
Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp
115 120 125
Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140

Arg Leu Leu Ser Gly Ser Ala Gly Gly Ser Pro Ala Gly Ser Pro Thr
145 150 155 160
Ser Thr Gly Thr Ser Gly Ser Gly Asn Asp Asp Glu Leu His Met Leu
165 170 175
Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
180 185 190
Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr
195 200 205

Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
210 215 220
Glu Leu Leu Glu Arg Leu Leu Ser
225 230
<210> 464
<211> 218

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 464

Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu Leu
1 5 10 15
Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro
50 55 60
Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly
65 70 75 80
Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg Leu
85 90 95

Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp Leu
100 105 110
Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu Ala
115 120 125
Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Ala Gly Ser
130 135 140
Pro Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr
145 150 155 160

Gly Gly Asp Lys Glu Trp Ile Leu Gln Lys Ile Tyr Glu Ile Met Arg
165 170 175
Leu Leu Asp Glu Leu Gly His Ala Glu Ala Ser Met Arg Val Ser Asp
180 185 190
Leu Ile Tyr Glu Phe Met Lys Lys Gly Asp Glu Arg Leu Leu Glu Glu
195 200 205
Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
210 215

<210> 465

<211> 242

<212

> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 465

Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe Gln Leu
20 25 30

Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Ser Ser Ala Gly Ser Pro Thr Ser Thr Gly Thr Ser Ser Ala
65 70 75 80

Thr Pro Ser Gly Ser Gly Thr Gly Gly Asn Asp Asp Glu Leu His Met
85 90 95

Leu Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu
100 105 110

Glu Ile Lys Lys Arg Val Phe Gln Leu Phe Glu Leu Ala Asp Lys Ala

115 120 125

Tyr Lys Asn Asn Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu
130 135 140

Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Ala Gly Ser
145 150 155 160

Pro Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr
165 170 175

Gly Gly Asn Asp Asp Glu Leu His Met Leu Met Thr Asp Leu Val Tyr

180 185 190

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Ile Lys Lys Arg Val Phe

195 200 205

Gln Leu Phe Glu Leu Ala Asp Lys Ala Tyr Lys Asn Asn Asp Arg Gln

210 215 220

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu

225 230 235 240

Leu Ser

<210> 466

<211> 137

<

212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 466

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu

1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Gly Gly Ser

50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser

65 70 75 80

Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr

85 90 95

Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu

100 105 110

Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala

115 120 125

Glu Arg Leu Leu Glu Glu Val Glu Arg

130 135

<210> 467

<211> 137

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 467

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro
50 55 60

Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly
65 70 75 80

Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr
85 90 95

Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
100 105 110

Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala
115 120 125

Glu Arg Leu Leu Glu Glu Val Glu Arg
130 135

<210> 468

<211> 137

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 468

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Glu Ala Ala

50 55 60

Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Gly Ser Ser Gly

65 70 75 80

Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr

85 90 95

Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu

100 105 110

Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala

115 120 125

Glu Arg Leu Leu Glu Glu Val Glu Arg

130 135

<210> 469

<211> 141

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 469

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu

1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Pro Ser Thr

50 55 60

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro

65 70 75 80

Gly Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu

85 90 95

Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln

100 105 110

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu

115 120 125

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg

130 135 140

<210> 470

<211> 197

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 470

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu

1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Gln Ile Phe

50 55 60

Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser

65 70 75 80

Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile

85 90 95

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp

100 105 110

Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His

115 120 125

Leu Val Leu Arg Leu Arg Gly Gly Gly Gly Ser Ser Gly Asp Lys Glu

130 135 140

Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu

145 150 155 160

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
165 170 175
Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu
180 185 190
Glu Glu Val Glu Arg
195

<210> 471
<211> 218
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 471

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Ala Gly Ser Pro
50 55 60
Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr Gly
65 70 75 80

Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr
85 90 95
Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
100 105 110
Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala
115 120 125
Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Ala Gly Ser
130 135 140

Pro Thr Ser Thr Gly Thr Ser Ser Ala Thr Pro Ser Gly Ser Gly Thr
145 150 155 160
Gly Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys
165 170 175
Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
180 185 190
Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
195 200 205

Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
210 215

<210> 472
<211> 218
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 472
Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15
Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu

35 40 45
Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Glu Ala Ala
50 55 60
Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Gly Ser Ser Gly
65 70 75 80
Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr
85 90 95
Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu

100 105 110
Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala
115 120 125

Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Glu Ala
130 135 140
Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Gly Ser Ser
145 150 155 160
Gly Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys

165 170 175
Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
180 185 190
Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu
195 200 205
Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
210 215

<210> 473

<211> 226

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400

> 473

Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15
Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Pro Ser Thr
50 55 60

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro
65 70 75 80
Gly Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu
85 90 95
Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln
100 105 110

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu
115 120 125

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser
130 135 140
Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
145 150 155 160
Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
165 170 175
Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
180 185 190

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
195 200 205
Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
210 215 220
Glu Arg
225
<210> 474
<211> 338
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 474
Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15

Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Gln Ile Phe
50 55 60
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser

65 70 75 80

Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
85 90 95

Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
100 105 110

Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
115 120 125

Leu Val Leu Arg Leu Arg Gly Gly Gly Gly Ser Ser Gly Asp Lys Glu
130 135 140

Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu
145 150 155 160

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
165 170 175

Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu
180 185 190

Glu Glu Val Glu Arg Gly Gly Ser Ser Gly Gln Ile Phe Val Lys Thr
195 200 205

Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser Asp Thr Ile
210 215 220

Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp
225 230 235 240

Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr
245 250 255

Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu
260 265 270

Arg Leu Arg Gly Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Ile Leu
275 280 285

Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala
290 295 300

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln
305 310 315 320

Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
325 330 335

Glu Arg

<210> 475
<211> 137
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 475
Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser
50 55 60
Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
65 70 75 80
Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
85 90 95
Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
100 105 110

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
115 120 125
Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135
<210> 476
<211> 141
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 476

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr
50 55 60

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro
65 70 75 80

Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

85 90 95

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

100 105 110

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
115 120 125

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 477

<211> 153

<212> PRT

<213> Artificial Sequence

<220

><223> Synthetic

<400> 477

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80
Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met
85 90 95
Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu
100 105 110
Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala
115 120 125

Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu
130 135 140
Lys Glu Leu Leu Glu Arg Leu Leu Ser
145 150
<210> 478
<211> 157
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 478
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
65 70 75 80
Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asn Leu Asp

85 90 95

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe

100 105 110

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys

115 120 125

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val

130 135 140

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

145 150 155

<210> 479

<211> 218

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 479

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser

50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser

65 70 75 80

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu

85 90 95

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu

100 105 110

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala

115 120 125

Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly

130 135 140

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser

145 150 155 160

Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys

165 170 175

Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp

180 185 190

Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu

195 200 205

Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

210 215

<210> 480

<211> 226

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 480

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr

50 55 60

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro

65 70 75 80

Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu

85 90 95

Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

100 105 110

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu

115 120 125

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser

130 135 140

Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr

145 150 155 160

Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu

165 170 175

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

180 185 190

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr

195 200 205

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

210 215 220

Lys Arg

225

<210> 481

<211> 242

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 481

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly

65 70 75 80

Gly Ser Ser Gly Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met

85 90 95

Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu

100 105 110

Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala

115 120 125

Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu

130 135 140

Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Ser Gly Gly Gly

145 150 155 160

Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser

165 170 175

Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr

180 185 190

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe

195 200 205

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln

210 215 220

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu

225 230 235 240

Leu Ser

<210> 482

<211> 250

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 482

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr

65 70 75 80

Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asn Leu Asp

85 90 95

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe

100 105 110

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys

115 120 125

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val

130 135 140

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser

145 150 155 160

Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr

165 170 175

Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His

180 185 190

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp

195 200 205

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys

210 215 220

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu

225 230 235 240

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

245 250

<210> 483

<211> 145

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 483

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser
50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser
65 70 75 80

Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu
85 90 95

Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln
100 105 110

Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys
115 120 125

Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu
130 135 140

Ser
145

<210> 484

<211> 149

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 484

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Pro Ser Thr

50 55 60

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Pro

65 70 75 80

Gly Gly Ser Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp

85 90 95

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys

100 105 110

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys

115 120 125

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu

130 135 140

Glu Arg Leu Leu Ser

145

<210> 485

<211> 145

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 485

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly

65 70 75 80

Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln
85 90 95
Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
100 105 110
Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
115 120 125
Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
130 135 140

Arg
145

<210> 486
<211> 149
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 486

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ser Ser Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr
65 70 75 80
Pro Pro Thr Pro Ser Pro Ser Pro Gly Gly Ser Ser Gly Asp Lys Glu
85 90 95
Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu
100 105 110

Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
115 120 125

Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
130 135 140

Glu Glu Val Lys Arg
145

<210> 487

<211> 130

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 487

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu
65 70 75 80

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
85 90 95

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
100 105 110

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
115 120 125

Lys Arg
130

<210> 488

<211> 130

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400

> 488

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
65 70 75 80

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
85 90 95

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
100 105 110

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
115 120 125

Lys Arg
130

<210> 489

<211> 135

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 489

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp
65 70 75 80
Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
85 90 95
Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
100 105 110

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
115 120 125
Leu Leu Glu Glu Val Lys Arg
130 135

<210> 490
<211> 140
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 490
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
65 70 75 80
Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
85 90 95

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
100 105 110
Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu
115 120 125
Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 491
<211> 122
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 491

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

1 5 10 15
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser
50 55 60
Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys

65 70 75 80
Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
85 90 95
Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
100 105 110
Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
115 120

<210> 492
<211> 127
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic

<400

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Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser
50 55 60

Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
65 70 75 80
Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
85 90 95
Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
100 105 110
Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
115 120 125

<210> 493
<211> 132
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 493
Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Ser Gly Gly Gly Ser

50 55 60

Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn
65 70 75 80
Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
85 90 95
His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110
Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

115 120 125
Glu Val Lys Arg
130

<210> 494
<211> 141
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 494
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80
Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
85 90 95
Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln

100 105 110
Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu
115 120 125

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 495

<211> 146

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 495

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
85 90 95

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
100 105 110

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
115 120 125

Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
130 135 140

Lys Arg
145

<210> 496

<211> 151

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 496

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp
85 90 95

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
100 105 110

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
115 120 125

Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg
130 135 140

Leu Leu Glu Glu Val Lys Arg
145 150

<210> 497

<211> 226

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 497

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp
85 90 95
Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu
100 105 110
Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met
115 120 125
Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu
130 135 140

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
145 150 155 160
Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys Glu Asn Val Leu
165 170 175
Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala
180 185 190
Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr
195 200 205

Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val
210 215 220
Lys Arg
225
<210> 498
<211> 236
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 498

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80
Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
85 90 95

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
100 105 110
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
115 120 125
Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
130 135 140
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
145 150 155 160

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
165 170 175
Gly Ser Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile
180 185 190
Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val
195 200 205
Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu
210 215 220

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235
<210> 499

<211> 246

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 499

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu
85 90 95

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala

100 105 110

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
115 120 125

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
130 135 140

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
145 150 155 160

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly

165 170 175

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Asp Lys
180 185 190

Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg
195 200 205

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu

210 215 220

Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu

225 230 235 240

Leu Glu Glu Val Lys Arg

245

<210> 500

<211> 160

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 500

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly

65 70 75 80

Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp

85 90 95

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

100 105 110

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

115 120 125

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

130 135 140

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

145 150 155 160

<210> 501

<211> 165

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 501

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val
85 90 95

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
100 105 110

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
115 120 125

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
130 135 140

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
145 150 155 160

Glu Leu Ala Arg Lys
165

<210> 502

<211> 170

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 502

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu
85 90 95

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
100 105 110

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
115 120 125

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
130 135 140

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
145 150 155 160

Leu Glu His Leu Glu Glu Leu Ala Arg Lys
165 170

<210> 503

<211> 245

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 503

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly

65 70 75 80

Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp

85 90 95

Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu

100 105 110

Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met

115 120 125

Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu

130 135 140

Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

145 150 155 160

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

165 170 175

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His

180 185 190

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp

195 200 205

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu

210 215 220

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

225 230 235 240

Glu Leu Ala Arg Lys

245

<210> 504

<211> 255

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 504

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly
65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu Glu Glu Gln Val

85 90 95

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
100 105 110

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
115 120 125

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
130 135 140

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu

145 150 155 160

Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly
165 170 175

Gly Ser Ser Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
180 185 190

Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
195 200 205

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu

210 215 220

Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu

225 230 235 240

Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

245 250 255

<210> 505

<211> 265

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 505

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly

65 70 75 80

Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu

85 90 95

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala

100 105 110

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala

115 120 125

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser

130 135 140

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile

145 150 155 160

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Ser Gly Gly

165 170 175

Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Glu Leu

180 185 190

Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His

195 200 205

Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr

210 215 220

Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp

225 230 235 240

Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu

245 250 255

Glu His Leu Glu Glu Leu Ala Arg Lys

260 265

<210> 506

<211> 174

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 506

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro

85 90 95

Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val

100 105 110

Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu

115 120 125

Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu

130 135 140

Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu

145 150 155 160

Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

165 170

<210> 507

<211> 144

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 507

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro

65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys

85 90 95

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala

100 105 110

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

115 120 125

Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 508
<211> 155
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 508

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95
Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met

100 105 110
Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
115 120 125
Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu
130 135 140
Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
145 150 155

<210> 509
<211> 273
<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 509

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val
100 105 110

Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu
115 120 125

Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu
130 135 140

Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu
145 150 155 160

Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly
165 170 175

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
180 185 190

Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu
195 200 205

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
210 215 220

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
225 230 235 240
Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
245 250 255

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
260 265 270
Lys

<210> 510
<211> 243
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 510
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80
Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His
85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
100 105 110
Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
115 120 125
Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
130 135 140

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
145 150 155 160

Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175
Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190
Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205
Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240
Val Lys Arg

<210> 511
<211> 243
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 511
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro

85 90 95

Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
100 105 110
Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
115 120 125
Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
130 135 140
Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175
Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190
Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205
Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240
Val Lys Arg

<210> 512
<211> 216
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 512
Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ala Ser Pro Ala Ala Pro
50 55 60
Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
65 70 75 80
Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
85 90 95

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
100 105 110
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
115 120 125
Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ala Ser Pro Ala Ala Pro
130 135 140
Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
145 150 155 160

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
165 170 175
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
180 185 190
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
195 200 205
Arg Leu Leu Glu Glu Val Lys Arg
210 215
<210> 513
<211> 240
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic
<400> 513
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80
Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln
85 90 95
Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
100 105 110
Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
115 120 125

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
130 135 140
Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro
145 150 155 160
Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
165 170 175
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
180 185 190

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
195 200 205
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
210 215 220
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
225 230 235 240
<210> 514
<211> 254
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 514

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro

85 90 95

Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val

100 105 110

Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu

115 120 125

Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu

130 135 140

Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu

145 150 155 160

Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly

165 170 175

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro

180 185 190

Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr

195 200 205

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met

210 215 220

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn

225 230 235 240

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

245 250

<210> 515

<211> 166

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 515

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Glu Leu Glu Glu Gln

85 90 95

Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu

100 105 110

His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp

115 120 125

Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg

130 135 140

Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu

145 150 155 160

Glu Glu Leu Ala Arg Lys

165

<210> 516

<211> 161

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 516

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu
85 90 95

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly
100 105 110

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met
115 120 125

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile
130 135 140

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg
145 150 155 160

Lys

<210> 517

<211> 136

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 517

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly
65 70 75 80

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
85 90 95

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
100 105 110

Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu
115 120 125

Arg Leu Leu Glu Glu Val Lys Arg
130 135

<210> 518

<211> 131

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 518

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
65 70 75 80

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
85 90 95

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
100 105 110

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
115 120 125

Val Lys Arg
130

<210> 519

<211> 147

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 519

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val
85 90 95

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
100 105 110

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

115 120 125

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
130 135 140
Val Lys Arg
145

<210> 520
<211> 142
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 520

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
85 90 95

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
100 105 110
Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Arg
115 120 125
Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 521
<211> 243
<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 521

Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser

50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro

65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His

85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu

100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr

115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg

130 135 140

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu

145 150 155 160

Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro

165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val

180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

210 215 220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240
Val Lys Arg

<210> 522
<211> 243
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 522
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80
Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95
Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile
100 105 110
Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
115 120 125
Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys

130 135 140
Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160
Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190
Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

195 200 205
Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220
Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240
Val Lys Arg

<210> 523
<211> 273
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 523
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro

65 70 75 80
Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95
Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val
100 105 110
Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu
115 120 125

Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu

130 135 140

Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu

145 150 155 160

Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly

165 170 175

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro

180 185 190

Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu

195 200 205

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly

210 215 220

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met

225 230 235 240

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile

245 250 255

Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg

260 265 270

Thr

<210> 524

<211> 216

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 524

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

35 40 45

Arg Leu Leu Glu Glu Val Thr Arg Gly Gly Ala Ser Pro Ala Ala Pro

50 55 60

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly

65 70 75 80

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

85 90 95

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

100 105 110

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

115 120 125

Arg Leu Leu Glu Glu Val Thr Arg Gly Gly Ala Ser Pro Ala Ala Pro

130 135 140

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly

145 150 155 160

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu

165 170 175

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

180 185 190

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

195 200 205

Arg Leu Leu Glu Glu Val Thr Arg

210 215

<210> 525

<211> 243

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 525

Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser

50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro

65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His

85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu

100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr

115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg

130 135 140

Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu

145 150 155 160

Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro

165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val

180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

210 215 220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

225 230 235 240

Val Lys Arg

<210> 526

<211> 243

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 526

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro

85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile

100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala

115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys

130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg

145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro

165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val

180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

210 215 220

Thr Lys Asp Glu Arg Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240
Val Lys Arg

<210> 527
<211> 243
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 527
Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala

1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu
20 25 30
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
50 55 60
Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro

65 70 75 80
Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His
85 90 95
Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
100 105 110
Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
115 120 125
Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg

130 135 140
Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu
145 150 155 160
Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190
Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

195 200 205
Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220
Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240
Val Lys Arg

<210> 528
<211> 243
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 528
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80
Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95
Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile
100 105 110
Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys

130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160
Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175
Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190
Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220
Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240
Val Lys Arg

<210> 529
<211> 243
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 529
Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu
20 25 30
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
50 55 60
Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro

65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His

85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu

100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr

115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg

130 135 140

Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu

145 150 155 160

Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro

165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val

180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

225 230 235 240

Val Lys Arg

<210> 530

<211> 243

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 530

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro

85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile

100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala

115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys

130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg

145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro

165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val

180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

225 230 235 240

Val Lys Arg

<210> 531

<211> 243

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 531

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro

85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile

100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala

115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys

130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg

145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro

165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val

180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

225 230 235 240

Val Lys Arg

<210> 532

<211> 235

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 532

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro

85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile

100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala

115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys

130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg

145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro

165 170 175

Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
180 185 190
Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser

195 200 205
Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
210 215 220
Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 533
<211> 227
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 533

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Ile Asp Glu Leu
85 90 95
Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys
100 105 110
Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr
115 120 125
Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu

130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro
145 150 155 160
Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val
165 170 175
Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
180 185 190
Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
195 200 205

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
210 215 220
Val Lys Arg
225

<210> 534
<211> 222
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 534
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr
85 90 95

Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110
Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125
Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140
Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro
145 150 155 160

Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
165 170 175
Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
180 185 190
Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
195 200 205
Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

<210> 535
<211> 230
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 535
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro

85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile

100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala

115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys

130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg

145 150 155 160

Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys

165 170 175

Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg

180 185 190

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu

195 200 205

Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu

210 215 220

Leu Glu Glu Val Lys Arg

225 230

<210> 536

<211> 222

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 536

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Ile Asp Glu Leu

85 90 95

Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys

100 105 110

Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr

115 120 125

Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu

130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro

145 150 155 160

Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr

165 170 175

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met

180 185 190

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn

195 200 205

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

210 215 220

<210> 537

<211> 217

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 537

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr
85 90 95

Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110
Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125
Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140
Leu Glu Arg Ile Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly
145 150 155 160

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
165 170 175
Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
180 185 190
Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
195 200 205
Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215

<210> 538
<211> 154
<212> PRT

<213> Artificial Sequence
<220><223> Synthetic
<400> 538

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Glu
65 70 75 80
Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
85 90 95
His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
100 105 110
Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser

115 120 125
Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
130 135 140
Leu Glu His Leu Glu Glu Leu Ala Arg Lys
145 150
<210> 539
<211> 152
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 539
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Glu Leu Glu
65 70 75 80

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
85 90 95
Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
100 105 110
Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp
115 120 125
Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu
130 135 140

His Leu Glu Glu Leu Ala Arg Lys
145 150
<210> 540
<211> 163
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 540
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr Asp Leu Ile
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Ala
115 120 125
Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Lys
130 135 140
Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160
Ile Leu Ser

<210> 541
<211> 155
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic

<400> 541
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Ile Asp Glu Leu
85 90 95
Leu Met Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys
100 105 110
Asp Glu Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr

115 120 125

Lys Ala Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu
130 135 140
Glu Leu Lys Glu Leu Leu Glu Arg Ile Leu Ser
145 150 155

<210> 542
<211> 150
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 542

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Gly Gly Asn Ile Asp Glu Leu Leu Met Gln Val Thr

85 90 95
Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110
Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125
Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140
Leu Glu Arg Ile Leu Ser
145 150

<210> 543

<211> 235

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 543

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ala Ser Pro Ala Ala Pro

50 55 60

Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly
65 70 75 80

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
85 90 95

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
100 105 110

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

115 120 125

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

130 135 140

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
145 150 155 160

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
165 170 175

Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met

180 185 190

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
195 200 205

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
210 215 220

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 544

<211> 243

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 544

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205
Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220
Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240
Val Lys Arg

<210> 545
<211> 235
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic

<400> 545
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95
Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
100 105 110
Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val

115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
130 135 140
Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160
Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175
Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
180 185 190

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
195 200 205
Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
210 215 220
Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 546
<211> 235
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 546

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu
85 90 95
His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
100 105 110
Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr
115 120 125
Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu

130 135 140
Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro
145 150 155 160
Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
165 170 175
Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
180 185 190
Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser

195 200 205
Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
210 215 220
Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
225 230 235

<210> 547
<211> 227
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 547

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu
85 90 95
His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
100 105 110
Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr
115 120 125
Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro
145 150 155 160
Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val
165 170 175
Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
180 185 190
Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
195 200 205

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
210 215 220
Val Lys Arg
225
<210> 548
<211> 222
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 548
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
85 90 95

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110
Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125
Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140
Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro
145 150 155 160

Ala Ser Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr
165 170 175
Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met
180 185 190
Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn
195 200 205
Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

<210> 549
<211> 230
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic

<400> 549

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val

115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Asp Lys
165 170 175

Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg

180 185 190

Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu
195 200 205

Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu
210 215 220

Leu Glu Glu Val Lys Arg
225 230

<210> 550

<211> 222

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 550

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Gly Gly Asn Leu Asp Glu Leu

85 90 95

His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys

100 105 110

Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr

115 120 125

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu

130 135 140

Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro

145 150 155 160

Ala Ala Pro Ala Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr

165 170 175

Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met

180 185 190

Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn

195 200 205

Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215 220

<210> 551

<211> 217

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 551

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
85 90 95

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu
130 135 140

Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly
145 150 155 160

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
165 170 175

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu
180 185 190

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
195 200 205

Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215

<210> 552

<211> 209

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 552

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Ala
65 70 75 80

Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
85 90 95

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
100 105 110

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln

115 120 125

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
130 135 140

Leu Ser Gly Gly Ala Ser Ala Gly Gly Asp Lys Glu Asn Val Leu Gln
145 150 155 160

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
165 170 175

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys

180 185 190

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys

195 200 205

Arg

<210> 553

<211> 211

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 553

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly

65 70 75 80

Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val

85 90 95

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val

100 105 110

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg

115 120 125

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg

130 135 140

Leu Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Asp Lys Glu Asn Val

145 150 155 160

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His

165 170 175

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys

180 185 190

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu

195 200 205

Val Lys Arg

210

<210> 554

<211> 204

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 554

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala

1 5 10 15

His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala

20 25 30

Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser

35 40 45

Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile

50 55 60

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Asn

65 70 75 80

Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu

85 90 95

His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe

100 105 110

Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu

115 120 125

Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly

130 135 140

Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile

145 150 155 160

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val

165 170 175

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu

180 185 190

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

195 200

<210> 555

<211> 217

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 555

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly

65 70 75 80

Ser Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr

85 90 95

Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln

100 105 110

Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn

115 120 125

Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu

130 135 140

Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly

145 150 155 160

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu

165 170 175

Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu

180 185 190

Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala

195 200 205

Glu Arg Leu Leu Glu Glu Val Lys Arg

210 215

<210> 556

<211> 247

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 556

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro

65 70 75 80

Ala Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu

85 90 95

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly

100 105 110

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met

115 120 125

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile

130 135 140

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg

145 150 155 160

Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Gly Gly Glu Leu Glu Glu

165 170 175

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu

180 185 190

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn

195 200 205

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu

210 215 220

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His

225 230 235 240

Leu Glu Glu Leu Ala Arg Lys

245

<210> 557

<211> 247

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 557

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly

65 70 75 80

Ser Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu

85 90 95

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly

100 105 110

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met

115 120 125

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile

130 135 140

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg

145 150 155 160

Lys Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Glu Leu Glu Glu

165 170 175

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu

180 185 190

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn

195 200 205

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu

210 215 220

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His

225 230 235 240

Leu Glu Glu Leu Ala Arg Lys

245

<210> 558

<211> 241

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 558

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly

65 70 75 80

Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val

85 90 95

Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu

100 105 110

Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu

115 120 125

Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu

130 135 140

Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly

145 150 155 160

Ser Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu

165 170 175

Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly

180 185 190

Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met

195 200 205

Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile

210 215 220

Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg

225 230 235 240

Lys

<210> 559

<211> 235

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 559

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
85 90 95

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
100 105 110

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

115 120 125

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
130 135 140

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
145 150 155 160

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
165 170 175

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

180 185 190

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
195 200 205

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
210 215 220

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys
225 230 235

<210> 560

<211> 225

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 560

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His
85 90 95

Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp
100 105 110

Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys
115 120 125

Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu
130 135 140

Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln
165 170 175

Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
180 185 190

Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
195 200 205

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
210 215 220

Arg
225

<210> 561

<211> 219

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 561

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Gly Gly Ser Gly Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln Met
85 90 95

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
100 105 110

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
115 120 125

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu

130 135 140

Leu Leu Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly
145 150 155 160
Gly Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
165 170 175
Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
180 185 190
Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
195 200 205

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215

<210> 562
<211> 213
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 562
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80
Gly Gly Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu
85 90 95
Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His

100 105 110

Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp
115 120 125
Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140
Arg Leu Leu Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Asp Lys Glu
145 150 155 160
Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu

165 170 175
Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe
180 185 190
Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu
195 200 205
Glu Glu Val Lys Arg
210

<210> 563
<211> 209
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 563
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly

65 70 75 80
Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
85 90 95

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
100 105 110
Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
115 120 125
Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu

130 135 140
Leu Ser Gly Gly Gly Ser Gly Gly Gly Asp Lys Glu Asn Val Leu Gln
145 150 155 160
Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
165 170 175
Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
180 185 190
Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys

195 200 205
Arg

<210> 564
<211> 137
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 564
Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

35 40 45
Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
65 70 75 80

Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu
85 90 95
Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu

100 105 110
Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala
115 120 125
Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135

<210> 565
<211> 132
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 565
Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn
65 70 75 80

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
85 90 95
His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110
Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
115 120 125
Glu Val Lys Arg
130

<210> 566

<211> 127

<212> PRT

<213> Artificial Sequence

<220><223

> Synthetic

<400> 566

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60

Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
65 70 75 80

Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
85 90 95

Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
100 105 110

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
115 120 125

<210> 567

<211> 122

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 567

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Ser Gly Gly Gly Gly Ser

50 55 60
Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys
65 70 75 80
Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp
85 90 95
Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu
100 105 110
Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
115 120

<210> 568
<211> 141
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 568
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80
Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
85 90 95
Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
100 105 110

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu

115 120 125

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

130 135 140

<210> 569

<211> 130

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 569

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu

65 70 75 80

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

85 90 95

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr

100 105 110

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

115 120 125

Lys Arg

130

<210> 570

<211> 149

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 570

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
85 90 95

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
100 105 110

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
115 120 125

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
130 135 140

Glu Arg Leu Leu Ser
145

<210> 571

<211> 149

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 571

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val
65 70 75 80
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
85 90 95
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
100 105 110

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
115 120 125
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
130 135 140
Glu Leu Ala Arg Lys
145

<210> 572
<211> 215
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 572
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly

65 70 75 80

Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
85 90 95

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
100 105 110

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
115 120 125

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
130 135 140

Glu Arg Leu Leu Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp
145 150 155 160

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
165 170 175

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
180 185 190

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
195 200 205

Leu Leu Glu Glu Val Lys Arg
210 215

<210> 573

<211> 215

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 573

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val
65 70 75 80
Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
85 90 95
Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
100 105 110

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
115 120 125
Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
130 135 140
Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp
145 150 155 160
Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
165 170 175

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr
180 185 190
Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
195 200 205
Leu Leu Glu Glu Val Lys Arg
210 215

<210> 574
<211> 225
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 574

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu
65 70 75 80

Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala
85 90 95
His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala
100 105 110
Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser
115 120 125
Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile
130 135 140

Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly Gly
145 150 155 160
Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Lys Glu Asn Val Leu Gln
165 170 175
Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
180 185 190
Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys
195 200 205

Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
210 215 220
Arg
225
<210> 575
<211> 132
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 575

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn
65 70 75 80
Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
85 90 95

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
100 105 110
Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
115 120 125
Glu Val Lys Arg
130

<210> 576
<211> 143
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 576
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
85 90 95
Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
100 105 110
Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
115 120 125
Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 577
<211> 151
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 577
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu Leu His Met Gln Met
85 90 95
Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
100 105 110
Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys

115 120 125

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu

130 135 140

Leu Leu Glu Arg Leu Leu Ser

145 150

<210> 578

<211> 151

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 578

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Glu Leu Glu Glu

65 70 75 80

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu

85 90 95

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn

100 105 110

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu

115 120 125

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His

130 135 140

Leu Glu Glu Leu Ala Arg Lys

145 150

<210> 579

<211> 219

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 579

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu Leu His Met Gln Met
85 90 95

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
100 105 110

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys

115 120 125

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
130 135 140

Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala
145 150 155 160

Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
165 170 175

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser

180 185 190

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
195 200 205

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

210 215

<210> 580

<211> 219

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 580

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Glu Leu Glu Glu
65 70 75 80

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
85 90 95

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn
100 105 110

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
115 120 125

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His
130 135 140

Leu Glu Glu Leu Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala
145 150 155 160

Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
165 170 175

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
180 185 190

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu

195 200 205

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

210 215

<210> 581

<211> 243

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 581

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro

65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His

85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu

100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr

115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg

130 135 140

Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu

145 150 155 160

Ala Arg Lys Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro

165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190
Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205
Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220
Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240
Val Lys Arg

<210> 582
<211> 143
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 582
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro
65 70 75 80
Ala Ala Pro Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile
85 90 95
Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser
100 105 110
Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu
115 120 125

Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
130 135 140

<210> 583

<211> 151

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 583

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu Leu His Met Gln Met
85 90 95

Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
100 105 110

Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
115 120 125

Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
130 135 140

Leu Leu Glu Arg Leu Leu Ser
145 150

<210> 584

<211> 151

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 584

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Glu Leu Glu Glu
65 70 75 80

Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
85 90 95

Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn
100 105 110

Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
115 120 125

Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His
130 135 140

Leu Glu Glu Leu Ala Arg Thr
145 150

<210> 585

<211> 219

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 585

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu Leu His Met Gln Met
85 90 95
Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe
100 105 110
Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys
115 120 125
Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu
130 135 140

Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala
145 150 155 160
Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
165 170 175
Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
180 185 190
Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
195 200 205

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215
<210> 586
<211> 219
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 586
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Gly Gly Glu Leu Glu Glu
65 70 75 80
Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu
85 90 95
Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn

100 105 110
Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu
115 120 125
Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His
130 135 140
Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala
145 150 155 160
Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met

165 170 175
Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser
180 185 190
Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
195 200 205
Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
210 215
<210> 587
<211> 243
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic

<400> 587

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser Pro
65 70 75 80

Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala Pro
85 90 95

Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val
100 105 110

Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val
115 120 125

Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg
130 135 140

Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg
145 150 155 160

Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 588

<211> 243

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 588

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Glu Leu Glu Glu Gln Val Met His
85 90 95

Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu
100 105 110

Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr
115 120 125

Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg
130 135 140

Glu Ile Glu Glu Glu Ala Ala Arg Ile Leu Glu His Leu Glu Glu Leu
145 150 155 160

Ala Arg Thr Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro
165 170 175

Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn Val
180 185 190

Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His
195 200 205

Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys
210 215 220

Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu
225 230 235 240

Val Lys Arg

<210> 589
<211> 85
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic

<400> 589
Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu
1 5 10 15

Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn
20 25 30

Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile
35 40 45

Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu
50 55 60

Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile
65 70 75 80

Ala Asp Glu Ser Arg
85

<210> 590
<211> 134
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 590
Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
115 120 125

Gln Lys Ala Leu Glu Leu
130

<210> 591

<211> 83

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 591

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln Lys Ala Leu Glu
50 55 60

Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys

65 70 75 80

Gln Lys Gln

<210> 592
<211> 83
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 592

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ile Glu Tyr Tyr Gln Lys Ala Leu Glu
50 55 60

Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys
65 70 75 80

Gln Lys Gln

<210> 593
<211> 116
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 593

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln Lys Ala Leu Glu

50 55 60

Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr

65 70 75 80

Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala

85 90 95

Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn

100 105 110

Lys Gln Lys Gln

115

<210> 594

<211> 73

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 594

Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr Ala

1 5 10 15

Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu Leu

20 25 30

Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile

35 40 45

Val Glu His Asn Ala Ile Ile Val Glu Asn Arg Ile Ile Ala Ala Val

50 55 60

Leu Glu Leu Ile Val Arg Ala Ile Lys

65 70

<210> 595

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 595

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
85 90 95

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
100 105

<210> 596

<211> 211

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 596

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

85 90 95

Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val

100 105 110

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr

115 120 125

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu

130 135 140

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu

145 150 155 160

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala

165 170 175

Arg Lys Gly Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg

180 185 190

Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser

195 200 205

Thr Phe Leu

210

<210> 597

<211> 107

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 597

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys

85 90 95

Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu

100 105

<210> 598

<211> 106

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 598

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp

85 90 95

Gly Glu Trp Val Leu Leu Ser Thr Phe Leu

100 105

<210> 599

<211> 105

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 599

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Gly Tyr

65 70 75 80

Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly

85 90 95

Glu Trp Val Leu Leu Ser Thr Phe Leu

100 105

<210> 600

<211> 208

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 600

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

85 90 95

Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val

100 105 110

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr

115 120 125

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu

130 135 140

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu

145 150 155 160

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala

165 170 175

Arg Lys Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln

180 185 190

Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu

195 200 205

<210> 601

<211> 164

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 601

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Ser

65 70 75 80

Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu

85 90 95

Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile

100 105 110

Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg

115 120 125

Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu

130 135 140

Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala

145 150 155 160

Asp Glu Ser Arg

<210> 602

<211> 165

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 602

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu

85 90 95

Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn

100 105 110

Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile

115 120 125

Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu

130 135 140

Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile

145 150 155 160

Ala Asp Glu Ser Arg

165

<210> 603

<211> 267

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 603

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

85 90 95

Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val

100 105 110

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr

115 120 125

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu

130 135 140

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu

145 150 155 160

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala

165 170 175

Arg Lys Gly Ser Gly Ser Ser Glu Glu Leu Arg Ala Val Ala Asp Leu

180 185 190

Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala

195 200 205

Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu

210 215 220

Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu

225 230 235 240

Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys

245 250 255

Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg

260 265

<210> 604

<211> 268

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 604

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

85 90 95

Ser Gly Ser Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val

100 105 110

Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr

115 120 125

Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu

130 135 140

Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu

145 150 155 160

Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala

165 170 175

Arg Lys Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp

180 185 190

Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val

195 200 205

Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu

210 215 220

Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu

225 230 235 240

Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala

245 250 255

Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg

260 265

<210> 605

<211> 97

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 605

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly
65 70 75 80
Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe
85 90 95

Leu

<210> 606
<211> 96
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 606
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Ser Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln
65 70 75 80
Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
85 90 95
<210> 607
<211> 95
<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 607

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala

65 70 75 80

Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu

85 90 95

<210> 608

<211> 154

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 608

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln

65 70 75 80

Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg

85 90 95

Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr
100 105 110
Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser
115 120 125
Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu
130 135 140
Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg
145 150

<210> 609

<211> 245

<212

> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 609

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
65 70 75 80
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Asp Glu
85 90 95
Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
100 105 110
Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala

115 120 125

Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val
130 135 140
Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser
145 150 155 160
Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu
165 170 175
Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn

180 185 190
Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile
195 200 205
Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu
210 215 220
Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile
225 230 235 240
Ala Asp Glu Ser Arg
245

<210
> 610
<211> 246
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 610
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15
Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
65 70 75 80

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Asp Glu
85 90 95
Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala
100 105 110
Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala

115 120 125
Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val
130 135 140
Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser
145 150 155 160
Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile
165 170 175
Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu

180 185 190
Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr
195 200 205
Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val
210 215 220
Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys
225 230 235 240
Ile Ala Asp Glu Ser Arg
245

<210> 611
<211> 196
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 611
Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15
Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu

50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly

100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr

115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn

130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly

145 150 155 160

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met

165 170 175

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

180 185 190

Glu Val Lys Arg

195

<210> 612

<211> 194

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 612

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg

20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu

50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly

100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr

115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Asp Lys Glu Asn Val Leu

130 135 140

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

145 150 155 160

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr

165 170 175

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

180 185 190

Lys Arg

<210> 613

<211> 192

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 613

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg

20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu

50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly

100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr

115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Asp Lys Glu Asn Val Leu Gln Lys

130 135 140

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala

145 150 155 160

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

165 170 175

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

180 185 190

<210> 614

<211> 241

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 614

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro

65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln

85 90 95

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu

100 105 110

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr

115 120 125

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys

130 135 140

Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Ser Glu Glu Leu

145 150 155 160

Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys

165 170 175

Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val

180 185 190

Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile

195 200 205

Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu

210 215 220

Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser

225 230 235 240

Arg

<210> 615

<211> 242

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 615

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro
65 70 75 80

Ala Pro Ser Ala Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln
85 90 95

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu
100 105 110

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr
115 120 125

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys
130 135 140

Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Glu Glu
145 150 155 160

Leu Arg Ala Val Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg
165 170 175

Lys Leu Leu Glu Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu
180 185 190

Val Arg Lys Thr Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu
195 200 205

Ile Arg Lys Val Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu
210 215 220

Glu Glu Ile Arg Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu
225 230 235 240

Ser Arg

<210> 616

<211> 172

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 616

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser
50 55 60

Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser
65 70 75 80

Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu
85 90 95

Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu
100 105 110

Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala
115 120 125

Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly
130 135 140

Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
145 150 155 160

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
165 170

<210> 617

<211> 190

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 617

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser
50 55 60
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
65 70 75 80
Gly Ser Gly Ser Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln

85 90 95
Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
100 105 110
Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
115 120 125
Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
130 135 140
Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly

145 150 155 160
Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr
165 170 175
Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
180 185 190

<210> 618

<211> 180

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 618

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Glu Leu Glu Glu Gln Val
65 70 75 80

Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu Leu Leu His
85 90 95

Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp
100 105 110

Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu
115 120 125

Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu His Leu Glu
130 135 140

Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro
145 150 155 160

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
165 170 175

Ser Thr Phe Leu
180

<210> 619

<211> 186

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 619

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
65 70 75 80

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
85 90 95

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
100 105 110

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
115 120 125

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
130 135 140

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
145 150 155 160

Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp
165 170 175

Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
180 185

<210> 620

<211> 288

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 620

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg

20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu

50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly

100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr

115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn

130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly

145 150 155 160

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met

165 170 175

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

180 185 190

Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser

195 200 205

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser

210 215 220

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala

225 230 235 240

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu

245 250 255

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu

260 265 270

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

275 280 285

<210> 621

<211> 269

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 621

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg

20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu

50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly

100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr

115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn

130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly

145 150 155 160

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met

165 170 175

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

180 185 190

Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser Gly Asn Leu Asp

195 200 205

Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe

210 215 220

Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys

225 230 235 240

Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val

245 250 255

Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser

260 265

<210> 622

<211> 299

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 622

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg

20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu

50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly

100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr

115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn

130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly

145 150 155 160

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met

165 170 175

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

180 185 190

Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser

195 200 205

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser

210 215 220

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

225 230 235 240

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

245 250 255

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

260 265 270

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

275 280 285

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys

290 295

<210> 623

<211> 280

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 623

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30
Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45
Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60
Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
85 90 95
Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
100 105 110
Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
115 120 125
Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn
130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
145 150 155 160
His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
165 170 175
Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
180 185 190
Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser Gly Glu Leu Glu
195 200 205

Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu Ala His Glu
210 215 220
Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala Ala Tyr Phe
225 230 235 240
Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys Ser Asp Asp
245 250 255

Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg Ile Leu Glu
260 265 270

His Leu Glu Glu Leu Ala Arg Lys
275 280

<210> 624

<211> 161

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 624

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser
50 55 60

Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr
65 70 75 80

Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe
85 90 95

Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln
100 105 110

Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu
115 120 125

Leu Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly
130 135 140

Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe
145 150 155 160

Leu

<210> 625

<211> 179

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 625

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser
50 55 60

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
65 70 75 80
Gly Ser Gly Ser Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu
85 90 95
Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His
100 105 110
Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp
115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140
Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg
145 150 155 160
Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser
165 170 175
Thr Phe Leu

<210> 626

<211> 180

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 626

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp
85 90 95

Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys
100 105 110

His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys
115 120 125

Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu
130 135 140

Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro
145 150 155 160

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
165 170 175

Ser Thr Phe Leu
180

<210> 627

<211> 186

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 627

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80
Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Asn Leu Asp Glu Leu
85 90 95
His Met Gln Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys
100 105 110
Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr
115 120 125

Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu
130 135 140
Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser Gly Ser Gly Ser Gly
145 150 155 160
Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp
165 170 175
Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
180 185

<210> 628

<211> 219

<212

> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 628

Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
1 5 10 15

Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
20 25 30

Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu
35 40 45

Arg Leu Leu Glu Glu Val Lys Arg Gly Ser Gly Ser Gly Ser Gly Ser

50 55 60

Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu
65 70 75 80

Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln
85 90 95

Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys
100 105 110

Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu

115 120 125

Ser Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val Ala Asp Leu
130 135 140

Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu Ala Val Ala
145 150 155 160

Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr Ser Glu Leu
165 170 175

Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val Lys Glu Glu

180 185 190

Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg Arg Ala Lys
195 200 205

Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg
210 215

<210> 629

<211> 238

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 629

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu
85 90 95

Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His
100 105 110

Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp
115 120 125

Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
130 135 140

Arg Leu Leu Ser Gly Ser Gly Ser Gly Ser Glu Glu Leu Arg Ala Val
145 150 155 160

Ala Asp Leu Gln Arg Leu Asn Ile Glu Leu Ala Arg Lys Leu Leu Glu
165 170 175

Ala Val Ala Arg Leu Gln Glu Leu Asn Ile Asp Leu Val Arg Lys Thr
180 185 190

Ser Glu Leu Thr Asp Glu Lys Thr Ile Arg Glu Glu Ile Arg Lys Val
195 200 205

Lys Glu Glu Ser Lys Arg Ile Val Glu Glu Ala Glu Glu Glu Ile Arg
210 215 220

Arg Ala Lys Glu Glu Ser Arg Lys Ile Ala Asp Glu Ser Arg

225 230 235

<210> 630

<211> 162

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 630

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Glu

65 70 75 80

Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly

85 90 95

Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp

100 105 110

Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys

115 120 125

Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln Lys Ala Leu Glu Leu

130 135 140

Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala Lys Gln

145 150 155 160

Lys Gln

<210> 631

<211> 164

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 631

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys
85 90 95

Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys
100 105 110

Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr
115 120 125

Tyr Lys Gln Gly Asp Tyr Asp Glu Ile Glu Tyr Tyr Gln Lys Ala Leu
130 135 140

Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala
145 150 155 160

Lys Gln Lys Gln

<210> 632

<211> 195

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 632

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Glu
65 70 75 80
Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu Gly
85 90 95
Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg Asp
100 105 110
Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr Lys

115 120 125
Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln Lys Ala Leu Glu Leu
130 135 140
Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
145 150 155 160
Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
165 170 175
Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Lys

180 185 190
Gln Lys Gln
195
<210> 633
<211> 197
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 633

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80
Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys
85 90 95
Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys

100 105 110
Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr
115 120 125
Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Tyr Tyr Gln Lys Ala Leu
130 135 140
Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
145 150 155 160
Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

165 170 175
Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly
180 185 190
Asn Lys Gln Lys Gln
195

<210> 634
<211> 154
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 634

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80
Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr

85 90 95
Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu
100 105 110
Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu
115 120 125
Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Arg Ile Ile Ala Ala
130 135 140
Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150

<210> 635
<211> 156
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 635
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala
85 90 95

Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser Thr
100 105 110

Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn

115 120 125

Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Arg Ile Ile
130 135 140

Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155

<210> 636

<211> 196

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 636

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly

100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr

115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Gly Ser Asp Lys Glu Asn

130 135 140

Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly

145 150 155 160

His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met

165 170 175

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu

180 185 190

Glu Val Lys Arg

195

<210> 637

<211> 194

<212> PRT

<213> Artificial Sequence

<220><223>

Synthetic

<400> 637

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg

20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu

50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly

100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr

115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Gly Ser Asp Lys Glu Asn Val Leu

130 135 140

Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala

145 150 155 160

Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr

165 170 175

Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val

180 185 190

Lys Arg

<210> 638

<211> 192

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 638

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu

1 5 10 15

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg

20 25 30

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

35 40 45

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu

50 55 60

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

65 70 75 80

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

85 90 95

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly

100 105 110

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr

115 120 125

Gln Lys Ala Leu Glu Leu Gly Ser Asp Lys Glu Asn Val Leu Gln Lys

130 135 140

Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala

145 150 155 160

Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp

165 170 175

Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

180 185 190

<210> 639

<211> 168

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 639

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala

85 90 95

Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala

100 105 110

Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn

115 120 125

Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln

130 135 140

Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu

145 150 155 160

Gly Asn Ala Lys Gln Lys Gln Gly

165

<210> 640

<211> 202

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 640

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala

85 90 95

Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala

100 105 110

Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn

115 120 125

Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln

130 135 140

Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu

145 150 155 160

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr

165 170 175

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln

180 185 190

Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly

195 200

<210> 641

<211> 159

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 641

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu

85 90 95

Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala

100 105 110

Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu

115 120 125

Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Asn

130 135 140

Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys

145 150 155

<210> 642

<211> 161

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 642

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu

85 90 95

Glu Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu

100 105 110

Arg Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu

115 120 125

Val Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu

130 135 140

Asn Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile

145 150 155 160

Lys

<210> 643

<211> 170

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 643

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu

85 90 95

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg

100 105 110

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu

115 120 125

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr

130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln

145 150 155 160

Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly

165 170

<210> 644

<211> 204

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 644

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu
85 90 95

Leu Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg
100 105 110

Ile Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
115 120 125

Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr
130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
145 150 155 160

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
165 170 175

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
180 185 190

Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 645

<

211> 112

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 645

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Arg
65 70 75 80

Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr
85 90 95

His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg
100 105 110

<210> 646

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 646

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80
Ser Gly Ser Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu
85 90 95
Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu
100 105 110
Ile Gly Glu Arg
115

<210> 647
<211> 155
<212> PRT
<213> Artificial Sequence
<220><223
> Synthetic
<400> 647
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80
Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser Thr
85 90 95
Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg Ala Ser Thr Glu Glu
100 105 110
Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu
115 120 125

Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn Asn Arg Ile Ile Ala
130 135 140

Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys

145 150 155

<210> 648

<211> 159

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 648

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu

85 90 95

Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg Ala

100 105 110

Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu

115 120 125

Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn Asn

130 135 140

Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys

145 150 155

<210> 649

<211> 200

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 649

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn Ala Met Tyr Arg
85 90 95

Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr Leu Ala Leu Leu
100 105 110

Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Ala
115 120 125

Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala Tyr Gln Lys Ala
130 135 140

Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn
145 150 155 160

Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln
165 170 175

Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu
180 185 190

Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 650

<211> 204

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 650

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly
65 70 75 80

Ser Gly Ser Gly Ser Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn
85 90 95

Ala Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr
100 105 110

Leu Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu
115 120 125

Gly Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala
130 135 140

Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr
145 150 155 160

Asn Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile
165 170 175

Glu Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala
180 185 190

Lys Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 651

<211> 111

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 651

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys

85 90 95

Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Gly

100 105 110

<210> 652

<211> 115

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 652

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser Gly

65 70 75 80

Ser Gly Ser Gly Ser Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala
85 90 95
Lys Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser
100 105 110
Leu Lys Gly
115

<210> 653
<211> 165
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 653

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
85 90 95
Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
100 105 110
Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr
115 120 125
Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
130 135 140

Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly Asn Ala
145 150 155 160
Lys Gln Lys Gln Gly
165

<210> 654
<211> 167
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 654

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80
Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr
85 90 95

Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu
100 105 110
Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
115 120 125
Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
130 135 140
Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly
145 150 155 160

Asn Ala Lys Gln Lys Gln Gly
165

<210> 655

<211> 169

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 655

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu
85 90 95

Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile
100 105 110

Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
115 120 125

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
130 135 140

Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn
145 150 155 160

Leu Gly Asn Ala Lys Gln Lys Gln Gly
165

<210> 656

<211> 199

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 656

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr Lys Leu
85 90 95

Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu Lys Arg
100 105 110

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Tyr Tyr

115 120 125

Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys Ala Leu
130 135 140

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
145 150 155 160

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
165 170 175

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly

180 185 190

Asn Ala Lys Gln Lys Gln Gly
195

<210> 657

<211> 201

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 657

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu Ala Tyr
85 90 95

Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile Ala Leu
100 105 110

Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala
115 120 125

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys
130 135 140

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
145 150 155 160

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
165 170 175

Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn
180 185 190

Leu Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 658

<211> 203

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 658

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Glu Glu Ala Glu Leu Ala Tyr Leu Leu Gly Glu Leu
85 90 95

Ala Tyr Lys Leu Gly Glu Tyr Arg Ile Ala Ile Arg Ala Tyr Arg Ile
100 105 110

Ala Leu Lys Arg Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
115 120 125

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
130 135 140

Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn
145 150 155 160

Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu
165 170 175

Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys
180 185 190

Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 659

<211> 156

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 659

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly
65 70 75 80

Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser
85 90 95

Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser Thr Glu
100 105 110

Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg

115 120 125

Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Asn Arg Ile Ile
130 135 140

Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155

<210> 660

<211> 158

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 660

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly

65 70 75 80

Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys

85 90 95

Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg Ala Ser

100 105 110

Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn

115 120 125

Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn Asn Arg

130 135 140

Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys

145 150 155

<210> 661

<211> 160

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 661

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser

65 70 75 80

Gly Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu

85 90 95

Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ala Thr Ala Ser Leu Arg

100 105 110

Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val

115 120 125

Glu Asn Asn Arg Leu Ile Val Glu His Asn Ala Ile Ile Val Glu Asn

130 135 140

Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys

145 150 155 160

<210> 662

<211> 113

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 662

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly

65 70 75 80

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile

85 90 95

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu

100 105 110

Arg

<210> 663

<211> 115

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 663

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80
Gly Gly Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser
85 90 95
Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile
100 105 110
Gly Glu Arg
115

<210> 664

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 664

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser

65 70 75 80

Gly Gly Gly Gly Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile

85 90 95

Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys

100 105 110

Leu Ile Gly Glu Arg

115

<210> 665

<211> 156

<212> PRT

<213> Artificial Sequence

<

220><223> Synthetic

<400> 665

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly

65 70 75 80

Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys Ala Ser

85 90 95

Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg Ala Ser Thr Glu

100 105 110

Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg

115 120 125

Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn Asn Arg Ile Ile

130 135 140

Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys

145 150 155

<210> 666

<211> 158

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 666

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly

65 70 75 80

Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu Leu Lys

85 90 95

Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg Ala Ser

100 105 110

Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn

115 120 125

Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn Asn Arg

130 135 140

Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys

145 150 155

<210> 667

<211> 160

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 667

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Gly Ser Glu Tyr Glu Ile Arg Lys Ala Leu Glu Glu
85 90 95

Leu Lys Ala Ser Thr Ala Glu Leu Lys Arg Ser Thr Ala Ser Leu Arg
100 105 110

Ala Ser Thr Glu Glu Leu Lys Lys Asn Pro Ser Glu Asp Ala Leu Val
115 120 125

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Ala Ile Ile Val Glu Asn
130 135 140

Asn Arg Ile Ile Ala Ala Val Leu Glu Leu Ile Val Arg Ala Ile Lys
145 150 155 160

<210> 668

<211> 199

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 668

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly

65 70 75 80

Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn Ala Met Tyr Arg Lys

85 90 95

Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr Leu Ala Leu Leu Lys

100 105 110

Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala Ala Tyr

115 120 125

Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala Tyr Gln Lys Ala Leu

130 135 140

Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

145 150 155 160

Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr Gln Lys

165 170 175

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn Leu Gly

180 185 190

Asn Ala Lys Gln Lys Gln Gly

195

<210> 669

<211> 201

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 669

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly
65 70 75 80

Gly Gly Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn Ala Met Tyr
85 90 95

Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr Leu Ala Leu
100 105 110

Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly Asn Ala

115 120 125

Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala Tyr Gln Lys
130 135 140

Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
145 150 155 160

Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu Tyr Tyr
165 170 175

Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys Gln Asn

180 185 190

Leu Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 670

<211> 203

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 670

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Asn Leu Ala Glu Lys Met Tyr Lys Ala Gly Asn Ala
85 90 95

Met Tyr Arg Lys Gly Gln Tyr Thr Ile Ala Ile Ile Ala Tyr Thr Leu
100 105 110

Ala Leu Leu Lys Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn Leu Gly
115 120 125

Asn Ala Ala Tyr Lys Lys Gly Glu Tyr Asp Glu Ala Ile Glu Ala Tyr
130 135 140

Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Trp Tyr Asn
145 150 155 160

Leu Gly Asn Ala Tyr Tyr Lys Gln Gly Asp Tyr Asp Glu Ala Ile Glu
165 170 175

Tyr Tyr Gln Lys Ala Leu Glu Leu Asp Pro Asn Asn Ala Glu Ala Lys
180 185 190

Gln Asn Leu Gly Asn Ala Lys Gln Lys Gln Gly
195 200

<210> 671

<211> 110

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 671

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Gly Gly

65 70 75 80

Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Glu

85 90 95

Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Gly

100 105 110

<210> 672

<211> 112

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 672

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu

1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Gly

65 70 75 80

Gly Gly Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Lys Ser Leu
85 90 95
Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser Leu Lys Gly
100 105 110

<210> 673
<211> 114
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 673
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80
Gly Gly Gly Gly Gly Glu Ile Ala Lys Ser Leu Lys Glu Ile Ala Lys

85 90 95
Ser Leu Lys Glu Ile Ala Trp Ser Leu Lys Glu Ile Ala Lys Ser Leu
100 105 110
Lys Gly

<210> 674
<211> 140
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic

<400> 674

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Glu Ala
65 70 75 80
Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
85 90 95
Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp
100 105 110
Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile
115 120 125
Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140

<210> 675

<211> 142

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 675

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg

50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Ser
65 70 75 80
Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser
85 90 95
Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser
100 105 110
Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys
115 120 125

Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140

<210> 676
<211> 144
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 676

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys

35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80
Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys
85 90 95
Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn

100 105 110

Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn
115 120 125

Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140

<210> 677

<211> 134

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 677

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Pro Glu
65 70 75 80

Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu
85 90 95

Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu Val
100 105 110

Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val
115 120 125

Leu Arg Ile Ile Ala Lys
130

<210> 678

<211> 136

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 678

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Ser
65 70 75 80

Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu
85 90 95

Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala
100 105 110

Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val
115 120 125

Glu Val Leu Arg Ile Ile Ala Lys
130 135

<210> 679

<211> 138

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 679

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80
Gly Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr
85 90 95
Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro
100 105 110

Glu Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile
115 120 125
Ile Val Glu Val Leu Arg Ile Ile Ala Lys
130 135

<210> 680
<211> 127
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 680
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala

20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Glu Lys
65 70 75 80
Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr

85 90 95
Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu Val Glu Asn Asn
100 105 110

Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg
115 120 125

<210> 681

<211> 129

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 681

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30

Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45

Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser Ser
65 70 75 80

Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg
85 90 95

Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu Val Glu
100 105 110

Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu
115 120 125

Arg

<210> 682

<211> 131

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 682

Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60

Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Gly Ser
65 70 75 80
Gly Ser Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu
85 90 95
Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu Ala Leu
100 105 110
Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu
115 120 125

Val Leu Arg
130

<210> 683
<211> 125
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 683
Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys
1 5 10 15
Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro
20 25 30
Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn
35 40 45

Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys Gly
50 55 60

Gly Gly Gly Ser Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu
65 70 75 80
Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln
85 90 95
Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu
100 105 110

Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
115 120 125

<210> 684
<211> 129
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 684
Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys
1 5 10 15
Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro
20 25 30
Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn

35 40 45
Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys Gly
50 55 60
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Glu Asn Val Leu Gln
65 70 75 80
Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu
85 90 95
Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys

100 105 110
Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys
115 120 125
Arg

<210> 685

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 685

Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
1 5 10 15

Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu

20 25 30

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile
35 40 45

Val Glu Val Leu Arg Ile Ile Ala Lys Gly Gly Gly Gly Ser Gly Asp
50 55 60

Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu
65 70 75 80

Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr

85 90 95

Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg
100 105 110

Leu Leu Glu Glu Val Lys Arg
115

<210> 686

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 686

Ser Pro Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
1 5 10 15

Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Gly Ser Pro Glu

20 25 30

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile
35 40 45
Val Glu Val Leu Arg Ile Ile Ala Lys Gly Gly Gly Gly Ser Gly Gly
50 55 60
Gly Gly Ser Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met
65 70 75 80
Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser

85 90 95
Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu
100 105 110
Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg
115 120

<210> 687
<211> 135
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 687
Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30
Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45
Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu
65 70 75 80

Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser
85 90 95
Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn
100 105 110

Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg
115 120 125

Ile Ile Ala Lys Val Leu Lys
130 135

<210> 688

<211> 133

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 688

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Gly Gly Ser Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala
65 70 75 80

Leu Arg Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu
85 90 95

Glu Leu Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg
100 105 110

Leu Ile Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile
115 120 125

Ala Lys Val Leu Lys
130

<210> 689

<211> 131

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 689

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60

Gly Gly Gly Ser Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg
65 70 75 80

Glu Leu Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu
85 90 95

Glu Lys Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile
100 105 110

Val Glu Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys
115 120 125

Val Leu Lys
130

<210> 690

<211> 129

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 690

Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu Val Tyr Glu Ala
1 5 10 15

Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His Val Phe Gln Leu
20 25 30

Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp Arg Gln Lys Leu
35 40 45

Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu Arg Leu Leu Ser
50 55 60
Gly Gly Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu
65 70 75 80
Lys Lys Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys
85 90 95

Asn Pro Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu
100 105 110
Asn Asn Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu
115 120 125
Lys

<210> 691
<211> 140
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 691
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15

Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg Arg
50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Glu Ala
65 70 75 80

Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
85 90 95
Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp
100 105 110

Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile
115 120 125
Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140
<210> 692
<
211> 140
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 692
Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu Leu
1 5 10 15
Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg Ala
20 25 30
Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile Lys
35 40 45
Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala Arg

50 55 60
Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ser Glu Ala
65 70 75 80
Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr Asp
85 90 95
Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu Asp
100 105 110
Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile Ile

115 120 125
Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140
<210> 693
<211> 141
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic

<400> 693

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
35 40 45

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg
50 55 60

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Ser Glu
65 70 75 80

Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys Ser Thr
85 90 95

Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro Ser Glu
100 105 110

Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn Lys Ile
115 120 125

Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys
130 135 140

<210> 694

<211> 220

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 694

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu

1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
35 40 45

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala

50 55 60

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser

65 70 75 80

Pro Ala Ala Pro Ala Pro Gly Gly Asn Leu Asp Glu Leu His Met Gln

85 90 95

Met Thr Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu

100 105 110

Phe Gln Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr

115 120 125

Lys Asn Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys

130 135 140

Glu Leu Leu Glu Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro

145 150 155 160

Ala Pro Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile

165 170 175

Met Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val

180 185 190

Ser Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu

195 200 205

Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

210 215 220

<210> 695

<211> 244

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 695

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu

1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg

20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
35 40 45
Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Ala
50 55 60
Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Thr Gly Gly Ala Ser
65 70 75 80
Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro Ser Ala
85 90 95

Pro Ala Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr Asp Leu
100 105 110
Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln Lys His
115 120 125
Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn Lys Asp
130 135 140
Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu Leu Glu
145 150 155 160

Arg Leu Leu Ser Gly Gly Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser
165 170 175
Pro Ala Ala Pro Ala Pro Ser Ala Pro Ala Gly Gly Asp Lys Glu Asn
180 185 190
Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu Glu Arg Leu Gly
195 200 205
His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile Tyr Glu Phe Met
210 215 220

Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu Arg Leu Leu Glu
225 230 235 240
Glu Val Lys Arg

<210> 696
<211> 143

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 696

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu

1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg

20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile

35 40 45

Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg

50 55 60

Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser

65 70 75 80

Ser Glu Ala Leu Glu Glu Leu Glu Lys Ala Leu Arg Glu Leu Lys Lys

85 90 95

Ser Thr Asp Glu Leu Glu Arg Ser Thr Glu Glu Leu Glu Lys Asn Pro

100 105 110

Ser Glu Asp Ala Leu Val Glu Asn Asn Arg Leu Ile Val Glu Asn Asn

115 120 125

Lys Ile Ile Val Glu Val Leu Arg Ile Ile Ala Lys Val Leu Lys

130 135 140

<210> 697

<211> 216

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<400> 697

Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu

1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg

20 25 30

Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile
35 40 45
Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg
50 55 60
Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Gly Gly Ser

65 70 75 80
Gly Gly Gly Ser Gly Gly Asn Leu Asp Glu Leu His Met Gln Met Thr
85 90 95
Asp Leu Val Tyr Glu Ala Leu His Phe Ala Lys Asp Glu Glu Phe Gln
100 105 110
Lys His Val Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala Tyr Lys Asn
115 120 125
Lys Asp Arg Gln Lys Leu Glu Lys Val Val Glu Glu Leu Lys Glu Leu

130 135 140
Leu Glu Arg Leu Leu Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
145 150 155 160
Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met Lys Glu Leu
165 170 175
Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile
180 185 190
Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu Glu Ala Glu

195 200 205
Arg Leu Leu Glu Glu Val Lys Arg
210 215
<210> 698
<211> 107
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 698
Met Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln Val Ser Glu
1 5 10 15

Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu Leu Glu Arg
20 25 30
Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu Glu Leu Ile

35 40 45
Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu Glu Ala Arg
50 55 60
Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly Ser Gly Ser
65 70 75 80
Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys
85 90 95
Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
100 105

<210> 699
<211> 235
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<220><221> MISC_FEATURE
<222> (1)..(20)
<223> optionally absent
<400> 699
Met Ser His His His His His His His His Ser Glu Asn Leu Tyr Phe
1 5 10 15
Gln Ser Gly Gly Glu Leu Glu Glu Gln Val Met His Val Leu Asp Gln
20 25 30
Val Ser Glu Leu Ala His Glu Leu Leu His Lys Leu Thr Gly Glu Glu
35 40 45

Leu Glu Arg Ala Ala Tyr Phe Asn Trp Trp Ala Thr Glu Met Met Leu
50 55 60
Glu Leu Ile Lys Ser Asp Asp Glu Arg Glu Ile Arg Glu Ile Glu Glu
65 70 75 80
Glu Ala Arg Arg Ile Leu Glu His Leu Glu Glu Leu Ala Arg Lys Gly

85 90 95

Gly Gly Ser Gly Gly Gly Ser Gly Gly Asn Ile Asp Glu Leu Leu Met

100 105 110

Gln Val Thr Asp Leu Ile Tyr Glu Ala Leu His Phe Ala Lys Asp Glu

115 120 125

Glu Phe Gln Lys His Ala Phe Gln Leu Phe Glu Lys Ala Thr Lys Ala

130 135 140

Tyr Lys Asn Lys Asp Lys Gln Lys Leu Glu Lys Val Val Glu Glu Leu

145 150 155 160

Lys Glu Leu Leu Glu Arg Ile Leu Ser Gly Gly Gly Ser Gly Gly Gly

165 170 175

Ser Gly Gly Asp Lys Glu Asn Val Leu Gln Lys Ile Tyr Glu Ile Met

180 185 190

Lys Glu Leu Glu Arg Leu Gly His Ala Glu Ala Ser Met Gln Val Ser

195 200 205

Asp Leu Ile Tyr Glu Phe Met Lys Thr Lys Asp Glu Asn Leu Leu Glu

210 215 220

Glu Ala Glu Arg Leu Leu Glu Glu Val Lys Arg

225 230 235

<210> 700

<211> 77

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic

<220><221> MISC_FEATURE

<222> (1)..(21)

<223> optionally absent

<400> 700

Met Ser His His His His His His His His Ser Glu Asn Leu Tyr Phe

1 5 10 15

Gln Ser Gly Gly Gly Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu

20 25 30

Ile Met Lys Thr Leu Glu Gln Leu Gly His Ala Glu Ala Ser Met Gln
35 40 45

Val Ser Asp Leu Ile Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu
50 55 60
Leu Glu Glu Ala Glu Arg Leu Leu Glu Glu Val Glu Arg
65 70 75
<210> 701
<211> 303
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic
<400> 701
Asp Lys Glu Asn Ile Leu Gln Lys Ile Tyr Glu Ile Met Lys Thr Leu
1 5 10 15
Asp Gln Leu Gly His Ala Glu Ala Ser Met Gln Val Ser Asp Leu Ile

20 25 30
Tyr Glu Phe Met Lys Gln Gly Asp Glu Arg Leu Leu Glu Glu Ala Glu
35 40 45
Arg Leu Leu Glu Glu Val Glu Arg Gly Gly Ser Gly Ser Gly Gly Ser
50 55 60
Gly Ser Gly Ser Gly Gly Ser Glu Pro Lys Ser Ser Asp Lys Thr His
65 70 75 80
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val

85 90 95
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
100 105 110
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
115 120 125
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
130 135 140
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser

145 150 155 160

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

165 170 175

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile

180 185 190

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro

195 200 205

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu

210 215 220

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn

225 230 235 240

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser

245 250 255

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg

260 265 270

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu

275 280 285

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

290 295 300